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(54) **IDENTIFICATION OF DISCRIMINANT PROTEINS THROUGH ANTIBODY PROFILING, METHODS AND APPARATUS FOR IDENTIFYING AN INDIVIDUAL**

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 None
 See application file for complete search history.

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(57) **ABSTRACT**

A method for determining a plurality of proteins for discriminating and positively identifying an individual based from a biological sample. The method may include profiling a biological sample from a plurality of individuals against a protein array including a plurality of proteins. The protein array may include proteins attached to a support in a preselected pattern such that locations of the proteins are known. The biological sample may be contacted with the protein array such that a portion of antibodies in the biological sample reacts with and binds to the proteins forming immune complexes. A statistical analysis method, such as discriminant analysis, may be performed to determine discriminating proteins for distinguishing individuals. Proteins of interest may be used to form a protein array. Such a protein array may be used, for example, to compare a forensic sample from an unknown source with a sample from a known source.

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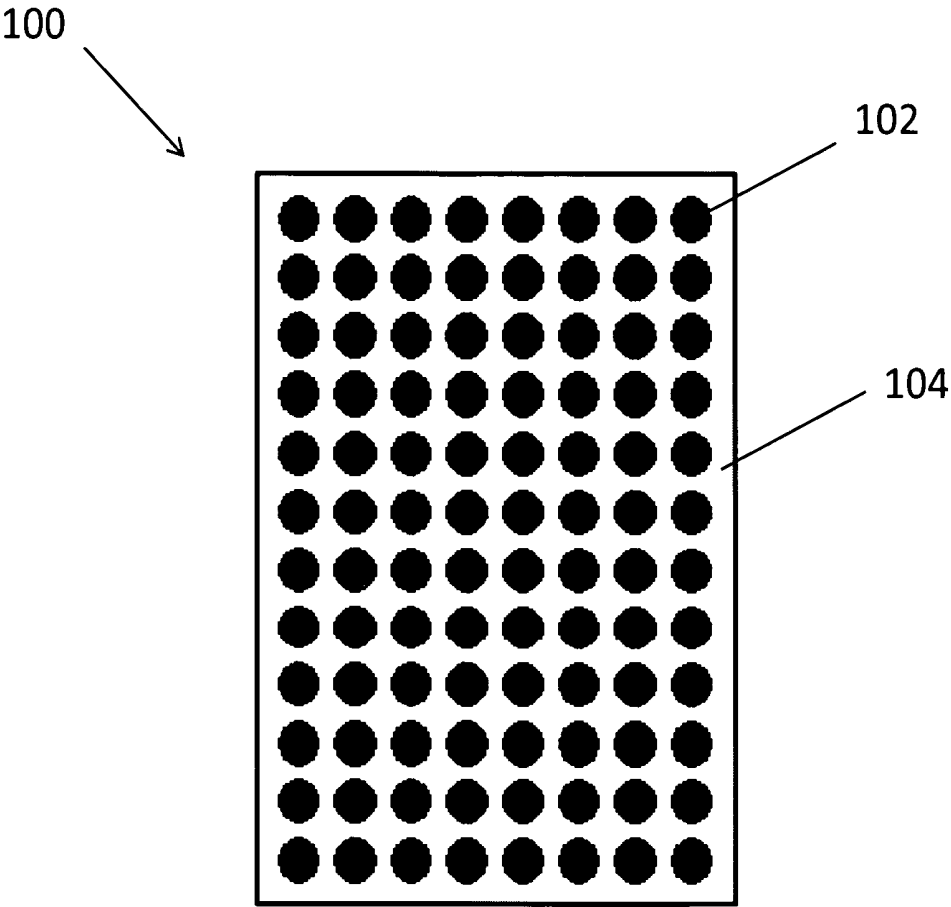
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**IDENTIFICATION OF DISCRIMINANT
PROTEINS THROUGH ANTIBODY
PROFILING, METHODS AND APPARATUS
FOR IDENTIFYING AN INDIVIDUAL**

GOVERNMENT RIGHTS

This invention was made with government support under Contract Number DE-AC07-05ID14517 awarded by the United States Department of Energy. The government has certain rights in the invention.

TECHNICAL FIELD

Embodiments of the present invention relate to analyzing biological samples to identify proteins useful in identifying individuals, and more particularly, to methods and apparatus for identifying an individual using such proteins.

BACKGROUND

The importance of differentiating and identifying individuals based on biological samples with a high degree of efficiency and accuracy is presented in various contexts. For example, the need for accurate means of identification is of increasing importance in law enforcement as it may be critical to link an individual to a forensic sample, such as blood, tissue, hair, saliva, or the like.

Many methods are known for identifying individuals or biological samples obtained from such individuals. For example, blood typing is based on the existence of antigens on the surface of red blood cells. The ABO system relates to four different conditions with respect to two antigens, A and B. Type A individuals exhibit the A antigen; Type B individuals exhibit the B antigen; Type AB individuals exhibit both the A and B antigens; and Type O individuals exhibit neither the A nor the B antigen. By analyzing a sample of a person's blood, it is possible to classify the blood as belonging to one of these blood groups. While this method may be used to identify one individual out of a small group of individuals, the method is limited when the group of individuals is larger because no distinction is made between persons of the same blood group. For example, the distribution of the ABO blood groups in the U.S. is approximately 45% O, 42% A, 10% B, and 3% AB. Tests based on other blood group antigens or isozymes present in body fluids suffer from the same disadvantages as the ABO blood typing tests. These methods may exclude certain individuals, but cannot differentiate between members of the same blood group.

A variety of immunological and biochemical tests based on genetics are routinely used in paternity testing, as well as for determining the compatibility of donors and recipients involved in transplant or transfusion procedures, and also sometimes as an aid in the identification of humans and animals. For example, serological testing of proteins encoded by the human leukocyte antigen (HLA) gene locus is well known. Although a good deal of information is known concerning the genetic makeup of the HLA locus, there are many drawbacks to using HLA serological typing for identifying individuals in a large group. Each of the HLA antigens must be tested for in a separate assay, and many such antigens must be assayed to identify an individual, an arduous process when identifying one individual in a large group.

In the past decade, DNA-based analysis methods, such as restriction fragment length polymorphisms (RFLPs) and polymerase chain reaction (PCR) have rapidly gained acceptance in forensic and paternity analyses for matching biologi-

cal samples to an individual. RFLP techniques are problematic, however, due to the need for relatively large sample sizes, specialized equipment, highly skilled technicians, and lengthy analysis times. For forensic applications there is often not enough sample available for this type of assay, and in remote areas the necessary equipment is often not available. In addition, the cost and length of time required to performed this technique may hinder a criminal investigation. Moreover, the cost of RFLP analysis may be prohibitory if screening of many samples is necessary. PCR techniques have the advantages over RFLP analysis of requiring much smaller sample sizes and permitting more rapid analysis, but they still require specialized equipment and skilled technicians, and they are also expensive.

Antibody profiling is an identification technique that has many advantages over conventional DNA-based analysis methods. For example, antibody profiling methods provide increased speed and ease of use and decreased costs in comparison to conventional DNA based analysis. Current antibody profiling methods for identifying individuals utilize an undefined mixture of proteins.

U.S. Pat. No. 4,880,750 and U.S. Pat. No. 5,270,167 each disclose antibody profiling as a method that purportedly overcomes many of the disadvantages associated with DNA analysis. The antibody profiling method is based on the discovery that every individual has a unique set of antibodies present in his or her bodily fluids. R. M. Bernstein et al., *Cellular Protein and RNA Antigens in Autoimmune Disease*, 2 Mol. Biol. Med. 105-120 (1984). Such antibodies, termed "individual-specific antibodies" or "ISAs," were found in blood, serum, saliva, urine, semen, perspiration, tears, and body tissues. A. M. Francoeur, *Antibody Fingerprinting: A Novel Method for Identifying Individual People and Animals*, 6 Bio/technology 821-825 (1988). The ISAs are not associated with disease and are thought to be directed against cellular components of the body. Individuals are born with an antibody profile that matches the mother's antibody profile. T. F. Unger & A. Strauss, *Individual-specific Antibody Profiles as a Means of Newborn Infant Identification*, 15 J. Perinatology 152-155 (1995). An individual's antibody profile gradually changes, however, until a stable unique pattern is obtained by about two years of age. It has been shown that even genetically identical individuals have different antibody profiles. An individual's profile is apparently stable for life and is not affected by short-term illnesses. A. M. Francoeur, supra. Few studies have been conducted on individuals with long-term diseases. Preliminary results, however, indicate that, although a few extra bands may appear, the overall pattern remains intact. This technique has been used in the medical field to track patient samples and avoid sample mix-ups. In addition, the technique has been used in hospitals in cases where switching of infants or abduction has been alleged.

WO 97/29206 discloses a method for identifying the source of a biological sample used for diagnostic testing by linking diagnostic test results to an antibody profile of the biological sample. By generating an antibody profile of each biological sample, the origin of the biological sample is identified.

Assays are also available that use specific nucleic acid probes or other biological molecules attached to surfaces such as glass, silicon, polymethacrylate, polymeric filters, microspheres, resins, and the like. In a configuration where the surface is planar, these assays are sometimes referred to as "biochips." Initially, biochips contained nucleic acid probes attached to glass or silicon substrates in microarrays. These DNA or RNA chips are made by microfabrication technolo-

gies initially developed for use in computer chip manufacturing. Leading DNA chip technologies include an in situ photochemical synthesis approach, P. S. Fodor, 277 Science 393-395 (1997); U.S. Pat. No. 5,445,934; an electrochemical positioning approach, U.S. Pat. No. 5,605,662; depositing gene probes on the chip using a sprayer that resembles an ink-jet printer; and the use of gels in a solution-based process. Arrays of other types of molecules, such as peptides, have been fabricated on biochips, e.g., U.S. Pat. No. 5,445,934.

BRIEF SUMMARY OF THE INVENTION

In some embodiments, the present invention includes a method of determining discriminant proteins useful for identifying an individual. For example, the method may be used to determine a set that includes one or more of such discriminant proteins. A plurality of samples may be obtained from a different individual and may include individual specific antibodies. Each of the plurality of samples may be contacted with an array including a plurality of antigens to form at least one immune complex, the immune complex including an individual specific antibody from the sample bound to an antigen of the array. Each antigen of the array is known and is immobilized at a known predetermined location in the array. At least one detection agent may be applied to the array and may include at least one interacting protein conjugated to a marker to detect the immune complexes. The immune complexes on the array may be detected to obtain an antibody profile corresponding to each of the different individuals and the antibody profiles corresponding to the different individuals may be compared using, for example, discriminant analysis, to determine at least one target antigen as a discriminant protein useful for indentifying an individual from at least one other individual or population of individuals.

In additional embodiments, the present invention includes a method for identifying source of a biological material. Less than about 200 antigens may be immobilized on a support to form an array. A sample of a biological material including individual-specific antibodies may be obtained and contacted with the array to bind at least a portion of the individual-specific antibodies to the multiple antigens of the array forming immune complexes. A blocking step may be performed prior to applying the sample to prevent binding of antigens, antibodies, and the like to the support wherein such antigens, antibodies, or other molecules are not intended to bind. The support may then be washed to remove any unbound antigens. A detection system such as those disclosed in U.S. Patent Application Nos. 2007/0190585 and 2008/0298667, each of which is incorporated herein by reference, may be used to detect the immune complexes. For example, at least one detection agent including at least one interacting protein conjugated to a marker may be applied to the array to detect the immune complexes. The support may then be washed to remove non-immobilized individual-specific antibodies and detection agent. The immune complexes on the array may be detected to obtain an antibody profile and the antibody profile may be compared to a known antibody profile obtained from an individual. For example, the antibody profile may be correlated to a single individual in a population of from about 1 million individuals to about 100 billion individuals.

In yet further embodiments, the present invention includes a method of designing a protein array useful in identifying an individual. A plurality of samples may be introduced to an array comprising a plurality of antigens, wherein each of the antigens is known and wherein each of the antigens is immobilized at a known predetermined location on a support. Each of the antigens may be known and may be immobilized at a

known predetermined location on a support. At least one detection agent including at least one interacting protein conjugated to a marker may be applied to the array to detect immune complexes formed between individual-specific antibodies and antigens of the plurality. The immune complexes formed on the array may be detected to obtain an antibody profile for each of the plurality of samples. The antibody profiles may be analyzed to determine a set of antigens useful in distinguishing an individual among a population.

In still further embodiments, the present invention includes a method of determining a relationship between a plurality of individuals. An array including less than about 200 antigens on a support may be formed. Each of the antigens is determined to distinguish between individuals. A sample of a biological material having individual-specific antibodies may be obtained from each of a plurality of individuals. The array may be contacted with the sample to bind at least a portion of the individual-specific antibodies therein to the multiple antigens of the array, at least one immune complex. At least one detection agent including at least one interacting protein conjugated to a marker may be applied to the array to detect the immune complexes. The support may be washed to remove non-immobilized individual-specific antibodies and detection agent and the immune complexes on the array detected to obtain an antibody profile.

BRIEF DESCRIPTION OF THE DRAWINGS

While the specification concludes with claims particularly pointing out and distinctly claiming that which is regarded as the present invention, advantages of this invention may be more readily ascertained from the following description of the invention when read in conjunction with the accompanying drawings in which:

FIG. 1 is an illustration of a protein array according to an embodiment of the invention.

DETAILED DESCRIPTION OF THE INVENTION

Before embodiments of the present invention are described in detail, it is to be understood that this invention is not limited to the particular configurations, process acts, and materials disclosed herein as such configurations, process acts, and materials may vary somewhat. It is also to be understood that the terminology employed herein is used for the purpose of describing particular embodiments only and is not limiting since the scope of the present invention will be limited only by the appended claims and equivalents thereof.

The publications and other reference materials referred to herein to describe the background of the invention and to provide additional detail regarding its practice are hereby incorporated by reference. The references discussed herein are provided solely for their disclosure prior to the filing date of the present application. Nothing herein is to be construed as an admission that such documents constitute prior art, or that the inventors are not entitled to antedate such disclosure by virtue of prior invention.

While the known methods for using antibody profiling are generally suitable for their limited purposes, they possess certain inherent deficiencies that detract from their overall utility in analyzing, characterizing, and identifying biological samples. For example, the known methods rely on fractionation of antigens by electrophoresis and then transfer of the fractionated antigens to a membrane. Due to differences in conditions from one fractionation procedure to another, there are lot-to-lot differences in the positions of the antigens on the membrane such that results obtained using membranes from

one lot cannot be compared with results obtained using membranes from another lot. Further, when colorimetric procedures are used for detecting immune complexes on the membrane, color determination may be subjective such that results may be interpreted differently by different observers.

It would be advantageous to provide a method identifying proteins capable of distinguishing an individual and methods for efficiently and accurately determining identity, distinguishing between individuals, as well as determining the source of biological fluids, especially those amenable to automation.

It must be noted that, as used in this specification and the appended claims, the singular forms "a," "an," and "the" include plural referents unless the context clearly dictates otherwise. Thus, for example, reference to a method for analyzing a biological sample from "an animal" includes reference to two or more of such animals, reference to "a support" includes reference to one or more of such supports, and reference to "an array" includes reference to two or more of such arrays.

As used herein, "blood" means and includes whole blood, plasma, serum, or any derivative of blood. A blood sample may be, for example, serum.

As used herein, "comprising," "including," "containing," "characterized by," and grammatical equivalents thereof are inclusive or open-ended terms that do not exclude additional, unrecited elements or method acts. "Comprising" is to be interpreted as including the more restrictive terms "consisting of" and "consisting essentially of."

As used herein, "consisting of" and grammatical equivalents thereof exclude any element, step, or ingredient not specified in the claim.

As used herein, "consisting essentially of" and grammatical equivalents thereof limit the scope of a claim to the specified materials or acts and those that do not materially affect the basic and novel characteristic or characteristics of the claimed invention.

As used herein, the terms "biological sample" and "sample" mean and include a sample comprising individual-specific antibodies obtained from an organism or from components (e.g., cells) of an organism. The sample may be of any biological material. Such samples include, but are not limited to, blood, blood fractions (e.g. serum, plasma), blood cells (e.g., white cells), tissue or fine needle biopsy samples, urine, saliva, perspiration or semen. Biological samples may also include sections of tissues such as frozen sections taken for histological purposes.

As used herein, "colorigenic" refers to a substrate that produces a colored product upon digestion with an appropriate enzyme. Such colored products include fluorescent and luminescent products.

The term "discriminant analysis" means and includes a set of statistical methods used to select features that optimally discriminate between two or more groups. Application of discriminant analysis to a data set allows the user to focus on the most discriminating features for further analysis.

As used herein, the terms "immobilized" or "affixed" mean and include an association between a protein or antigen and a substrate at the molecular level (i.e., through a covalent or non-covalent bond or interaction). For example, a protein may be immobilized to a support by covalent bonding directly to a surface of the support which may or may not be modified to enhance such covalent bonding. Also, the protein may be immobilized to the support by use of a linker molecule between the protein and the support. Proteins may further be immobilized on the support by steric hindrance within a polymerized gel or by covalent bonding within a polymerized gel.

Proteins may also be immobilized on a support through hybridization between the protein and a molecule immobilized on the support.

The term "protein array" as used herein refers to a protein array, a protein macroarray, a protein microarray or a protein nanoarray. A protein array may include, for example, but is not limited to, ProtoArray™ high density protein array, which is commercially available from Invitrogen (Carlsbad, Calif.). The ProtoArray™ high density protein array may be used to screen complex biological mixtures, such as serum, to assay for the presence of autoantibodies directed against human proteins. Alternatively, a custom protein array that includes autoantigens, such as those provided herein, for the detection of autoantibody biomarkers, may be used to assay for the presence of autoantibodies directed against human proteins. In certain disease states including autoimmune diseases and cancer, autoantibodies are expressed at altered levels relative to those observed in healthy individuals.

As used herein, "support" means a generally or substantially planar substrate onto which an array of antigens is disposed. A support may comprise any material or combination of materials suitable for carrying the array. Materials used to construct these supports need to meet several requirements, such as (1) the presence of surface groups that may be easily derivatized, (2) inertness to reagents used in the assay, (3) stability over time, and (4) compatibility with biological samples. For example, suitable materials include glass, silicon, silicon dioxide (i.e., silica), plastics, polymers, hydrophilic inorganic supports, and ceramic materials. Illustrative plastics and polymers include poly(tetrafluoroethylene), poly(vinylidenedifluoride), polystyrene, polycarbonate, polymethacrylate, and combinations thereof. Illustrative hydrophilic inorganic supports include alumina, zirconia, titania, and nickel oxide. An example of a glass substrate would be a microscope slide. Silicon wafers used to make computer chips have also been used to make biochips. See, for example, U.S. Pat. No. 5,605,662. The supports may further include a coating, such as, nitrocellulose, gelatin, a polymer (i.e., polyvinyl difluoride) or an aldehyde.

In some embodiments, a method of determining proteins useful in discriminating one individual from 1 or more other individuals and/or positively identifying an individual is provided. Such proteins may be referred to herein as "discriminant proteins." The method may employ a protein array including a plurality of proteins immobilized on a support. As a non-limiting example, the protein array may be a ProtoArray™ human protein microarray, which is commercially available from Invitrogen Corporation (Carlsbad, Calif.). The plurality of proteins immobilized on the support may include a plurality of antigens.

In a typical assay, a plurality of biological samples including individual-specific antibodies may each be physically contacted with a protein array, under conditions that permit high affinity binding, but that minimize non-specific interactions. In one embodiment, the biological samples are introduced to the protein array that includes a plurality of antigens immobilized in predetermined locations on a support. The protein array may be washed free of unbound material, and the presence of bound antibodies may be detected, and correlated with the cognate antigen.

The data collected from each of the plurality of biological samples profiled on a protein array may be used to determine an antibody profile for the individual. The antibody profiles may be analyzed using, for example, conventional discriminant analysis methods, to determine proteins relevant in discriminating and positively identifying an individual (i.e., discriminant proteins) from a population of one or more other

individuals. The discriminant proteins may be used to generate a test panel for identifying an individual or determining a source of a biological sample. In some embodiments, the test panel may be, for example, a protein array **100**, as shown in FIG. 1, including a plurality of the discriminant proteins arranged as spots **102** in predetermined locations on a support **104**.

Protein Array

The protein array may be prepared by attaching the antigens to the surface of the support in a preselected pattern such that the locations of antigens in the array are known. As used herein, an antigen is a substance that is bound by an antibody. Antigens may include proteins, carbohydrates, nucleic acids, hormones, drugs, receptors, tumor markers, and the like, and mixtures thereof. An antigen may also be a group of antigens, such as a particular fraction of proteins eluted from a size exclusion chromatography column. Still further, an antigen may also be identified as a designated clone from an expression library or a random epitope library.

In one embodiment, antigens may be isolated from HeLa cells as generally described in A. M. Francoeur et al., *Identification of Ki (Ku, p70/p80) Autoantigens and Analysis of Anti-Ki Autoantibody Reactivity*, 136 J. Immunol. 1648 (1986). Briefly, HeLa cells may be grown in standard medium under standard tissue culture conditions. Confluent HeLa cell cultures may then be rinsed, preferably with phosphate-buffered saline (PBS), lysed with detergent, and centrifuged to remove insoluble cellular debris. The supernate contains approximately 10,000 immunologically distinct antigens suitable for generating an array.

There is no requirement that the antigens used to generate the array be known. All that is required is that the source of the antigens be consistent such that a reproducible array may be generated. For example, the HeLa cell supernate containing the antigens may be fractionated on a size exclusion column, electrophoretic gel, density gradient, or the like, as is well known in the art. Fractions may be collected, and each fraction collected could represent a unique set of antigens for the purpose of generating the array. Thus, even though the antigens may be unknown, a reproducible array may be generated if the HeLa cell antigens may be isolated and fractionated using the same method and conditions.

Other methods, such as preparation of random peptide libraries or epitope libraries are well known in the art and may be used to reproducibly produce antigens (e.g., J. K. Scott and G. P. Smith, *Searching for Peptide Ligands with an Epitope Library*, 249 Science 386 (1990); J. J. Devlin et al., *Random Peptide Libraries: A Source of Specific Protein Binding Molecules*, 249 Science 404-406 (1990); S. E. Cwirla et al., *Peptides on Phage: A Vast Library of Peptides for Identifying Ligands*, 87 Proc. Nat'l Acad. Sci. USA 6378-6382 (1990); K. S. Lam et al., *A New Type of Synthetic Peptide Library for Identifying Ligand-binding Activity*, 354 Nature 82-84 (1991); S. Cabilly, *Combinatorial Peptide Library Protocols*, Humana Press, 304 p.p., 129-154 1997; and U.S. Pat. No. 5,885,780). Such libraries may be constructed by ligating synthetic oligonucleotides into an appropriate fusion phage. Fusion phages may be filamentous bacteriophage vectors in which foreign sequences may be cloned into phage gene III and displayed as part of the gene III protein (pIII) at one tip of the virion. Each phage encodes a single random sequence and expresses it as a fusion complex with pIII, a minor coat protein present at about five molecules per phage. For example, in the fusion phage techniques of J. K. Scott and G. P. Smith, supra, a library was constructed of phage containing a variable cassette of six amino acid residues. The hexapeptide modules fused to bacteriophage proteins provided a

library for the screening methodology that may examine $>10^{12}$ phages (or about 10^8 - 10^{10} different clones) at one time, each with a test sequence on the virion surface. The library obtained was used to screen monoclonal antibodies specific for particular hexapeptide sequences. The fusion phage system has also been used by other groups, and libraries containing longer peptide inserts have been constructed. Fusion phage prepared according to this methodology may be selected randomly or non-randomly for inclusion in the array of antigens. The fusion phages selected for inclusion in the array may be propagated by standard methods to result in what is virtually an endless supply of the selected antigens.

Other methods for producing antigens are also known in the art. For example, expression libraries may be prepared by random cloning of DNA fragments or cDNA into an expression vector (e.g., R. A. Young and R. W. Davis, *Yeast RNA Polymerase II Genes: Isolation with Antibody Probes*, 222 Science 778-782 (1983); G. M. Santangelo et al., *Cloning of Open Reading Frames and Promoters from the Saccharomyces cerevisiae Genome: Construction of Genomic Libraries of Random Small Fragments*, 46 Gene 181-186 (1986). Expression vectors that could be used for making such libraries are commercially available from a variety of sources. For example, random fragments of HeLa cell DNA or cDNA may be cloned into an expression vector, and then clones expressing HeLa cell proteins may be selected. These clones may then be propagated by methods well known in the art. The expressed proteins may then be isolated or purified and may be used in the making of the array.

Alternatively, antigens may be synthesized using recombinant DNA technology well known in the art. Genes that code for many proteins from a gamut of organisms including viruses, bacteria, and mammals have been cloned, and thus large quantities of highly pure proteins may be synthesized quickly and inexpensively. For example, the genes that code for many eukaryotic and mammalian membrane-bound receptors, growth factors, cell adhesion molecules, and regulatory proteins have been cloned and may be useful as antigens. Many proteins produced by such recombinant techniques, such as transforming growth factor, acidic and basic fibroblast growth factors, interferon, insulin-like growth factor, and various interleukins from different species, are commercially available. In most instances, the entire polypeptide need not be used as an antigen. For example, any size or portion of the polypeptide that contains at least one epitope, i.e., antigenic determinant or portion of an antigen that specifically interacts with an antibody, will suffice for use in the array. In addition, a particular antigen may be purified or isolated from any natural or synthetic source of the antigen by methods known in the art.

The antigens, whether selected randomly or non-randomly, may be disposed on the support to result in the array. The pattern of the antigens on the support should be reproducible. In embodiments, the location and identity of each antigen on the support may be known. For example, in a 10×10 array one skilled in the art might place antigens 1-100 in locations 1-100, respectively, of the array. As a non-limiting example, each of the antigens of the array may be deposited on the support as a spot having a diameter of from about 10 microns to about 500 microns and, more particularly, from about 50 microns to about 300 microns.

The proteins may be placed in arrays on the surface of the support using a pipetting device or a machine or device configured for placing liquid samples on a support, for example, using a commercially available microarrayer, such as those from Arrayit Corporation (Sunnyvale, Calif.); Genomic Solutions, Inc. (Ann Arbor, Mich.); Gene Machines (San Carlos,

Calif.); Genetic MicroSystems, Inc. (Woburn, Mass.); GenePack DNA (Cambridge, UK); Genetix Ltd. (Christchurch, Dorset, UK); and Packard Instrument Company (Meriden, Conn.).

Relevant methods to array a series of proteins onto a surface include contact printing processes, non-contact printing processes and in silico protein synthesis arrayer processes. Commercially available instruments are available for both methods. In some embodiments, conventional contact printing processes, such as contact pin printing and microstamping, in which the printing device may physically contact a surface may be used to apply the proteins to the surface of a support. For example, a pin printing device such as that commercially available from Arrayit Corporation may be used to deposit spots having an average diameter of 65 microns or larger. As another non-limiting example, Genomic Solutions offers several nanoliter dispensing instruments that may dispense liquid volumes from 20 nL up to 250 μ L from 96-, 384-, 1536-, 3456-, and 9600-well microtiter plates and place them precisely on a surface with densities up to 400 spots/cm². The instruments will spot onto surfaces in a variety of patterns. In additional embodiments, the protein antigens may be applied to the surface without physical contact between the printing device and the surface using conventional non-contact printing processes including, but not limited to, photochemistry-based methods, laser writing, electrospray deposition, and inkjet. As the name implies, inkjet technology utilizes the same principles as those used in inkjet printers. MicroFab Technologies, Inc. (Plano, Tex.), offers a ten-fluid print head that may dispense picoliter quantities of liquids onto a surface in a variety of patterns. An illustrative pattern for the present application would be a simple array ranging from 10 \times 10 up to 100 \times 100. The protein antigens may be applied to the surface using a serial deposition process or a parallel deposition process.

There are a number of methods that may be used to attach proteins or other antigens to the surface of a support. The simplest of these is simple adsorption through hydrophobic, ionic, and van der Waals forces. As a non-limiting example, bifunctional organosilanes may be used in attachment of proteins to the surface of the support (e.g., Thompson and Maragos, *Fiber-Optic Immunosensor for the Detection of Fumonisin B₁*, 44 J. Agric. Food Chem. 1041-1046 (1996)). One end of the organosilane reacts with exposed —OH groups on the surface of the support to form a silanol bond. The other end of the organosilane contains a group that is reactive with various groups on the protein surface, such as —NH₂ and —SH groups. This method of attaching proteins to the support results in the formation of a covalent linkage between the protein and the support. Other suitable methods that have been used for protein attachment to surfaces include arylazide, nitrobenzyl, and diazirine photochemistry methodologies. Exposure of the above chemicals to UV light causes the formation of reactive groups that may react with proteins to form a covalent bond. The arylazide chemistry forms a reactive nitrene group that may insert into C—H bonds, while the diazirine chemistry results in a reactive carbene group. The nitrobenzyl chemistry is referred to as caging chemistry whereby the caging group inactivates a reactive molecule. Exposure to UV light frees the molecule and makes it available for reaction. Still other methods for attaching proteins to supports are well known in the art, (e.g., S. S. Wong, *Chemistry of Protein Conjugation and Cross-Linking* CRC Press, 340, 1991).

Following attachment of the antigens on the support in the selected array, the support may be washed. The wash solution may include, for example, one or more of a surfactant or a

non-specific protein such as bovine serum albumin (BSA). Appropriate liquids for washing include, but are not limited to, phosphate buffered saline (PBS) and the like, i.e., relatively low ionic strength, biocompatible salt solutions buffered at or near neutrality. Many of such appropriate wash liquids are known in the art or may be devised by a person skilled in the art without undue experimentation (e.g., N.E. Good and S. Izawa, *Hydrogen Ion Buffers*, 24 Methods Enzymology 53-68 (1972)).

The support may be processed for blocking of nonspecific binding of proteins and other molecules to the support. This blocking step may prevent the binding of antigens, antibodies, and the like to the support wherein such antigens, antibodies, or other molecules are not intended to bind. Blocking may reduce the background that might swamp out the signal, thus increasing the signal-to-noise ratio. The support may be blocked by incubating the support in a medium that contains inert molecules that bind to sites where nonspecific binding might otherwise occur. Examples of suitable blockers include, but are not limited to, bovine serum albumin, human albumin, gelatin, nonfat dry milk, polyvinyl alcohol, TWEEN® 20, and various commercial blocking buffers, such as SEABLOCK™ blocking buffer from EastCoast Bio, Inc., (West Berwick, Me.) and SUPERBLOCK® blocking buffer from Pierce Chemical Co., (Rockford, Ill.). In some embodiments, one or more of the suitable blockers may be incorporated into the wash solution described above.

Antibody Profile

The array may be contacted with a sample of the biological material to be tested. For example, the biological sample may be obtained from various bodily fluids and solids, including blood, saliva, semen, serum, plasma, urine, amniotic fluid, pleural fluid, cerebrospinal fluid, and mixtures thereof. These samples may be obtained according to methods well known in the art. Depending on the detection method used, it may be required to manipulate the biological sample to attain optimal reaction conditions. For example, the ionic strength or hydrogen ion concentration or the concentration of the biological sample may be adjusted for optimal immune complex formation, enzymatic catalysis, and the like.

As described in detail in U.S. Pat. No. 5,270,167 to Francoeur, when ISAs are allowed to react with a set of random antigens, a certain number of immune complexes form. For example, using a panel of about 1000 unique antigens, about 30 immune complexes between ISAs in a biological sample that has been diluted 20-fold may be detected. If the biological sample is undiluted, the total number of possible detectable immune complexes that could form would be greater than 10²³. The total number of possible immune complexes may also be increased by selecting “larger” antigens, i.e., proteins instead of peptides) that have multiple epitopes. Therefore, it will be appreciated that depending on the antigens and number thereof used, the dilution of the biological sample, and the detection method, one skilled in the art may regulate the number of immune complexes that will form and be detected. As used herein, an “antibody profile” refers to the set of unique immune complexes that form and fail to form between the ISAs in the biological sample and the antigens in the array.

Detection and/or Quantification of Reactions

Methods for detecting antibody/antigen or immune complexes are well known in the art. The present invention may be modified by one skilled in the art to accommodate the various detection methods known in the art. The particular detection method chosen by one skilled in the art depends on several factors, including the amount of biological sample available, the type of biological sample, the stability of the biological

sample, the stability of the antigen, and the affinity between the antibody and antigen. Moreover, as discussed above, depending on the detection methods chosen, it may be required to modify the biological sample. While these techniques are well known in the art, non-limiting examples of a few of the detection methods that may be used to practice the present invention are briefly described below.

There are many types of immunoassays known in the art. The most common types of immunoassay are competitive and non-competitive heterogeneous assays, such as, for example, enzyme-linked immunosorbent assays (ELISAs). In a non-competitive ELISA, unlabeled antigen is bound to a support. A biological sample may be combined with antigens bound to the reaction vessel, and antibodies (primary antibodies) in the biological sample may be allowed to bind to the antigens, forming the immune complexes. After the immune complexes have formed, excess biological sample may be removed and the array may be washed to remove nonspecifically bound antibodies. The immune complexes may then be reacted with an appropriate enzyme-labeled anti-immunoglobulin (secondary antibody). The secondary antibody reacts with antibodies in the immune complexes, not with other antigens bound to the array. Secondary antibodies specific for binding antibodies of different species, including humans, are well known in the art and are commercially available, such as from Sigma Chemical Co. (St. Louis, Mo.) and Santa Cruz Biotechnology, Inc. (Santa Cruz, Calif.). After an optional further wash, the enzyme substrate may be added. The enzyme linked to the secondary antibody catalyzes a reaction that converts the substrate into a product. When excess antigen is present, the amount of product is directly proportional to the amount of primary antibody present in the biological sample. By way of non-limiting example, the product may be fluorescent or luminescent, which may be measured using technology and equipment well known in the art. It is also possible to use reaction schemes that result in a colored product, which may be measured spectrophotometrically.

In other embodiments of the invention, the secondary antibody may not be labeled to facilitate detection. Additional antibodies may be layered (i.e., tertiary, quaternary, etc.) such that each additional antibody specifically recognizes the antibody previously added to the immune complex. Any one of these additional (i.e., tertiary, quaternary, etc.) may be labeled so as to allow detection of the immune complex as described herein.

Sandwich or capture assays may also be used to identify and quantify immune complexes. Sandwich assays are a mirror image of non-competitive ELISAs in that antibodies are bound to the solid phase and antigen in the biological sample is measured. These assays may be particularly useful in detecting antigens having multiple epitopes that are present at low concentrations. This technique requires excess antibody to be attached to a solid phase. The bound antibody is then incubated with the biological samples, and the antigens in the sample may be allowed to form immune complexes with the bound antibody. The immune complex is incubated with an enzyme-linked secondary antibody, which recognizes the same or a different epitope on the antigen as the primary antibody. Hence, enzyme activity is directly proportional to the amount of antigen in the biological sample. D. M. Kemeny and S. J. Challacombe, *ELISA and Other Solid Phase Immunoassays*, (John Wiley & Sons Ltd.) (1988).

Typical enzymes that may be linked to secondary antibodies include, but are not limited to, horseradish peroxidase, glucose oxidase, glucose-6-phosphate dehydrogenase, alkaline phosphatase, β -galactosidase, and urease. Secondary

antigen-specific antibodies linked to various enzymes are commercially available from, for example, Sigma Chemical Co. and Amersham Life Sciences (Arlington Heights, Ill.).

Competitive ELISAs are similar to noncompetitive ELISAs except that enzyme linked antibodies compete with unlabeled antibodies in the biological sample for limited antigen binding sites. Briefly, a limited number of antigens may be bound to the support. Biological sample and enzyme-labeled antibodies may be added to the support. Antigen-specific antibodies in the biological sample compete with enzyme-labeled antibodies for the limited number of antigens bound to the support. After immune complexes have formed, nonspecifically bound antibodies may be removed by washing, enzyme substrate is added, and the enzyme activity is measured. No secondary antibody is required. Because the assay is competitive, enzyme activity is inversely proportional to the amount of antibodies in the biological sample.

Another competitive ELISA may also be used within the scope of the present invention. In this embodiment, limited amounts of antibodies from the biological sample may be bound to the surface of the support as described herein. Labeled and unlabeled antigens may be then brought into contact with the support such that the labeled and unlabeled antigens compete with each other for binding to the antibodies on the surface of the support. After immune complexes have formed, nonspecifically bound antigens may be removed by washing. The immune complexes may be detected by incubation with an enzyme-linked secondary antibody, which recognizes the same or a different epitope on the antigen as the primary antibody, as described above. The activity of the enzyme is then assayed, which yields a signal that is inversely proportional to the amount of antigen present.

Homogeneous immunoassays may also be used when practicing the method of the present invention. Homogeneous immunoassays may be preferred for detection of low molecular weight compounds, such as hormones, therapeutic drugs, and illegal drugs that cannot be analyzed by other methods, or compounds found in high concentration. Homogeneous assays may be particularly useful because no separation step is necessary. R. C. Boguslaski et al., *Clinical Immunochimistry Principles of Methods and Applications*, (1984).

In homogeneous techniques, bound or unbound antigens may be enzyme-linked. When antibodies in the biological sample bind to the enzyme-linked antigen, steric hindrances inactivate the enzyme. This results in a measurable loss in enzyme activity. Free antigens (i.e., not enzyme-linked) compete with the enzyme-linked antigen for limited antibody binding sites. Thus, enzyme activity is directly proportional to the concentration of antigen in the biological sample.

Enzymes useful in homogeneous immunoassays include, but are not limited to, lysozyme, neuraminidase, trypsin, papain, bromelain, glucose-6-phosphate dehydrogenase, and β -galactosidase. T. Persoon, "Immunochemical Assays in the Clinical Laboratory," 5 *Clinical Laboratory Science* 31 (1992). Enzyme-linked antigens are commercially available or may be linked using various chemicals well known in the art, including glutaraldehyde and maleimide derivatives.

Prior antibody profiling technology involved an alkaline phosphatase labeled secondary antibody with 5-bromo-4-chloro-3'-indolylphosphate p-toluidine salt (BCIP) and nitro-blue tetrazolium chloride (NBT), both of which are commercially available from a variety of sources, such as from Pierce Chemical Co. (Rockford, Ill.). The enzymatic reaction forms an insoluble colored product that is deposited on the surface of membrane strips to form bands wherever antigen-antibody complexes occur. As a non-limiting example, the array may be scanned to detect a colored product using one of a variety

of conventional desktop scanners, which are commercially available from a variety of sources, such as from Canon U.S.A. (Lake Success, N.Y.). The intensity of the colored product may be quantified by calculating the median feature pixel intensity minus median background pixel intensity.

As another non-limiting example, gold nanoparticle labeled antibodies may be employed and may be detected using a scanning, transmission electron microscopy, and/or dark-field zoom stereomicroscopy. Compared to conventional fluorescent labels, the gold nanoparticles scatter incident white light to generate monochromatic light which may be easily detected. The light intensity generated by the gold nanoparticles may be up to 100,000 times greater than that generated by fluorescent-labeled molecules. For example, the gold nanoparticles may be detected using a conventional desktop scanner. Han et al., *Detection of Analyte Binding to Microarrays Using Gold Nanoparticle Labels and a Desktop Scanner*, 3 Lab Chip 329; 329-332 (2003).

Fluorescent immunoassays may also be used when practicing the method of the present invention. Fluorescent immunoassays are similar to ELISAs except the enzyme is substituted for fluorescent compounds called fluorophores or fluorochromes. These compounds have the ability to absorb energy from incident light and emit the energy as light of a longer wavelength and lower energy. Fluorescein and rhodamine, usually in the form of isothiocyanates that may be readily coupled to antigens and antibodies, are most commonly used in the art. D. P. Stites et al., *Basic and Clinical Immunology*, (1994). Fluorescein absorbs light of 490 to 495 nm in wavelength and emits light at 520 nm in wavelength. Tetramethylrhodamine absorbs light of 550 nm in wavelength and emits light at 580 nm in wavelength. Illustrative fluorescence-based detection methods include ELF-97 alkaline phosphatase substrate (Molecular Probes, Inc., Eugene, Oreg.); PBXL-1 and PBXL-3 (phycobilisomes conjugated to streptavidin) (Martek Biosciences Corp., Columbia, Md.); FITC (fluorescein isothiocyanate) and Texas Red labeled goat anti-human IgG (Jackson ImmunoResearch Laboratories, Inc., West Grove, Pa.); and B-Phycocerythrin and R-Phycocerythrin conjugated to streptavidin (Molecular Probes Inc.). ELF-97 is a nonfluorescent chemical that is digested by alkaline phosphatase to form a fluorescent molecule. Because of turnover of the alkaline phosphatase, use of the ELF-97 substrate results in signal amplification. Fluorescent molecules attached to secondary antibodies do not exhibit this amplification.

Phycobiliproteins isolated from algae, porphyrins, and chlorophylls, which all fluoresce at about 600 nm, are also being used in the art. I. Hemmila, *Fluoroimmunoassays and Immunofluorometric Assays*, 31 Clin. Chem. 359 (1985); U.S. Pat. No. 4,542,104. Phycobiliproteins and derivatives thereof are commercially available under the names R-phycocerythrin (PE) and QUANTUM RED™ from Sigma Chemical Co.

In addition, Cy-conjugated secondary antibodies and antigens may be useful in immunoassays and are commercially available. Cy3, for example, is maximally excited at 554 nm and emits light at between 568 and 574 nm. Cy3 is more hydrophilic than other fluorophores and thus has less of a tendency to bind nonspecifically or aggregate. Cy-conjugated compounds are commercially available from Amersham Life Sciences.

Illustrative luminescence-based detection methods include CSPD® and CDP star alkaline phosphatase substrates from Roche Molecular Biochemicals, (Indianapolis, Ind.) and SUPERSIGNAL® horseradish peroxidase substrate from Pierce Chemical Co., (Rockford, Ill.).

Chemiluminescence, electroluminescence, and electrochemiluminescence (ECL) detection methods may also be attractive means for quantifying antigens and antibodies in a

biological sample. Luminescent compounds have the ability to absorb energy, which is released in the form of visible light upon excitation. In chemiluminescence, the excitation source is a chemical reaction; in electroluminescence the excitation source is an electric field; and in ECL an electric field induces a luminescent chemical reaction.

Molecules used with ECL detection methods generally comprise an organic ligand and a transition metal. The organic ligand forms a chelate with one or more transition metal atoms forming an organometallic complex. Various organometallic and transition metal-organic ligand complexes have been used as ECL labels for detecting and quantifying analytes in biological samples. Due to their thermal, chemical, and photochemical stability, their intense emissions and long emission lifetimes, ruthenium, osmium, rhenium, iridium, and rhodium transition metals are favored in the art. The types of organic ligands are numerous and include anthracene and polypyridyl molecules and heterocyclic organic compounds. For example, bipyridyl, bipyrazyl, terpyridyl, and phenanthrolyl, and derivatives thereof, are common organic ligands in the art. A common organometallic complex used in the art includes tris-bipyridine ruthenium (II), commercially available from IGEN, Inc. (Rockville, Md.) and Sigma Chemical Co.

ECL may be performed under aqueous conditions and under physiological pH, thus minimizing biological sample handling. J. K. Leland et al., *Electrogenerated Chemiluminescence: An Oxidative-Reduction Type ECL Reactions Sequence Using Tripropyl Amine*, 137 J. Electrochemical Soc. 3127-3131 (1990); WO 90/05296; and U.S. Pat. No. 5,541,113. Moreover, the luminescence of these compounds may be enhanced by the addition of various cofactors, such as amines.

A tris-bipyridine ruthenium (II) complex, for example, may be attached to a secondary antibody using strategies well known in the art, including attachment to lysine amino groups, cysteine sulfhydryl groups, and histidine imidazole groups. In a typical ELISA immunoassay, secondary antibodies would recognize antibodies bound to antigens, but not unbound antigens. After washing nonspecific binding complexes, the tris-bipyridine ruthenium (II) complex may be excited by chemical, photochemical, and electrochemical excitation means, such as by applying current to the array (e.g., WO 86/02734). The excitation would result in a double oxidation reaction of the tris-bipyridine ruthenium (II) complex, resulting in luminescence that could be detected by, for example, a photomultiplier tube. Instruments for detecting luminescence are well known in the art and are commercially available, for example, from IGEN, Inc. (Rockville, Md.).

Solid state color detection circuitry may also be used to monitor the color reactions on the array and, on command, compare the color patterns before and after the sample application. A color camera image may also be used and the pixel information analyzed to obtain the same information.

Still another method involves detection using a surface plasmon resonance (SPR) chip. The surface of the chip is scanned before and after sample application and a comparison is made. The SPR chip relies on the refraction of light when the molecules of interest may be exposed to a light source. Each molecule has its own refraction index by which it may be identified. This method requires precise positioning and control circuitry to scan the chip accurately.

Yet another method involves a fluid rinse of the array with a fluorescing reagent. The antigens that combine with the biological sample will fluoresce and may be detected with a charge-coupled device (CCD) array. The output of such a CCD array is analyzed to determine the unique pattern associated with each sample. Speed is not a factor with any of the methods since the chemical combining of sample and reference takes minutes to occur.

Moreover, array scanners are commercially available, such as from Genetic MicroSystems, Inc. The GMS 418 Array Scanner uses laser optics to rapidly move a focused beam of light over the array. This system uses a dual-wavelength system including high-powered, solid-state lasers that generate high excitation energy to allow for reduced excitation time. At a scanning speed of 30 Hz, the GMS 418 may scan a 22×75-mm slide with 10-μm resolution in about four minutes.

Software for image analysis obtained with an array scanner is readily available. Available software packages include ImageGene (BioDiscovery, Los Angeles, Calif.); ScanAlyze (available at no charge; developed by Mike Eisen, Stanford University, Palo Alto, Calif.); De-Array (developed by Yidong Chen and Jeff Trent of the National Institutes of Health; used with IP Lab from Scanalytics, Inc., Fairfax, Va.); Pathways (Research Genetics, Huntsville, Ala.); GEM Tools (Incyte Pharmaceuticals, Inc., Palo Alto, Calif.); and Imaging Research (Amersham Pharmacia Biotech, Inc., Piscataway, N.J.).

Once interactions between the antigens and antibodies have been identified and quantified, the signals may be digitized. The digitized antibody profile may serve as a signature that identifies the source of the biological sample. Depending on the array used, the digitized data may take numerous forms. For example, the array may include 10 columns and 10 rows for a total number of 100 spots, each including at least one antigen. After the biological sample including the antibodies is added to the array and allowed to incubate, interactions between antigens and antibodies in the biological sample may be identified and quantified. In each spot, an interaction between the antigen in the spot and the antibody in the biological sample will either result in or not result in a quantifiable signal. In one embodiment, the results of the antibody profile may be digitized by, by way of non limiting example, ascribing each one of the 100 spots a numerical value of either "0," if a quantifiable signal was not obtained, or "1," if a quantifiable signal was obtained. Using this method, the digitized antibody profile may comprise a unique set of zeroes and ones. It will be understood that the use of 1 and 0 is merely exemplary and that any set of values or indicators may be used to signify the absence, presence, or intensity of a particular signal.

The numerical values "0" or "1" may, of course, be normalized to signals obtained in internal control spots so that digitized antibody profiles obtained at a later time may be properly compared. For example, one or several of the spots may contain a known antigen, which will remain constant over time. Therefore, if a subsequent biological sample is more or less dilute than a previous biological sample, the signals may be normalized using the signals from the known antigen.

It will be appreciated by one skilled in the art that other methods of digitizing the antibody profile exist and may be used. For example, rather than ascribing each spot with a numerical value of "0" or "1," the numerical value may be incremental and directly proportional to the strength of the signal.

Statistical Analysis

The antibody profiles obtained from the plurality of individuals may be analyzed using conventional discriminant analysis methods to determine proteins useful in discriminating or identifying an individual from one or more other individuals. For example, discriminant proteins may be determined using forward selection, backward elimination, or stepwise selection to determine a subset of proteins that best reveals differences among the classes (i.e., the individuals). The STEPDISC procedure, which is available from SAS Institute, Inc. (Cary, N.C.), may be used to perform a stepwise discriminant analysis to select a subset of the proteins useful in discriminating among individuals. Signals from a set of

proteins that make up each class may be assumed to be multivariate normal with a common covariance matrix.

Using the STEPDISC procedure, variables (in particular, signals from particular proteins) may be chosen to enter or leave the model according to the significance level of an F-test from an analysis of covariance, where the variables already chosen act as covariates and the variable under consideration is the dependent variable. In other embodiments, a variable could be chosen to enter or leave the model according to whether the squared partial correlation for its prediction using the class variable (and controlling for the effects of the other variables already in the model) is high.

In some embodiments, the discriminant proteins useful in discriminating or identifying an individual may be determined by calculating various discriminant functions for classifying observations using the protein signals. Linear or quadratic discriminant functions may be used for data with approximately multivariate normal within-class distributions. Nonparametric methods may be used without making any assumptions about these distributions.

One or more of the discriminant proteins may be used to identify an individual, to distinguish between individuals, or to establish or rule out the source of a biological sample. In some embodiments, one or more of the discriminant proteins may be used as part of a test panel. For example, discriminant proteins may be immobilized on a support in the form of an array as described above to form a protein array useful in discriminating among individuals and/or sources of a biological sample. However, other methods of detecting an interaction between a discriminant protein and an antibody present in a biological sample, such as conventional protein affinity chromatography methods, affinity blotting methods, immunoprecipitation methods, and cross-linking methods, may also be used. In embodiments, the array or test panel may be used to generate an antibody profile which may be used to distinguish between individuals in a population, or to establish or rule out the source of a biological sample within a population, wherein the population may comprise 1 million, 10 million, 100 million, 1 billion, 10 billion, 100 billion, or more individuals.

The array may include several discriminant proteins, each of which may be immobilized on a support. The array may include less than about 200, 175, 150, 125, 100, 75, or 50 discriminant proteins. For example, the test panel for discriminating or identifying an individual may include from about 20 to about 90 discriminant proteins, and more particularly, from about 45 to about 80 discriminant proteins. With "X" different profiles that are each independent, the probability that no two different people have the same profile among "m" people can be shown to be equal to $\exp[-m^2/(2X)]$. As a non-limiting example, greater than about 76 independent discriminant proteins may be used to distinguish an individual among a population of about 10 billion individuals, the probability of a match between two different individuals being less than about 0.0001. As another non-limiting example, greater than about 86 independent discriminant proteins may be used to distinguish an individual among a population of about 100 billion individuals, the probability of a match between two different individuals being less than about 0.0001. Examples of discriminant proteins include, but are not limited to, those proteins presented in Table 1.

In an embodiment of the invention, a protein array including discriminant proteins may be used for forensic analysis for matching a biological sample to an individual such as, for example, a criminal suspect. Forensic samples obtained from crime scenes are often subject to drying of the samples, small sample sizes, mixing with samples from more than one individual, adulteration with chemicals, and the like. The present method provides the advantages of rapid analysis, simplicity, low cost, and accuracy for matching forensic samples with

suspects. For example, the forensic sample and a sample from one or more suspects may be obtained according to methods well known in the art. The samples may be tested against the array and compared. If the discriminant proteins obtained from the samples match, it may be concluded that the forensic sample was obtained from the matching suspect. If no match of discriminant proteins is obtained, then none of the suspects was the source of the forensic sample.

Example

Serum samples from ninety-four (94) individuals were profiled against a high throughput protein array with over 8000 proteins and the data from these chips was statistically analyzed to determine proteins useful for discriminating among sets of individuals in a population. The ninety-four (94) individuals included nineteen (19) Asian individuals, twenty (20) African American individuals, twenty (20) Native American individuals, and thirty-five (35) Caucasian individuals. For quality assurance (QA), the arrays contained the immobilized proteins in pairs on a support. Thus, each array provided two opportunities for antigen/antibody binding for each protein.

The serum samples were diluted 1:150 and used to probe human ProtoArray™. The arrays were blocked for 1 hour and then incubated with the serum samples for 90 minutes at

about 4° C. without shaking. The arrays were then transferred to ice and washed about three times by adding about 20 ml buffer (1×PBS, 5 mM MgCl₂, 0.5 mM DTT, 0.05% Triton X-100, 5% Glycerol, 1% BSA) to the arrays, incubating the arrays with the buffer for 8 minutes at 4° C., and decanting the buffer from the arrays by inverting. The arrays were incubated with anti-human IgG antibody conjugated to AlexaFluor 647 for about 90 minutes, washed as above and dried. The arrays were scanned using a ScanArray Express® 3.0 HT microarray scanner, which is available commercially from Perkin Elmer, Inc. (Waltham, Mass.). The images were captured from the microarray scanner using a 633 nm laser with the scanner set to 10 μm resolution. Following scanning, data was acquired using ImaGene 8.0 microarray analysis software from BioDiscovery (El Segundo, Calif.). Background-subtracted signals from each population were normalized utilizing a quantile normalization strategy. Subjects were distinguished from one another using conventional discriminant analysis. The STEPDISC procedure from SAS Institute, Inc. was utilized to identify discriminant proteins based on the logarithms of the intensities detected. The discriminant proteins of interest were identified as significant in distinguishing between individuals. A list of 80 discriminating proteins from among the over 8,000 on the arrays was determined. The 80 discriminating proteins are listed in Table 1.

TABLE 1

SEQ ID NO	Protein ID	SelOrdAll	MinPSeeOrNot	sRatio	maxCorrAfter
SEQ ID NO: 1	PM_2149	16	0.45	22.1	0.683
SEQ ID NO: 2	PM_2151	99	0.25	13.4	0.585
SEQ ID NO: 3	BC010125.1	62	0.23	15.6	0.500
SEQ ID NO: 4	BC011414.1	15	0.40	19.9	0.482
SEQ ID NO: 5	BC012945.1	38	0.33	18.4	0.570
SEQ ID NO: 6	BC014409.1	—	0.32	10.7	0.448
SEQ ID NO: 7	BC015219.1	76	0.29	15.6	0.652
SEQ ID NO: 8	BC016470.2	74	0.19	14.6	0.579
SEQ ID NO: 9	BC018206.1	31	0.38	16.1	0.551
SEQ ID NO: 10	BC018404.1	93	0.27	19.0	0.754
SEQ ID NO: 11	BC019039.2	33	0.41	17.2	0.544
SEQ ID NO: 12	BC019315.1	27	0.48	17.8	0.846
SEQ ID NO: 13	BC021189.2	29	0.34	17.2	0.488
SEQ ID NO: 14	BC023152.1	6	0.10	25.3	0.752
SEQ ID NO: 15	BC026175.1	50	0.39	15.6	0.582
SEQ ID NO: 16	BC026346.1	78	0.48	16.4	0.360
SEQ ID NO: 17	BC032825.2	13	0.10	18.9	0.491
SEQ ID NO: 18	BC033711.1	72	0.29	14.6	0.567
SEQ ID NO: 19	BC036123.1	101	0.35	15.0	0.649
SEQ ID NO: 20	BC040949.1	45	0.37	17.9	0.523
SEQ ID NO: 21	BC050377.1	70	0.14	11.0	0.310
SEQ ID NO: 22	BC052805.1	56	0.29	16.6	0.501
SEQ ID NO: 23	BC053602.1	42	0.32	16.1	0.621
SEQ ID NO: 24	BC060824.1	12	0.28	19.4	0.421
SEQ ID NO: 25	NM_015138.2	91	0.33	13.3	0.607
SEQ ID NO: 26	NM_175887.2	34	0.43	15.4	0.537
SEQ ID NO: 27	NM_000394.2	44	0.38	20.2	0.737
SEQ ID NO: 28	NM_000723.3	200	0.22	9.4	0.580
SEQ ID NO: 29	NM_001008220.1	17	0.22	21.7	0.405
SEQ ID NO: 30	NM_001106.2	22	0.41	20.3	0.303
SEQ ID NO: 31	NM_001312.2	81	0.42	13.2	0.619
SEQ ID NO: 32	NM_001537.1	84	0.49	23.5	0.733
SEQ ID NO: 33	NM_002737	73	0.47	10.0	0.300
SEQ ID NO: 34	NM_002740	79	0.28	12.4	0.620
SEQ ID NO: 35	NM_002744	3	0.42	22.4	0.215
SEQ ID NO: 36	NM_003907.1	57	0.37	14.8	0.440
SEQ ID NO: 37	NM_003910.2	63	0.12	12.7	0.594
SEQ ID NO: 38	NM_004064.2	54	0.20	13.8	0.422
SEQ ID NO: 39	NM_004394.1	58	0.48	16.3	0.641
SEQ ID NO: 40	NM_004845.3	30	0.25	18.0	0.432
SEQ ID NO: 41	NM_004965.3	97	0.46	11.4	0.648
SEQ ID NO: 42	NM_005030	95	0.41	14.2	0.683
SEQ ID NO: 43	NM_005246.1	77	0.22	9.3	0.625
SEQ ID NO: 44	NM_006007.1	80	0.24	13.3	0.417
SEQ ID NO: 45	NM_006218.2	90	0.24	8.2	0.573
SEQ ID NO: 46	NM_006628.4	66	0.29	15.0	0.538

TABLE 1-continued

SEQ ID NO	Protein ID	SelOrdAll	MinPSeeOrNot	sRatio	maxCorrAfter
SEQ ID NO: 47	NM_006819.1	4	0.22	17.9	0.356
SEQ ID NO: 48	NM_012472.1	11	0.49	23.0	0.578
SEQ ID NO: 49	NM_014240.1	19	0.44	18.9	0.459
SEQ ID NO: 50	NM_014245.1	18	0.29	22.9	0.676
SEQ ID NO: 51	NM_014460.2	21	0.32	19.7	0.414
SEQ ID NO: 52	NM_014622.4	65	0.49	15.7	0.566
SEQ ID NO: 53	NM_014891.1	32	0.23	19.1	0.343
SEQ ID NO: 54	NM_014943.3	71	0.16	12.7	0.519
SEQ ID NO: 55	NM_015149.2	96	0.18	11.4	0.665
SEQ ID NO: 56	NM_015417.2	8	0.12	19.3	0.353
SEQ ID NO: 57	NM_015509.2	43	0.23	12.8	0.554
SEQ ID NO: 58	NM_016096.1	41	0.28	16.0	0.516
SEQ ID NO: 59	NM_016520.1	60	0.38	13.3	0.471
SEQ ID NO: 60	NM_017855.2	69	0.29	14.2	0.578
SEQ ID NO: 61	NM_017949.1	49	0.16	16.2	0.630
SEQ ID NO: 62	NM_018326.1	26	0.39	17.5	0.254
SEQ ID NO: 63	NM_018584.4	7	0.37	21.7	0.448
SEQ ID NO: 64	NM_024718.2	103	0.17	11.0	0.495
SEQ ID NO: 65	NM_024826.1	20	0.41	17.8	0.328
SEQ ID NO: 66	NM_025241.1	48	0.43	13.2	0.268
SEQ ID NO: 67	NM_032345.1	85	0.16	13.4	0.765
SEQ ID NO: 68	NM_032368.3	39	0.36	19.2	0.635
SEQ ID NO: 69	NM_079420.1	51	0.45	14.0	0.643
SEQ ID NO: 70	NM_080390.3	86	0.23	15.3	0.582
SEQ ID NO: 71	NM_138623.2	67	0.12	14.4	0.538
SEQ ID NO: 72	NM_145796.2	64	0.26	11.4	0.590
SEQ ID NO: 73	NM_153757.1	46	0.46	16.8	0.402
SEQ ID NO: 74	NM_177973.1	10	0.26	18.5	0.290
SEQ ID NO: 75	NM_178010.1	9	0.31	16.8	0.124
SEQ ID NO: 76	NM_199124.1	28	0.38	14.0	0.252
SEQ ID NO: 77	NM_201262.1	14	0.27	17.5	0.118
SEQ ID NO: 78	NM_203284.1	5	0.31	26.9	0.277
SEQ ID NO: 79	NM_205853.1	25	0.44	17.7	0.208
SEQ ID NO: 80	NM_212540.1	75	0.17	12.4	—

The discriminant proteins of Table 1 were selected to discriminate an individual based on the primary criterion that the logarithms of the associated intensity signals appear as selected variables in a STEPDISC model. Several STEPDISC models were tested. One used only data from the first QA sample associated with each protein. A second model used only data from the other QA sample. A third model used average values, and a fourth used all the data (a total of 198 sets of protein intensity data from 99 non-blank arrays). The “SelOrdAll” column in Table 1 shows the order of selection of proteins from the fourth model. The values are ranked, so “1” corresponds to the first protein selected, “2” for the second, and so forth. The protein (SEQ. ID NO: 6) with no value in this column was selected in a fifth STEPDISC model that used just data from subjects with replication (specifically, data from the two individuals with more than one array in the data set were used in this model). The fourth run identified a total of 197 proteins. The filter sought proteins among the first 100 selected using this model. For later protein lists that needed more proteins than just the 80, additional proteins selected in the first three STEPDISC models were included in the screening list.

The initial list was refined using three additional filters. First, proteins retained on the list had to have the between-subject standard deviation as the largest of the estimated standard deviations. The standard deviations for this filter were obtained using a conventional “components of variance” analysis for each protein that sought variation between subjects, arrays, spots on the array and the QA sampling variation. The ratio of the between-subject estimate divided by the QA sample standard deviation estimate is shown in the “sRatio” column of Table 1. This ratio was used as a further criteria in narrowing the selection (see further below).

The second criterion used in refining the list of discriminant proteins to get just 80 was related to the probability of detection. For the example embodiment of the invention, a

median intensity of greater than 1500 was assumed to be required in order to observe the presence of antigen/antibody bonding for a protein. The fraction of array data exceeding 1500 was tabulated for each protein. In initial data screening, this fraction was required to be at least 0.1 and less than 0.9. If nearly all the sample intensities are invisible, or nearly all are visible, there is less potential for discriminating between people. The minimum of the probability of visibility, and 1-this probability, was used further as described below. This attribute of a protein is denoted as “MinPSeeOrNot” in Table 1.

To determine the subset of 45 discriminant proteins listed in Table 2 below, pairwise correlation coefficients for all pairs among the 80 proteins were evaluated. The correlations were estimated using the data set of people with just one array per person (92 arrays), so that complete independence in the results would be ideal. The correlations were estimated using JMP® statistical software from SAS Institute. For each of the 80 proteins, a maximum correlation was identified. The pair of proteins in the array with the maximum correlation of all of these was identified. The protein in this pair with other relatively high correlations was identified as the worst protein from the correlation standpoint. This protein was recorded and then all correlations associated with it were removed from further consideration. This process was repeated using the remaining data, leading to identification of the second-worst protein and its highest correlation, conditioned on the first (worst) protein being omitted. This process was repeated until only two proteins remained in the set of data being considered. These are the two most “independent” proteins among the set of 80. The maximum correlation estimated between a given protein and some other protein, given that the more highly-correlated proteins have been removed from the data set, is shown as “MaxCorrAfter” in Table 1. The most discriminating proteins have the lowest values for “MaxCorrAfter.”

The 45 discriminant proteins in Table 2 were identified using the following cutoff values for the three filters discussed above: sRatio greater than or equal to about 11, a “MaxCorr-

rAfter” less than about 0.6, and “MinPSeeOrNot” greater than about 0.2. The numbers in this filter were selected by trial and error to retain exactly 45 proteins.

TABLE 2

45 proteins, sorted on sRatio.					
Protein ID	SEQ ID NO	selOrdAll	MinPSeeOrNot	sRatio	maxCorrAfter
NM_203284.1	SEQ ID NO: 78	5	0.3131	26.9	0.277
NM_012472.1	SEQ ID NO: 48	11	0.4949	23.0	0.578
NM_002744	SEQ ID NO: 35	3	0.4192	22.4	0.215
NM_018584.4	SEQ ID NO: 63	7	0.3737	21.7	0.448
NM_001008220.1	SEQ ID NO: 29	17	0.2172	21.7	0.405
NM_001106.2	SEQ ID NO: 30	22	0.4091	20.3	0.303
BC011414.1	SEQ ID NO: 4	15	0.4040	19.9	0.482
NM_014460.2	SEQ ID NO: 51	21	0.3182	19.7	0.414
BC060824.1	SEQ ID NO: 24	12	0.2828	19.4	0.421
NM_014891.1	SEQ ID NO: 53	32	0.2323	19.1	0.343
NM_014240.1	SEQ ID NO: 49	19	0.4444	18.9	0.459
NM_177973.1	SEQ ID NO: 74	10	0.2576	18.5	0.290
BC012945.1	SEQ ID NO: 5	38	0.3333	18.4	0.570
NM_004845.3	SEQ ID NO: 40	30	0.2525	18.0	0.432
NM_006819.1	SEQ ID NO: 47	4	0.2222	17.9	0.356
BC040949.1	SEQ ID NO: 20	45	0.3737	17.9	0.523
NM_024826.1	SEQ ID NO: 65	20	0.4141	17.8	0.328
NM_205853.1	SEQ ID NO: 79	25	0.4394	17.7	0.208
NM_018326.1	SEQ ID NO: 62	26	0.3939	17.5	0.254
NM_201262.1	SEQ ID NO: 77	14	0.2727	17.5	0.118
BC021189.2	SEQ ID NO: 13	29	0.3434	17.2	0.488
BC019039.2	SEQ ID NO: 11	33	0.4091	17.2	0.544
NM_178010.1	SEQ ID NO: 75	9	0.3081	16.8	0.124
NM_153757.1	SEQ ID NO: 73	46	0.4596	16.8	0.402
BC052805.1	SEQ ID NO: 22	56	0.2879	16.6	0.501
BC026346.1	SEQ ID NO: 16	78	0.4798	16.4	0.360
BC018206.1	SEQ ID NO: 9	31	0.3838	16.1	0.551
NM_016096.1	SEQ ID NO: 58	41	0.2828	16.0	0.516
NM_014622.4	SEQ ID NO: 52	65	0.4899	15.7	0.566
BC026175.1	SEQ ID NO: 15	50	0.3889	15.6	0.582
BC010125.1	SEQ ID NO: 3	62	0.2323	15.6	0.500
NM_175887.2	SEQ ID NO: 26	34	0.4293	15.4	0.537
NM_080390.3	SEQ ID NO: 70	86	0.2273	15.3	0.582
NM_006628.4	SEQ ID NO: 46	66	0.2929	15.0	0.538
NM_003907.1	SEQ ID NO: 36	57	0.3737	14.8	0.440
BC033711.1	SEQ ID NO: 18	72	0.2929	14.6	0.567
NM_017855.2	SEQ ID NO: 60	69	0.2879	14.2	0.578
NM_199124.1	SEQ ID NO: 76	28	0.3788	14.0	0.252
NM_004064.2	SEQ ID NO: 38	54	0.2020	13.8	0.422
PM_2151	SEQ ID NO: 2	99	0.2475	13.4	0.585
NM_016520.1	SEQ ID NO: 59	60	0.3838	13.3	0.471
NM_006007.1	SEQ ID NO: 44	80	0.2424	13.3	0.417
NM_025241.1	SEQ ID NO: 66	48	0.4343	13.2	0.268
NM_015509.2	SEQ ID NO: 57	43	0.2273	12.8	0.554
NM_145796.2	SEQ ID NO: 72	64	0.2576	11.4	0.590

50 While the invention is susceptible to various modifications and implementation in alternative forms, specific embodiments have been shown by way of non-limiting example in the drawings and have been described in detail herein. However, it should be understood that the invention is not intended to be limited to the particular forms disclosed. Rather, the invention includes all modifications, equivalents, and alternatives falling within the scope of the invention as defined by the following appended claims and their legal equivalents.

SEQUENCE LISTING

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<211> LENGTH: 2768

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

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 Asn Asp Gly Arg Ser Cys Trp Cys Val Gly Ala Asn Gly Ser Glu Val
 65 70 75 80
 Leu Gly Ser Arg Gln Pro Gly Arg Pro Val Ala Cys Leu Ser Phe Cys
 85 90 95
 Gln Leu Gln Lys Gln Gln Ile Leu Leu Ser Gly Tyr Ile Asn Ser Thr
 100 105 110
 Asp Thr Ser Tyr Leu Pro Gln Cys Gln Asp Ser Gly Asp Tyr Ala Pro
 115 120 125
 Val Gln Cys Asp Val Gln Gln Val Gln Cys Trp Cys Val Asp Ala Glu
 130 135 140
 Gly Met Glu Val Tyr Gly Thr Arg Gln Leu Gly Arg Pro Lys Arg Cys
 145 150 155 160
 Pro Arg Ser Cys Glu Ile Arg Asn Arg Arg Leu Leu His Gly Val Gly
 165 170 175
 Asp Lys Ser Pro Pro Gln Cys Ser Ala Glu Gly Glu Phe Met Pro Val
 180 185 190
 Gln Cys Lys Phe Val Asn Thr Thr Asp Met Met Ile Phe Asp Leu Val
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 His Ser Tyr Asn Arg Phe Pro Asp Ala Phe Val Thr Phe Ser Ser Phe
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 Gln Arg Arg Phe Pro Glu Val Ser Gly Tyr Cys His Cys Ala Asp Ser
 225 230 235 240
 Gln Gly Arg Glu Leu Ala Glu Thr Gly Leu Glu Leu Leu Leu Asp Glu
 245 250 255
 Ile Tyr Asp Thr Ile Phe Ala Gly Leu Asp Leu Pro Ser Thr Phe Thr
 260 265 270
 Glu Thr Thr Leu Tyr Arg Ile Leu Gln Arg Arg Phe Leu Ala Val Gln
 275 280 285
 Ser Val Ile Ser Gly Arg Phe Arg Cys Pro Thr Lys Cys Glu Val Glu
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 Arg Phe Thr Ala Thr Ser Phe Gly His Pro Tyr Val Pro Ser Cys Arg
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 Arg Asn Gly Asp Tyr Gln Ala Val Gln Cys Gln Thr Glu Gly Pro Cys
 325 330 335
 Trp Cys Val Asp Ala Gln Gly Lys Glu Met His Gly Thr Arg Gln Gln
 340 345 350
 Gly Glu Pro Pro Ser Cys Ala Glu Gly Gln Ser Cys Ala Ser Glu Arg
 355 360 365
 Gln Gln Ala Leu Ser Arg Leu Tyr Phe Gly Thr Ser Gly Tyr Phe Ser
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 Gln His Asp Leu Phe Ser Ser Pro Glu Lys Arg Trp Ala Ser Pro Arg
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Phe Ser Val Ser Glu Asn Leu Leu Lys Glu Ala Ile Arg Ala Ile Phe
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Pro Ser Arg Gly Leu Ala Arg Leu Ala Leu Gln Phe Thr Thr Asn Pro
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Lys Arg Leu Gln Gln Asn Leu Phe Gly Gly Lys Phe Leu Val Asn Val
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Gly Gln Phe Asn Leu Ser Gly Ala Leu Gly Thr Arg Gly Thr Phe Asn
 485 490 495

Phe Ser Gln Phe Phe Gln Gln Leu Gly Leu Ala Ser Phe Leu Asn Gly
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Gly Arg Gln Glu Asp Leu Ala Lys Pro Leu Ser Val Gly Leu Asp Ser
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Asn Lys Pro Thr Val Gly Ser Phe Gly Phe Glu Ile Asn Leu Gln Glu
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Asn Gln Asn Ala Leu Lys Phe Leu Ala Ser Leu Leu Glu Leu Pro Glu
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Arg Asp Leu Gly Asp Val Met Glu Thr Val Leu Ser Ser Gln Thr Cys
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Ser Trp Gly Lys Glu Leu Pro Gly Ser Arg Val Arg Gly Gly Gln Pro
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Ser Glu Gly His Phe Leu Pro Val Gln Cys Phe Asn Ser Glu Cys Tyr
 690 695 700

Cys Val Asp Ala Glu Gly Gln Ala Ile Pro Gly Thr Arg Ser Ala Ile
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Gly Lys Pro Lys Lys Cys Pro Thr Pro Cys Gln Leu Gln Ser Glu Gln
 725 730 735

Ala Phe Leu Arg Thr Val Gln Ala Leu Leu Ser Asn Ser Ser Met Leu
 740 745 750

Pro Thr Leu Ser Asp Thr Tyr Ile Pro Gln Cys Ser Thr Asp Gly Gln
 755 760 765

Trp Arg Gln Val Gln Cys Asn Gly Pro Pro Glu Gln Val Phe Glu Leu
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Tyr Gln Arg Trp Glu Ala Gln Asn Lys Gly Gln Asp Leu Thr Pro Ala
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Lys Leu Leu Val Lys Ile Met Ser Tyr Arg Glu Ala Ala Ser Gly Asn
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 820 825 830

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Pro Tyr Leu Phe Trp Gln Ile Leu Asn Gly Gln Leu Ser Gln Tyr Pro
 865 870 875 880

Gly Ser Tyr Ser Asp Phe Ser Thr Pro Leu Ala His Phe Asp Leu Arg
 885 890 895

Asn Cys Trp Cys Val Asp Glu Ala Gly Gln Glu Leu Glu Gly Met Arg
 900 905 910

Ser Glu Pro Ser Lys Leu Pro Thr Cys Pro Gly Ser Cys Glu Glu Ala
 915 920 925

Lys Leu Arg Val Leu Gln Phe Ile Arg Glu Thr Glu Glu Ile Val Ser
 930 935 940

Ala Ser Asn Ser Ser Arg Phe Pro Leu Gly Glu Ser Phe Leu Val Ala
 945 950 955 960

Lys Gly Ile Arg Leu Arg Asn Glu Asp Leu Gly Leu Pro Pro Leu Phe
 965 970 975

Pro Pro Arg Glu Ala Phe Ala Glu Gln Phe Leu Arg Gly Ser Asp Tyr
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Ala Ile Arg Leu Ala Ala Gln Ser Thr Leu Ser Phe Tyr Gln Arg Arg
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Gln Ile Pro Gln Cys Pro Thr Thr Cys Glu Lys Ser Arg Thr Ser
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 1085 1090 1095

Ser Pro Lys Asp Leu Phe Val Pro Ala Cys Leu Glu Thr Gly Glu
 1100 1105 1110

Tyr Ala Arg Leu Gln Ala Ser Gly Ala Gly Thr Trp Cys Val Asp
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Pro Ala Ser Gly Glu Glu Leu Arg Pro Gly Ser Ser Ser Ser Ala
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Thr Gly Gly Gln Pro Ala Cys Glu Ser Pro Arg Cys Pro Leu Pro
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Arg Ala Cys Gln Arg Pro 1280	Gln Leu Trp Gln Thr 1285	Ile Gln Thr Gln 1290
Gly His Phe Gln Leu Gln 1295	Leu Pro Pro Gly Lys 1300	Met Cys Ser Ala 1305
Asp Tyr Ala Asp Leu Leu 1310	Gln Thr Phe Gln Val 1315	Phe Ile Leu Asp 1320
Glu Leu Thr Ala Arg Gly 1325	Phe Cys Gln Ile Gln 1330	Val Lys Thr Phe 1335
Gly Thr Leu Val Ser Ile 1340	Pro Val Cys Asn Asn 1345	Ser Ser Val Gln 1350
Val Gly Cys Leu Thr Arg 1355	Glu Arg Leu Gly Val 1360	Asn Val Thr Trp 1365
Lys Ser Arg Leu Glu Asp 1370	Ile Pro Val Ala Ser 1375	Leu Pro Asp Leu 1380
His Asp Ile Glu Arg Ala 1385	Leu Val Gly Lys Asp 1390	Leu Leu Gly Arg 1395
Phe Thr Asp Leu Ile Gln 1400	Ser Gly Ser Phe Gln 1405	Leu His Leu Asp 1410
Ser Lys Thr Phe Pro Ala 1415	Glu Thr Ile Arg Phe 1420	Leu Gln Gly Asp 1425
His Phe Gly Thr Ser Pro 1430	Arg Thr Trp Phe Gly 1435	Cys Ser Glu Gly 1440
Phe Tyr Gln Val Leu Thr 1445	Ser Glu Ala Ser Gln 1450	Asp Gly Leu Gly 1455
Cys Val Lys Cys Pro Glu 1460	Gly Ser Tyr Ser Gln 1465	Asp Glu Glu Cys 1470
Ile Pro Cys Pro Val Gly 1475	Phe Tyr Gln Glu Gln 1480	Ala Gly Ser Leu 1485
Ala Cys Val Pro Cys Pro 1490	Val Gly Arg Thr Thr 1495	Ile Ser Ala Gly 1500
Ala Phe Ser Gln Thr His 1505	Cys Val Thr Asp Cys 1510	Gln Arg Asn Glu 1515
Ala Gly Leu Gln Cys Asp 1520	Gln Asn Gly Gln Tyr 1525	Arg Ala Ser Gln 1530
Lys Asp Arg Gly Ser Gly 1535	Lys Ala Phe Cys Val 1540	Asp Gly Glu Gly 1545
Arg Arg Leu Pro Trp Trp 1550	Glu Thr Glu Ala Pro 1555	Leu Glu Asp Ser 1560
Gln Cys Leu Met Met Gln 1565	Lys Phe Glu Lys Val 1570	Pro Glu Ser Lys 1575
Val Ile Phe Asp Ala Asn 1580	Ala Pro Val Ala Val 1585	Arg Ser Lys Val 1590
Pro Asp Ser Glu Phe Pro 1595	Val Met Gln Cys Leu 1600	Thr Asp Cys Thr 1605
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Glu Ile Ser Cys Asp Phe 1625	Tyr Ala Trp Thr Ser 1630	Asp Asn Val Ala 1635

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Ser Thr	Thr Thr Leu Gln	Lys Arg Phe Glu Pro	Thr Gly Phe Gln	
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Gly Gly	Ala Ile Ile Cys	Gly Leu Leu Ser Ser	Pro Ser Val Leu	
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Val Ile	Leu Arg Leu Gly	Asp Gln Glu Phe Ile	Lys Ser Leu Thr	
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Arg Cys	Asp Ala Asp Pro	Cys Cys Thr Gly Phe	Gly Phe Leu Asn	
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Val Ser	Gln Leu Lys Gly	Gly Glu Val Thr Cys	Leu Thr Leu Asn	
2015		2020	2025	

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

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Trp Gly Pro Val Ile Asp Gly His Phe Leu Arg Glu Pro Pro Ala 2480	2485	2490
Arg Ala Leu Lys Arg Ser Leu Trp Val Glu Val Asp Leu Leu Ile 2495	2500	2505
Gly Ser Ser Gln Asp Asp Gly Leu Ile Asn Arg Ala Lys Ala Val 2510	2515	2520
Lys Gln Phe Glu Glu Ser Arg Gly Arg Thr Ser Ser Lys Thr Ala 2525	2530	2535
Phe Tyr Gln Ala Leu Gln Asn Ser Leu Gly Gly Glu Asp Ser Asp 2540	2545	2550
Ala Arg Val Glu Ala Ala Ala Thr Trp Tyr Tyr Ser Leu Glu His 2555	2560	2565
Ser Thr Asp Asp Tyr Ala Ser Phe Ser Arg Ala Leu Glu Asn Ala 2570	2575	2580
Thr Arg Asp Tyr Phe Ile Ile Cys Pro Ile Ile Asp Met Ala Ser 2585	2590	2595
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Phe Ser Leu Glu Glu Lys Ser Leu Ser Leu Lys Ile Met Gln Tyr 2645	2650	2655
Phe Ser His Phe Ile Arg Ser Gly Asn Pro Asn Tyr Pro Tyr Glu 2660	2665	2670
Phe Ser Arg Lys Val Pro Thr Phe Ala Thr Pro Trp Pro Asp Phe 2675	2680	2685
Val Pro Arg Ala Gly Gly Glu Asn Tyr Lys Glu Phe Ser Glu Leu 2690	2695	2700
Leu Pro Asn Arg Gln Gly Leu Lys Lys Ala Asp Cys Ser Phe Trp 2705	2710	2715
Ser Lys Tyr Ile Ser Ser Leu Lys Thr Ser Ala Asp Gly Ala Lys 2720	2725	2730
Gly Gly Gln Ser Ala Glu Ser Glu Glu Glu Glu Leu Thr Ala Gly 2735	2740	2745
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 Lys Lys Lys Asp Arg Phe Tyr Arg Ser Ile Leu Pro Gly Asp Lys Thr
 50 55 60
 Asn Lys Lys Lys Glu Lys Glu Arg Pro Glu Ile Ser Leu Pro Ser Asp
 65 70 75 80
 Phe Glu His Thr Ile His Val Gly Phe Asp Ala Val Thr Gly Glu Phe
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 Thr Gly Met Pro Glu Gln Trp Ala Arg Leu Leu Gln Thr Ser Asn Ile
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 Thr Lys Ser Glu Gln Lys Lys Asn Pro Gln Ala Val Leu Asp Val Leu
 115 120 125
 Glu Phe Tyr Asn Ser Lys Lys Thr Ser Asn Ser Gln Lys Tyr Met Ser
 130 135 140
 Phe Thr Asp Lys Ser Ala Glu Asp Tyr Asn Ser Ser Asn Ala Leu Asn
 145 150 155 160
 Val Lys Ala Val Ser Glu Thr Pro Ala Val Pro Pro Val Ser Glu Asp
 165 170 175
 Glu Asp Asp Asp Asp Asp Ala Thr Pro Pro Pro Val Ile Ala Pro
 180 185 190
 Arg Pro Glu His Thr Lys Ser Val Tyr Thr Arg Ser Val Ile Glu Pro
 195 200 205
 Leu Pro Val Thr Pro Thr Arg Asp Val Ala Thr Ser Pro Ile Ser Pro
 210 215 220
 Thr Glu Asn Asn Thr Thr Pro Pro Asp Ala Leu Thr Arg Asn Thr Glu
 225 230 235 240
 Lys Gln Lys Lys Lys Pro Lys Met Ser Asp Glu Glu Ile Leu Glu Lys
 245 250 255
 Leu Arg Ser Ile Val Ser Val Gly Asp Pro Lys Lys Lys Tyr Thr Arg
 260 265 270
 Phe Glu Lys Ile Gly Gln Gly Ala Ser Gly Thr Val Tyr Thr Ala Met
 275 280 285
 Asp Val Ala Thr Gly Gln Glu Val Ala Ile Lys Gln Met Asn Leu Gln
 290 295 300
 Gln Gln Pro Lys Lys Glu Leu Ile Ile Asn Glu Ile Leu Val Met Arg
 305 310 315 320
 Glu Asn Lys Asn Pro Asn Ile Val Asn Tyr Leu Asp Ser Tyr Leu Val
 325 330 335
 Gly Asp Glu Leu Trp Val Val Met Glu Tyr Leu Ala Gly Gly Ser Leu
 340 345 350
 Thr Asp Val Val Thr Glu Thr Cys Met Asp Glu Gly Gln Ile Ala Ala
 355 360 365
 Val Cys Arg Glu Cys Leu Gln Ala Leu Glu Phe Leu His Ser Asn Gln
 370 375 380
 Val Ile His Arg Asp Ile Lys Ser Asp Asn Ile Leu Leu Gly Met Asp
 385 390 395 400
 Gly Ser Val Lys Leu Thr Asp Phe Gly Phe Cys Ala Gln Ile Thr Pro
 405 410 415
 Glu Gln Ser Lys Arg Ser Thr Met Val Gly Thr Pro Tyr Trp Met Ala

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420 425 430
 Pro Glu Val Val Thr Arg Lys Ala Tyr Gly Pro Lys Val Asp Ile
 435 440 445

<210> SEQ ID NO 3
 <211> LENGTH: 354
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 3

Met Cys Gly Arg Thr Ser Cys His Leu Pro Arg Asp Val Leu Thr Arg
 1 5 10 15

Ala Cys Ala Tyr Gln Asp Arg Arg Gly Gln Gln Arg Leu Pro Glu Trp
 20 25 30

Arg Asp Pro Asp Lys Tyr Cys Pro Ser Tyr Asn Lys Ser Pro Gln Ser
 35 40 45

Asn Ser Pro Val Leu Leu Ser Arg Leu His Phe Glu Lys Asp Ala Asp
 50 55 60

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

Trp Phe Lys Glu Ser Asp Pro Ser Lys Leu Gln Phe Asn Thr Thr Asn
 85 90 95

Cys Arg Ser Asp Thr Val Met Glu Lys Arg Ser Phe Lys Val Pro Leu
 100 105 110

Gly Lys Gly Arg Arg Cys Val Val Leu Ala Asp Gly Phe Tyr Glu Trp
 115 120 125

Gln Arg Cys Gln Gly Thr Asn Gln Arg Gln Pro Tyr Phe Ile Tyr Phe
 130 135 140

Pro Gln Ile Lys Thr Glu Lys Ser Gly Ser Ile Gly Ala Ala Asp Ser
 145 150 155 160

Pro Glu Asn Trp Glu Lys Val Trp Asp Asn Trp Arg Leu Leu Thr Met
 165 170 175

Ala Gly Ile Phe Asp Cys Trp Glu Pro Pro Glu Gly Gly Asp Val Leu
 180 185 190

Tyr Ser Tyr Thr Ile Ile Thr Val Asp Ser Cys Lys Gly Leu Ser Asp
 195 200 205

Ile His His Arg Met Pro Ala Ile Leu Asp Gly Glu Glu Ala Val Ser
 210 215 220

Lys Trp Leu Asp Phe Gly Glu Val Ser Thr Gln Glu Ala Leu Lys Leu
 225 230 235 240

Ile His Pro Thr Glu Asn Ile Thr Phe His Ala Val Ser Ser Val Val
 245 250 255

Asn Asn Ser Arg Asn Asn Thr Pro Glu Cys Leu Ala Pro Val Asp Leu
 260 265 270

Val Val Lys Lys Glu Leu Arg Ala Ser Gly Ser Ser Gln Arg Met Leu
 275 280 285

Gln Trp Leu Ala Thr Lys Ser Pro Lys Lys Glu Asp Ser Lys Thr Pro
 290 295 300

Gln Lys Glu Glu Ser Asp Val Pro Gln Trp Ser Ser Gln Phe Leu Gln
 305 310 315 320

Lys Ser Pro Leu Pro Thr Lys Arg Gly Thr Ala Gly Leu Leu Glu Gln
 325 330 335

Trp Leu Lys Arg Glu Lys Glu Glu Glu Pro Val Ala Lys Arg Pro Tyr
 340 345 350

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Ser Gln

<210> SEQ ID NO 4

<211> LENGTH: 505

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 4

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Met Ser Asp Lys Asp Asp Ile Glu Thr Pro Leu Leu Thr Glu Ala Ala
1           5           10           15

Pro Ile Leu Glu Asp Gly Asn Cys Glu Pro Ala Lys Asn Ser Glu Ser
           20           25           30

Val Asp Gln Gly Ala Lys Pro Glu Ser Lys Ser Glu Pro Val Val Ser
           35           40           45

Thr Arg Lys Arg Pro Glu Thr Lys Pro Ser Ser Asp Leu Glu Thr Ser
           50           55           60

Lys Val Leu Pro Ile Gln Asp Asn Val Ser Lys Asp Val Pro Gln Thr
65           70           75           80

Arg Trp Gly Tyr Trp Gly Ser Trp Gly Lys Ser Ile Leu Ser Ser Ala
           85           90           95

Ser Ala Thr Val Ala Thr Val Gly Gln Gly Ile Ser Asn Val Ile Glu
           100          105          110

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

Glu Val Lys Tyr Val Ala Gly Glu Thr Asn Ala Lys Glu Asn Glu Asn
130          135          140

Ser Ser Pro Val Ala Gly Ala Phe Gly Val Phe Ser Thr Ile Ser Thr
145          150          155          160

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

Leu Glu Phe Ile Gly Lys Lys Thr Met Asp Val Ile Ala Glu Gly Asp
           180          185          190

Pro Gly Phe Lys Arg Thr Lys Gly Leu Met Asn Arg Asn Ala Thr Leu
           195          200          205

Ser Gln Val Leu Arg Glu Ala Lys Glu Lys Glu Glu Ile Arg Thr Ser
210          215          220

Asn Glu Val Thr Val Glu Thr Asp Lys Lys Thr His Tyr Gly Leu Leu
225          230          235          240

Phe Asp Glu Phe Gln Gly Leu Ser His Leu Glu Ala Leu Glu Met Leu
           245          250          255

Ser Gln Glu Ser Glu Ile Lys Val Lys Ser Ile Leu Asn Ser Leu Ser
           260          265          270

Gly Glu Glu Leu Glu Thr Leu Lys Val Glu Leu Glu Gln Leu Lys Glu
           275          280          285

Thr Phe Ser Leu Ala Glu Phe Cys Glu Glu Glu Glu Glu Glu Lys Lys
290          295          300

Gly Asp Glu Asp Phe Thr Lys Asp Ile Thr Glu Leu Phe Ser Gln Leu
305          310          315          320

His Val Ser Ser Lys Pro Glu Lys Leu Ala Arg Ala Arg Asn Thr Ala
           325          330          335

His Glu Trp Ile Arg Lys Ser Leu Thr Lys Pro Leu Ala Glu Asn Glu
           340          345          350

Glu Gly Glu Lys Gln Ser Glu Ala Glu Asn Thr Glu Gln Val Asn Lys
           355          360          365

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Asn Ser Ile Glu Asp Ile His Ala Phe Ala Ile Arg Ser Leu Ala Glu
 370                               375                               380

Leu Thr Ala Cys Ser Ile Glu Leu Phe His Lys Thr Ala Ala Leu Val
385                               390                               395                               400

Leu His Gly Arg Lys Gln Glu Val Thr Ala Ile Glu Arg Ser Gln Thr
                               405                               410                               415

Leu Ser Gln Met Thr Ile Val Leu Cys Lys Glu Leu Ser Ser Leu Ser
                               420                               425                               430

Lys Glu Phe Thr Thr Cys Leu Thr Thr Ala Gly Val Lys Glu Met Ala
                               435                               440                               445

Asp Val Leu Asn Pro Leu Ile Thr Ala Val Phe Leu Glu Ala Ser Asn
450                               455                               460

Ser Ala Ser Tyr Ile Gln Asp Ala Phe Gln Leu Leu Leu Pro Val Leu
465                               470                               475                               480

Glu Ile Ser Leu Ile Glu Asn Lys Ile Glu Ser His Arg His Glu Leu
                               485                               490                               495

Gln Gly Gln Lys Pro Leu Leu Glu His
                               500                               505

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<210> SEQ ID NO 5

<211> LENGTH: 546

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 5

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Asp Arg Gly Ser Gly Ala Phe Ser Leu Glu Thr Ile Ala Glu Ser Ser
1           5           10           15

Ala Gln Ser Pro Gly Cys Gln Leu Leu Val Glu Thr Leu Gly Val Pro
          20           25           30

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

Arg Pro Glu Gln Ser Ser Gln Ser Pro Val Gln Ala Val Pro Gly Ser
          50           55           60

Gly Asp Ser Gln Pro Asp Asp Pro Pro Asp Arg Gly Thr Gly Leu Ser
65           70           75           80

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

Asp Ser Lys Pro Glu Thr Asp Arg Val Pro Gly Asp Gly Gly Gln Lys
          100          105          110

Glu His Leu Pro Ser Ile Asp Ser Glu Gly Glu Lys Pro Asp Arg Gly
          115          120          125

Ala Pro Gln Glu Gly Gly Ala Gln Arg Thr Ala Gly Ala Gly Leu Pro
          130          135          140

Arg Gly Pro Gln Glu Glu Gly Asp Gly Val Pro Cys Thr Pro Ala Ser
          145          150          155          160

Ala Pro Thr Ser Gly Pro Ala Pro Gly Leu Gly Pro Ala Ser Trp Cys
          165          170          175

Leu Glu Pro Gly Ser Val Ala Gln Gly Ser Pro Asp Pro Gln Gln Thr
          180          185          190

Pro Ser Arg Met Gly Arg Glu Gly Glu Gly Thr His Ser Ser Leu Gly
          195          200          205

Cys Ser Ser Leu Gly Met Val Val Ile Ala Asp Leu Ser Thr Asp Pro
          210          215          220

Thr Glu Leu Glu Glu Arg Ala Leu Glu Val Ala Gly Pro Asp Gly Gln
          225          230          235          240

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Ala Ser Ala Ile Ser Pro Ala Ser Pro Arg Arg Lys Ala Ala Asp Gly
 245 250 255

Gly His Arg Arg Ala Leu Pro Gly Cys Thr Ser Leu Thr Gly Glu Thr
 260 265 270

Thr Gly Glu Ser Gly Glu Ala Gly Gln Asp Gly Lys Pro Pro Gly Asp
 275 280 285

Val Leu Val Gly Pro Thr Ala Ser Leu Ala Leu Ala Pro Gly Ser Gly
 290 295 300

Glu Ser Met Met Gly Ala Gly Asp Ser Gly His Ala Ser Pro Asp Thr
 305 310 315 320

Gly Pro Cys Val Asn Gln Lys Gln Glu Pro Gly Pro Ala Gln Glu Glu
 325 330 335

Ala Glu Leu Gly Gly Gln Asn Leu Glu Arg Asp Leu Glu Gly Phe Arg
 340 345 350

Val Ser Pro Gln Ala Ser Val Val Leu Glu His Arg Glu Ile Ala Asp
 355 360 365

Asp Pro Leu Gln Glu Pro Gly Ala Gln Arg Gly Ile Pro Asp Thr Thr
 370 375 380

Ser Glu Leu Ala Gly Gln Arg Asp His Leu Pro His Ser Ala Asp Gln
 385 390 395 400

Gly Thr Trp Ala Asp Ser Leu Ala Val Glu Leu Asp Phe Leu Leu Asp
 405 410 415

Ser Gln Ile Gln Asp Ala Leu Asp Ala Ser Asp Phe Glu Ala Pro Pro
 420 425 430

Glu Gln Leu Phe Pro Ser Gly Asn Lys Pro Gly Pro Cys Trp Pro Gly
 435 440 445

Pro Ser Ser His Ala Asn Gly Asp Pro Val Ala Val Ala Lys Ala Gln
 450 455 460

Pro Arg Thr Phe Val Gly Ile Gln Ala Ser Glu Ala Ser Arg Met Glu
 465 470 475 480

Asp Ala Thr Asn Val Val Arg Gly Leu Ile Val Glu Leu Ser Asn Leu
 485 490 495

Asn Arg Leu Ile Met Gly Thr His Arg Asp Leu Glu Ala Phe Lys Arg
 500 505 510

Leu Asn Tyr Arg Lys Thr Lys Leu Gly Gly Lys Ala Pro Leu Pro Tyr
 515 520 525

Pro Ser Lys Gly Pro Gly Asn Ile Pro Arg Gly Asp Pro Pro Trp Arg
 530 535 540

Glu Leu
 545

<210> SEQ ID NO 6
 <211> LENGTH: 204
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 6

Met Glu Pro Lys Ala Ser Cys Pro Ala Ala Ala Pro Leu Met Glu Arg
 1 5 10 15

Lys Phe His Val Leu Val Gly Val Thr Gly Ser Val Ala Ala Leu Lys
 20 25 30

Leu Pro Leu Leu Val Ser Lys Leu Leu Asp Ile Pro Gly Leu Glu Val
 35 40 45

Ala Val Val Thr Thr Glu Arg Ala Lys His Phe Tyr Ser Pro Gln Asp

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

<210> SEQ ID NO 7
<211> LENGTH: 510
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 7
Met Asp Glu Lys Thr Lys Lys Ala Glu Glu Met Ala Leu Ser Leu Thr
1          5          10          15
Arg Ala Val Ala Gly Gly Asp Glu Gln Val Ala Met Lys Cys Ala Ile
20         25         30
Trp Leu Ala Glu Gln Arg Val Pro Leu Ser Val Gln Leu Lys Pro Glu
35         40         45
Val Ser Pro Thr Gln Asp Ile Arg Leu Trp Val Ser Val Glu Asp Ala
50         55         60
Gln Met His Thr Val Thr Ile Trp Leu Thr Val Arg Pro Asp Met Thr
65         70         75         80
Val Ala Ser Leu Lys Asp Met Val Phe Leu Asp Tyr Gly Phe Pro Pro
85         90         95
Val Leu Gln Gln Trp Val Ile Gly Gln Arg Leu Ala Arg Asp Gln Glu
100        105        110
Thr Leu His Ser His Gly Val Arg Gln Asn Gly Asp Ser Ala Tyr Leu
115        120        125
Tyr Leu Leu Ser Ala Arg Asn Thr Ser Leu Asn Pro Gln Glu Leu Gln
130        135        140
Arg Glu Arg Gln Leu Arg Met Leu Glu Asp Leu Gly Phe Lys Asp Leu
145        150        155        160
Thr Leu Gln Pro Arg Gly Pro Leu Glu Pro Gly Pro Pro Lys Pro Gly
165        170        175
Val Pro Gln Glu Pro Gly Arg Gly Gln Pro Asp Ala Val Pro Glu Pro
180        185        190
Pro Pro Val Gly Trp Gln Cys Pro Gly Cys Thr Phe Ile Asn Lys Pro
195        200        205
Thr Arg Pro Gly Cys Glu Met Cys Cys Arg Ala Arg Pro Glu Ala Tyr
210        215        220

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Gln Val Pro Ala Ser Tyr Gln Pro Asp Glu Glu Glu Arg Ala Arg Leu
 225 230 235 240

Ala Gly Glu Glu Glu Ala Leu Arg Gln Tyr Gln Gln Arg Lys Gln Gln
 245 250 255

Gln Gln Glu Gly Asn Tyr Leu Gln His Val Gln Leu Asp Gln Arg Ser
 260 265 270

Leu Val Leu Asn Thr Glu Pro Ala Glu Cys Pro Val Cys Tyr Ser Val
 275 280 285

Leu Ala Pro Gly Glu Ala Val Val Leu Arg Glu Cys Leu His Thr Phe
 290 295 300

Cys Arg Glu Cys Leu Gln Gly Thr Ile Arg Asn Ser Gln Glu Ala Glu
 305 310 315 320

Val Ser Cys Pro Phe Ile Asp Asn Thr Tyr Ser Cys Ser Gly Lys Leu
 325 330 335

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

Phe Leu Asp Leu Gly Ile Ser Ile Ala Glu Asn Arg Ser Ala Phe Ser
 355 360 365

Tyr His Cys Lys Thr Pro Asp Cys Lys Gly Trp Cys Phe Phe Glu Asp
 370 375 380

Asp Val Asn Glu Phe Thr Cys Pro Val Cys Phe His Val Asn Cys Leu
 385 390 395 400

Leu Cys Lys Ala Ile His Glu Gln Met Asn Cys Lys Glu Tyr Gln Glu
 405 410 415

Asp Leu Ala Leu Arg Ala Gln Asn Asp Val Ala Ala Arg Gln Thr Thr
 420 425 430

Glu Met Leu Lys Val Met Leu Gln Gln Gly Glu Ala Met Arg Cys Pro
 435 440 445

Gln Cys Gln Ile Val Val Gln Lys Lys Asp Gly Cys Asp Trp Ile Arg
 450 455 460

Cys Thr Val Cys His Thr Glu Ile Cys Trp Val Thr Lys Gly Pro Arg
 465 470 475 480

Trp Gly Pro Gly Gly Pro Gly Asp Thr Ser Gly Gly Cys Arg Cys Arg
 485 490 495

Val Asn Gly Ile Pro Cys His Pro Ser Cys Gln Asn Cys His
 500 505 510

<210> SEQ ID NO 8

<211> LENGTH: 583

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 8

Met Ala Leu Lys Lys Ser Ser Pro Ser Leu Asp Ser Gly Asp Ser Asp
 1 5 10 15

Ser Glu Glu Leu Pro Thr Phe Ala Phe Leu Lys Lys Glu Pro Ser Ser
 20 25 30

Thr Lys Arg Arg Gln Pro Glu Arg Glu Glu Lys Ile Val Val Val Asp
 35 40 45

Ile Ser Asp Cys Glu Ala Ser Cys Pro Pro Ala Pro Glu Leu Phe Ser
 50 55 60

Pro Pro Val Pro Asp Ile Ala Glu Thr Val Thr Gln Thr Gln Pro Val
 65 70 75 80

Arg Leu Leu Ser Ser Glu Ser Glu Asp Glu Glu Glu Phe Ile Pro Leu
 85 90 95

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Ala Gln Arg Leu Thr Cys Lys Phe Leu Thr His Lys Gln Leu Ser Pro
100 105 110

Glu Asp Ser Ser Ser Pro Val Lys Ser Val Leu Asp His Gln Asn Asn
115 120 125

Glu Gly Ala Ser Cys Asp Trp Lys Lys Pro Phe Pro Lys Ile Pro Glu
130 135 140

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

Leu Ile Leu Asp Pro Cys Cys Gln Leu Pro Ala Tyr Leu Ser Thr Cys
165 170 175

Pro Gly Gln Ser Ser Ser Leu Ala Val Thr Lys Thr Asn Ser Asp Ile
180 185 190

Leu Pro Pro Gln Lys Lys Thr Lys Pro Ser Gln Lys Val Gln Gly Arg
195 200 205

Gly Ser His Gly Cys Arg Gln Gln Arg Gln Ala Arg Gln Lys Glu Ser
210 215 220

Thr Leu Arg Arg Gln Glu Arg Lys Asn Ala Ala Leu Val Thr Arg Met
225 230 235 240

Lys Ala Gln Arg Pro Glu Glu Cys Leu Lys His Ile Ile Val Val Leu
245 250 255

Asp Pro Val Leu Leu Gln Met Glu Gly Gly Gly Gln Leu Leu Gly Ala
260 265 270

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

Cys Ser Val Thr Trp Arg Arg Arg Ala Gly Pro Ser Glu Asp Arg Glu
290 295 300

Asp Trp Val Glu Glu Pro Thr Val Leu Val Leu Leu Arg Ala Glu Ala
305 310 315 320

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

Met Lys Gly Lys Glu Thr Leu Gln Gly Phe Val Thr Asp Ile Thr Ala
340 345 350

Lys Thr Ala Gly Lys Ala Leu Ser Leu Val Ile Val Asp Gln Glu Lys
355 360 365

Cys Phe Ser Leu Glu Leu Leu Phe Phe Asp Phe Leu Pro Cys Thr Ser
370 375 380

Ala Gln Asn Pro Pro Arg Arg Gly Lys Gln Gly Ala Asn Lys Gln Thr
385 390 395 400

Lys Lys Gln Gln Gln Arg Gln Pro Glu Ala Ser Ile Gly Ser Met Val
405 410 415

Ser Arg Val Asp Ala Glu Glu Ala Leu Val Asp Leu Gln Leu His Thr
420 425 430

Glu Ala Gln Ala Gln Ile Val Gln Ser Trp Lys Glu Leu Ala Asp Phe
435 440 445

Thr Cys Ala Phe Thr Lys Ala Val Ala Glu Ala Pro Phe Lys Lys Leu
450 455 460

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

Gly Val Lys Val Asp Leu Ala Gly Arg Gly Leu Ala Leu Val Trp Arg
485 490 495

Arg Gln Ile Gln Gln Leu Asn Arg Val Ser Leu Glu Met Ala Ser Ala
500 505 510

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Val Val Asn Ala Tyr Pro Ser Pro Gln Leu Leu Val Gln Ala Tyr Gln
 515 520 525

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

Val Arg Arg Gly Glu Gly Val Thr Ser Thr Ser Arg Arg Ile Gly Pro
 545 550 555 560

Glu Leu Ser Arg Arg Ile Tyr Leu Gln Met Thr Thr Leu Gln Pro His
 565 570 575

Leu Ser Leu Asp Ser Ala Asp
 580

<210> SEQ ID NO 9
 <211> LENGTH: 158
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 9

Met Ala Ala Gln Gly Val Gly Pro Gly Pro Gly Ser Ala Ala Pro Pro
 1 5 10 15

Gly Leu Glu Ala Ala Arg Gln Lys Leu Ala Leu Arg Arg Lys Lys Val
 20 25 30

Leu Ser Thr Glu Glu Met Glu Leu Tyr Glu Leu Ala Gln Ala Ala Gly
 35 40 45

Gly Gly Ile Asp Pro Asp Val Phe Lys Ile Leu Val Asp Leu Leu Lys
 50 55 60

Leu Asn Val Ala Pro Leu Ala Val Phe Gln Met Leu Lys Ser Met Cys
 65 70 75 80

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

Leu Pro Thr Ser Ser Val Pro Glu Thr Arg Gly Arg Asp Lys Gly Ser
 100 105 110

Ala Ala Leu Gly Gly Val Leu Ala Leu Ala Glu Arg Ser Asn His Glu
 115 120 125

Gly Ser Ser Gln Arg Met Pro Arg Gln Pro Ser Ala Thr Arg Leu Pro
 130 135 140

Lys Gly Gly Gly Pro Gly Lys Ser Pro Thr Gln Gly Ser Thr
 145 150 155

<210> SEQ ID NO 10
 <211> LENGTH: 209
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 10

Met Asp Ser Asp Glu Thr Gly Phe Glu His Ser Gly Leu Trp Val Ser
 1 5 10 15

Val Leu Ala Gly Leu Leu Leu Gly Ala Cys Gln Ala His Pro Ile Pro
 20 25 30

Asp Ser Ser Pro Leu Leu Gln Phe Gly Gly Gln Val Arg Gln Arg Tyr
 35 40 45

Leu Tyr Thr Asp Asp Ala Gln Thr Glu Ala His Leu Glu Ile Arg
 50 55 60

Glu Asp Gly Thr Val Gly Gly Ala Ala Asp Gln Ser Pro Glu Ser Leu
 65 70 75 80

Leu Gln Leu Lys Ala Leu Lys Pro Gly Val Ile Gln Ile Leu Gly Val
 85 90 95

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Lys Thr Ser Arg Phe Leu Cys Gln Arg Pro Asp Gly Ala Leu Tyr Gly
 100 105 110

Ser Leu His Phe Asp Pro Glu Ala Cys Ser Phe Arg Glu Leu Leu Leu
 115 120 125

Glu Asp Gly Tyr Asn Val Tyr Gln Ser Glu Ala His Gly Leu Pro Leu
 130 135 140

His Leu Pro Gly Asn Lys Ser Pro His Arg Asp Pro Ala Pro Arg Gly
 145 150 155 160

Pro Ala Arg Phe Leu Pro Leu Pro Gly Leu Pro Pro Ala Pro Pro Glu
 165 170 175

Pro Pro Gly Ile Leu Ala Pro Gln Pro Pro Asp Val Gly Ser Ser Asp
 180 185 190

Pro Leu Ser Met Val Gly Pro Ser Gln Gly Arg Ser Pro Ser Tyr Ala
 195 200 205

Ser

<210> SEQ ID NO 11
 <211> LENGTH: 235
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 11

Gln Arg Ala Cys Val Ala Ala Ala Cys Thr Val Ala Ala Arg Cys Pro
 1 5 10 15

Gly Arg Gly Val Gly Asp Arg Ser Gln Ser Gly Ala Ser Tyr Arg Pro
 20 25 30

Ile Cys Gly Pro Lys Val Gly Gly Pro Thr Glu Met Leu Arg Gly Met
 35 40 45

Tyr Leu Thr Arg Asn Gly Asn Leu Gln Arg Arg His Thr Met Lys Glu
 50 55 60

Ala Lys Asp Met Lys Asn Lys Leu Gly Ile Phe Arg Arg Arg Asn Glu
 65 70 75 80

Ser Pro Gly Ala Pro Pro Ala Gly Lys Ala Asp Lys Met Met Lys Ser
 85 90 95

Phe Lys Pro Thr Ser Glu Glu Ala Leu Lys Trp Gly Glu Ser Leu Glu
 100 105 110

Lys Leu Leu Val His Lys Tyr Gly Leu Ala Val Phe Gln Ala Phe Leu
 115 120 125

Arg Thr Glu Phe Ser Glu Glu Asn Leu Glu Phe Trp Leu Ala Cys Glu
 130 135 140

Asp Phe Lys Lys Val Lys Ser Gln Ser Lys Met Ala Ser Lys Ala Lys
 145 150 155 160

Lys Ile Phe Ala Glu Tyr Ile Ala Ile Gln Ala Cys Lys Glu Val Asn
 165 170 175

Leu Asp Ser Tyr Thr Arg Glu His Thr Lys Asp Asn Leu Gln Ser Val
 180 185 190

Thr Arg Gly Cys Phe Asp Leu Ala Gln Lys Arg Ile Phe Gly Leu Met
 195 200 205

Glu Lys Asp Ser Tyr Pro Arg Phe Leu Arg Ser Asp Leu Tyr Leu Asp
 210 215 220

Leu Ile Asn Gln Lys Lys Met Ser Pro Pro Leu
 225 230 235

<210> SEQ ID NO 12
 <211> LENGTH: 359

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<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 12

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

His Pro Cys Phe Ile Ile Ala Glu Ile Gly Gln Asn His Gln Gly Asp
          20          25          30

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

Asp Cys Ala Lys Phe Gln Lys Ser Glu Leu Glu Phe Lys Phe Asn Arg
          50          55          60

Lys Ala Leu Asp Arg Pro Tyr Thr Ser Lys His Ser Trp Gly Lys Thr
          65          70          75          80

Tyr Gly Glu His Lys Arg His Leu Glu Phe Ser His Asp Gln Tyr Arg
          85          90          95

Glu Leu Gln Arg Tyr Ala Glu Glu Val Gly Ile Phe Phe Thr Ala Ser
          100          105          110

Gly Met Asp Glu Met Ala Val Glu Phe Leu His Glu Leu Asn Val Pro
          115          120          125

Phe Phe Lys Val Gly Ser Gly Asp Thr Asn Asn Phe Pro Tyr Leu Glu
          130          135          140

Lys Thr Ala Lys Lys Gly Arg Pro Met Val Ile Ser Ser Gly Met Gln
          145          150          155          160

Ser Met Asp Thr Met Lys Gln Val Tyr Gln Ile Val Lys Pro Leu Asn
          165          170          175

Pro Asn Phe Cys Phe Leu Gln Cys Thr Ser Ala Tyr Pro Leu Gln Pro
          180          185          190

Glu Asp Val Asn Leu Arg Val Ile Ser Glu Tyr Gln Lys Leu Phe Pro
          195          200          205

Asp Ile Pro Ile Gly Tyr Ser Gly His Glu Thr Gly Ile Ala Ile Ser
          210          215          220

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

Leu Asp Lys Thr Trp Lys Gly Ser Asp His Ser Ala Ser Leu Glu Pro
          245          250          255

Gly Glu Leu Ala Glu Leu Val Arg Ser Val Arg Leu Val Glu Arg Ala
          260          265          270

Leu Gly Ser Pro Thr Lys Gln Leu Leu Pro Cys Glu Met Ala Cys Asn
          275          280          285

Glu Lys Leu Gly Lys Ser Val Val Ala Lys Val Lys Ile Pro Glu Gly
          290          295          300

Thr Ile Leu Thr Met Asp Met Leu Thr Val Lys Val Gly Glu Pro Lys
          305          310          315          320

Gly Tyr Pro Pro Glu Asp Ile Phe Asn Leu Val Gly Lys Lys Val Leu
          325          330          335

Val Thr Val Glu Glu Asp Asp Thr Ile Met Glu Glu Leu Val Asp Asn
          340          345          350

His Gly Lys Lys Ile Lys Ser
          355

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<210> SEQ ID NO 13
<211> LENGTH: 91
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 13

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

<210> SEQ ID NO 14

<211> LENGTH: 470

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 14

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

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

<210> SEQ ID NO 15
 <211> LENGTH: 209
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 15

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

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                165                170                175
Thr Ser Ser Asp Ser Ser Val Ile Ile Gln Gln Ala Val Pro Ser Pro
   180                185                190

Thr Ser Ser Thr Val Ile Thr Gln Ala Pro Ser Ser Asn Arg Pro Ile
   195                200                205

Val

<210> SEQ ID NO 16
<211> LENGTH: 292
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 16
Met Gly Asn Gln Leu Asp Arg Ile Thr His Leu Asn Tyr Ser Glu Leu
 1                5                10                15
Pro Thr Gly Asp Pro Ser Gly Ile Glu Lys Asp Glu Leu Arg Val Gly
   20                25                30
Val Ala Tyr Phe Phe Ser Asp Asp Glu Glu Asp Leu Asp Glu Arg Gly
   35                40                45
Gln Pro Asp Lys Phe Gly Val Lys Ala Pro Pro Gly Cys Thr Pro Cys
 50                55                60
Pro Glu Ser Pro Ser Arg His His His His Leu Leu His Gln Leu Val
 65                70                75                80
Leu Asn Glu Thr Gln Phe Ser Ala Phe Arg Gly Gln Glu Cys Ile Phe
   85                90                95
Ser Lys Val Ser Gly Gly Pro Gln Gly Ala Asp Leu Ser Val Tyr Ala
 100                105                110
Val Thr Ala Leu Pro Ala Leu Cys Glu Pro Gly Asp Leu Leu Glu Leu
 115                120                125
Leu Trp Leu Gln His Ala Pro Glu Pro Pro Ala Pro Ala Pro His Trp
 130                135                140
Ala Val Tyr Val Gly Gly Gly Gln Ile Ile His Leu His Gln Gly Glu
 145                150                155                160
Ile Arg Gln Asp Ser Leu Tyr Glu Ala Gly Ala Ala Asn Val Gly Arg
 165                170                175
Val Val Asn Ser Trp Tyr Arg Tyr Arg Pro Leu Val Ala Glu Leu Val
 180                185                190
Val Gln Asn Ala Cys Gly His Leu Gly Leu Lys Ser Glu Glu Ile Cys
 195                200                205
Trp Thr Asn Ser Glu Ser Phe Ala Ala Trp Cys Arg Phe Gly Lys Arg
 210                215                220
Glu Phe Lys Ala Gly Gly Glu Val Pro Ala Gly Thr Gln Pro Pro Gln
 225                230                235                240
Gln Gln Tyr Tyr Leu Lys Val His Leu Gly Glu Asn Lys Val His Thr
 245                250                255
Ala Arg Phe His Ser Leu Glu Asp Leu Ile Arg Glu Lys Arg Arg Ile
 260                265                270
Asp Ala Ser Gly Arg Leu Arg Val Leu Gln Glu Leu Ala Asp Leu Val
 275                280                285

Asp Asp Lys Glu
 290

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<210> SEQ ID NO 17
<211> LENGTH: 279
<212> TYPE: PRT

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<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 17
Met Ser Val Ala Gly Leu Lys Lys Gln Phe His Lys Ala Thr Gln Lys
1          5          10          15
Val Ser Glu Lys Val Gly Gly Ala Glu Gly Thr Lys Leu Asp Asp Asp
          20          25          30
Phe Lys Glu Met Glu Arg Lys Val Asp Val Thr Ser Arg Ala Val Met
          35          40          45
Glu Ile Met Thr Lys Thr Ile Glu Tyr Leu Gln Pro Asn Pro Ala Ser
          50          55          60
Arg Ala Lys Leu Ser Met Ile Asn Thr Met Ser Lys Ile Arg Gly Gln
65          70          75          80
Glu Lys Gly Pro Gly Tyr Pro Gln Ala Glu Ala Leu Leu Ala Glu Ala
          85          90          95
Met Leu Lys Phe Gly Arg Glu Leu Gly Asp Asp Cys Asn Phe Gly Pro
          100          105          110
Ala Leu Gly Glu Val Gly Glu Ala Met Arg Glu Leu Ser Glu Val Lys
          115          120          125
Asp Ser Leu Asp Ile Glu Val Lys Gln Asn Phe Ile Asp Pro Leu Gln
130          135          140
Asn Leu His Asp Lys Asp Leu Arg Glu Ile Gln His His Leu Lys Lys
145          150          155          160
Leu Glu Gly Arg Arg Leu Asp Phe Asp Tyr Lys Lys Glu Arg Gln Gly
          165          170          175
Lys Ile Pro Asp Glu Glu Leu Arg Gln Ala Leu Glu Lys Phe Asp Glu
          180          185          190
Ser Lys Glu Ile Ala Glu Ser Ser Met Phe Asn Leu Leu Glu Met Asp
          195          200          205
Ile Glu Gln Val Ser Gln Leu Ser Ala Leu Val Gln Ala Gln Leu Glu
210          215          220
Tyr His Lys Gln Ala Val Gln Ile Leu Gln Gln Val Thr Val Arg Leu
225          230          235          240
Glu Glu Arg Ile Arg Gln Ala Ser Ser Gln Pro Arg Arg Glu Tyr Gln
          245          250          255
Pro Lys Pro Arg Met Ser Leu Glu Phe Pro Thr Gly Asp Ser Thr Gln
          260          265          270
Pro Asn Gly Gly Leu Ser His
          275

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<210> SEQ ID NO 18
<211> LENGTH: 370
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 18

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

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

<210> SEQ ID NO 19

<211> LENGTH: 467

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 19

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

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Val His Ile Ser Arg Val Lys Ser Val Asn Leu Asp Gln Trp Thr Ala
 65 70 75 80

Glu Gln Ile Gln Cys Met Gln Asp Met Gly Asn Thr Lys Ala Arg Leu
 85 90 95

Leu Tyr Glu Ala Asn Leu Pro Glu Asn Phe Arg Arg Pro Gln Thr Asp
 100 105 110

Gln Ala Val Glu Phe Phe Ile Arg Asp Lys Tyr Glu Lys Lys Lys Tyr
 115 120 125

Tyr Asp Lys Asn Ala Ile Ala Ile Thr Asn Ile Ser Ser Ser Asp Ala
 130 135 140

Pro Leu Gln Pro Leu Val Ser Ser Pro Ser Leu Gln Ala Ala Val Asp
 145 150 155 160

Lys Asn Lys Leu Glu Lys Glu Lys Glu Lys Lys Lys Glu Glu Lys Lys
 165 170 175

Arg Glu Lys Glu Pro Glu Lys Pro Ala Lys Pro Leu Thr Ala Glu Lys
 180 185 190

Leu Gln Lys Lys Asp Gln Gln Leu Glu Pro Lys Lys Ser Thr Ser Pro
 195 200 205

Lys Lys Ala Ala Glu Pro Thr Val Asp Leu Leu Gly Leu Asp Gly Pro
 210 215 220

Ala Val Ala Pro Val Thr Asn Gly Asn Thr Thr Val Pro Pro Leu Asn
 225 230 235 240

Asp Asp Leu Asp Ile Phe Gly Pro Met Ile Ser Asn Pro Leu Pro Ala
 245 250 255

Thr Val Met Pro Pro Ala Gln Gly Thr Pro Ser Ala Pro Ala Ala Ala
 260 265 270

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

Thr Thr Lys Ser Glu Glu Val Ala Lys Lys Gln Leu Ser Lys Asp Ser
 290 295 300

Ile Leu Ser Leu Tyr Gly Thr Gly Thr Ile Gln Gln Gln Ser Thr Pro
 305 310 315 320

Gly Val Phe Met Gly Pro Thr Asn Ile Pro Phe Thr Ser Gln Ala Pro
 325 330 335

Ala Ala Phe Gln Gly Phe Pro Ser Met Gly Val Pro Val Pro Ala Ala
 340 345 350

Pro Gly Leu Ile Gly Asn Val Met Gly Gln Ser Pro Ser Met Met Val
 355 360 365

Gly Met Pro Met Pro Asn Gly Phe Met Gly Asn Ala Gln Thr Gly Val
 370 375 380

Met Pro Leu Pro Gln Asn Val Val Gly His Gln Gly Gly Met Val Gly
 385 390 395 400

Gln Met Gly Ala Pro Gln Ser Lys Phe Gly Leu Pro Gln Ala Gln Gln
 405 410 415

Pro Gln Trp Ser Leu Ser Gln Met Asn Gln Gln Met Ala Gly Met Ser
 420 425 430

Ile Ser Ser Ala Thr Pro Thr Ala Gly Phe Gly Gln Pro Ser Ser Thr
 435 440 445

Thr Ala Gly Trp Ser Gly Ser Ser Ser Gly Gln Thr Leu Ser Thr Gln
 450 455 460

Leu Trp Lys
 465

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<210> SEQ ID NO 20
<211> LENGTH: 514
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 20

Met Gly Arg Lys Lys Ile Gln Ile Gln Arg Ile Thr Asp Glu Arg Asn
1           5           10           15
Arg Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala
                20           25           30
Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe
            35           40           45
Asn His Ser Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys
    50           55           60
Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr
65           70           75           80
Asn Ala Asp Ile Ile Glu Thr Leu Arg Lys Lys Gly Phe Asn Gly Cys
            85           90           95
Asp Ser Pro Glu Pro Asp Gly Glu Asp Ser Leu Glu Gln Ser Pro Leu
    100           105           110
Leu Glu Asp Lys Tyr Arg Arg Ala Ser Glu Glu Leu Asp Gly Leu Phe
    115           120           125
Arg Arg Tyr Gly Ser Thr Val Pro Ala Pro Asn Phe Ala Met Pro Val
    130           135           140
Thr Val Pro Val Ser Asn Gln Ser Ser Leu Gln Phe Ser Asn Pro Ser
145           150           155           160
Gly Ser Leu Val Thr Pro Ser Leu Val Thr Ser Ser Leu Thr Asp Pro
    165           170           175
Arg Leu Leu Ser Pro Gln Gln Pro Ala Leu Gln Arg Asn Ser Val Ser
    180           185           190
Pro Gly Leu Pro Gln Arg Pro Ala Ser Ala Gly Ala Met Leu Gly Gly
    195           200           205
Asp Leu Asn Ser Ala Asn Gly Ala Cys Pro Ser Pro Val Gly Asn Gly
    210           215           220
Tyr Val Ser Ala Arg Ala Ser Pro Gly Leu Leu Pro Val Ala Asn Gly
225           230           235           240
Asn Ser Leu Asn Lys Val Ile Pro Ala Lys Ser Pro Pro Pro Pro Thr
    245           250           255
His Ser Thr Gln Leu Gly Ala Pro Ser Arg Lys Pro Asp Leu Arg Val
    260           265           270
Ile Thr Ser Gln Ala Gly Lys Gly Leu Met His His Leu Asn Asn Ala
    275           280           285
Gln Arg Leu Gly Val Ser Gln Ser Thr His Ser Leu Thr Thr Pro Val
    290           295           300
Val Ser Val Ala Thr Pro Ser Leu Leu Ser Gln Gly Leu Pro Phe Ser
305           310           315           320
Ser Met Pro Thr Ala Tyr Asn Thr Asp Tyr Gln Leu Thr Ser Ala Glu
    325           330           335
Leu Ser Ser Leu Pro Ala Phe Ser Ser Pro Gly Gly Leu Ser Leu Gly
    340           345           350
Asn Val Thr Ala Trp Gln Gln Pro Gln Gln Pro Gln Gln Pro Gln Gln
    355           360           365
Pro Gln Pro Pro Gln Gln Gln Pro Pro Gln Pro Gln Gln Pro Gln Pro
    370           375           380

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Gln Gln Pro Gln Gln Pro Gln Gln Pro Pro Gln Gln Gln Ser His Leu
385 390 395 400

Val Pro Val Ser Leu Ser Asn Leu Ile Pro Gly Ser Pro Leu Pro His
405 410 415

Val Gly Ala Ala Leu Thr Val Thr Thr His Pro His Ile Ser Ile Lys
420 425 430

Ser Glu Pro Val Ser Pro Ser Arg Glu Arg Ser Pro Ala Pro Pro Pro
435 440 445

Pro Ala Val Phe Pro Ala Ala Arg Pro Glu Pro Gly Asp Gly Leu Ser
450 455 460

Ser Pro Ala Gly Gly Ser Tyr Glu Thr Gly Asp Arg Asp Asp Gly Arg
465 470 475 480

Gly Asp Phe Gly Pro Thr Leu Gly Leu Leu Arg Pro Ala Pro Glu Pro
485 490 495

Glu Ala Glu Gly Ser Ala Val Lys Arg Met Arg Leu Asp Thr Trp Thr
500 505 510

Leu Lys

<210> SEQ ID NO 21

<211> LENGTH: 447

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 21

Met Ser Asn Asn Gly Leu Asp Ile Gln Asp Lys Pro Pro Ala Pro Pro
1 5 10 15

Met Arg Asn Thr Ser Thr Met Ile Gly Ala Gly Ser Lys Asp Ala Gly
20 25 30

Thr Leu Asn His Gly Ser Lys Pro Leu Pro Pro Asn Pro Glu Glu Lys
35 40 45

Lys Lys Lys Asp Arg Phe Tyr Arg Ser Ile Leu Pro Gly Asp Lys Thr
50 55 60

Asn Lys Lys Lys Glu Lys Glu Arg Pro Glu Ile Ser Leu Pro Ser Asp
65 70 75 80

Phe Glu His Thr Ile His Val Gly Phe Asp Ala Val Thr Gly Glu Phe
85 90 95

Thr Gly Met Pro Glu Gln Trp Ala Arg Leu Leu Gln Thr Ser Asn Ile
100 105 110

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

Glu Phe Tyr Asn Ser Lys Lys Thr Ser Asn Ser Gln Lys Tyr Met Ser
130 135 140

Phe Thr Asp Lys Ser Ala Glu Asp Tyr Asn Ser Ser Asn Ala Leu Asn
145 150 155 160

Val Lys Ala Val Ser Glu Thr Pro Ala Val Pro Pro Val Ser Glu Asp
165 170 175

Glu Asp Asp Asp Asp Asp Ala Thr Pro Pro Pro Val Ile Ala Pro
180 185 190

Arg Pro Glu His Thr Lys Ser Val Tyr Thr Arg Ser Val Ile Glu Pro
195 200 205

Leu Pro Val Thr Pro Thr Arg Asp Val Ala Thr Ser Pro Ile Ser Pro
210 215 220

Thr Glu Asn Asn Thr Thr Pro Pro Asp Ala Leu Thr Arg Asn Thr Glu
225 230 235 240

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Lys Gln Lys Lys Lys Pro Lys Met Ser Asp Glu Glu Ile Leu Glu Lys
 245 250 255

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

Phe Glu Lys Ile Gly Gln Gly Ala Ser Gly Thr Val Tyr Thr Ala Met
 275 280 285

Asp Val Ala Thr Gly Gln Glu Val Ala Ile Lys Gln Met Asn Leu Gln
 290 295 300

Gln Gln Pro Lys Lys Glu Leu Ile Ile Asn Glu Ile Leu Val Met Arg
 305 310 315 320

Glu Asn Lys Asn Pro Asn Ile Val Asn Tyr Leu Asp Ser Tyr Leu Val
 325 330 335

Gly Asp Glu Leu Trp Val Val Met Glu Tyr Leu Ala Gly Gly Ser Leu
 340 345 350

Thr Asp Val Val Thr Glu Thr Cys Met Asp Glu Gly Gln Ile Ala Ala
 355 360 365

Val Cys Arg Glu Cys Leu Gln Ala Leu Glu Phe Leu His Ser Asn Gln
 370 375 380

Val Ile His Arg Asp Ile Lys Ser Asp Asn Ile Leu Leu Gly Met Asp
 385 390 395 400

Gly Ser Val Lys Leu Thr Asp Phe Gly Phe Cys Ala Gln Ile Thr Pro
 405 410 415

Glu Gln Ser Lys Arg Ser Thr Met Val Gly Thr Pro Tyr Trp Met Ala
 420 425 430

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

<210> SEQ ID NO 22
 <211> LENGTH: 383
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 22

Met Glu Arg Leu Gln Lys Gln Pro Leu Thr Ser Pro Gly Ser Val Ser
 1 5 10 15

Pro Ser Arg Asp Ser Ser Val Pro Gly Ser Pro Ser Ser Ile Val Ala
 20 25 30

Lys Met Asp Asn Gln Val Leu Gly Tyr Lys Asp Leu Ala Ala Ile Pro
 35 40 45

Lys Asp Lys Ala Ile Leu Asp Ile Glu Arg Pro Asp Leu Met Ile Tyr
 50 55 60

Glu Pro His Phe Thr Tyr Ser Leu Leu Glu His Val Glu Leu Pro Arg
 65 70 75 80

Ser Arg Glu Arg Ser Leu Ser Pro Lys Ser Thr Ser Pro Pro Pro Ser
 85 90 95

Pro Glu Val Trp Ala Asp Ser Arg Ser Pro Gly Ile Ile Ser Gln Ala
 100 105 110

Ser Ala Pro Arg Thr Thr Gly Thr Pro Arg Thr Ser Leu Pro His Phe
 115 120 125

His His Pro Glu Thr Ser Arg Pro Asp Ser Asn Ile Tyr Lys Lys Pro
 130 135 140

Pro Ile Tyr Lys Gln Arg Glu Ser Val Gly Gly Ser Pro Gln Thr Lys
 145 150 155 160

His Leu Ile Glu Asp Leu Ile Ile Glu Ser Ser Lys Phe Pro Ala Ala
 165 170 175

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

<210> SEQ ID NO 23
 <211> LENGTH: 226
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 23

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

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165	170	175
Ala Gly Thr Val Thr Lys Cys Asn Phe Thr Gly Asp Gly Lys Thr Gly 180	185	190
Ala Ser Trp Thr Asp Asn Ile Met Ala Gln Lys Cys Ser Lys Gly Ala 195	200	205
Ala Ala Glu Ile Arg Glu Gln Gly Asp Gly Ala Glu Asp Glu Glu Trp 210	215	220
Asp Asp 225		

<210> SEQ ID NO 24
 <211> LENGTH: 253
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 24

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

<210> SEQ ID NO 25
 <211> LENGTH: 585
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 25

Met Lys Lys Gln Ala Asn Lys Thr Ala Ser Ser Gly Ser Ser Asp Lys

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1	5	10	15
Asp Ser Ser Ala Glu Ser Ser Ala Pro Glu Glu Gly Glu Val Ser Asp	20	25	30
Ser Asp Ser Ser Asn Ser Ser Ser Ser Ser Ser Asp Ser Asp Ser Ser Ser	35	40	45
Glu Asp Glu Glu Phe His Asp Gly Tyr Gly Glu Asp Leu Met Gly Asp	50	55	60
Glu Glu Asp Arg Ala Arg Leu Glu Gln Met Thr Glu Lys Glu Arg Glu	65	70	80
Gln Glu Leu Phe Asn Arg Ile Glu Lys Arg Glu Val Leu Lys Arg Arg	85	90	95
Phe Glu Ile Lys Lys Lys Leu Lys Thr Ala Lys Lys Lys Glu Lys Lys	100	105	110
Glu Lys Lys Lys Lys Gln Glu Glu Glu Gln Glu Lys Lys Lys Leu Thr	115	120	125
Gln Ile Gln Glu Ser Gln Val Thr Ser His Asn Lys Glu Arg Arg Ser	130	135	140
Lys Arg Asp Glu Lys Leu Asp Lys Lys Ser Gln Ala Met Glu Glu Leu	145	150	160
Lys Ala Glu Arg Glu Lys Arg Lys Asn Arg Thr Ala Glu Leu Leu Ala	165	170	175
Lys Lys Gln Pro Leu Lys Thr Ser Glu Val Tyr Ser Asp Asp Glu Glu	180	185	190
Glu Glu Glu Asp Asp Lys Ser Ser Glu Lys Ser Asp Arg Ser Ser Arg	195	200	205
Thr Ser Ser Ser Asp Glu Glu Glu Glu Lys Glu Glu Ile Pro Pro Lys	210	215	220
Ser Gln Pro Val Ser Leu Pro Glu Glu Leu Asn Arg Val Arg Leu Ser	225	230	240
Arg His Lys Leu Glu Arg Trp Cys His Met Pro Phe Phe Ala Lys Thr	245	250	255
Val Thr Gly Cys Phe Val Arg Ile Gly Ile Gly Asn His Asn Ser Lys	260	265	270
Pro Val Tyr Arg Val Ala Glu Ile Thr Gly Val Val Glu Thr Ala Lys	275	280	285
Val Tyr Gln Leu Gly Gly Thr Arg Thr Asn Lys Gly Leu Gln Leu Arg	290	295	300
His Gly Asn Asp Gln Arg Val Phe Arg Leu Glu Phe Val Ser Asn Gln	305	310	315
Glu Phe Thr Glu Ser Glu Phe Met Lys Trp Lys Glu Ala Met Phe Ser	325	330	335
Ala Gly Met Gln Leu Pro Thr Leu Asp Glu Ile Asn Lys Lys Glu Leu	340	345	350
Ser Ile Lys Glu Ala Leu Asn Tyr Lys Phe Asn Asp Gln Asp Ile Glu	355	360	365
Glu Ile Val Lys Glu Lys Glu Arg Phe Arg Lys Ala Pro Pro Asn Tyr	370	375	380
Ala Met Lys Lys Thr Gln Leu Leu Lys Glu Lys Ala Met Ala Glu Asp	385	390	395
Leu Gly Asp Gln Asp Lys Ala Lys Gln Ile Gln Asp Gln Leu Asn Glu	405	410	415
Leu Glu Glu Arg Ala Glu Ala Leu Asp Arg Gln Arg Thr Lys Asn Ile	420	425	430

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Ser Ala Ile Ser Tyr Ile Asn Gln Arg Asn Arg Glu Trp Asn Ile Val
 435 440 445

Glu Ser Glu Lys Ala Leu Val Ala Glu Ser His Asn Met Lys Asn Gln
 450 455 460

Gln Met Asp Pro Phe Thr Arg Arg Gln Cys Lys Pro Thr Ile Val Ser
 465 470 475 480

Asn Ser Arg Asp Pro Ala Val Gln Ala Ala Ile Leu Ala Gln Leu Asn
 485 490 495

Ala Lys Tyr Gly Ser Gly Val Leu Pro Asp Ala Pro Lys Glu Met Ser
 500 505 510

Lys Gly Gln Gly Lys Asp Lys Asp Leu Asn Ser Lys Ser Ala Ser Asp
 515 520 525

Leu Ser Glu Asp Leu Phe Lys Val His Asp Phe Asp Val Lys Ile Asp
 530 535 540

Leu Gln Val Pro Ser Ser Glu Ser Lys Ala Leu Ala Ile Thr Ser Lys
 545 550 555 560

Ala Pro Pro Ala Lys Asp Gly Ala Pro Arg Arg Ser Leu Asn Leu Glu
 565 570 575

Asp Tyr Lys Lys Arg Arg Gly Leu Ile
 580 585

<210> SEQ ID NO 26
 <211> LENGTH: 129
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 26

Met Ala Asp Ser Gly Asp Ala Gly Ser Ser Gly Pro Trp Trp Lys Ser
 1 5 10 15

Leu Thr Asn Ser Arg Lys Lys Ser Lys Glu Ala Ala Val Gly Val Pro
 20 25 30

Pro Pro Ala Gln Pro Ala Pro Gly Glu Pro Thr Pro Pro Ala Pro Pro
 35 40 45

Ser Pro Asp Trp Thr Ser Ser Ser Arg Glu Asn Gln His Pro Asn Leu
 50 55 60

Leu Gly Gly Ala Gly Glu Pro Pro Lys Pro Asp Lys Leu Tyr Gly Asp
 65 70 75 80

Lys Ser Gly Ser Ser Arg Arg Asn Leu Lys Ile Ser Arg Ser Gly Arg
 85 90 95

Phe Lys Glu Lys Arg Lys Val Arg Ala Thr Leu Leu Pro Glu Ala Gly
 100 105 110

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

Gln

<210> SEQ ID NO 27
 <211> LENGTH: 173
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 27

Met Asp Val Thr Ile Gln His Pro Trp Phe Lys Arg Thr Leu Gly Pro
 1 5 10 15

Phe Tyr Pro Ser Arg Leu Phe Asp Gln Phe Phe Gly Glu Gly Leu Phe
 20 25 30

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

<210> SEQ ID NO 28

<211> LENGTH: 598

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 28

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

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

 <210> SEQ ID NO 30
 <211> LENGTH: 512
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

 <400> SEQUENCE: 30

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

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His Glu Asn Leu Leu Gln Phe Ile Ala Ala Glu Lys Arg Gly Ser Asn
 245 250 255

Leu Glu Val Glu Leu Trp Leu Ile Thr Ala Phe His Asp Lys Gly Ser
 260 265 270

Leu Thr Asp Tyr Leu Lys Gly Asn Ile Ile Thr Trp Asn Glu Leu Cys
 275 280 285

His Val Ala Glu Thr Met Ser Arg Gly Leu Ser Tyr Leu His Glu Asp
 290 295 300

Val Pro Trp Cys Arg Gly Glu Gly His Lys Pro Ser Ile Ala His Arg
 305 310 315 320

Asp Phe Lys Ser Lys Asn Val Leu Leu Lys Ser Asp Leu Thr Ala Val
 325 330 335

Leu Ala Asp Phe Gly Leu Ala Val Arg Phe Glu Pro Gly Lys Pro Pro
 340 345 350

Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg Tyr Met Ala Pro Glu
 355 360 365

Val Leu Glu Gly Ala Ile Asn Phe Gln Arg Asp Ala Phe Leu Arg Ile
 370 375 380

Asp Met Tyr Ala Met Gly Leu Val Leu Trp Glu Leu Val Ser Arg Cys
 385 390 395 400

Lys Ala Ala Asp Gly Pro Val Asp Glu Tyr Met Leu Pro Phe Glu Glu
 405 410 415

Glu Ile Gly Gln His Pro Ser Leu Glu Glu Leu Gln Glu Val Val Val
 420 425 430

His Lys Lys Met Arg Pro Thr Ile Lys Asp His Trp Leu Lys His Pro
 435 440 445

Gly Leu Ala Gln Leu Cys Val Thr Ile Glu Glu Cys Trp Asp His Asp
 450 455 460

Ala Glu Ala Arg Leu Ser Ala Gly Cys Val Glu Glu Arg Val Ser Leu
 465 470 475 480

Ile Arg Arg Ser Val Asn Gly Thr Thr Ser Asp Cys Leu Val Ser Leu
 485 490 495

Val Thr Ser Val Thr Asn Val Asp Leu Pro Pro Lys Glu Ser Ser Ile
 500 505 510

<210> SEQ ID NO 31
 <211> LENGTH: 206
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 31

Ser Lys Cys Pro Lys Cys Asp Lys Thr Val Tyr Phe Ala Glu Lys Val
 1 5 10 15

Ser Ser Leu Gly Lys Asp Trp His Lys Phe Cys Leu Lys Cys Glu Arg
 20 25 30

Cys Ser Lys Thr Leu Thr Pro Gly Gly His Ala Glu His Asp Gly Lys
 35 40 45

Pro Phe Cys His Lys Pro Cys Tyr Ala Thr Leu Phe Gly Pro Lys Gly
 50 55 60

Val Asn Ile Gly Gly Ala Gly Ser Tyr Ile Tyr Glu Lys Pro Leu Ala
 65 70 75 80

Glu Gly Pro Gln Val Thr Gly Pro Ile Glu Val Pro Ala Ala Arg Ala
 85 90 95

Glu Glu Arg Lys Ala Ser Gly Pro Pro Lys Gly Pro Ser Arg Ala Ser
 100 105 110

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Ser Val Thr Thr Phe Thr Gly Glu Pro Asn Thr Cys Pro Arg Cys Ser
 115 120 125

Lys Lys Val Tyr Phe Ala Glu Lys Val Thr Ser Leu Gly Lys Asp Trp
 130 135 140

His Arg Pro Cys Leu Arg Cys Glu Arg Cys Gly Lys Thr Leu Thr Pro
 145 150 155 160

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

Tyr Gly Ile Leu Phe Gly Pro Lys Gly Val Asn Thr Gly Ala Val Gly
 180 185 190

Ser Tyr Ile Tyr Asp Arg Asp Pro Glu Gly Lys Val Gln Pro
 195 200 205

<210> SEQ ID NO 32
 <211> LENGTH: 76
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 32

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

Gln Thr Leu Leu Gln Gln Met Gln Asp Lys Phe Gln Thr Met Ser Asp
 20 25 30

Gln Ile Ile Gly Arg Ile Asp Asp Met Ser Ser Arg Ile Asp Asp Leu
 35 40 45

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

Glu Ser Glu Asn Lys Ile Pro Ala Thr Gln Lys Ser
 65 70 75

<210> SEQ ID NO 33
 <211> LENGTH: 672
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 33

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

Ala Asn Arg Phe Ala Arg Lys Gly Ala Leu Arg Gln Lys Asn Val His
 20 25 30

Glu Val Lys Asp His Lys Phe Ile Ala Arg Phe Phe Lys Gln Pro Thr
 35 40 45

Phe Cys Ser His Cys Thr Asp Phe Ile Trp Gly Phe Gly Lys Gln Gly
 50 55 60

Phe Gln Cys Gln Val Cys Cys Phe Val Val His Lys Arg Cys His Glu
 65 70 75 80

Phe Val Thr Phe Ser Cys Pro Gly Ala Asp Lys Gly Pro Asp Thr Asp
 85 90 95

Asp Pro Arg Ser Lys His Lys Phe Lys Ile His Thr Tyr Gly Ser Pro
 100 105 110

Thr Phe Cys Asp His Cys Gly Ser Leu Leu Tyr Gly Leu Ile His Gln
 115 120 125

Gly Met Lys Cys Asp Thr Cys Asp Met Asn Val His Lys Gln Cys Val
 130 135 140

Ile Asn Val Pro Ser Leu Cys Gly Met Asp His Thr Glu Lys Arg Gly
 145 150 155 160

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Arg Ile Tyr Leu Lys Ala Glu Val Ala Asp Glu Lys Leu His Val Thr
 165 170 175
 Val Arg Asp Ala Lys Asn Leu Ile Pro Met Asp Pro Asn Gly Leu Ser
 180 185 190
 Asp Pro Tyr Val Lys Leu Lys Leu Ile Pro Asp Pro Lys Asn Glu Ser
 195 200 205
 Lys Gln Lys Thr Lys Thr Ile Arg Ser Thr Leu Asn Pro Gln Trp Asn
 210 215 220
 Glu Ser Phe Thr Phe Lys Leu Lys Pro Ser Asp Lys Asp Arg Arg Leu
 225 230 235 240
 Ser Val Glu Ile Trp Asp Trp Asp Arg Thr Thr Arg Asn Asp Phe Met
 245 250 255
 Gly Ser Leu Ser Phe Gly Val Ser Glu Leu Met Lys Met Pro Ala Ser
 260 265 270
 Gly Trp Tyr Lys Leu Leu Asn Gln Glu Glu Gly Glu Tyr Tyr Asn Val
 275 280 285
 Pro Ile Pro Glu Gly Asp Glu Glu Gly Asn Met Glu Leu Arg Gln Lys
 290 295 300
 Phe Glu Lys Ala Lys Leu Gly Pro Ala Gly Asn Lys Val Ile Ser Pro
 305 310 315 320
 Ser Glu Asp Arg Lys Gln Pro Ser Asn Asn Leu Asp Arg Val Lys Leu
 325 330 335
 Thr Asp Phe Asn Phe Leu Met Val Leu Gly Lys Gly Ser Phe Gly Lys
 340 345 350
 Val Met Leu Ala Asp Arg Lys Gly Thr Glu Glu Leu Tyr Ala Ile Lys
 355 360 365
 Ile Leu Lys Lys Asp Val Val Ile Gln Asp Asp Asp Val Glu Cys Thr
 370 375 380
 Met Val Glu Lys Arg Val Leu Ala Leu Leu Asp Lys Pro Pro Phe Leu
 385 390 395 400
 Thr Gln Leu His Ser Cys Phe Gln Thr Val Asp Arg Leu Tyr Phe Val
 405 410 415
 Met Glu Tyr Val Asn Gly Gly Asp Leu Met Tyr His Ile Gln Gln Val
 420 425 430
 Gly Lys Phe Lys Glu Pro Gln Ala Val Phe Tyr Ala Ala Glu Ile Ser
 435 440 445
 Ile Gly Leu Phe Phe Leu His Lys Arg Gly Ile Ile Tyr Arg Asp Leu
 450 455 460
 Lys Leu Asp Asn Val Met Leu Asp Ser Glu Gly His Ile Lys Ile Ala
 465 470 475 480
 Asp Phe Gly Met Cys Lys Glu His Met Met Asp Gly Val Thr Thr Arg
 485 490 495
 Thr Phe Cys Gly Thr Pro Asp Tyr Ile Ala Pro Glu Ile Ile Ala Tyr
 500 505 510
 Gln Pro Tyr Gly Lys Ser Val Asp Trp Trp Ala Tyr Gly Val Leu Leu
 515 520 525
 Tyr Glu Met Leu Ala Gly Gln Pro Pro Phe Asp Gly Glu Asp Glu Asp
 530 535 540
 Glu Leu Phe Gln Ser Ile Met Glu His Asn Val Ser Tyr Pro Lys Ser
 545 550 555 560
 Leu Ser Lys Glu Ala Val Ser Ile Cys Lys Gly Leu Met Thr Lys His
 565 570 575

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Pro Ala Lys Arg Leu Gly Cys Gly Pro Glu Gly Glu Arg Asp Val Arg
580 585 590

Glu His Ala Phe Phe Arg Arg Ile Asp Trp Glu Lys Leu Glu Asn Arg
595 600 605

Glu Ile Gln Pro Pro Phe Lys Pro Lys Val Cys Gly Lys Gly Ala Glu
610 615 620

Asn Phe Asp Lys Phe Phe Thr Arg Gly Gln Pro Val Leu Thr Pro Pro
625 630 635 640

Asp Gln Leu Val Ile Ala Asn Ile Asp Gln Ser Asp Phe Glu Gly Phe
645 650 655

Ser Tyr Val Asn Pro Gln Phe Val His Pro Ile Leu Gln Ser Ala Val
660 665 670

<210> SEQ ID NO 34
 <211> LENGTH: 596
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 34

Met Pro Thr Gln Arg Asp Ser Ser Thr Met Ser His Thr Val Ala Gly
1 5 10 15

Gly Gly Ser Gly Asp His Ser His Gln Val Arg Val Lys Ala Tyr Tyr
20 25 30

Arg Gly Asp Ile Met Ile Thr His Phe Glu Pro Ser Ile Ser Phe Glu
35 40 45

Gly Leu Cys Asn Glu Val Arg Asp Met Cys Ser Phe Asp Asn Glu Gln
50 55 60

Leu Phe Thr Met Lys Trp Ile Asp Glu Glu Gly Asp Pro Cys Thr Val
65 70 75 80

Ser Ser Gln Leu Glu Leu Glu Glu Ala Phe Arg Leu Tyr Glu Leu Asn
85 90 95

Lys Asp Ser Glu Leu Leu Ile His Val Phe Pro Cys Val Pro Glu Arg
100 105 110

Pro Gly Met Pro Cys Pro Gly Glu Asp Lys Ser Ile Tyr Arg Arg Gly
115 120 125

Ala Arg Arg Trp Arg Lys Leu Tyr Cys Ala Asn Gly His Thr Phe Gln
130 135 140

Ala Lys Arg Phe Asn Arg Arg Ala His Cys Ala Ile Cys Thr Asp Arg
145 150 155 160

Ile Trp Gly Leu Gly Arg Gln Gly Tyr Lys Cys Ile Asn Cys Lys Leu
165 170 175

Leu Val His Lys Lys Cys His Lys Leu Val Thr Ile Glu Cys Gly Arg
180 185 190

His Ser Leu Pro Gln Glu Pro Val Met Pro Met Asp Gln Ser Ser Met
195 200 205

His Ser Asp His Ala Gln Thr Val Ile Pro Tyr Asn Pro Ser Ser His
210 215 220

Glu Ser Leu Asp Gln Val Gly Glu Glu Lys Glu Ala Met Asn Thr Arg
225 230 235 240

Glu Ser Gly Lys Ala Ser Ser Ser Leu Gly Leu Gln Asp Phe Asp Leu
245 250 255

Leu Arg Val Ile Gly Arg Gly Ser Tyr Ala Lys Val Leu Leu Val Arg
260 265 270

Leu Lys Lys Thr Asp Arg Ile Tyr Ala Met Lys Val Val Lys Lys Glu
275 280 285

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

<210> SEQ ID NO 35
 <211> LENGTH: 592
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 35

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

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50					55					60					
Gly	Asp	Pro	Cys	Thr	Val	Ser	Ser	Gln	Met	Glu	Leu	Glu	Glu	Ala	Phe
65					70					75					80
Arg	Leu	Ala	Arg	Gln	Cys	Arg	Asp	Glu	Gly	Leu	Ile	Ile	His	Val	Phe
				85					90					95	
Pro	Ser	Thr	Pro	Glu	Gln	Pro	Gly	Leu	Pro	Cys	Pro	Gly	Glu	Asp	Lys
			100					105						110	
Ser	Ile	Tyr	Arg	Arg	Gly	Ala	Arg	Arg	Trp	Arg	Lys	Leu	Tyr	Arg	Ala
		115					120					125			
Asn	Gly	His	Leu	Phe	Gln	Ala	Lys	Arg	Phe	Asn	Arg	Arg	Ala	Tyr	Cys
							135							140	
Gly	Gln	Cys	Ser	Glu	Arg	Ile	Trp	Gly	Leu	Ala	Arg	Gln	Gly	Tyr	Arg
145						150					155				160
Cys	Ile	Asn	Cys	Lys	Leu	Leu	Val	His	Lys	Arg	Cys	His	Gly	Leu	Val
				165					170					175	
Pro	Leu	Thr	Cys	Arg	Lys	His	Met	Asp	Ser	Val	Met	Pro	Ser	Gln	Glu
			180					185						190	
Pro	Pro	Val	Asp	Asp	Lys	Asn	Glu	Asp	Ala	Asp	Leu	Pro	Ser	Glu	Glu
		195					200							205	
Thr	Asp	Gly	Ile	Ala	Tyr	Ile	Ser	Ser	Ser	Arg	Lys	His	Asp	Ser	Ile
						215							220		
Lys	Asp	Asp	Ser	Glu	Asp	Leu	Lys	Pro	Val	Ile	Asp	Gly	Met	Asp	Gly
225						230					235				240
Ile	Lys	Ile	Ser	Gln	Gly	Leu	Gly	Leu	Gln	Asp	Phe	Asp	Leu	Ile	Arg
				245					250					255	
Val	Ile	Gly	Arg	Gly	Ser	Tyr	Ala	Lys	Val	Leu	Leu	Val	Arg	Leu	Lys
			260					265						270	
Lys	Asn	Asp	Gln	Ile	Tyr	Ala	Met	Lys	Val	Val	Lys	Lys	Glu	Leu	Val
			275				280						285		
His	Asp	Asp	Glu	Asp	Ile	Asp	Trp	Val	Gln	Thr	Glu	Lys	His	Val	Phe
			290				295						300		
Glu	Gln	Ala	Ser	Ser	Asn	Pro	Phe	Leu	Val	Gly	Leu	His	Ser	Cys	Phe
						310					315				320
Gln	Thr	Thr	Ser	Arg	Leu	Phe	Leu	Val	Ile	Glu	Tyr	Val	Asn	Gly	Gly
				325					330					335	
Asp	Leu	Met	Phe	His	Met	Gln	Arg	Gln	Arg	Lys	Leu	Pro	Glu	Glu	His
			340					345						350	
Ala	Arg	Phe	Tyr	Ala	Ala	Glu	Ile	Cys	Ile	Ala	Leu	Asn	Phe	Leu	His
			355				360						365		
Glu	Arg	Gly	Ile	Ile	Tyr	Arg	Asp	Leu	Lys	Leu	Asp	Asn	Val	Leu	Leu
						375					380				
Asp	Ala	Asp	Gly	His	Ile	Lys	Leu	Thr	Asp	Tyr	Gly	Met	Cys	Lys	Glu
385						390					395				400
Gly	Leu	Gly	Pro	Gly	Asp	Thr	Thr	Ser	Thr	Phe	Cys	Gly	Thr	Pro	Asn
				405					410					415	
Tyr	Ile	Ala	Pro	Glu	Ile	Leu	Arg	Gly	Glu	Glu	Tyr	Gly	Phe	Ser	Val
			420						425					430	
Asp	Trp	Trp	Ala	Leu	Gly	Val	Leu	Met	Phe	Glu	Met	Met	Ala	Gly	Arg
			435				440						445		
Ser	Pro	Phe	Asp	Ile	Ile	Thr	Asp	Asn	Pro	Asp	Met	Asn	Thr	Glu	Asp
						455							460		
Tyr	Leu	Phe	Gln	Val	Ile	Leu	Glu	Lys	Pro	Ile	Arg	Ile	Pro	Arg	Phe
465						470					475				480

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Leu Ser Val Lys Ala Ser His Val Leu Lys Gly Phe Leu Asn Lys Asp
 485 490 495

Pro Lys Glu Arg Leu Gly Cys Arg Pro Gln Thr Gly Phe Ser Asp Ile
 500 505 510

Lys Ser His Ala Phe Phe Arg Ser Ile Asp Trp Asp Leu Leu Glu Lys
 515 520 525

Lys Gln Ala Leu Pro Pro Phe Gln Pro Gln Ile Thr Asp Asp Tyr Gly
 530 535 540

Leu Asp Asn Phe Asp Thr Gln Phe Thr Ser Glu Pro Val Gln Leu Thr
 545 550 555 560

Pro Asp Asp Glu Asp Ala Ile Lys Arg Ile Asp Gln Ser Glu Phe Glu
 565 570 575

Gly Phe Glu Tyr Ile Asn Pro Leu Leu Leu Ser Thr Glu Glu Ser Val
 580 585 590

<210> SEQ ID NO 36
 <211> LENGTH: 721
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 36

Met Ala Ala Pro Val Val Ala Pro Pro Gly Val Val Val Ser Arg Ala
 1 5 10 15

Asn Lys Arg Ser Gly Ala Gly Pro Gly Gly Ser Gly Gly Gly Ala
 20 25 30

Arg Gly Ala Glu Glu Glu Pro Pro Pro Leu Gln Ala Val Leu Val
 35 40 45

Ala Asp Ser Phe Asp Arg Arg Phe Phe Pro Ile Ser Lys Asp Gln Pro
 50 55 60

Arg Val Leu Leu Pro Leu Ala Asn Val Ala Leu Ile Asp Tyr Thr Leu
 65 70 75 80

Glu Phe Leu Thr Ala Thr Gly Val Gln Glu Thr Phe Val Phe Cys Cys
 85 90 95

Trp Lys Ala Ala Gln Ile Lys Glu His Leu Leu Lys Ser Lys Trp Cys
 100 105 110

Arg Pro Thr Ser Leu Asn Val Val Arg Ile Ile Thr Ser Glu Leu Tyr
 115 120 125

Arg Ser Leu Gly Asp Val Leu Arg Asp Val Asp Ala Lys Ala Leu Val
 130 135 140

Arg Ser Asp Phe Leu Leu Val Tyr Gly Asp Val Ile Ser Asn Ile Asn
 145 150 155 160

Ile Thr Arg Ala Leu Glu Glu His Arg Leu Arg Arg Lys Leu Glu Lys
 165 170 175

Asn Val Ser Val Met Thr Met Ile Phe Lys Glu Ser Ser Pro Ser His
 180 185 190

Pro Thr Arg Cys His Glu Asp Asn Val Val Val Ala Val Asp Ser Thr
 195 200 205

Thr Asn Arg Val Leu His Phe Gln Lys Thr Gln Gly Leu Arg Arg Phe
 210 215 220

Ala Phe Pro Leu Ser Leu Phe Gln Gly Ser Ser Asp Gly Val Glu Val
 225 230 235 240

Arg Tyr Asp Leu Leu Asp Cys His Ile Ser Ile Cys Ser Pro Gln Val
 245 250 255

Ala Gln Leu Phe Thr Asp Asn Phe Asp Tyr Gln Thr Arg Asp Asp Phe

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260					265					270					
Val	Arg	Gly	Leu	Leu	Val	Asn	Glu	Glu	Ile	Leu	Gly	Asn	Gln	Ile	His
		275					280					285			
Met	His	Val	Thr	Ala	Lys	Glu	Tyr	Gly	Ala	Arg	Val	Ser	Asn	Leu	His
		290					295					300			
Met	Tyr	Ser	Ala	Val	Cys	Ala	Asp	Val	Ile	Arg	Arg	Trp	Val	Tyr	Pro
		305					310					315			
Leu	Thr	Pro	Glu	Ala	Asn	Phe	Thr	Asp	Ser	Thr	Thr	Gln	Ser	Cys	Thr
				325								330			335
His	Ser	Arg	His	Asn	Ile	Tyr	Arg	Gly	Pro	Glu	Val	Ser	Leu	Gly	His
				340										350	
Gly	Ser	Ile	Leu	Glu	Glu	Asn	Val	Leu	Leu	Gly	Ser	Gly	Thr	Val	Ile
			355									365			
Gly	Ser	Asn	Cys	Phe	Ile	Thr	Asn	Ser	Val	Ile	Gly	Pro	Gly	Cys	His
			370									380			
Ile	Gly	Asp	Asn	Val	Val	Leu	Asp	Gln	Thr	Tyr	Leu	Trp	Gln	Gly	Val
				390								395			400
Arg	Val	Ala	Ala	Gly	Ala	Gln	Ile	His	Gln	Ser	Leu	Leu	Cys	Asp	Asn
				405								410			415
Ala	Glu	Val	Lys	Glu	Arg	Val	Thr	Leu	Lys	Pro	Arg	Ser	Val	Leu	Thr
				420										430	
Ser	Gln	Val	Val	Val	Gly	Pro	Asn	Ile	Thr	Leu	Pro	Glu	Gly	Ser	Val
				435								445			
Ile	Ser	Leu	His	Pro	Pro	Asp	Ala	Glu	Glu	Asp	Glu	Asp	Asp	Gly	Glu
				450								460			
Phe	Ser	Asp	Asp	Ser	Gly	Ala	Asp	Gln	Glu	Lys	Asp	Lys	Val	Lys	Met
				465								475			480
Lys	Gly	Tyr	Asn	Pro	Ala	Glu	Val	Gly	Ala	Ala	Gly	Lys	Gly	Tyr	Leu
				485								490			495
Trp	Lys	Ala	Ala	Gly	Met	Asn	Met	Glu	Glu	Glu	Glu	Glu	Glu	Leu	Gln
				500								505			510
Asn	Leu	Trp	Gly	Leu	Lys	Ile	Asn	Met	Glu	Glu	Glu	Glu	Ser	Glu	Ser
				515								520			525
Ser	Glu	Gln	Ser	Met	Asp	Ser	Glu	Glu	Pro	Asp	Ser	Arg	Gly	Gly	Ser
				530								540			
Pro	Gln	Met	Asp	Asp	Ile	Lys	Val	Phe	Gln	Asn	Glu	Val	Leu	Gly	Thr
				545								555			560
Leu	Gln	Arg	Gly	Lys	Glu	Glu	Asn	Ile	Ser	Cys	Asp	Asn	Leu	Val	Leu
				565								570			575
Glu	Ile	Asn	Ser	Leu	Lys	Tyr	Ala	Tyr	Asn	Val	Ser	Leu	Lys	Glu	Val
				580								585			590
Met	Gln	Val	Leu	Ser	His	Val	Val	Leu	Glu	Phe	Pro	Leu	Gln	Gln	Met
				595								600			605
Asp	Ser	Pro	Leu	Asp	Ser	Ser	Arg	Tyr	Cys	Ala	Leu	Leu	Leu	Pro	Leu
				610								615			620
Leu	Lys	Ala	Trp	Ser	Pro	Val	Phe	Arg	Asn	Tyr	Ile	Lys	Arg	Ala	Ala
				625								630			635
Asp	His	Leu	Glu	Ala	Leu	Ala	Ala	Ile	Glu	Asp	Phe	Phe	Leu	Glu	His
				645								650			655
Glu	Ala	Leu	Gly	Ile	Ser	Met	Ala	Lys	Val	Leu	Met	Ala	Phe	Tyr	Gln
				660								665			670
Leu	Glu	Ile	Leu	Ala	Glu	Glu	Thr	Ile	Leu	Ser	Trp	Phe	Ser	Gln	Arg
				675								680			685

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Asp Thr Thr Asp Lys Gly Gln Gln Leu Arg Lys Asn Gln Gln Leu Gln
690 695 700

Arg Phe Ile Gln Trp Leu Lys Glu Ala Glu Glu Glu Ser Ser Glu Asp
705 710 715 720

Asp

<210> SEQ ID NO 37

<211> LENGTH: 143

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 37

Met Pro Lys Val Lys Arg Ser Arg Lys Ala Pro Pro Asp Gly Trp Glu
1 5 10 15

Leu Ile Glu Pro Thr Leu Asp Glu Leu Asp Gln Lys Met Arg Glu Ala
20 25 30

Glu Thr Glu Pro His Glu Gly Lys Arg Lys Val Glu Ser Leu Trp Pro
35 40 45

Ile Phe Arg Ile His His Gln Lys Thr Arg Tyr Ile Phe Asp Leu Phe
50 55 60

Tyr Lys Arg Lys Ala Ile Ser Arg Glu Leu Tyr Glu Tyr Cys Ile Lys
65 70 75 80

Glu Gly Tyr Ala Asp Lys Asn Leu Ile Ala Lys Trp Lys Lys Gln Gly
85 90 95

Tyr Glu Asn Leu Cys Cys Leu Arg Cys Ile Gln Thr Arg Asp Thr Asn
100 105 110

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

Gly Arg Ile Ile Glu Cys Thr His Cys Gly Cys Arg Gly Cys Ser
130 135 140

<210> SEQ ID NO 38

<211> LENGTH: 198

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 38

Met Ser Asn Val Arg Val Ser Asn Gly Ser Pro Ser Leu Glu Arg Met
1 5 10 15

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

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

Cys Arg Asp Met Glu Glu Ala Ser Gln Arg Lys Trp Asn Phe Asp Phe
50 55 60

Gln Asn His Lys Pro Leu Glu Gly Lys Tyr Glu Trp Gln Glu Val Glu
65 70 75 80

Lys Gly Ser Leu Pro Glu Phe Tyr Tyr Arg Pro Pro Arg Pro Pro Lys
85 90 95

Gly Ala Cys Lys Val Pro Ala Gln Glu Ser Gln Asp Val Ser Gly Ser
100 105 110

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

His Leu Val Asp Pro Lys Thr Asp Pro Ser Asp Ser Gln Thr Gly Leu
130 135 140

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Ala Glu Gln Cys Ala Gly Ile Arg Lys Arg Pro Ala Thr Asp Asp Ser
 145 150 155 160

Ser Thr Gln Asn Lys Arg Ala Asn Arg Thr Glu Glu Asn Val Ser Asp
 165 170 175

Gly Ser Pro Asn Ala Gly Ser Val Glu Gln Thr Pro Lys Lys Pro Gly
 180 185 190

Leu Arg Arg Arg Gln Thr
 195

<210> SEQ ID NO 39
 <211> LENGTH: 102
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 39

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

Pro Ala Val Lys Ala Gly Gly Met Arg Ile Val Gln Lys His Pro His
 20 25 30

Thr Gly Asp Thr Lys Glu Glu Lys Asp Lys Asp Asp Gln Glu Trp Glu
 35 40 45

Ser Pro Ser Pro Pro Lys Pro Thr Val Phe Ile Ser Gly Val Ile Ala
 50 55 60

Arg Gly Asp Lys Asp Phe Pro Pro Ala Ala Ala Gln Val Ala His Gln
 65 70 75 80

Lys Pro His Ala Ser Met Asp Lys His Pro Ser Pro Arg Thr Gln His
 85 90 95

Ile Gln Gln Pro Arg Lys
 100

<210> SEQ ID NO 40
 <211> LENGTH: 369
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 40

Met Pro Val Val Thr Thr Asp Ala Glu Ser Glu Thr Gly Ile Pro Lys
 1 5 10 15

Ser Leu Ser Asn Glu Pro Pro Ser Glu Thr Met Glu Glu Ile Glu His
 20 25 30

Thr Cys Pro Gln Pro Arg Leu Thr Leu Thr Ala Pro Ala Pro Phe Ala
 35 40 45

Asp Glu Thr Asn Cys Gln Cys Gln Ala Pro His Glu Lys Leu Thr Ile
 50 55 60

Ala Gln Ala Arg Leu Gly Thr Pro Ala Asp Arg Pro Val Arg Val Tyr
 65 70 75 80

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

Met Gln Ala Lys Thr Leu Phe Pro Asn Ser Tyr Leu Leu Val Gly Val
 100 105 110

Cys Ser Asp Asp Leu Thr His Lys Phe Lys Gly Phe Thr Val Met Asn
 115 120 125

Glu Ala Glu Arg Tyr Glu Ala Leu Arg His Cys Arg Tyr Val Asp Glu
 130 135 140

Val Ile Arg Asp Ala Pro Trp Thr Leu Thr Pro Glu Phe Leu Glu Lys
 145 150 155 160

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His Lys Ile Asp Phe Val Ala His Asp Asp Ile Pro Tyr Ser Ser Ala
 165 170 175

Gly Ser Asp Asp Val Tyr Lys His Ile Lys Glu Ala Gly Met Phe Val
 180 185 190

Pro Thr Gln Arg Thr Glu Gly Ile Ser Thr Ser Asp Ile Ile Thr Arg
 195 200 205

Ile Val Arg Asp Tyr Asp Val Tyr Ala Arg Arg Asn Leu Gln Arg Gly
 210 215 220

Tyr Thr Ala Lys Glu Leu Asn Val Ser Phe Ile Asn Glu Lys Arg Tyr
 225 230 235 240

Arg Phe Gln Asn Gln Val Asp Lys Met Lys Glu Lys Val Lys Asn Val
 245 250 255

Glu Glu Arg Ser Lys Glu Phe Val Asn Arg Val Glu Glu Lys Ser His
 260 265 270

Asp Leu Ile Gln Lys Trp Glu Glu Lys Ser Arg Glu Phe Ile Gly Asn
 275 280 285

Phe Leu Glu Leu Phe Gly Pro Asp Gly Ala Trp Lys Gln Met Phe Gln
 290 295 300

Glu Arg Ser Ser Arg Met Leu Gln Ala Leu Ser Pro Lys Gln Ser Pro
 305 310 315 320

Val Ser Ser Pro Thr Arg Ser Arg Ser Pro Ser Arg Ser Pro Ser Pro
 325 330 335

Thr Phe Ser Trp Leu Pro Leu Lys Thr Ser Pro Pro Ser Ser Pro Lys
 340 345 350

Ala Ala Ser Ala Ser Ile Ser Ser Met Ser Glu Gly Asp Glu Asp Glu
 355 360 365

Lys

<210> SEQ ID NO 41
 <211> LENGTH: 100
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 41

Met Pro Lys Arg Lys Val Ser Ser Ala Glu Gly Ala Ala Lys Glu Glu
 1 5 10 15

Pro Lys Arg Arg Ser Ala Arg Leu Ser Ala Lys Pro Pro Ala Lys Val
 20 25 30

Glu Ala Lys Pro Lys Lys Ala Ala Ala Lys Asp Lys Ser Ser Asp Lys
 35 40 45

Lys Val Gln Thr Lys Gly Lys Arg Gly Ala Lys Gly Lys Gln Ala Glu
 50 55 60

Val Ala Asn Gln Glu Thr Lys Glu Asp Leu Pro Ala Glu Asn Gly Glu
 65 70 75 80

Thr Lys Thr Glu Glu Ser Pro Ala Ser Asp Glu Ala Gly Glu Lys Glu
 85 90 95

Ala Lys Ser Asp
 100

<210> SEQ ID NO 42
 <211> LENGTH: 603
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 42

Met Ser Ala Ala Val Thr Ala Gly Lys Leu Ala Arg Ala Pro Ala Asp

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1	5	10	15
Pro Gly Lys	Ala Gly Val	Pro Gly Val Ala Ala	Pro Gly Ala Pro Ala
	20	25	30
Ala Ala Pro	Pro Ala Lys Glu Ile	Pro Glu Val Leu Val Asp	Pro Arg
	35	40	45
Ser Arg Arg	Arg Tyr Val Arg Gly Arg Phe Leu Gly Lys Gly Gly Phe		
	50	55	60
Ala Lys Cys Phe Glu Ile Ser Asp Ala Asp Thr Lys Glu Val Phe Ala			
	65	70	75
Gly Lys Ile Val Pro Lys Ser Leu Leu Leu Lys Pro His Gln Arg Glu			
	85	90	95
Lys Met Ser Met Glu Ile Ser Ile His Arg Ser Leu Ala His Gln His			
	100	105	110
Val Val Gly Phe His Gly Phe Phe Glu Asp Asn Asp Phe Val Phe Val			
	115	120	125
Val Leu Glu Leu Cys Arg Arg Arg Ser Leu Leu Glu Leu His Lys Arg			
	130	135	140
Arg Lys Ala Leu Thr Glu Pro Glu Ala Arg Tyr Tyr Leu Arg Gln Ile			
	145	150	155
Val Leu Gly Cys Gln Tyr Leu His Arg Asn Arg Val Ile His Arg Asp			
	165	170	175
Leu Lys Leu Gly Asn Leu Phe Leu Asn Glu Asp Leu Glu Val Lys Ile			
	180	185	190
Gly Asp Phe Gly Leu Ala Thr Lys Val Glu Tyr Asp Gly Glu Arg Lys			
	195	200	205
Lys Thr Leu Cys Gly Thr Pro Asn Tyr Ile Ala Pro Glu Val Leu Ser			
	210	215	220
Lys Lys Gly His Ser Phe Glu Val Asp Val Trp Ser Ile Gly Cys Ile			
	225	230	235
Met Tyr Thr Leu Leu Val Gly Lys Pro Pro Phe Glu Thr Ser Cys Leu			
	245	250	255
Lys Glu Thr Tyr Leu Arg Ile Lys Lys Asn Glu Tyr Ser Ile Pro Lys			
	260	265	270
His Ile Asn Pro Val Ala Ala Ser Leu Ile Gln Lys Met Leu Gln Thr			
	275	280	285
Asp Pro Thr Ala Arg Pro Thr Ile Asn Glu Leu Leu Asn Asp Glu Phe			
	290	295	300
Phe Thr Ser Gly Tyr Ile Pro Ala Arg Leu Pro Ile Thr Cys Leu Thr			
	305	310	315
Ile Pro Pro Arg Phe Ser Ile Ala Pro Ser Ser Leu Asp Pro Ser Asn			
	325	330	335
Arg Lys Pro Leu Thr Val Leu Asn Lys Gly Leu Glu Asn Pro Leu Pro			
	340	345	350
Glu Arg Pro Arg Glu Lys Glu Glu Pro Val Val Arg Glu Thr Gly Glu			
	355	360	365
Val Val Asp Cys His Leu Ser Asp Met Leu Gln Gln Leu His Ser Val			
	370	375	380
Asn Ala Ser Lys Pro Ser Glu Arg Gly Leu Val Arg Gln Glu Glu Ala			
	385	390	395
Glu Asp Pro Ala Cys Ile Pro Ile Phe Trp Val Ser Lys Trp Val Asp			
	405	410	415
Tyr Ser Asp Lys Tyr Gly Leu Gly Tyr Gln Leu Cys Asp Asn Ser Val			
	420	425	430

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Gly Val Leu Phe Asn Asp Ser Thr Arg Leu Ile Leu Tyr Asn Asp Gly
 435 440 445
 Asp Ser Leu Gln Tyr Ile Glu Arg Asp Gly Thr Glu Ser Tyr Leu Thr
 450 455 460
 Val Ser Ser His Pro Asn Ser Leu Met Lys Lys Ile Thr Leu Leu Lys
 465 470 475 480
 Tyr Phe Arg Asn Tyr Met Ser Glu His Leu Leu Lys Ala Gly Ala Asn
 485 490 495
 Ile Thr Pro Arg Glu Gly Asp Glu Leu Ala Arg Leu Pro Tyr Leu Arg
 500 505 510
 Thr Trp Phe Arg Thr Arg Ser Ala Ile Ile Leu His Leu Ser Asn Gly
 515 520 525
 Ser Val Gln Ile Asn Phe Phe Gln Asp His Thr Lys Leu Ile Leu Cys
 530 535 540
 Pro Leu Met Ala Ala Val Thr Tyr Ile Asp Glu Lys Arg Asp Phe Arg
 545 550 555 560
 Thr Tyr Arg Leu Ser Leu Leu Glu Glu Tyr Gly Cys Cys Lys Glu Leu
 565 570 575
 Ala Ser Arg Leu Arg Tyr Ala Arg Thr Met Val Asp Lys Leu Leu Ser
 580 585 590
 Ser Arg Ser Ala Ser Asn Arg Leu Lys Ala Ser
 595 600

<210> SEQ ID NO 43
 <211> LENGTH: 822
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 43

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

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195					200					205					
Asp	Ser	Leu	Gln	Lys	Met	Gln	Glu	Glu	Met	Ile	Lys	Ala	Leu	Lys	Gly
210						215					220				
Ile	Phe	Asp	Glu	Tyr	Ser	Gln	Ile	Thr	Ser	Leu	Val	Thr	Glu	Glu	Ile
225					230					235					240
Val	Asn	Val	His	Lys	Glu	Ile	Gln	Met	Ser	Val	Glu	Gln	Ile	Asp	Pro
				245					250					255	
Ser	Thr	Glu	Tyr	Asn	Asn	Phe	Ile	Asp	Val	His	Arg	Thr	Thr	Ala	Ala
			260					265						270	
Lys	Glu	Gln	Glu	Ile	Glu	Phe	Asp	Thr	Ser	Leu	Leu	Glu	Glu	Asn	Glu
		275					280						285		
Asn	Leu	Gln	Ala	Asn	Glu	Ile	Met	Trp	Asn	Asn	Leu	Thr	Ala	Glu	Ser
290						295					300				
Leu	Gln	Val	Met	Leu	Lys	Thr	Leu	Ala	Glu	Glu	Leu	Met	Gln	Thr	Gln
305					310						315				320
Gln	Met	Leu	Leu	Asn	Lys	Glu	Glu	Ala	Val	Leu	Glu	Leu	Glu	Lys	Arg
				325					330					335	
Ile	Glu	Glu	Ser	Ser	Glu	Thr	Cys	Glu	Lys	Lys	Ser	Asp	Ile	Val	Leu
			340					345					350		
Leu	Leu	Ser	Gln	Lys	Gln	Ala	Leu	Glu	Glu	Leu	Lys	Gln	Ser	Val	Gln
		355					360					365			
Gln	Leu	Arg	Cys	Thr	Glu	Ala	Lys	Phe	Ser	Ala	Gln	Lys	Glu	Leu	Leu
370						375					380				
Glu	Gln	Lys	Val	Gln	Glu	Asn	Asp	Gly	Lys	Glu	Pro	Pro	Pro	Val	Val
385						390				395					400
Asn	Tyr	Glu	Glu	Asp	Ala	Arg	Ser	Val	Thr	Ser	Met	Glu	Arg	Lys	Glu
				405					410					415	
Arg	Leu	Ser	Lys	Phe	Glu	Ser	Ile	Arg	His	Ser	Ile	Ala	Gly	Ile	Ile
			420					425					430		
Arg	Ser	Pro	Lys	Ser	Ala	Val	Gly	Ser	Ser	Ala	Leu	Ser	Asp	Met	Ile
		435					440					445			
Ser	Ile	Ser	Glu	Lys	Pro	Leu	Ala	Glu	Gln	Asp	Trp	Tyr	His	Gly	Ala
450						455					460				
Ile	Pro	Arg	Ile	Glu	Ala	Gln	Glu	Leu	Leu	Lys	Lys	Gln	Gly	Asp	Phe
465					470						475				480
Leu	Val	Arg	Glu	Ser	His	Gly	Lys	Pro	Gly	Glu	Tyr	Val	Leu	Ser	Val
					485				490					495	
Tyr	Ser	Asp	Gly	Gln	Arg	Arg	His	Phe	Ile	Ile	Gln	Tyr	Val	Asp	Asn
			500					505					510		
Met	Tyr	Arg	Phe	Glu	Gly	Thr	Gly	Phe	Ser	Asn	Ile	Pro	Gln	Leu	Ile
		515					520					525			
Asp	His	His	Tyr	Thr	Thr	Lys	Gln	Val	Ile	Thr	Lys	Lys	Ser	Gly	Val
530						535					540				
Val	Leu	Leu	Asn	Pro	Ile	Pro	Lys	Asp	Lys	Lys	Trp	Ile	Leu	Ser	His
545					550						555				560
Glu	Asp	Val	Ile	Leu	Gly	Glu	Leu	Leu	Gly	Lys	Gly	Asn	Phe	Gly	Glu
				565					570					575	
Val	Tyr	Lys	Gly	Thr	Leu	Lys	Asp	Lys	Thr	Ser	Val	Ala	Val	Lys	Thr
			580					585						590	
Cys	Lys	Glu	Asp	Leu	Pro	Gln	Glu	Leu	Lys	Ile	Lys	Phe	Leu	Gln	Glu
		595					600					605			
Ala	Lys	Ile	Leu	Lys	Gln	Tyr	Asp	His	Pro	Asn	Ile	Val	Lys	Leu	Ile
610						615					620				

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Gly Val Cys Thr Gln Arg Gln Pro Val Tyr Ile Ile Met Glu Leu Val
 625 630 635 640
 Ser Gly Gly Asp Phe Leu Thr Phe Leu Arg Arg Lys Lys Asp Glu Leu
 645 650 655
 Lys Leu Lys Gln Leu Val Lys Phe Ser Leu Asp Ala Ala Ala Gly Met
 660 665 670
 Leu Tyr Leu Glu Ser Lys Asn Cys Ile His Arg Asp Leu Ala Ala Arg
 675 680 685
 Asn Cys Leu Val Gly Glu Asn Asn Val Leu Lys Ile Ser Asp Phe Gly
 690 695 700
 Met Ser Arg Gln Glu Asp Gly Gly Val Tyr Ser Ser Ser Gly Leu Lys
 705 710 715 720
 Gln Ile Pro Ile Lys Trp Thr Ala Pro Glu Ala Leu Asn Tyr Gly Arg
 725 730 735
 Tyr Ser Ser Glu Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Trp Glu
 740 745 750
 Thr Phe Ser Leu Gly Val Cys Pro Tyr Pro Gly Met Thr Asn Gln Gln
 755 760 765
 Ala Arg Glu Gln Val Glu Arg Gly Tyr Arg Met Ser Ala Pro Gln His
 770 775 780
 Cys Pro Glu Asp Ile Ser Lys Ile Met Met Lys Cys Trp Asp Tyr Lys
 785 790 795 800
 Pro Glu Asn Arg Pro Lys Phe Ser Glu Leu Gln Lys Glu Leu Thr Ile
 805 810 815
 Ile Lys Arg Lys Leu Thr
 820
 <210> SEQ ID NO 44
 <211> LENGTH: 213
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 44
 Met Ala Gln Glu Thr Asn Gln Thr Pro Gly Pro Met Leu Cys Ser Thr
 1 5 10 15
 Gly Cys Gly Phe Tyr Gly Asn Pro Arg Thr Asn Gly Met Cys Ser Val
 20 25 30
 Cys Tyr Lys Glu His Leu Gln Arg Gln Gln Asn Ser Gly Arg Met Ser
 35 40 45
 Pro Met Gly Thr Ala Ser Gly Ser Asn Ser Pro Thr Ser Asp Ser Ala
 50 55 60
 Ser Val Gln Arg Ala Asp Thr Ser Leu Asn Asn Cys Glu Gly Ala Ala
 65 70 75 80
 Gly Ser Thr Ser Glu Lys Ser Arg Asn Val Pro Val Ala Ala Leu Pro
 85 90 95
 Val Thr Gln Gln Met Thr Glu Met Ser Ile Ser Arg Glu Asp Lys Ile
 100 105 110
 Thr Thr Pro Lys Thr Glu Val Ser Glu Pro Val Val Thr Gln Pro Ser
 115 120 125
 Pro Ser Val Ser Gln Pro Ser Thr Ser Gln Ser Glu Glu Lys Ala Pro
 130 135 140
 Glu Leu Pro Lys Pro Lys Lys Asn Arg Cys Phe Met Cys Arg Lys Lys
 145 150 155 160
 Val Gly Leu Thr Gly Phe Asp Cys Arg Cys Gly Asn Leu Phe Cys Gly

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740				745				750							
Ser	Pro	Leu	Asn	Pro	Ala	His	Gln	Leu	Gly	Asn	Leu	Arg	Leu	Glu	Glu
		755					760					765			
Cys	Arg	Ile	Met	Ser	Ser	Ala	Lys	Arg	Pro	Leu	Trp	Leu	Asn	Trp	Glu
	770				775						780				
Asn	Pro	Asp	Ile	Met	Ser	Glu	Leu	Leu	Phe	Gln	Asn	Asn	Glu	Ile	Ile
785					790					795				800	
Phe	Lys	Asn	Gly	Asp	Asp	Leu	Arg	Gln	Asp	Met	Leu	Thr	Leu	Gln	Ile
			805						810					815	
Ile	Arg	Ile	Met	Glu	Asn	Ile	Trp	Gln	Asn	Gln	Gly	Leu	Asp	Leu	Arg
			820						825				830		
Met	Leu	Pro	Tyr	Gly	Cys	Leu	Ser	Ile	Gly	Asp	Cys	Val	Gly	Leu	Ile
		835					840					845			
Glu	Val	Val	Arg	Asn	Ser	His	Thr	Ile	Met	Gln	Ile	Gln	Cys	Lys	Gly
	850					855					860				
Gly	Leu	Lys	Gly	Ala	Leu	Gln	Phe	Asn	Ser	His	Thr	Leu	His	Gln	Trp
865					870					875					880
Leu	Lys	Asp	Lys	Asn	Lys	Gly	Glu	Ile	Tyr	Asp	Ala	Ala	Ile	Asp	Leu
			885						890					895	
Phe	Thr	Arg	Ser	Cys	Ala	Gly	Tyr	Cys	Val	Ala	Thr	Phe	Ile	Leu	Gly
			900						905				910		
Ile	Gly	Asp	Arg	His	Asn	Ser	Asn	Ile	Met	Val	Lys	Asp	Asp	Gly	Gln
		915				920						925			
Leu	Phe	His	Ile	Asp	Phe	Gly	His	Phe	Leu	Asp	His	Lys	Lys	Lys	Lys
	930				935						940				
Phe	Gly	Tyr	Lys	Arg	Glu	Arg	Val	Pro	Phe	Val	Leu	Thr	Gln	Asp	Phe
945					950					955					960
Leu	Ile	Val	Ile	Ser	Lys	Gly	Ala	Gln	Glu	Cys	Thr	Lys	Thr	Arg	Glu
			965						970					975	
Phe	Glu	Arg	Phe	Gln	Glu	Met	Cys	Tyr	Lys	Ala	Tyr	Leu	Ala	Ile	Arg
			980						985				990		
Gln	His	Ala	Asn	Leu	Phe	Ile	Asn	Leu	Phe	Ser	Met	Met	Leu	Gly	Ser
		995					1000					1005			
Gly	Met	Pro	Glu	Leu	Gln	Ser	Phe	Asp	Asp	Ile	Ala	Tyr	Ile	Arg	
	1010					1015					1020				
Lys	Thr	Leu	Ala	Leu	Asp	Lys	Thr	Glu	Gln	Glu	Ala	Leu	Glu	Tyr	
	1025					1030					1035				
Phe	Met	Lys	Gln	Met	Asn	Asp	Ala	His	His	Gly	Gly	Trp	Thr	Thr	
	1040				1045						1050				
Lys	Met	Asp	Trp	Ile	Phe	His	Thr	Ile	Lys	Gln	His	Ala	Leu	Asn	
	1055				1060						1065				
<210> SEQ ID NO 46															
<211> LENGTH: 112															
<212> TYPE: PRT															
<213> ORGANISM: Homo sapiens															
<400> SEQUENCE: 46															
Met	Ser	Ala	Glu	Val	Pro	Glu	Ala	Ala	Ser	Ala	Glu	Glu	Gln	Lys	Glu
1			5						10					15	
Met	Glu	Asp	Lys	Val	Thr	Ser	Pro	Glu	Lys	Ala	Glu	Glu	Ala	Lys	Leu
			20						25				30		
Lys	Ala	Arg	Tyr	Pro	His	Leu	Gly	Gln	Lys	Pro	Gly	Gly	Ser	Asp	Phe
	35					40						45			

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

<210> SEQ ID NO 48

<211> LENGTH: 463

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 48

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

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

<210> SEQ ID NO 49
 <211> LENGTH: 676
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 49

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

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Leu Gln Glu Glu Thr Leu Pro Arg Gly Ser Arg Gly Pro Val Asn Gly
 65 70 75 80
 Gly Gly Arg Leu Gly Pro Gln Ala Arg Trp Glu Val Val Gly Ser Lys
 85 90 95
 Leu Thr Val Asp Gly Ala Ala Lys Pro Pro Leu Ala Ala Ser Thr Gly
 100 105 110
 Ala Pro Gly Ala Val Thr Thr Leu Ala Ala Gly Gln Pro Pro Tyr Pro
 115 120 125
 Pro Gln Glu Gln Arg Ser Arg Pro Tyr Leu His Gly Thr Arg His Gly
 130 135 140
 Ser Gln Asp Cys Gly Ser Arg Glu Ser Leu Ala Thr Ser Glu Met Ser
 145 150 155 160
 Ala Phe His Gln Pro Gly Pro Cys Glu Asp Pro Ser Cys Leu Thr His
 165 170 175
 Gly Asp Tyr Tyr Asp Asn Leu Ser Leu Ala Ser Pro Lys Trp Gly Asp
 180 185 190
 Lys Pro Gly Val Ser Pro Ser Ile Gly Leu Ser Val Gly Ser Gly Trp
 195 200 205
 Pro Ser Ser Pro Gly Ser Asp Pro Pro Leu Pro Lys Pro Cys Gly Asp
 210 215 220
 His Pro Leu Asn His Arg Gln Leu Ser Leu Ser Ser Ser Arg Ser Ser
 225 230 235 240
 Glu Gly Ser Leu Gly Gly Gln Asn Ser Gly Ile Gly Gly Arg Ser Ser
 245 250 255
 Glu Lys Pro Thr Gly Leu Trp Ser Thr Ala Ser Ser Gln Arg Val Ser
 260 265 270
 Pro Gly Leu Pro Ser Pro Asn Leu Glu Asn Gly Ala Pro Ala Val Gly
 275 280 285
 Pro Val Gln Pro Arg Thr Pro Ser Val Ser Ala Pro Leu Ala Leu Ser
 290 295 300
 Cys Pro Arg Gln Gly Gly Leu Pro Arg Ser Asn Ser Gly Leu Gly Gly
 305 310 315 320
 Glu Val Ser Gly Val Met Ser Lys Pro Asn Val Asp Pro Gln Pro Trp
 325 330 335
 Phe Gln Asp Gly Pro Lys Ser Tyr Leu Ser Ser Ser Ala Pro Ser Ser
 340 345 350
 Ser Pro Ala Gly Leu Asp Gly Ser Gln Gln Gly Ala Val Pro Gly Leu
 355 360 365
 Gly Pro Lys Pro Gly Cys Thr Asp Leu Gly Thr Gly Pro Lys Leu Ser
 370 375 380
 Pro Thr Ser Leu Val His Pro Val Met Ser Thr Leu Pro Glu Leu Ser
 385 390 395 400
 Cys Lys Glu Gly Pro Leu Gly Trp Ser Ser Asp Gly Ser Leu Gly Ser
 405 410 415
 Val Leu Leu Asp Ser Pro Ser Ser Pro Arg Val Arg Leu Pro Cys Gln
 420 425 430
 Pro Leu Val Pro Gly Pro Glu Leu Arg Pro Ser Ala Ala Glu Leu Lys
 435 440 445
 Leu Glu Ala Leu Thr Gln Arg Leu Glu Arg Glu Met Asp Ala His Pro
 450 455 460
 Lys Ala Asp Tyr Phe Gly Ala Cys Val Lys Cys Ser Lys Gly Val Phe
 465 470 475 480
 Gly Ala Gly Gln Ala Cys Gln Ala Met Gly Asn Leu Tyr His Asp Thr

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

<210> SEQ ID NO 52

<211> LENGTH: 786

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 52

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

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225	230	235	240
Ser Val Val Leu Glu Met Gly Met Pro Asn Met Lys Pro Gly His Leu	245	250	255
Met Gly Asp Pro Ser Ala Met Val Ser Phe Tyr Pro Asn Ile Pro Glu	260	265	270
Asp Gln Pro Ser Asn Thr Cys Gly Glu Phe Ile Phe Leu Met Asp Arg	275	280	285
Ser Gly Ser Met Gln Ser Pro Met Ser Ser Gln Asp Thr Ser Gln Leu	290	295	300
Arg Ile Gln Ala Ala Lys Glu Thr Leu Ile Leu Leu Leu Lys Ser Leu	305	310	315
Pro Ile Gly Cys Tyr Phe Asn Ile Tyr Gly Phe Gly Ser Ser Tyr Glu	325	330	335
Ala Cys Phe Pro Glu Ser Val Lys Tyr Thr Gln Gln Thr Met Glu Glu	340	345	350
Ala Leu Gly Arg Val Lys Leu Met Gln Ala Asp Leu Gly Gly Thr Glu	355	360	365
Ile Leu Ala Pro Leu Gln Asn Ile Tyr Arg Gly Pro Ser Ile Pro Gly	370	375	380
His Pro Leu Gln Leu Phe Val Phe Thr Asp Gly Glu Val Thr Asp Thr	385	390	395
Phe Ser Val Ile Lys Glu Val Arg Ile Asn Arg Gln Lys His Arg Cys	405	410	415
Phe Ser Phe Gly Ile Gly Glu Gly Thr Ser Thr Ser Leu Ile Lys Gly	420	425	430
Ile Ala Arg Ala Ser Gly Gly Thr Ser Glu Phe Ile Thr Gly Lys Asp	435	440	445
Arg Met Gln Ser Lys Ala Leu Arg Thr Leu Lys Arg Ser Leu Gln Pro	450	455	460
Val Val Glu Asp Val Ser Leu Ser Trp His Leu Pro Pro Gly Leu Ser	465	470	475
Ala Lys Met Leu Ser Pro Glu Gln Thr Val Ile Phe Arg Gly Gln Arg	485	490	495
Leu Ile Ser Tyr Ala Gln Leu Thr Gly Arg Met Pro Ala Ala Glu Thr	500	505	510
Thr Gly Glu Val Cys Leu Lys Tyr Thr Leu Gln Gly Lys Thr Phe Glu	515	520	525
Asp Lys Val Thr Phe Pro Leu Gln Pro Lys Pro Asp Val Asn Leu Thr	530	535	540
Ile His Arg Leu Ala Ala Lys Ser Leu Leu Gln Thr Lys Asp Met Gly	545	550	555
Leu Arg Glu Thr Pro Ala Ser Asp Lys Lys Asp Ala Leu Asn Leu Ser	565	570	575
Leu Glu Ser Gly Val Ile Ser Ser Phe Thr Ala Phe Ile Ala Ile Asn	580	585	590
Lys Glu Leu Asn Lys Pro Val Gln Gly Pro Leu Ala His Arg Asp Val	595	600	605
Pro Arg Pro Ile Leu Leu Gly Ala Ser Ala Pro Leu Lys Ile Lys Cys	610	615	620
Gln Ser Gly Phe Arg Lys Ala Leu His Ser Asp Arg Pro Pro Ser Ala	625	630	635
Ser Gln Pro Arg Gly Glu Leu Met Cys Tyr Lys Ala Lys Thr Phe Gln	645	650	655

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Met Asp Asp Tyr Ser Leu Cys Gly Leu Ile Ser His Lys Asp Gln His
660 665 670

Ser Pro Gly Phe Gly Glu Asn His Leu Val Gln Leu Ile Tyr His Gln
675 680 685

Asn Ala Asn Gly Ser Trp Asp Leu Asn Glu Asp Leu Ala Lys Ile Leu
690 695 700

Gly Met Ser Leu Glu Glu Ile Met Ala Ala Gln Pro Ala Glu Leu Val
705 710 715 720

Asp Ser Ser Gly Trp Ala Thr Ile Leu Ala Val Ile Trp Leu His Ser
725 730 735

Asn Gly Lys Asp Leu Lys Cys Glu Trp Glu Leu Leu Glu Arg Lys Ala
740 745 750

Val Ala Trp Met Arg Ala His Ala Gly Ser Thr Met Pro Ser Val Val
755 760 765

Lys Ala Ala Ile Thr Phe Leu Lys Ser Ser Val Asp Pro Ala Ile Phe
770 775 780

Ala Phe
785

<210> SEQ ID NO 53
<211> LENGTH: 181
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 53

Met Pro Lys Gly Gly Arg Lys Gly Gly His Lys Gly Arg Ala Arg Gln
1 5 10 15

Tyr Thr Ser Pro Glu Glu Ile Asp Ala Gln Leu Gln Ala Glu Lys Gln
20 25 30

Lys Ala Arg Glu Glu Glu Glu Gln Lys Glu Gly Gly Asp Gly Ala Ala
35 40 45

Gly Asp Pro Lys Lys Glu Lys Lys Ser Leu Asp Ser Asp Glu Ser Glu
50 55 60

Asp Glu Glu Asp Asp Tyr Gln Gln Lys Arg Lys Gly Val Glu Gly Leu
65 70 75 80

Ile Asp Ile Glu Asn Pro Asn Arg Val Ala Gln Thr Thr Lys Lys Val
85 90 95

Thr Gln Leu Asp Leu Asp Gly Pro Lys Glu Leu Ser Arg Arg Glu Arg
100 105 110

Glu Glu Ile Glu Lys Gln Lys Ala Lys Glu Arg Tyr Met Lys Met His
115 120 125

Leu Ala Gly Lys Thr Glu Gln Ala Lys Ala Asp Leu Ala Arg Leu Ala
130 135 140

Ile Ile Arg Lys Gln Arg Glu Glu Ala Ala Arg Lys Lys Glu Glu Glu
145 150 155 160

Arg Lys Ala Lys Asp Asp Ala Thr Leu Ser Gly Lys Arg Met Gln Ser
165 170 175

Leu Ser Leu Asn Lys
180

<210> SEQ ID NO 54
<211> LENGTH: 837
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 54

-continued

Met Ala Ser Lys Arg Lys Ser Thr Thr Pro Cys Met Val Arg Thr Ser
 1 5 10 15
 Gln Val Val Glu Gln Asp Val Pro Glu Glu Val Asp Arg Ala Lys Glu
 20 25 30
 Lys Gly Ile Gly Thr Pro Gln Pro Asp Val Ala Lys Asp Ser Trp Ala
 35 40 45
 Ala Glu Leu Glu Asn Ser Ser Lys Glu Asn Glu Val Ile Glu Val Lys
 50 55 60
 Ser Met Gly Glu Ser Gln Ser Lys Lys Leu Gln Gly Gly Tyr Glu Cys
 65 70 75 80
 Lys Tyr Cys Pro Tyr Ser Thr Gln Asn Leu Asn Glu Phe Thr Glu His
 85 90 95
 Val Asp Met Gln His Pro Asn Val Ile Leu Asn Pro Leu Tyr Val Cys
 100 105 110
 Ala Glu Cys Asn Phe Thr Thr Lys Lys Tyr Asp Ser Leu Ser Asp His
 115 120 125
 Asn Ser Lys Phe His Pro Gly Glu Ala Asn Phe Lys Leu Lys Leu Ile
 130 135 140
 Lys Arg Asn Asn Gln Thr Val Leu Glu Gln Ser Ile Glu Thr Thr Asn
 145 150 155 160
 His Val Val Ser Ile Thr Thr Ser Gly Pro Gly Thr Gly Asp Ser Asp
 165 170 175
 Ser Gly Ile Ser Val Ser Lys Thr Pro Ile Met Lys Pro Gly Lys Pro
 180 185 190
 Lys Ala Asp Ala Lys Lys Val Pro Lys Lys Pro Glu Glu Ile Thr Pro
 195 200 205
 Glu Asn His Val Glu Gly Thr Ala Arg Leu Val Thr Asp Thr Ala Glu
 210 215 220
 Ile Leu Ser Arg Leu Gly Gly Val Glu Leu Leu Gln Asp Thr Leu Gly
 225 230 235 240
 His Val Met Pro Ser Val Gln Leu Pro Pro Asn Ile Asn Leu Val Pro
 245 250 255
 Lys Val Pro Val Pro Leu Asn Thr Thr Lys Tyr Asn Ser Ala Leu Asp
 260 265 270
 Thr Asn Ala Thr Met Ile Asn Ser Phe Asn Lys Phe Pro Tyr Pro Thr
 275 280 285
 Gln Ala Glu Leu Ser Trp Leu Thr Ala Ala Ser Lys His Pro Glu Glu
 290 295 300
 His Ile Arg Ile Trp Phe Ala Thr Gln Arg Leu Lys His Gly Ile Ser
 305 310 315 320
 Trp Ser Pro Glu Glu Val Glu Glu Ala Arg Lys Lys Met Phe Asn Gly
 325 330 335
 Thr Ile Gln Ser Val Pro Pro Thr Ile Thr Val Leu Pro Ala Gln Leu
 340 345 350
 Ala Pro Thr Lys Val Thr Gln Pro Ile Leu Gln Thr Ala Leu Pro Cys
 355 360 365
 Gln Ile Leu Gly Gln Thr Ser Leu Val Leu Thr Gln Val Thr Ser Gly
 370 375 380
 Ser Thr Thr Val Ser Cys Ser Pro Ile Thr Leu Ala Val Ala Gly Val
 385 390 395 400
 Thr Asn His Gly Gln Lys Arg Pro Leu Val Thr Pro Gln Ala Ala Pro
 405 410 415

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Glu Pro Lys Arg Pro His Ile Ala Gln Val Pro Glu Pro Pro Pro Lys
 420 425 430

Val Ala Asn Pro Pro Leu Thr Pro Ala Ser Asp Arg Lys Lys Thr Lys
 435 440 445

Glu Gln Ile Ala His Leu Lys Ala Ser Phe Leu Gln Ser Gln Phe Pro
 450 455 460

Asp Asp Ala Glu Val Tyr Arg Leu Ile Glu Val Thr Gly Leu Ala Arg
 465 470 475 480

Ser Glu Ile Lys Lys Trp Phe Ser Asp His Arg Tyr Arg Cys Gln Arg
 485 490 495

Gly Ile Val His Ile Thr Ser Glu Ser Leu Ala Lys Asp Gln Leu Ala
 500 505 510

Ile Ala Ala Ser Arg His Gly Arg Thr Tyr His Ala Tyr Pro Asp Phe
 515 520 525

Ala Pro Gln Lys Phe Lys Glu Lys Thr Gln Gly Gln Val Lys Ile Leu
 530 535 540

Glu Asp Ser Phe Leu Lys Ser Ser Phe Pro Thr Gln Ala Glu Leu Asp
 545 550 555 560

Arg Leu Arg Val Glu Thr Lys Leu Ser Arg Arg Glu Ile Asp Ser Trp
 565 570 575

Phe Ser Glu Arg Arg Lys Leu Arg Asp Ser Met Glu Gln Ala Val Leu
 580 585 590

Asp Ser Met Gly Ser Gly Lys Lys Gly Gln Asp Val Gly Ala Pro Asn
 595 600 605

Gly Ala Leu Ser Arg Leu Asp Gln Leu Ser Gly Ala Gln Leu Thr Ser
 610 615 620

Ser Leu Pro Ser Pro Ser Pro Ala Ile Ala Lys Ser Gln Glu Gln Val
 625 630 635 640

His Leu Leu Arg Ser Thr Phe Ala Arg Thr Gln Trp Pro Thr Pro Gln
 645 650 655

Glu Tyr Asp Gln Leu Ala Ala Lys Thr Gly Leu Val Arg Thr Glu Ile
 660 665 670

Val Arg Trp Phe Lys Glu Asn Arg Cys Leu Leu Lys Thr Gly Thr Val
 675 680 685

Lys Trp Met Glu Gln Tyr Gln His Gln Pro Met Ala Asp Asp His Gly
 690 695 700

Tyr Asp Ala Val Ala Arg Lys Ala Thr Lys Pro Met Ala Glu Ser Pro
 705 710 715 720

Lys Asn Gly Gly Asp Val Val Pro Gln Tyr Tyr Lys Asp Pro Lys Lys
 725 730 735

Leu Cys Glu Glu Asp Leu Glu Lys Leu Val Thr Arg Val Lys Val Gly
 740 745 750

Ser Glu Pro Ala Lys Asp Cys Leu Pro Ala Lys Pro Ser Glu Ala Thr
 755 760 765

Ser Asp Arg Ser Glu Gly Ser Ser Arg Asp Gly Gln Gly Ser Asp Glu
 770 775 780

Asn Glu Glu Ser Ser Val Val Asp Tyr Val Glu Val Thr Val Gly Glu
 785 790 795 800

Glu Asp Ala Ile Ser Asp Arg Ser Asp Ser Trp Ser Gln Ala Ala Ala
 805 810 815

Glu Gly Val Ser Glu Leu Ala Glu Ser Asp Ser Asp Cys Val Pro Ala
 820 825 830

Glu Ala Gly Gln Ala

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835

<210> SEQ ID NO 55
 <211> LENGTH: 803
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 55

Met Glu Val Lys Pro Val Gly Glu Pro Thr Gln Glu Val Ser Lys Phe
 1 5 10 15
 Lys Leu Ser Thr Lys Val Glu Ser Thr Gly His Trp Leu Val Glu Asp
 20 25 30
 His Val Arg Ile Trp Glu Val Leu Lys Thr Glu Glu Ser Ser Ile Gln
 35 40 45
 Asp Trp Gly Glu Glu Val Glu Glu Gly Ala Val Tyr His Val Thr Leu
 50 55 60
 Lys Arg Val Gln Ile Gln Gln Ala Ala Asn Lys Gly Ala Arg Trp Leu
 65 70 75 80
 Gly Val Glu Gly Asp Gln Leu Pro Pro Gly His Thr Val Ser Gln Tyr
 85 90 95
 Glu Thr Cys Lys Ile Arg Thr Ile Lys Ala Gly Thr Leu Glu Lys Leu
 100 105 110
 Val Glu Asn Leu Leu Thr Ala Phe Gly Asp Asn Asp Phe Thr Tyr Ile
 115 120 125
 Ser Ile Phe Leu Ser Thr Tyr Arg Gly Phe Ala Ser Thr Lys Glu Val
 130 135 140
 Leu Glu Leu Leu Leu Asp Arg Tyr Gly Asn Leu Thr Ser Pro Asn Cys
 145 150 155 160
 Glu Glu Asp Gly Ser Gln Ser Ser Ser Glu Ser Lys Met Val Ile Arg
 165 170 175
 Asn Ala Ile Ala Ser Ile Leu Arg Ala Trp Leu Asp Gln Cys Ala Glu
 180 185 190
 Asp Phe Arg Glu Pro Pro His Phe Pro Cys Leu Gln Lys Leu Leu Asp
 195 200 205
 Tyr Leu Thr Arg Met Met Pro Gly Ser Asp Pro Glu Arg Arg Ala Gln
 210 215 220
 Asn Leu Leu Glu Gln Phe Gln Lys Gln Glu Val Glu Thr Asp Asn Gly
 225 230 235 240
 Leu Pro Asn Thr Ile Ser Phe Ser Leu Glu Glu Glu Glu Glu Leu Glu
 245 250 255
 Gly Gly Glu Ser Ala Glu Phe Thr Cys Phe Ser Glu Asp Leu Val Ala
 260 265 270
 Glu Gln Leu Thr Tyr Met Asp Ala Gln Leu Phe Lys Lys Val Val Pro
 275 280 285
 His His Cys Leu Gly Cys Ile Trp Ser Arg Arg Asp Lys Lys Glu Asn
 290 295 300
 Lys His Leu Ala Pro Thr Ile Arg Ala Thr Ile Ser Gln Phe Asn Thr
 305 310 315 320
 Leu Thr Lys Cys Val Val Ser Thr Ile Leu Gly Gly Lys Glu Leu Lys
 325 330 335
 Thr Gln Gln Arg Ala Lys Ile Ile Glu Lys Trp Ile Asn Ile Ala His
 340 345 350
 Glu Cys Arg Leu Leu Lys Asn Phe Ser Ser Leu Arg Ala Ile Val Ser
 355 360 365

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Ala Leu Gln Ser Asn Ser Ile Tyr Arg Leu Lys Lys Thr Trp Ala Ala
370 375 380

Val Pro Arg Asp Arg Met Leu Met Phe Glu Glu Leu Ser Asp Ile Phe
385 390 395 400

Ser Asp His Asn Asn His Leu Thr Ser Arg Glu Leu Leu Met Lys Glu
405 410 415

Gly Thr Ser Lys Phe Ala Asn Leu Asp Ser Ser Val Lys Glu Asn Gln
420 425 430

Lys Arg Thr Gln Arg Arg Leu Gln Leu Gln Lys Asp Met Gly Val Met
435 440 445

Gln Gly Thr Val Pro Tyr Leu Gly Thr Phe Leu Thr Asp Leu Thr Met
450 455 460

Leu Asp Thr Ala Leu Gln Asp Tyr Ile Glu Gly Gly Leu Ile Asn Phe
465 470 475 480

Glu Lys Arg Arg Arg Glu Phe Glu Val Ile Ala Gln Ile Lys Leu Leu
485 490 495

Gln Ser Ala Cys Asn Ser Tyr Cys Met Thr Pro Asp Gln Lys Phe Ile
500 505 510

Gln Trp Phe Gln Arg Gln Gln Leu Leu Thr Glu Glu Glu Ser Tyr Ala
515 520 525

Leu Ser Cys Glu Ile Glu Ala Ala Ala Asp Ala Ser Thr Thr Ser Pro
530 535 540

Lys Pro Arg Lys Ser Met Val Lys Arg Leu Ser Leu Leu Phe Leu Gly
545 550 555 560

Ser Asp Met Ile Thr Ser Pro Thr Pro Thr Lys Glu Gln Pro Lys Ser
565 570 575

Thr Ala Ser Gly Ser Ser Gly Glu Ser Met Asp Ser Val Ser Val Ser
580 585 590

Ser Cys Glu Ser Asn His Ser Glu Ala Glu Glu Gly Ser Ile Thr Pro
595 600 605

Met Asp Thr Pro Asp Glu Pro Gln Lys Lys Leu Ser Glu Ser Ser Ser
610 615 620

Ser Cys Ser Ser Ile His Ser Met Asp Thr Asn Ser Ser Gly Met Ser
625 630 635 640

Ser Leu Ile Asn Pro Leu Ser Ser Pro Pro Ser Cys Asn Asn Asn Pro
645 650 655

Lys Ile His Lys Arg Ser Val Ser Val Thr Ser Ile Thr Ser Thr Val
660 665 670

Leu Pro Pro Val Tyr Asn Gln Gln Asn Glu Asp Thr Cys Ile Ile Arg
675 680 685

Ile Ser Val Glu Asp Asn Asn Gly Asn Met Tyr Lys Ser Ile Met Leu
690 695 700

Thr Ser Gln Asp Lys Thr Pro Ala Val Ile Gln Arg Ala Met Leu Lys
705 710 715 720

His Asn Leu Asp Ser Asp Pro Ala Glu Glu Tyr Glu Leu Val Gln Val
725 730 735

Ile Ser Glu Asp Lys Glu Leu Val Ile Pro Asp Ser Ala Asn Val Phe
740 745 750

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

Asn Ser Met Glu Glu Gln Val Lys Leu Arg Ser Arg Thr Ser Leu Thr
770 775 780

Leu Pro Arg Thr Ala Lys Arg Gly Cys Trp Ser Tyr Arg His Ser Lys

-continued

 785 790 795 800

Ile Thr Leu

<210> SEQ ID NO 56

<211> LENGTH: 162

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 56

Met Ala Ser Ser Val Asp Glu Glu Ala Leu His Gln Leu Tyr Leu Trp
 1 5 10 15

Val Asp Asn Ile Pro Leu Ser Arg Pro Lys Arg Asn Leu Ser Arg Asp
 20 25 30

Phe Ser Asp Gly Val Leu Val Ala Glu Val Ile Lys Phe Tyr Phe Pro
 35 40 45

Lys Met Val Glu Met His Asn Tyr Val Pro Ala Asn Ser Leu Gln Gln
 50 55 60

Lys Leu Ser Asn Trp Gly His Leu Asn Arg Lys Val Leu Lys Arg Leu
 65 70 75 80

Asn Phe Ser Val Pro Asp Asp Val Met Arg Lys Ile Ala Gln Cys Ala
 85 90 95

Pro Gly Val Val Glu Leu Val Leu Ile Pro Leu Arg Gln Arg Leu Glu
 100 105 110

Glu Arg Gln Arg Arg Arg Lys Gln Gly Ala Gly Ser Leu Gln Glu Leu
 115 120 125

Ala Pro Gln Asp Gly Ser Gly Tyr Met Asp Val Gly Lys Val Ala Phe
 130 135 140

Ser Ile Ser Pro Ser Arg Leu Glu Leu Ser Phe Cys Pro Ser Ser Cys
 145 150 155 160

His Leu

<210> SEQ ID NO 57

<211> LENGTH: 275

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 57

Met Ala Thr Glu Leu Glu Tyr Glu Ser Val Leu Cys Val Lys Pro Asp
 1 5 10 15

Val Ser Val Tyr Arg Ile Pro Pro Arg Ala Ser Asn Arg Gly Tyr Arg
 20 25 30

Ala Ser Asp Trp Lys Leu Asp Gln Pro Asp Trp Thr Gly Arg Leu Arg
 35 40 45

Ile Thr Ser Lys Gly Lys Thr Ala Tyr Ile Lys Leu Glu Asp Lys Val
 50 55 60

Ser Gly Glu Leu Phe Ala Gln Ala Pro Val Glu Gln Tyr Pro Gly Ile
 65 70 75 80

Ala Val Glu Thr Val Thr Asp Ser Ser Arg Tyr Phe Val Ile Arg Ile
 85 90 95

Gln Asp Gly Thr Gly Arg Ser Ala Phe Ile Gly Ile Gly Phe Thr Asp
 100 105 110

Arg Gly Asp Ala Phe Asp Phe Asn Val Ser Leu Gln Asp His Phe Lys
 115 120 125

Trp Val Lys Gln Glu Ser Glu Ile Ser Lys Glu Ser Gln Glu Met Asp
 130 135 140

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Ala Arg Pro Lys Leu Asp Leu Gly Phe Lys Glu Gly Gln Thr Ile Lys
 145 150 155 160

Leu Cys Ile Gly Asn Ile Thr Asn Lys Lys Gly Gly Ala Ser Lys Pro
 165 170 175

Arg Thr Ala Arg Gly Gly Gly Leu Ser Leu Leu Pro Pro Pro Pro Gly
 180 185 190

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

His Val Thr Pro Pro Pro Ile Pro Lys Ser Asn His Gly Gly Ser Asp
 210 215 220

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

Ala Pro Thr Pro Val Ser Val Ser Asn Asp Leu Trp Gly Asp Phe Ser
 245 250 255

Thr Ala Ser Ser Ser Val Pro Asn Gln Ala Pro Gln Pro Ser Asn Trp
 260 265 270

Val Gln Phe
 275

<210> SEQ ID NO 58
 <211> LENGTH: 76
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 58

Met Ala Arg Gly Gln Gln Lys Ile Gln Ser Gln Gln Lys Asn Ala Lys
 1 5 10 15

Lys Gln Ala Gly Gln Lys Lys Lys Gln Gly His Asp Gln Lys Ala Ala
 20 25 30

Ala Lys Ala Ala Leu Ile Tyr Thr Cys Thr Val Cys Arg Thr Gln Met
 35 40 45

Pro Asp Pro Lys Thr Phe Lys Gln His Phe Glu Ser Lys His Pro Lys
 50 55 60

Thr Pro Leu Pro Pro Glu Leu Ala Asp Val Gln Ala
 65 70 75

<210> SEQ ID NO 59
 <211> LENGTH: 289
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 59

Met Pro Val Val Arg Lys Ile Phe Arg Arg Arg Arg Gly Asp Ser Glu
 1 5 10 15

Ser Glu Glu Asp Glu Gln Asp Ser Glu Glu Val Arg Leu Lys Leu Glu
 20 25 30

Glu Thr Arg Glu Val Gln Asn Leu Arg Lys Arg Pro Asn Gly Val Ser
 35 40 45

Ala Val Ala Leu Leu Val Gly Glu Lys Val Gln Glu Glu Thr Thr Leu
 50 55 60

Val Asp Asp Pro Phe Gln Met Lys Thr Gly Gly Met Val Asp Met Lys
 65 70 75 80

Lys Leu Lys Glu Arg Gly Lys Asp Lys Ile Ser Glu Glu Glu Asp Leu
 85 90 95

His Leu Gly Thr Ser Phe Ser Ala Glu Thr Asn Arg Arg Asp Glu Asp
 100 105 110

-continued

Ala Asp Met Met Lys Tyr Ile Glu Thr Glu Leu Lys Lys Arg Lys Gly
 115 120 125

Ile Val Glu His Glu Glu Gln Lys Val Lys Pro Lys Asn Ala Glu Asp
 130 135 140

Cys Leu Tyr Glu Leu Pro Glu Asn Ile Arg Val Ser Ser Ala Lys Lys
 145 150 155 160

Thr Glu Glu Met Leu Ser Asn Gln Met Leu Ser Gly Ile Pro Glu Val
 165 170 175

Asp Leu Gly Ile Asp Ala Lys Ile Lys Asn Ile Ile Ser Thr Glu Asp
 180 185 190

Ala Lys Ala Arg Leu Leu Ala Glu Gln Gln Asn Lys Lys Lys Asp Ser
 195 200 205

Glu Thr Ser Phe Val Pro Thr Asn Met Ala Val Asn Tyr Val Gln His
 210 215 220

Asn Arg Phe Tyr His Glu Glu Leu Asn Ala Pro Ile Arg Arg Asn Lys
 225 230 235 240

Glu Glu Pro Lys Ala Arg Pro Leu Arg Val Gly Asp Thr Glu Lys Pro
 245 250 255

Glu Pro Glu Arg Ser Pro Pro Asn Arg Lys Arg Pro Ala Asn Glu Lys
 260 265 270

Ala Thr Asp Asp Tyr His Tyr Glu Lys Phe Lys Lys Met Asn Arg Arg
 275 280 285

Tyr

<210> SEQ ID NO 60
 <211> LENGTH: 153
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 60

Met Pro Tyr Val Phe Ser Phe Lys Met Pro Gln Glu Gln Gly Gln Met
 1 5 10 15

Phe Gln Tyr Tyr Pro Val Tyr Met Val Leu Pro Trp Glu Gln Pro Gln
 20 25 30

Gln Thr Val Pro Arg Ser Pro Gln Gln Thr Arg Gln Gln Gln Tyr Glu
 35 40 45

Glu Gln Ile Pro Phe Tyr Ala Gln Phe Gly Tyr Ile Pro Gln Leu Ala
 50 55 60

Glu Pro Ala Ile Ser Gly Gly Gln Gln Gln Leu Ala Phe Asp Pro Gln
 65 70 75 80

Leu Gly Thr Ala Pro Glu Ile Ala Val Met Ser Thr Gly Glu Glu Ile
 85 90 95

Pro Tyr Leu Gln Lys Glu Ala Ile Asn Phe Arg His Asp Ser Ala Gly
 100 105 110

Val Phe Met Pro Ser Thr Ser Pro Lys Pro Ser Thr Thr Asn Val Phe
 115 120 125

Thr Ser Ala Val Asp Gln Thr Ile Thr Pro Glu Leu Pro Glu Glu Lys
 130 135 140

Asp Lys Thr Asp Ser Leu Arg Glu Pro
 145 150

<210> SEQ ID NO 61
 <211> LENGTH: 386
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 61

Met Thr Ser Leu Phe Arg Arg Ser Ser Ser Gly Ser Gly Gly Gly Gly
 1 5 10 15
 Thr Ala Gly Ala Arg Gly Gly Gly Gly Gly Thr Ala Ala Pro Gln Glu
 20 25 30
 Leu Asn Asn Ser Arg Pro Ala Arg Gln Val Arg Arg Leu Glu Phe Asn
 35 40 45
 Gln Ala Met Asp Asp Phe Lys Thr Met Phe Pro Asn Met Asp Tyr Asp
 50 55 60
 Ile Ile Glu Cys Val Leu Arg Ala Asn Ser Gly Ala Val Asp Ala Thr
 65 70 75 80
 Ile Asp Gln Leu Leu Gln Met Asn Leu Glu Gly Gly Gly Ser Ser Gly
 85 90 95
 Gly Val Tyr Glu Asp Ser Ser Asp Ser Glu Asp Ser Ile Pro Pro Glu
 100 105 110
 Ile Leu Glu Arg Thr Leu Glu Pro Asp Ser Ser Asp Glu Glu Pro Pro
 115 120 125
 Pro Val Tyr Ser Pro Pro Ala Tyr His Met His Val Phe Asp Arg Pro
 130 135 140
 Tyr Pro Leu Ala Pro Pro Thr Pro Pro Pro Arg Ile Asp Ala Leu Gly
 145 150 155 160
 Ser Gly Ala Pro Thr Ser Gln Arg Arg Tyr Arg Asn Trp Asn Pro Pro
 165 170 175
 Leu Leu Gly Asn Leu Pro Asp Asp Phe Leu Arg Ile Leu Pro Gln Gln
 180 185 190
 Leu Asp Ser Ile Gln Gly Asn Ala Gly Gly Pro Lys Pro Gly Ser Gly
 195 200 205
 Glu Gly Cys Pro Pro Ala Met Ala Gly Pro Gly Pro Gly Asp Gln Glu
 210 215 220
 Ser Arg Trp Lys Gln Tyr Leu Glu Asp Glu Arg Ile Ala Leu Phe Leu
 225 230 235 240
 Gln Asn Glu Glu Phe Met Lys Glu Leu Gln Arg Asn Arg Asp Phe Leu
 245 250 255
 Leu Ala Leu Glu Arg Asp Arg Leu Lys Tyr Glu Ser Gln Lys Ser Lys
 260 265 270
 Ser Ser Ser Val Ala Val Gly Asn Asp Phe Gly Phe Ser Ser Pro Val
 275 280 285
 Pro Gly Thr Gly Asp Ala Asn Pro Ala Val Ser Glu Asp Ala Leu Phe
 290 295 300
 Arg Asp Lys Leu Lys His Met Gly Lys Ser Thr Arg Arg Lys Leu Phe
 305 310 315 320
 Glu Leu Ala Arg Ala Phe Ser Glu Lys Thr Lys Met Arg Lys Ser Lys
 325 330 335
 Arg Lys His Leu Leu Lys His Gln Ser Leu Gly Ala Ala Ala Ser Thr
 340 345 350
 Ala Asn Leu Leu Asp Asp Val Glu Gly His Ala Cys Asp Glu Asp Phe
 355 360 365
 Arg Gly Arg Arg Gln Glu Ala Pro Lys Val Glu Glu Gly Leu Arg Glu
 370 375 380

Gly Gln
385

<210> SEQ ID NO 62

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<211> LENGTH: 329
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 62

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

Ile Leu Leu Arg Leu Phe Ala Glu Asp
325

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<210> SEQ ID NO 63
<211> LENGTH: 78
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 63

Met Ser Glu Val Leu Pro Tyr Gly Asp Glu Lys Leu Ser Pro Tyr Gly
1          5          10          15

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Asp Gly Gly Asp Val Gly Gln Ile Phe Ser Cys Arg Leu Gln Asp Thr
 20 25 30
 Asn Asn Phe Phe Gly Ala Gly Gln Asn Lys Arg Pro Pro Lys Leu Gly
 35 40 45
 Gln Ile Gly Arg Ser Lys Arg Val Val Ile Glu Asp Asp Arg Ile Asp
 50 55 60
 Asp Val Leu Lys Asn Met Thr Asp Lys Ala Pro Pro Gly Val
 65 70 75

<210> SEQ ID NO 64
 <211> LENGTH: 686
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 64

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

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305				310				315				320			
Thr	Ser	Pro	Ala	Thr	Glu	Ala	Ala	Pro	Pro	Pro	Pro	Glu	Pro	Val	Pro
				325				330						335	
Ala	Ala	Glu	Gly	Pro	Ala	Thr	Val	Gln	Ser	Val	Glu	Asp	Phe	Val	Pro
			340					345					350		
Asp	Asp	Arg	Leu	Asp	Arg	Ser	Phe	Leu	Glu	Asp	Thr	Thr	Pro	Ala	Arg
		355					360					365			
Asp	Glu	Lys	Lys	Val	Gly	Ala	Lys	Ala	Ala	Gln	Gln	Asp	Ser	Asp	Ser
	370					375					380				
Asp	Gly	Glu	Ala	Leu	Gly	Gly	Asn	Pro	Met	Val	Ala	Gly	Phe	Gln	Asp
	385				390					395					400
Asp	Val	Asp	Leu	Glu	Asp	Gln	Pro	Arg	Gly	Ser	Pro	Pro	Leu	Pro	Ala
			405						410				415		
Gly	Pro	Val	Pro	Ser	Gln	Asp	Ile	Thr	Leu	Ser	Ser	Glu	Glu	Glu	Ala
			420						425				430		
Glu	Val	Ala	Ala	Pro	Thr	Lys	Gly	Pro	Ala	Pro	Ala	Pro	Gln	Gln	Cys
		435					440					445			
Ser	Glu	Pro	Glu	Thr	Lys	Trp	Ser	Ser	Ile	Pro	Ala	Ser	Lys	Pro	Arg
	450					455					460				
Arg	Gly	Thr	Ala	Pro	Thr	Arg	Thr	Ala	Ala	Pro	Pro	Trp	Pro	Gly	Gly
	465				470					475					480
Val	Ser	Val	Arg	Thr	Gly	Pro	Glu	Lys	Arg	Ser	Ser	Thr	Arg	Pro	Pro
			485						490					495	
Ala	Glu	Met	Glu	Pro	Gly	Lys	Gly	Glu	Gln	Ala	Ser	Ser	Ser	Glu	Ser
		500						505					510		
Asp	Pro	Glu	Gly	Pro	Ile	Ala	Ala	Gln	Met	Leu	Ser	Phe	Val	Met	Asp
		515					520					525			
Asp	Pro	Asp	Phe	Glu	Ser	Glu	Gly	Ser	Asp	Thr	Gln	Arg	Arg	Ala	Asp
		530				535					540				
Asp	Phe	Pro	Val	Arg	Asp	Asp	Pro	Ser	Asp	Val	Thr	Asp	Glu	Asp	Glu
		545			550					555					560
Gly	Pro	Ala	Glu	Pro	Pro	Pro	Pro	Pro	Lys	Leu	Pro	Leu	Pro	Ala	Phe
			565						570					575	
Arg	Leu	Lys	Asn	Asp	Ser	Asp	Leu	Phe	Gly	Leu	Gly	Leu	Glu	Glu	Ala
			580					585					590		
Gly	Pro	Lys	Glu	Ser	Ser	Glu	Glu	Gly	Lys	Glu	Gly	Lys	Thr	Pro	Ser
		595					600					605			
Lys	Glu	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Gly	Lys	Glu	Glu	Glu	Glu	Lys
	610					615					620				
Ala	Ala	Lys	Lys	Lys	Ser	Lys	His	Lys	Lys	Ser	Lys	Asp	Lys	Glu	Glu
			625		630					635					640
Gly	Lys	Glu	Glu	Arg	Arg	Arg	Arg	Gln	Gln	Arg	Pro	Pro	Arg	Ser	Arg
			645						650					655	
Glu	Arg	Thr	Ala	Ala	Asp	Glu	Leu	Glu	Ala	Phe	Leu	Gly	Gly	Gly	Ala
			660						665					670	
Pro	Gly	Gly	Arg	His	Pro	Gly	Gly	Gly	Asp	Tyr	Glu	Glu	Leu		
		675					680					685			

<210> SEQ ID NO 65

<211> LENGTH: 376

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 65

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Met Ser Asp Glu Val Phe Ser Thr Thr Leu Ala Tyr Thr Lys Ser Pro
1          5          10          15

Lys Val Thr Lys Arg Thr Thr Phe Gln Asp Glu Leu Ile Arg Ala Ile
20          25          30

Thr Ala Arg Ser Ala Arg Gln Arg Ser Ser Glu Tyr Ser Asp Asp Phe
35          40          45

Asp Ser Asp Glu Ile Val Ser Leu Gly Asp Phe Ser Asp Thr Ser Ala
50          55          60

Asp Glu Asn Ser Val Asn Lys Lys Met Asn Asp Phe His Ile Ser Asp
65          70          75          80

Asp Glu Glu Lys Asn Pro Ser Lys Leu Leu Phe Leu Lys Thr Asn Lys
85          90          95

Ser Asn Gly Asn Ile Thr Lys Asp Glu Pro Val Cys Ala Ile Lys Asn
100         105         110

Glu Glu Glu Met Ala Pro Asp Gly Cys Glu Asp Ile Val Val Lys Ser
115         120         125

Phe Ser Glu Ser Gln Asn Lys Asp Glu Glu Phe Glu Lys Asp Lys Ile
130         135         140

Lys Met Lys Pro Lys Pro Arg Ile Leu Ser Ile Lys Ser Thr Ser Ser
145         150         155         160

Ala Glu Asn Asn Ser Leu Asp Thr Asp Asp His Phe Lys Pro Ser Pro
165         170         175

Trp Pro Arg Ser Met Leu Lys Lys Lys Ser His Met Glu Glu Lys Asp
180         185         190

Gly Leu Glu Asp Lys Glu Thr Ala Leu Ser Glu Glu Leu Glu Leu His
195         200         205

Ser Ala Pro Ser Ser Leu Pro Thr Pro Asn Gly Ile Gln Leu Glu Ala
210         215         220

Glu Lys Lys Ala Phe Ser Glu Asn Leu Asp Pro Glu Asp Ser Cys Leu
225         230         235         240

Thr Ser Leu Ala Ser Ser Ser Leu Lys Gln Ile Leu Gly Asp Ser Phe
245         250         255

Ser Pro Gly Ser Glu Gly Asn Ala Ser Gly Lys Asp Pro Asn Glu Glu
260         265         270

Ile Thr Glu Asn His Asn Ser Leu Lys Ser Asp Glu Asn Lys Glu Asn
275         280         285

Ser Phe Ser Ala Asp His Val Thr Thr Ala Val Glu Lys Ser Lys Glu
290         295         300

Ser Gln Val Thr Ala Asp Asp Leu Glu Glu Glu Lys Ala Lys Ala Glu
305         310         315         320

Leu Ile Met Asp Asp Asp Arg Thr Val Asp Pro Leu Leu Ser Lys Ser
325         330         335

Gln Ser Ile Leu Ile Ser Thr Ser Ala Thr Ala Ser Ser Lys Lys Thr
340         345         350

Ile Glu Asp Arg Asn Ile Lys Asn Lys Lys Ser Thr Asn Asn Arg Ala
355         360         365

Ser Ser Ala Ser Ala Arg Ser Gly
370         375

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<210> SEQ ID NO 66

<211> LENGTH: 441

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 66

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Met Lys Lys Phe Phe Gln Glu Phe Lys Ala Asp Ile Lys Phe Lys Ser
 1 5 10 15
 Ala Gly Pro Gly Gln Lys Leu Lys Glu Ser Val Gly Glu Lys Ala His
 20 25 30
 Lys Glu Lys Pro Asn Gln Pro Ala Pro Arg Pro Pro Arg Gln Gly Pro
 35 40 45
 Thr Asn Glu Ala Gln Met Ala Ala Ala Ala Ala Leu Ala Arg Leu Glu
 50 55 60
 Gln Lys Gln Ser Arg Ala Trp Gly Pro Thr Ser Gln Asp Thr Ile Arg
 65 70 75 80
 Asn Gln Val Arg Lys Glu Leu Gln Ala Glu Ala Thr Val Ser Gly Ser
 85 90 95
 Pro Glu Ala Pro Gly Thr Asn Val Val Ser Glu Pro Arg Glu Glu Gly
 100 105 110
 Ser Ala His Leu Ala Val Pro Gly Val Tyr Phe Thr Cys Pro Leu Thr
 115 120 125
 Gly Ala Thr Leu Arg Lys Asp Gln Arg Asp Ala Cys Ile Lys Glu Ala
 130 135 140
 Ile Leu Leu His Phe Ser Thr Asp Pro Val Ala Ala Ser Ile Met Lys
 145 150 155 160
 Ile Tyr Thr Phe Asn Lys Asp Gln Asp Arg Val Lys Leu Gly Val Asp
 165 170 175
 Thr Ile Ala Lys Tyr Leu Asp Asn Ile His Leu His Pro Glu Glu Glu
 180 185 190
 Lys Tyr Arg Lys Ile Lys Leu Gln Asn Lys Val Phe Gln Glu Arg Ile
 195 200 205
 Asn Cys Leu Glu Gly Thr His Glu Phe Phe Glu Ala Ile Gly Phe Gln
 210 215 220
 Lys Val Leu Leu Pro Ala Gln Asp Gln Glu Asp Pro Glu Glu Phe Tyr
 225 230 235 240
 Val Leu Ser Glu Thr Thr Leu Ala Gln Pro Gln Ser Leu Glu Arg His
 245 250 255
 Lys Glu Gln Leu Leu Ala Ala Glu Pro Val Arg Ala Lys Leu Asp Arg
 260 265 270
 Gln Arg Arg Val Phe Gln Pro Ser Pro Leu Ala Ser Gln Phe Glu Leu
 275 280 285
 Pro Gly Asp Phe Phe Asn Leu Thr Ala Glu Glu Ile Lys Arg Glu Gln
 290 295 300
 Arg Leu Arg Ser Glu Ala Val Glu Arg Leu Ser Val Leu Arg Thr Lys
 305 310 315 320
 Ala Met Arg Glu Lys Glu Glu Gln Arg Gly Leu Arg Lys Tyr Asn Tyr
 325 330 335
 Thr Leu Leu Arg Val Arg Leu Pro Asp Gly Cys Leu Leu Gln Gly Thr
 340 345 350
 Phe Tyr Ala Arg Glu Arg Leu Gly Ala Val Tyr Gly Phe Val Arg Glu
 355 360 365
 Ala Leu Gln Ser Asp Trp Leu Pro Phe Glu Leu Leu Ala Ser Gly Gly
 370 375 380
 Gln Lys Leu Ser Glu Asp Glu Asn Leu Ala Leu Asn Glu Cys Gly Leu
 385 390 395 400
 Val Pro Ser Ala Leu Leu Thr Phe Ser Trp Asp Met Ala Val Leu Glu
 405 410 415

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Asp Ile Lys Ala Ala Gly Ala Glu Pro Asp Ser Ile Leu Lys Pro Glu
 420 425 430

Leu Leu Ser Ala Ile Glu Lys Leu Leu
 435 440

<210> SEQ ID NO 67
 <211> LENGTH: 204
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 67

Met Glu Ala Ala Gly Ser Pro Ala Ala Thr Glu Thr Gly Lys Tyr Ile
 1 5 10 15

Ala Ser Thr Gln Arg Pro Asp Gly Thr Trp Arg Lys Gln Arg Arg Val
 20 25 30

Lys Glu Gly Tyr Val Pro Gln Glu Glu Val Pro Val Tyr Glu Asn Lys
 35 40 45

Tyr Val Lys Phe Phe Lys Ser Lys Pro Glu Leu Pro Pro Gly Leu Ser
 50 55 60

Pro Glu Ala Thr Ala Pro Val Thr Pro Ser Arg Pro Glu Gly Gly Glu
 65 70 75 80

Pro Gly Leu Ser Lys Thr Ala Lys Arg Asn Leu Lys Arg Lys Glu Lys
 85 90 95

Arg Arg Gln Gln Gln Glu Lys Gly Glu Ala Glu Ala Leu Ser Arg Thr
 100 105 110

Leu Asp Lys Val Ser Leu Glu Glu Thr Ala Gln Leu Pro Ser Ala Pro
 115 120 125

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

Ala Ala Thr Thr Glu Lys Ala Lys Lys Ile Lys Asn Leu Lys Lys Lys
 145 150 155 160

Leu Arg Gln Val Glu Glu Leu Gln Gln Arg Ile Gln Ala Gly Glu Val
 165 170 175

Ser Gln Pro Ser Lys Glu Gln Leu Glu Lys Leu Ala Arg Arg Arg Ala
 180 185 190

Leu Glu Glu Glu Leu Glu Asp Leu Glu Leu Gly Leu
 195 200

<210> SEQ ID NO 68
 <211> LENGTH: 190
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 68

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

Glu Glu Gln Leu Asp Arg Leu Met Gln Gln Leu Gln Asp Leu Glu Glu
 20 25 30

Cys Arg Glu Glu Leu Asp Thr Asp Glu Tyr Glu Glu Thr Lys Lys Glu
 35 40 45

Thr Leu Glu Gln Leu Ser Glu Phe Asn Asp Ser Leu Lys Lys Ile Met
 50 55 60

Ser Gly Asn Met Thr Leu Val Asp Glu Leu Ser Gly Met Gln Leu Ala
 65 70 75 80

Ile Gln Ala Ala Ile Ser Gln Ala Phe Lys Thr Pro Glu Val Ile Arg
 85 90 95

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Leu Phe Ala Lys Lys Gln Pro Gly Gln Leu Arg Thr Arg Leu Ala Glu
 100 105 110

Met Asp Arg Asp Leu Met Val Gly Lys Leu Glu Arg Asp Leu Tyr Thr
 115 120 125

Gln Gln Lys Val Glu Ile Leu Thr Ala Leu Arg Lys Leu Gly Glu Lys
 130 135 140

Leu Thr Ala Asp Asp Glu Ala Phe Leu Ser Ala Asn Ala Gly Ala Ile
 145 150 155 160

Leu Ser Gln Phe Glu Lys Val Ser Thr Asp Leu Gly Ser Gly Asp Lys
 165 170 175

Ile Leu Ala Leu Ala Ser Phe Glu Val Glu Lys Thr Lys Lys
 180 185 190

<210> SEQ ID NO 69
 <211> LENGTH: 194
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 69

Met Ala Pro Lys Lys Asp Val Lys Lys Pro Val Ala Ala Ala Ala Ala
 1 5 10 15

Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Lys
 20 25 30

Pro Lys Glu Glu Lys Ile Asp Leu Ser Ala Ile Lys Ile Glu Phe Ser
 35 40 45

Lys Glu Gln Gln Asp Glu Phe Lys Glu Ala Phe Leu Leu Phe Asp Arg
 50 55 60

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

Ala Leu Gly Thr Asn Pro Thr Asn Ala Glu Val Arg Lys Val Leu Gly
 85 90 95

Asn Pro Ser Asn Glu Glu Leu Asn Ala Lys Lys Ile Glu Phe Glu Gln
 100 105 110

Phe Leu Pro Met Met Gln Ala Ile Ser Asn Asn Lys Asp Gln Ala Thr
 115 120 125

Tyr Glu Asp Phe Val Glu Gly Leu Arg Val Phe Asp Lys Glu Gly Asn
 130 135 140

Gly Thr Val Met Gly Ala Glu Leu Arg His Val Leu Ala Thr Leu Gly
 145 150 155 160

Glu Lys Met Lys Glu Glu Glu Val Glu Ala Leu Met Ala Gly Gln Glu
 165 170 175

Asp Ser Asn Gly Cys Ile Asn Tyr Glu Ala Phe Val Lys His Ile Met
 180 185 190

Ser Ile

<210> SEQ ID NO 70
 <211> LENGTH: 227
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 70

Met Glu Lys Leu Phe Asn Glu Asn Glu Gly Met Pro Ser Asn Gln Gly
 1 5 10 15

Lys Ile Asp Asn Glu Glu Gln Pro Pro His Glu Gly Lys Pro Glu Val
 20 25 30

Ala Cys Ile Leu Glu Asp Lys Lys Leu Glu Asn Glu Gly Asn Thr Glu

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

Pro Tyr Val
225

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<210> SEQ ID NO 71
<211> LENGTH: 109
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 71

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

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<210> SEQ ID NO 72
<211> LENGTH: 363
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 72

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Met Ala Asp Thr Asp Leu Phe Met Glu Cys Glu Glu Glu Leu Glu
 1          5          10          15
Pro Trp Gln Lys Ile Ser Asp Val Ile Glu Asp Ser Val Val Glu Asp

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-continued

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

<210> SEQ ID NO 73
 <211> LENGTH: 182
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 73

Met	Ala	Asp	Ser	Glu	Asn	Gln	Gly	Pro	Ala	Glu	Pro	Ser	Gln	Ala	Ala
1				5					10					15	
Ala	Ala	Ala	Glu	Ala	Ala	Ala	Glu	Glu	Val	Met	Ala	Glu	Gly	Gly	Ala
			20					25						30	

-continued

Gln Gly Gly Asp Cys Asp Ser Ala Ala Gly Asp Pro Asp Ser Ala Ala
 35 40 45

Gly Gln Met Ala Glu Glu Pro Gln Thr Pro Ala Glu Asn Ala Pro Lys
 50 55 60

Pro Lys Asn Asp Phe Ile Glu Ser Leu Pro Asn Ser Val Lys Cys Arg
 65 70 75 80

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

Lys Phe Asp Lys Glu Phe Gln Ala Leu Glu Lys Lys Tyr Asn Asp Ile
 100 105 110

Tyr Lys Pro Leu Leu Ala Lys Ile Gln Glu Leu Thr Gly Glu Met Glu
 115 120 125

Gly Cys Ala Trp Thr Leu Glu Gly Glu Glu Glu Glu Glu Glu Tyr
 130 135 140

Glu Asp Asp Glu Glu Glu Gly Glu Asp Glu Glu Glu Glu Glu Ala Ala
 145 150 155 160

Ala Glu Ala Ala Ala Gly Ala Lys His Asp Asp Ala His Ala Glu Met
 165 170 175

Pro Asp Asp Ala Lys Lys
 180

<210> SEQ ID NO 74

<211> LENGTH: 365

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 74

Met Asp Gly Pro Ala Glu Pro Gln Ile Pro Gly Leu Trp Asp Thr Tyr
 1 5 10 15

Glu Asp Asp Ile Ser Glu Ile Ser Gln Lys Leu Pro Gly Glu Tyr Phe
 20 25 30

Arg Tyr Lys Gly Val Pro Phe Pro Val Gly Leu Tyr Ser Leu Glu Ser
 35 40 45

Ile Ser Leu Ala Glu Asn Thr Gln Asp Val Arg Asp Asp Asp Ile Phe
 50 55 60

Ile Ile Thr Tyr Pro Lys Ser Gly Thr Thr Trp Met Ile Glu Ile Ile
 65 70 75 80

Cys Leu Ile Leu Lys Glu Gly Asp Pro Ser Trp Ile Arg Ser Val Pro
 85 90 95

Ile Trp Glu Arg Ala Pro Trp Cys Glu Thr Ile Val Gly Ala Phe Ser
 100 105 110

Leu Pro Asp Gln Tyr Ser Pro Arg Leu Met Ser Ser His Leu Pro Ile
 115 120 125

Gln Ile Phe Thr Lys Ala Phe Phe Ser Ser Lys Ala Lys Val Ile Tyr
 130 135 140

Met Gly Arg Asn Pro Arg Asp Val Val Val Ser Leu Tyr His Tyr Ser
 145 150 155 160

Lys Ile Ala Gly Gln Leu Lys Asp Pro Gly Thr Pro Asp Gln Phe Leu
 165 170 175

Arg Asp Phe Leu Lys Gly Glu Val Gln Phe Gly Ser Trp Phe Asp His
 180 185 190

Ile Lys Gly Trp Leu Arg Met Lys Gly Lys Asp Asn Phe Leu Phe Ile
 195 200 205

Thr Tyr Glu Glu Leu Gln Gln Asp Leu Gln Gly Ser Val Glu Arg Ile
 210 215 220

-continued

Cys Gly Phe Leu Gly Arg Pro Leu Gly Lys Glu Ala Leu Gly Ser Val
 225 230 235 240
 Val Ala His Ser Thr Phe Ser Ala Met Lys Ala Asn Thr Met Ser Asn
 245 250 255
 Tyr Thr Leu Leu Pro Pro Ser Leu Leu Asp His Arg Arg Gly Ala Phe
 260 265 270
 Leu Arg Lys Gly Val Cys Gly Asp Trp Lys Asn His Phe Thr Val Ala
 275 280 285
 Gln Ser Glu Ala Phe Asp Arg Ala Tyr Arg Lys Gln Met Arg Gly Met
 290 295 300
 Pro Thr Phe Pro Trp Asp Glu Asp Pro Glu Glu Asp Gly Ser Pro Asp
 305 310 315 320
 Pro Glu Pro Ser Pro Glu Pro Glu Pro Lys Pro Ser Leu Glu Pro Asn
 325 330 335
 Thr Ser Leu Glu Arg Glu Pro Arg Pro Asn Ser Ser Pro Ser Pro Ser
 340 345 350
 Pro Gly Gln Ala Ser Glu Thr Pro His Pro Arg Pro Ser
 355 360 365

<210> SEQ ID NO 75
 <211> LENGTH: 377
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 75

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

-continued

Leu Ser Pro Tyr Val Lys Ser Ser Ser Ser His Asn Glu Val Phe Leu
 225 230 235 240

Pro Gly Ser Arg Gly Pro Arg Arg Arg Lys Ser Lys Gln His Phe Val
 245 250 255

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

Tyr Leu Gln Leu His Asn Lys Lys Arg Gly Glu Ser His Pro Glu Gln
 275 280 285

Val Ile Leu Arg Val Asn Ser Leu Pro Arg Asp Gly Phe Lys Thr Phe
 290 295 300

Trp Ser Gln
 305

<210> SEQ ID NO 77
 <211> LENGTH: 107
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 77

Met Asp Ala Ile Leu Asn Tyr Arg Ser Glu Asp Thr Glu Asp Tyr Tyr
 1 5 10 15

Thr Leu Leu Gly Cys Asp Glu Leu Ser Ser Val Glu Gln Ile Leu Ala
 20 25 30

Glu Phe Lys Val Arg Ala Leu Glu Cys His Pro Asp Lys His Pro Glu
 35 40 45

Asn Pro Lys Ala Val Glu Thr Phe Gln Lys Leu Gln Lys Ala Lys Glu
 50 55 60

Ile Leu Thr Asn Glu Glu Ser Arg Ala Arg Tyr Asp His Trp Arg Arg
 65 70 75 80

Ser Gln Met Ser Met Pro Phe Gln Gln Trp Glu Ala Leu Asn Asp Ser
 85 90 95

Val Lys Thr Val Gly Phe Ser Leu Gly Ala Thr
 100 105

<210> SEQ ID NO 78
 <211> LENGTH: 486
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 78

Met Ala Trp Ile Lys Arg Lys Phe Gly Glu Arg Pro Pro Pro Lys Arg
 1 5 10 15

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

Thr Val Leu Ile Leu His Ala Lys Val Ala Gln Lys Ser Tyr Gly Asn
 35 40 45

Glu Lys Arg Phe Phe Cys Pro Pro Pro Cys Val Tyr Leu Met Gly Ser
 50 55 60

Gly Trp Lys Lys Lys Lys Glu Gln Met Glu Arg Asp Gly Cys Ser Glu
 65 70 75 80

Gln Glu Ser Gln Pro Cys Ala Phe Ile Gly Ile Gly Asn Ser Asp Gln
 85 90 95

Glu Met Gln Gln Leu Asn Leu Glu Gly Lys Asn Tyr Cys Thr Ala Lys
 100 105 110

Thr Leu Tyr Ile Ser Asp Ser Asp Lys Arg Lys His Phe Met Leu Ser
 115 120 125

-continued

Val Lys Met Phe Tyr Gly Asn Ser Asp Asp Ile Gly Val Phe Leu Ser
 130 135 140

Lys Arg Ile Lys Val Ile Ser Lys Pro Ser Lys Lys Lys Gln Ser Leu
 145 150 155 160

Lys Asn Ala Asp Leu Cys Ile Ala Ser Gly Thr Lys Val Ala Leu Phe
 165 170 175

Asn Arg Leu Arg Ser Gln Thr Val Ser Thr Arg Tyr Leu His Val Glu
 180 185 190

Gly Gly Asn Phe His Ala Ser Ser Gln Gln Trp Gly Ala Phe Phe Ile
 195 200 205

His Leu Leu Asp Asp Asp Glu Ser Glu Gly Glu Glu Phe Thr Val Arg
 210 215 220

Asp Gly Tyr Ile His Tyr Gly Gln Thr Val Lys Leu Val Cys Ser Val
 225 230 235 240

Thr Gly Met Ala Leu Pro Arg Leu Ile Ile Arg Lys Val Asp Lys Gln
 245 250 255

Thr Ala Leu Leu Asp Ala Asp Asp Pro Val Ser Gln Leu His Lys Cys
 260 265 270

Ala Phe Tyr Leu Lys Asp Thr Glu Arg Met Tyr Leu Cys Leu Ser Gln
 275 280 285

Glu Arg Ile Ile Gln Phe Gln Ala Thr Pro Cys Pro Lys Glu Pro Asn
 290 295 300

Lys Glu Met Ile Asn Asp Gly Ala Ser Trp Thr Ile Ile Ser Thr Asp
 305 310 315 320

Lys Ala Glu Tyr Thr Phe Tyr Glu Gly Met Gly Pro Val Leu Ala Pro
 325 330 335

Val Thr Pro Val Pro Val Val Glu Ser Leu Gln Leu Asn Gly Gly Gly
 340 345 350

Asp Val Ala Met Leu Glu Leu Thr Gly Gln Asn Phe Thr Pro Asn Leu
 355 360 365

Arg Val Trp Phe Gly Asp Val Glu Ala Glu Thr Met Tyr Arg Cys Gly
 370 375 380

Glu Ser Met Leu Cys Val Val Pro Asp Ile Ser Ala Phe Arg Glu Gly
 385 390 395 400

Trp Arg Trp Val Arg Gln Pro Val Gln Val Pro Val Thr Leu Val Arg
 405 410 415

Asn Asp Gly Ile Ile Tyr Ser Thr Ser Leu Thr Phe Thr Tyr Thr Pro
 420 425 430

Glu Pro Gly Pro Arg Pro His Cys Ser Ala Ala Gly Ala Ile Leu Arg
 435 440 445

Ala Asn Ser Ser Gln Val Pro Pro Asn Glu Ser Asn Thr Asn Ser Glu
 450 455 460

Gly Ser Tyr Thr Asn Ala Ser Thr Asn Ser Thr Ser Val Thr Ser Ser
 465 470 475 480

Thr Ala Thr Val Val Ser
 485

<210> SEQ ID NO 79

<211> LENGTH: 82

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

-continued

<400> SEQUENCE: 79

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

<210> SEQ ID NO 80

<211> LENGTH: 129

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 80

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

What is claimed is:

1. A protein array for identifying an individual comprising proteins immobilized on a support, wherein no more than about 200 proteins are in the array, wherein each protein is known, wherein each protein is immobilized at a known predetermined location on the support, and wherein each protein is useful in identifying an individual.
2. The protein array of claim 1, wherein each of the proteins is immobilized on the support to form a spot having a diameter of greater than about at least 50 microns to form an array.
3. The protein array of claim 1, wherein at least one of the proteins is one of SEQ ID NOs: 1-80, or a fragment thereof comprising an epitope.
4. The protein array of claim 1, wherein at least one of the proteins is one of SEQ ID NOs: 1-45, or a fragment thereof comprising an epitope.
5. The protein array of claim 1, wherein the array comprises each of the proteins of SEQ ID NOs: 1-80.
6. The protein array of claim 1, wherein the array comprises each of the proteins of SEQ ID NOs: 1-45.
7. The protein array of claim 1, wherein less than about 100 proteins are immobilized on the support.
8. The protein array of claim 1, wherein about from 45 to about 80 proteins are immobilized on the support.
9. A method for analyzing biological material having individual-specific antibodies, the method comprising:
 - obtaining a sample of the biological material having individual-specific antibodies;
 - contacting the array of claim 1 with the sample to bind at least a portion of the individual-specific antibodies to the multiple proteins of the array, to form immune complexes;
 - applying at least one detection agent to the array, the detection agent comprising at least one interacting protein conjugated to a marker to detect the immune complexes;
 - washing the support to remove non-immobilized individual-specific antibodies and the detection agent; and
 - detecting the immune complexes on the array to obtain an antibody profile.
10. The method of claim 9, wherein obtaining a sample of the biological material having individual-specific antibodies comprises obtaining a plurality of samples from each of a plurality of individuals.

11. The method of claim 9, wherein no more than about 100 proteins are in the array.

12. The method of claim 9, wherein each of the proteins of the array has a spot diameter sufficient to be detected with a color scanner.

13. The method of claim 9, wherein each of the proteins of the array has a spot diameter of at least 300 microns.

14. The method of claim 9, wherein obtaining a sample of a biological material comprises obtaining a sample of a biological material selected from the group of biological material consisting of tissue, blood, saliva, urine, perspiration, tears, semen, serum, plasma, amniotic fluid, pleural fluid, cerebrospinal fluid, and combinations thereof.

15. The method of claim 9, wherein applying at least one detection agent to the array comprises applying a detection agent comprising at least one interacting protein conjugated to at least one of a chemiluminescent marker, a fluorescent marker, and a colorigenic marker.

16. The method of claim 9, wherein detecting the immune complexes on the array to obtain an antibody profile comprises detecting at least one of a chemiluminescent marker, a fluorescent marker, and a colorigenic marker using a portable device.

17. The method of claim 9, further comprising comparing the antibody profile to a known antibody profile obtained from an individual.

18. A method for analyzing biological material comprising antibodies, the method comprising:

obtaining a sample of a biological material comprising antibodies;

contacting the sample with the array of claim 1 to bind at least a portion of the antibodies to the proteins to form immune complexes;

applying at least one detection agent to the array, the detection agent comprising at least one interacting protein conjugated to a marker to detect the immune complexes;

washing the support to remove non-immobilized antibodies and detection agent; and

detecting the immune complexes on the array, to obtain an antibody profile.

19. The method of claim 18, wherein each of the proteins of the array is selected from Table 1 or Table 2.

20. The method of claim 18, further comprising correlating the antibody profile to a single individual in a population of from about 1 million individuals to about 100 billion individuals.

21. The method of claim 20, wherein correlating the antibody profile to a single individual in a population of from about 1 million individuals to about 100 billion individuals comprises correlating the antibody profile to the single individual in a population of about 10 million individuals.

22. The method of claim 20, wherein correlating the antibody profile to a single individual in a population of from about 1 million individuals to about 100 billion individuals comprises correlating the antibody profile to an individual among a population of about 10 billion individuals.

23. A method of analyzing biological material from each of the plurality of individuals, comprising:

obtaining a plurality of samples of a biological material from each of the plurality of individuals, each of the plurality of samples having individual-specific antibodies;

contacting the array of claim 1 with each of the plurality of samples to bind at least a portion of the individual-specific antibodies to the multiple proteins of the array, to form immune complexes;

applying at least one detection agent to the array, the detection agent comprising at least one interacting protein conjugated to a marker to detect the immune complexes;

washing the support to remove non-immobilized individual-specific antibodies and detection agent; and

detecting the immune complexes on the array, to obtain an antibody profile.

24. The method of claim 23, further comprising comparing the antibody profile obtained from each of the plurality of individuals to determine a relationship.

* * * * *

专利名称(译)	通过抗体谱分析鉴定鉴别蛋白，鉴定个体的方法和装置		
公开(公告)号	US8969009	公开(公告)日	2015-03-03
申请号	US12/586109	申请日	2009-09-17
[标]申请(专利权)人(译)	巴特勒能源同盟有限公司		
申请(专利权)人(译)	BATTELLE ENERGY ALLIANCE, LLC		
当前申请(专利权)人(译)	BATTELLE ENERGY ALLIANCE, LLC		
[标]发明人	THOMPSON VICKI S LACEY JEFFREY A GENTILLON CYNTHIA A APEL WILLIAM A		
发明人	THOMPSON, VICKI S. LACEY, JEFFREY A. GENTILLON, CYNTHIA A. APEL, WILLIAM A.		
IPC分类号	G01N33/53 G01N33/68		
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其他公开文献	US20110065594A1		
外部链接	Espacenet USPTO		

摘要(译)

一种用于基于生物样品确定用于区分和肯定识别个体的多种蛋白质的方法。该方法可以包括针对包括多种蛋白质的蛋白质阵列分析来自多个个体的生物样品。蛋白质阵列可包括以预选模式附着于支持物的蛋白质，使得蛋白质的位置是已知的。可以使生物样品与蛋白质阵列接触，使得生物样品中的一部分抗体与形成免疫复合物的蛋白质反应并结合。可以进行统计分析方法，例如判别分析，以确定用于区分个体的区分蛋白质。感兴趣的蛋白质可用于形成蛋白质阵列。例如，这种蛋白质阵列可用于将来自未知来源的法医样品与来自已知来源的样品进行比较。

