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- (54) **BIOMARKERS FOR CHAGAS DISEASE RELATED CARDIOMYOPATHY**
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G01N 33/53 (2006.01)
G01N 33/68 (2006.01)
G01N 33/569 (2006.01)
- (52) **U.S. Cl.**
CPC ... **G01N 33/6896** (2013.01); **G01N 33/56905** (2013.01); **G01N 2800/28** (2013.01)
- (58) **Field of Classification Search**
None
See application file for complete search history.
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(57) **ABSTRACT**

Certain embodiments include methods for assessing a subject having a trypanosome infection for the presence or absence of indications of cardiomyopathy.

5 Claims, 16 Drawing Sheets

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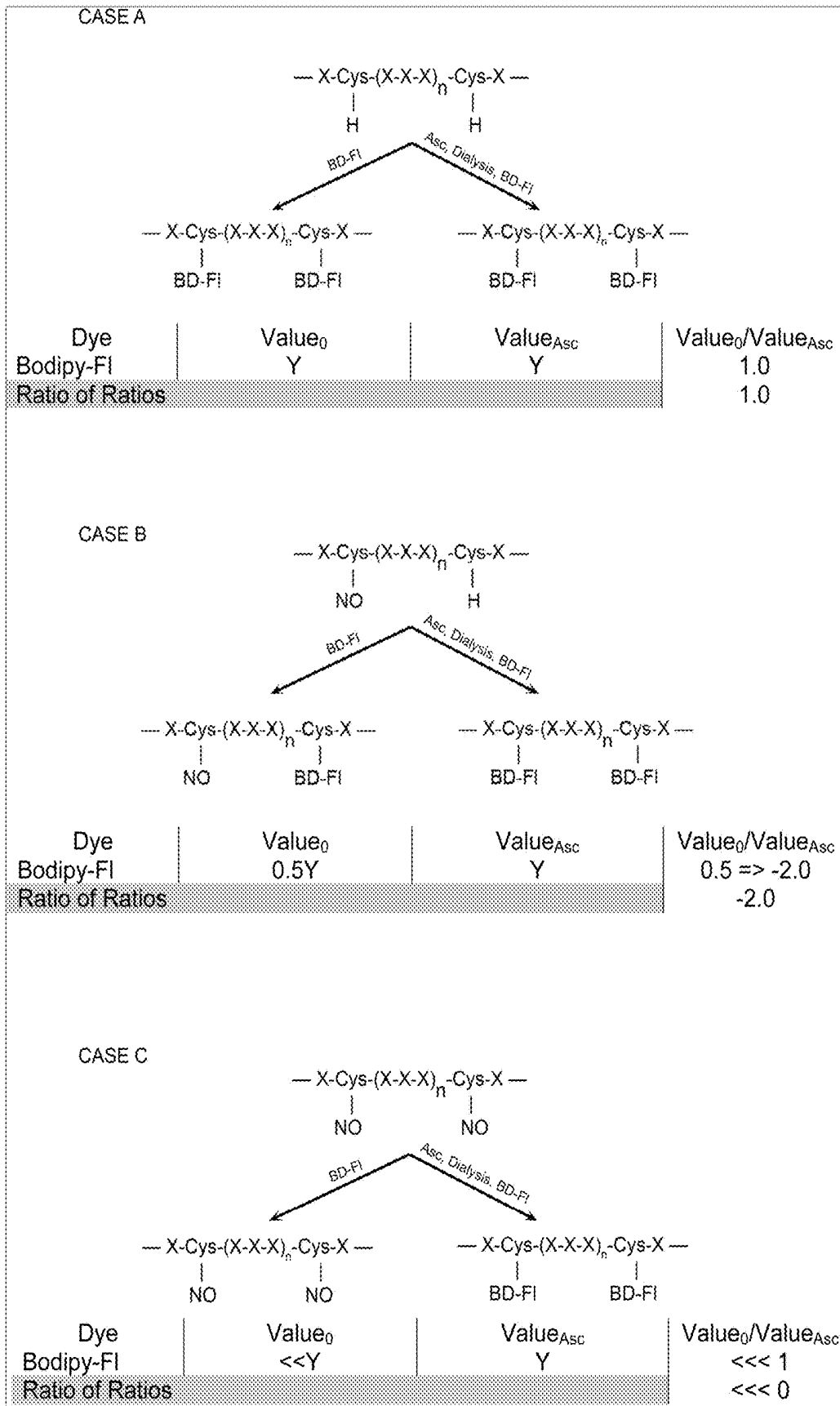


FIG. 1

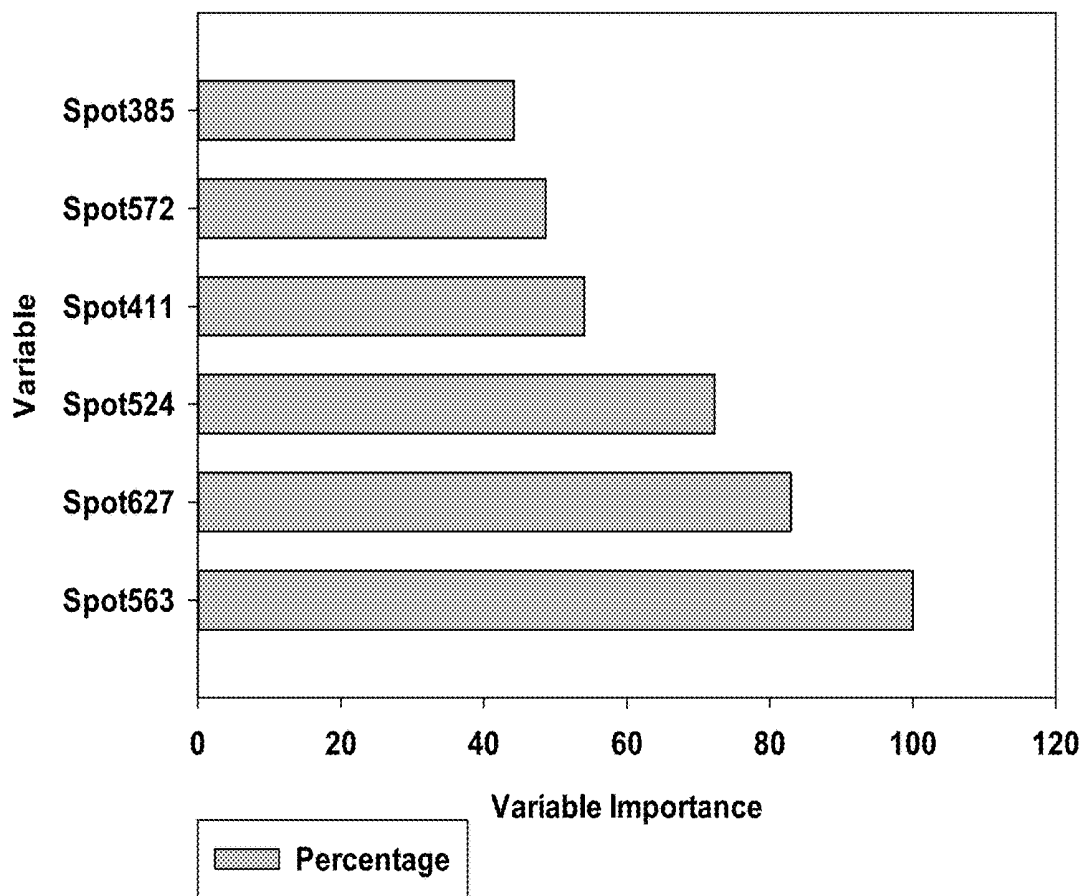


FIG. 2

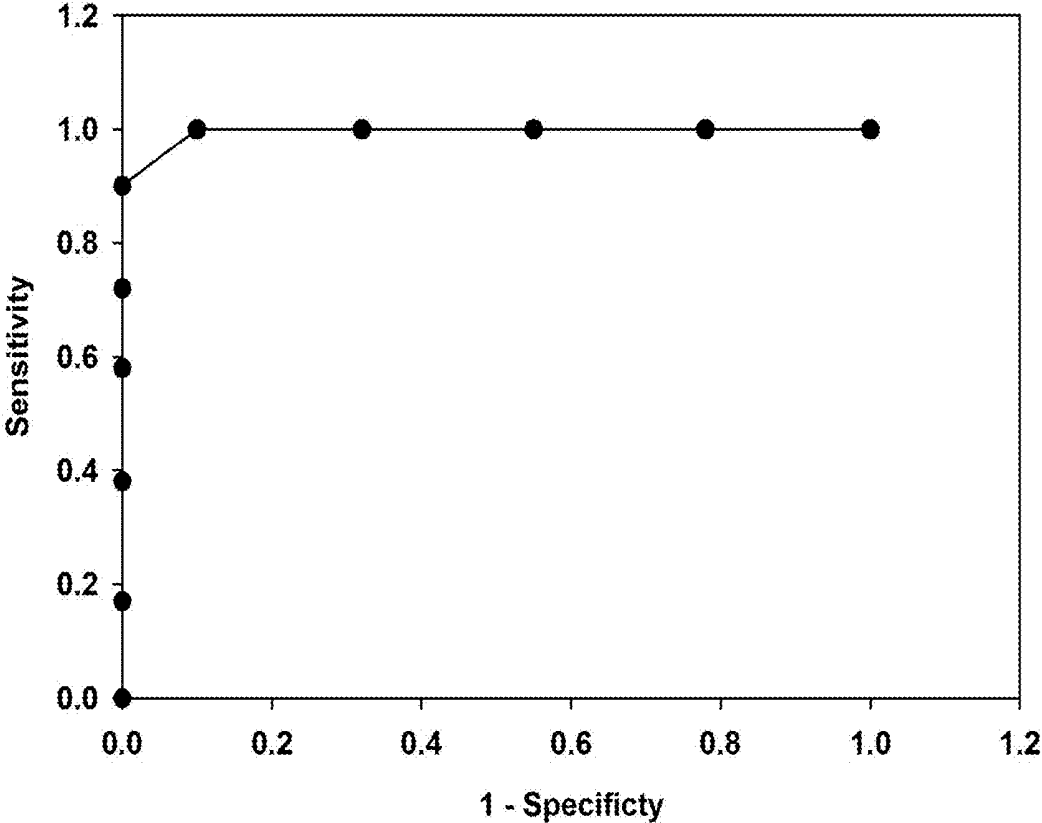


FIG. 3

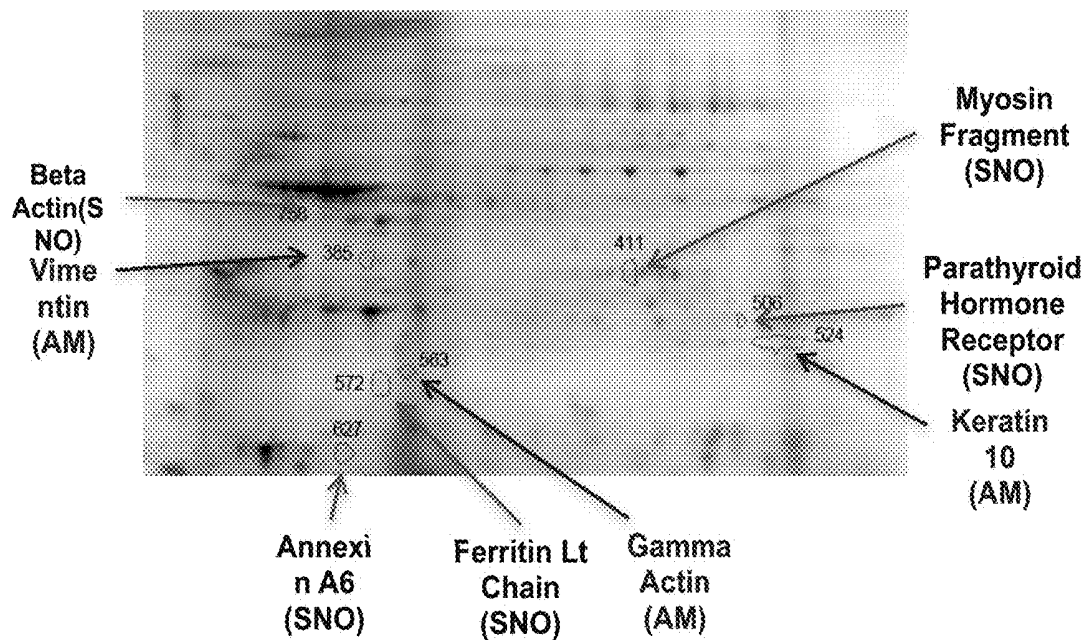


FIG. 4

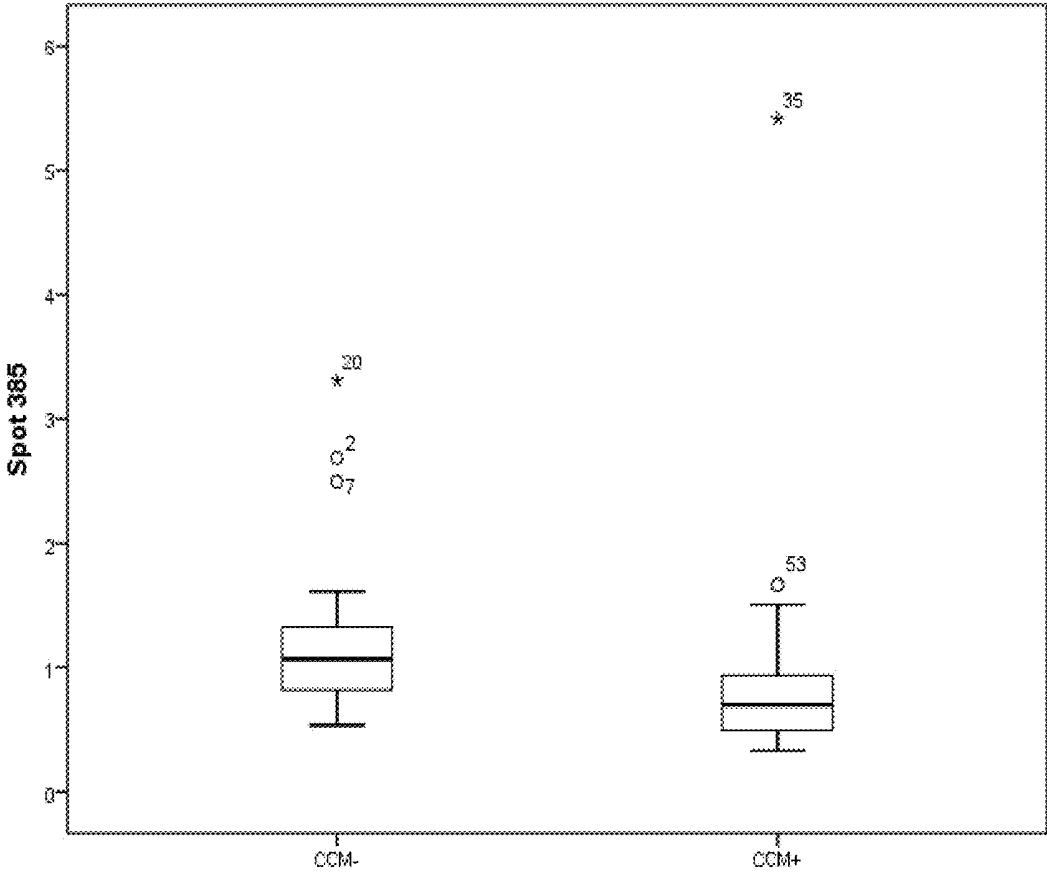


FIG. 5

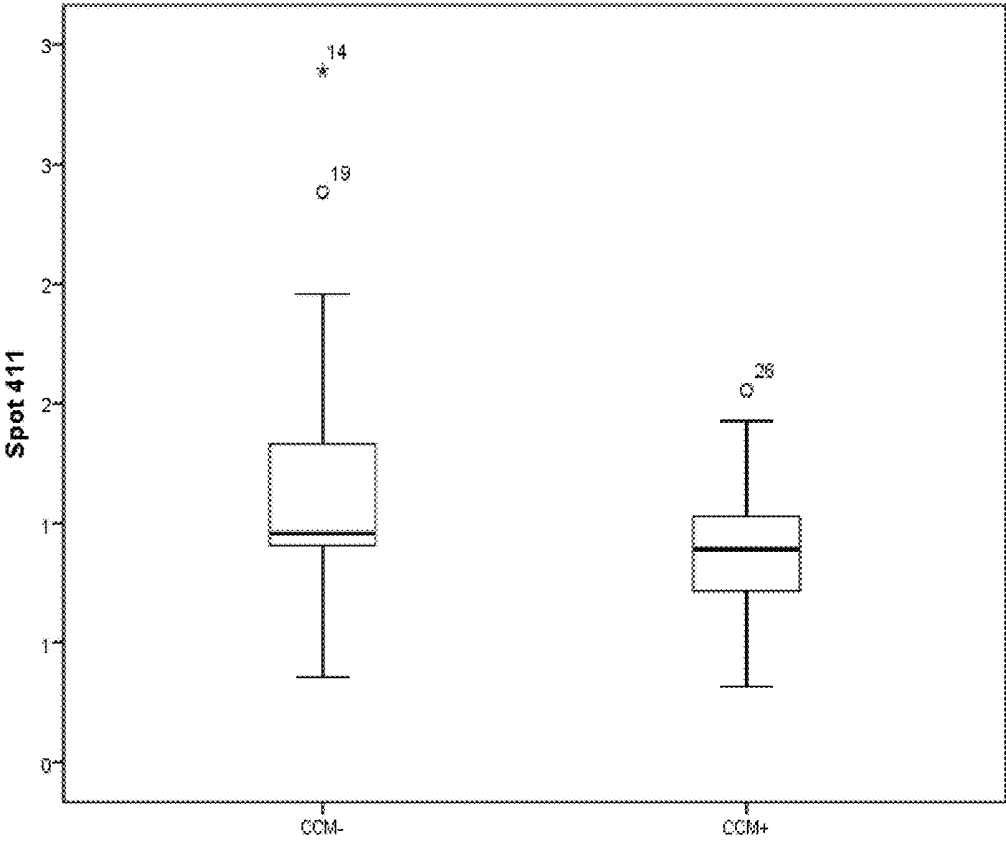


FIG. 6

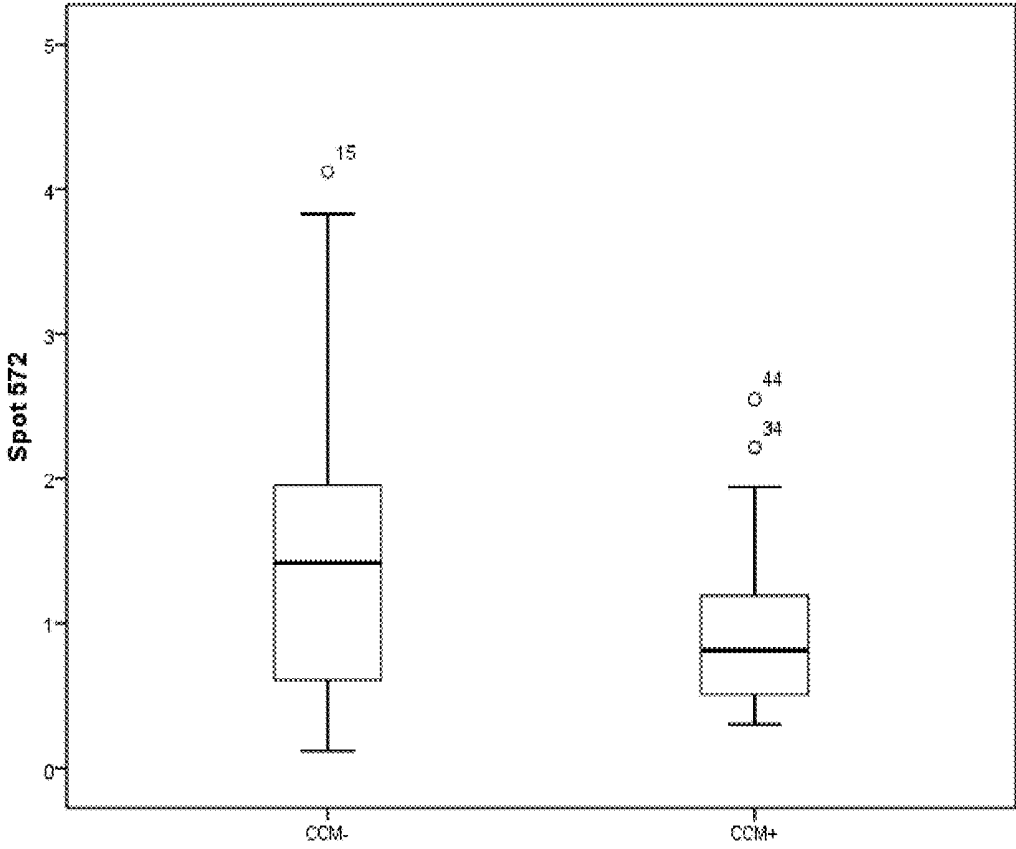


FIG. 7

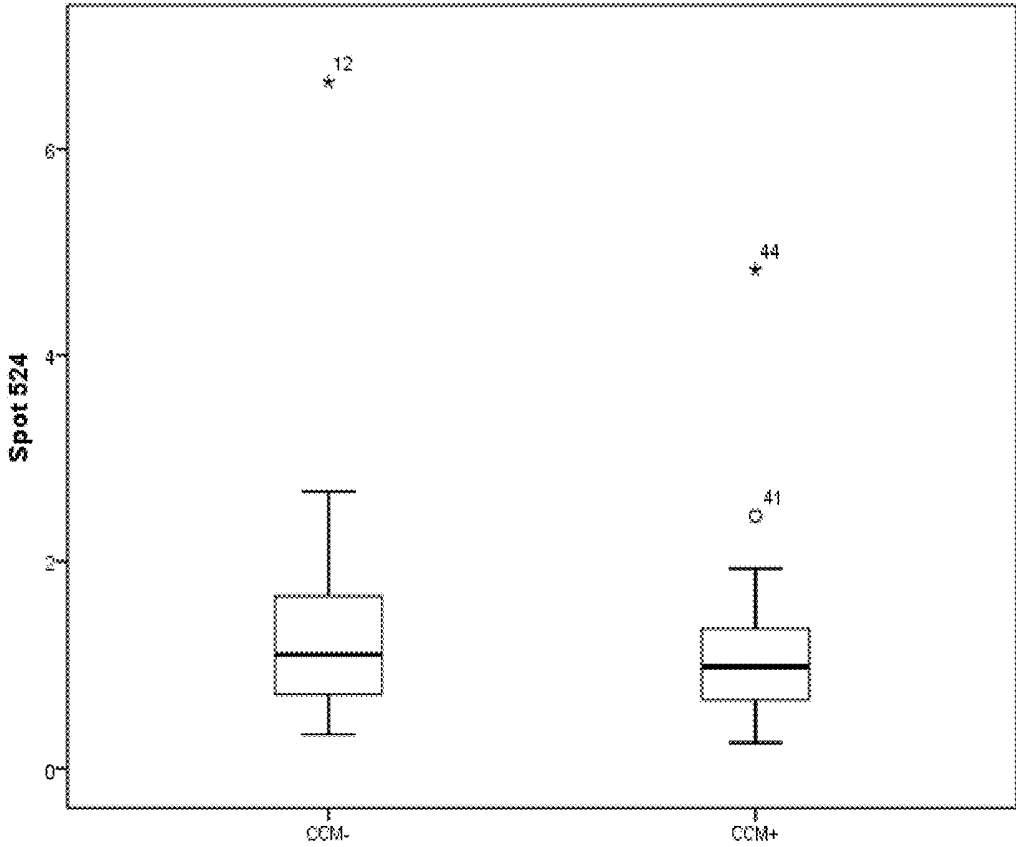


FIG. 8

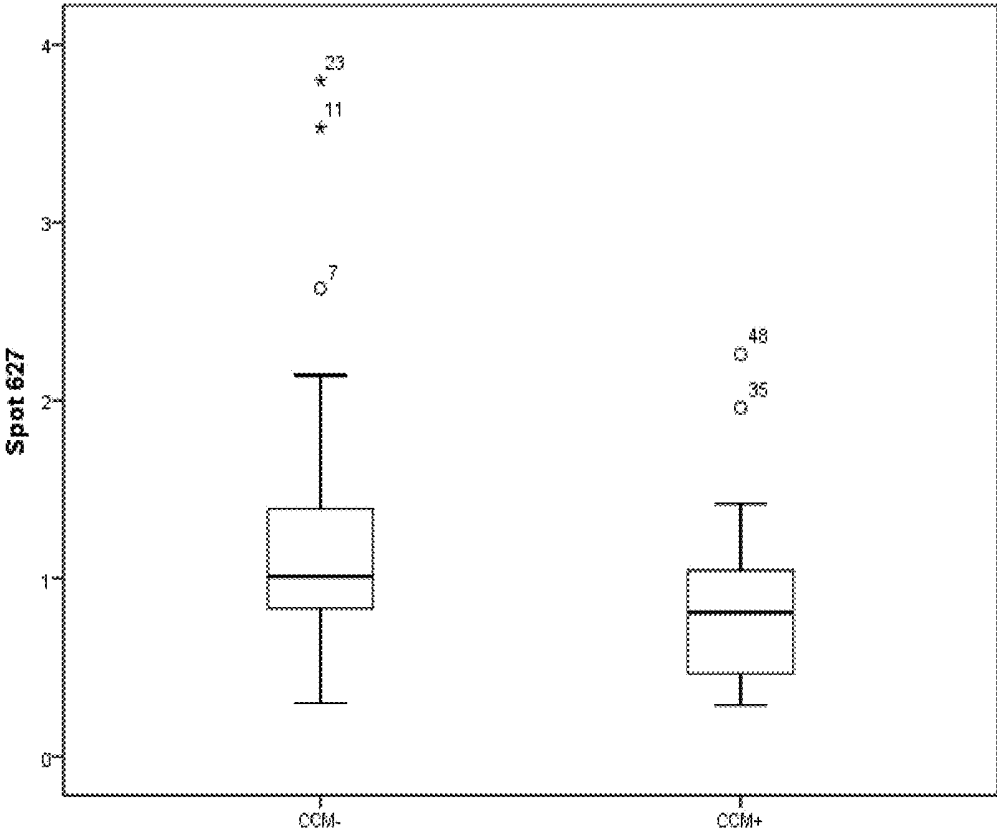


FIG. 9

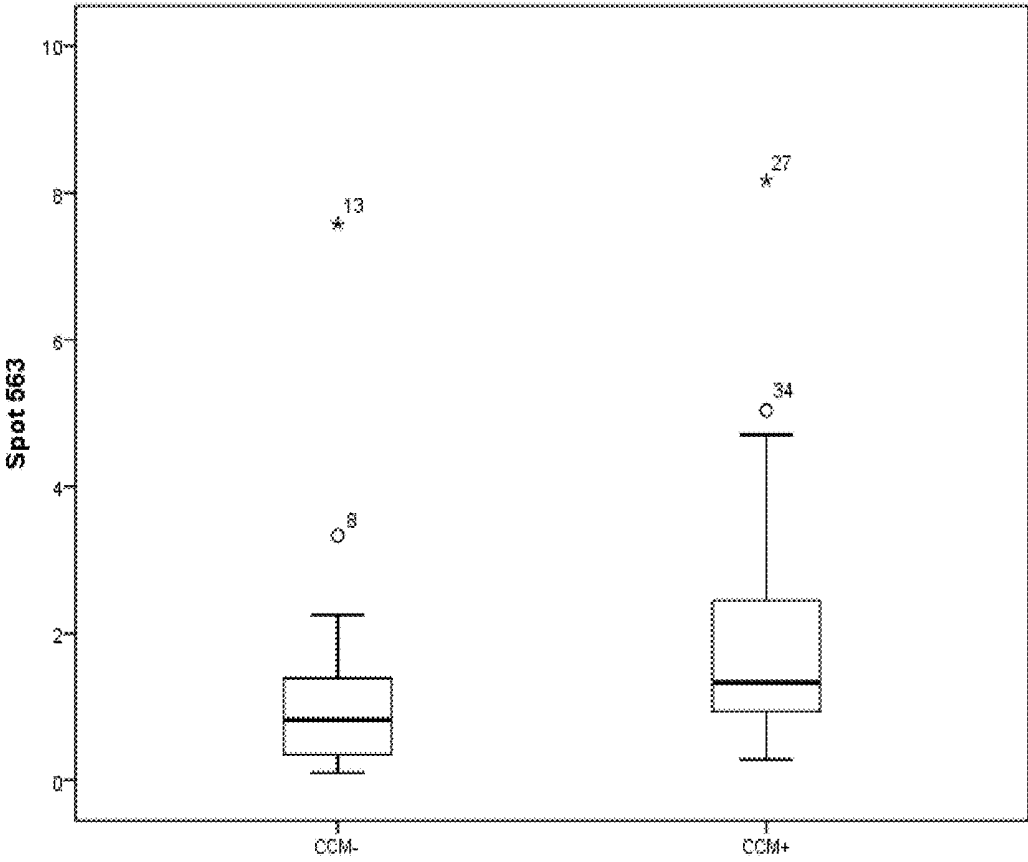


FIG. 10

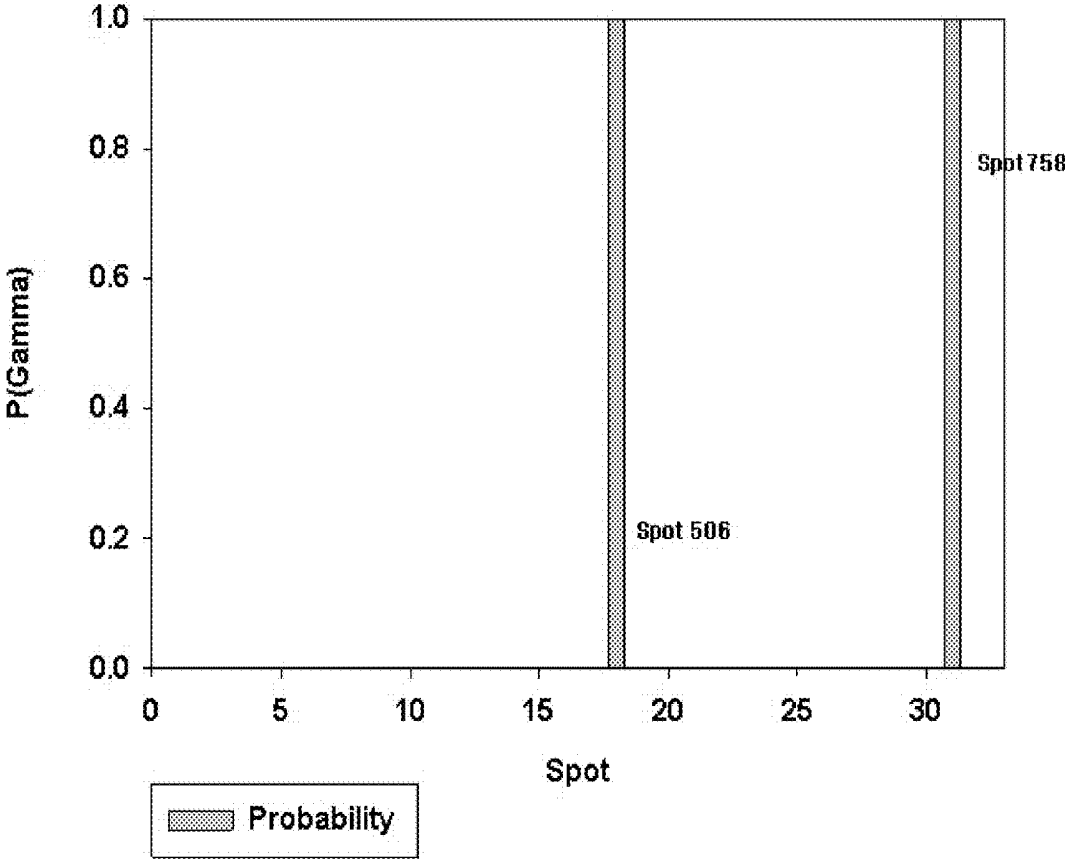


FIG. 11

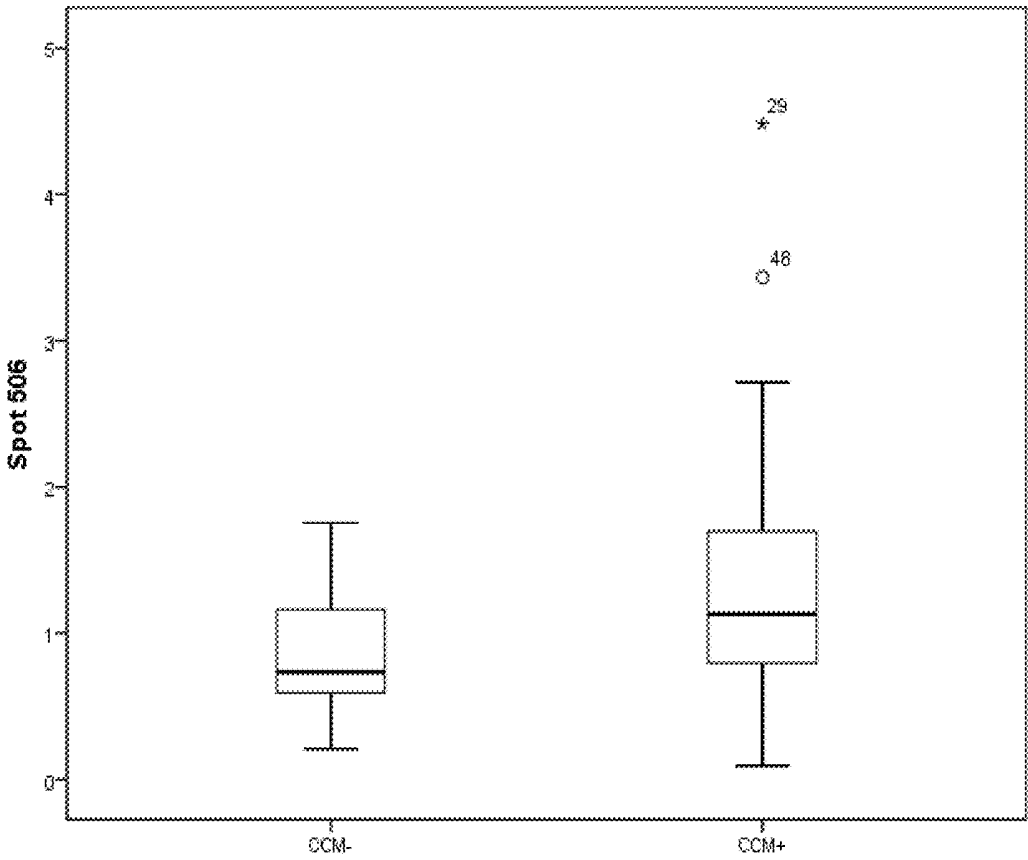


FIG. 12

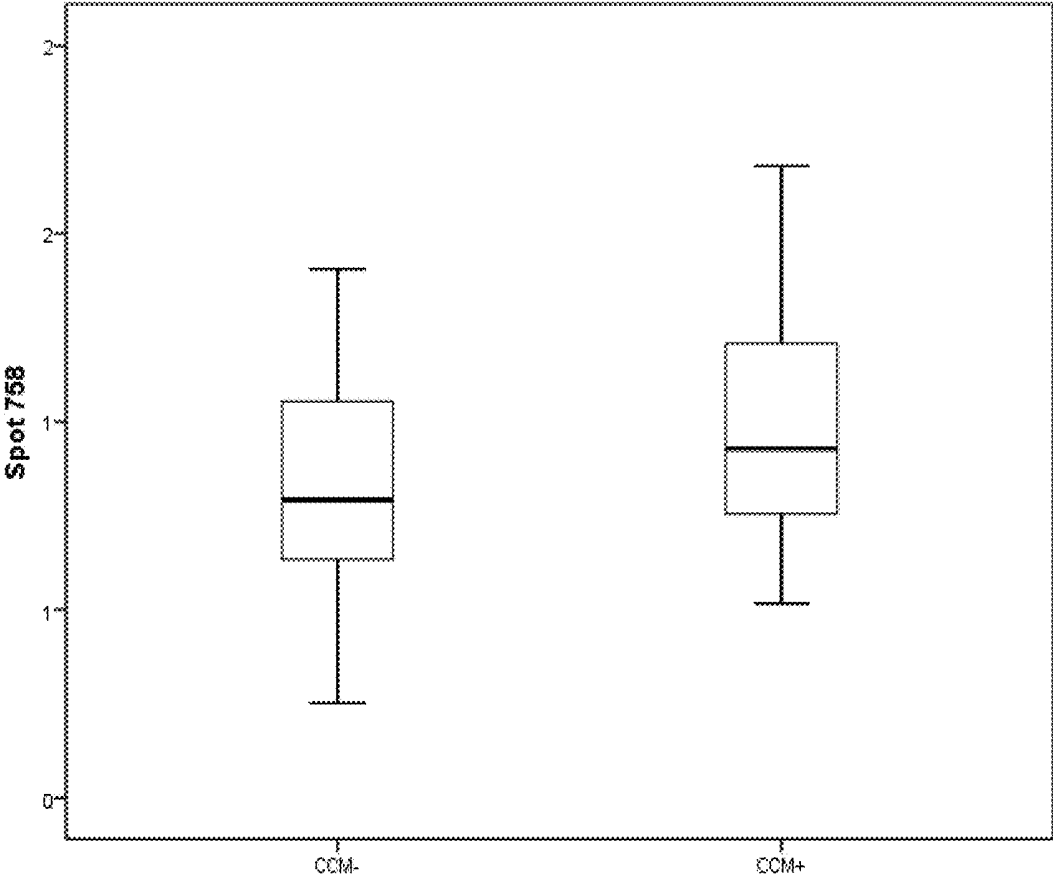


FIG. 13

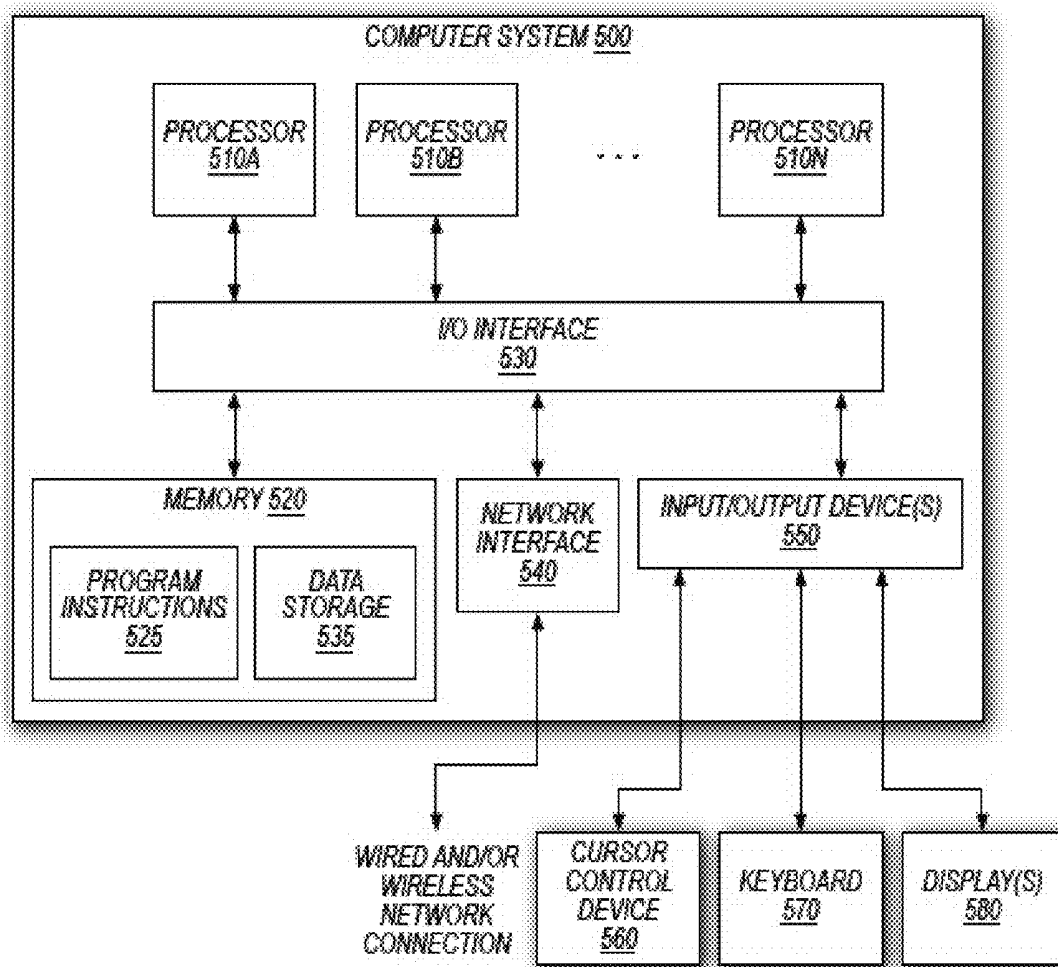


FIG. 14

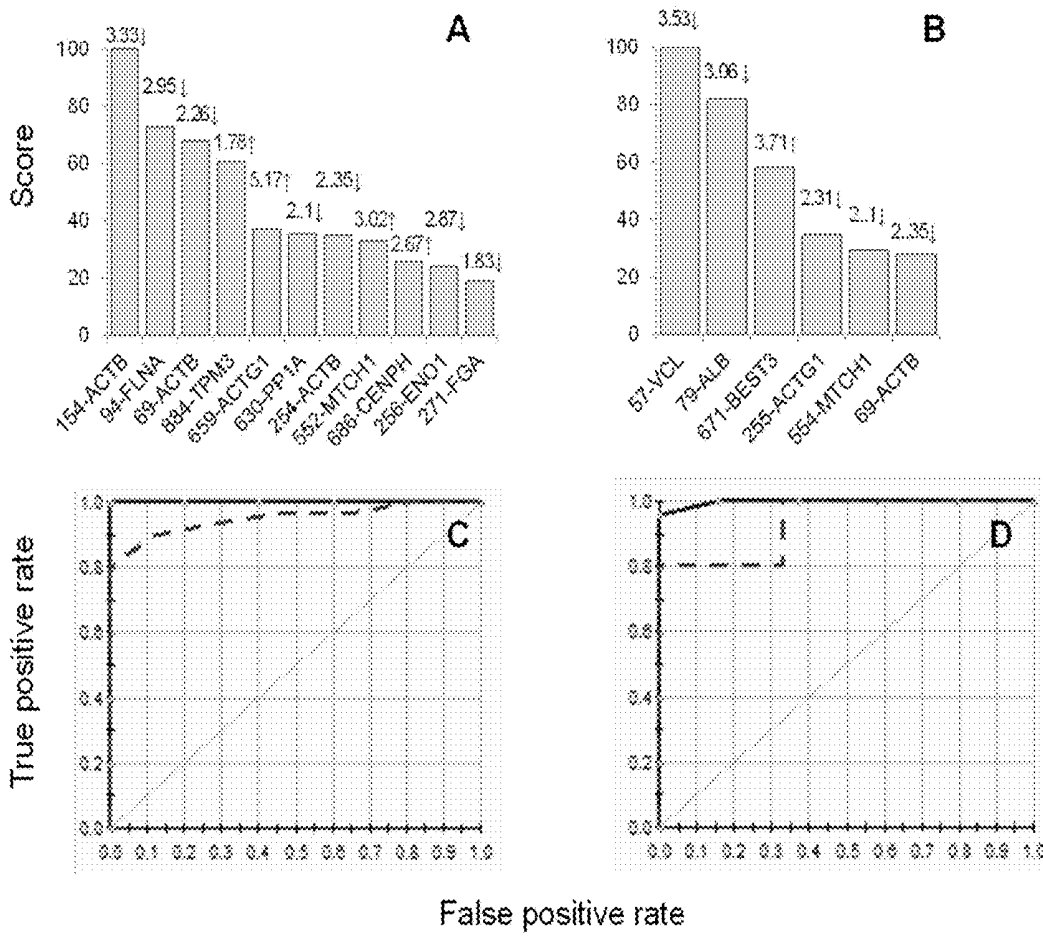


FIG. 15A-15D

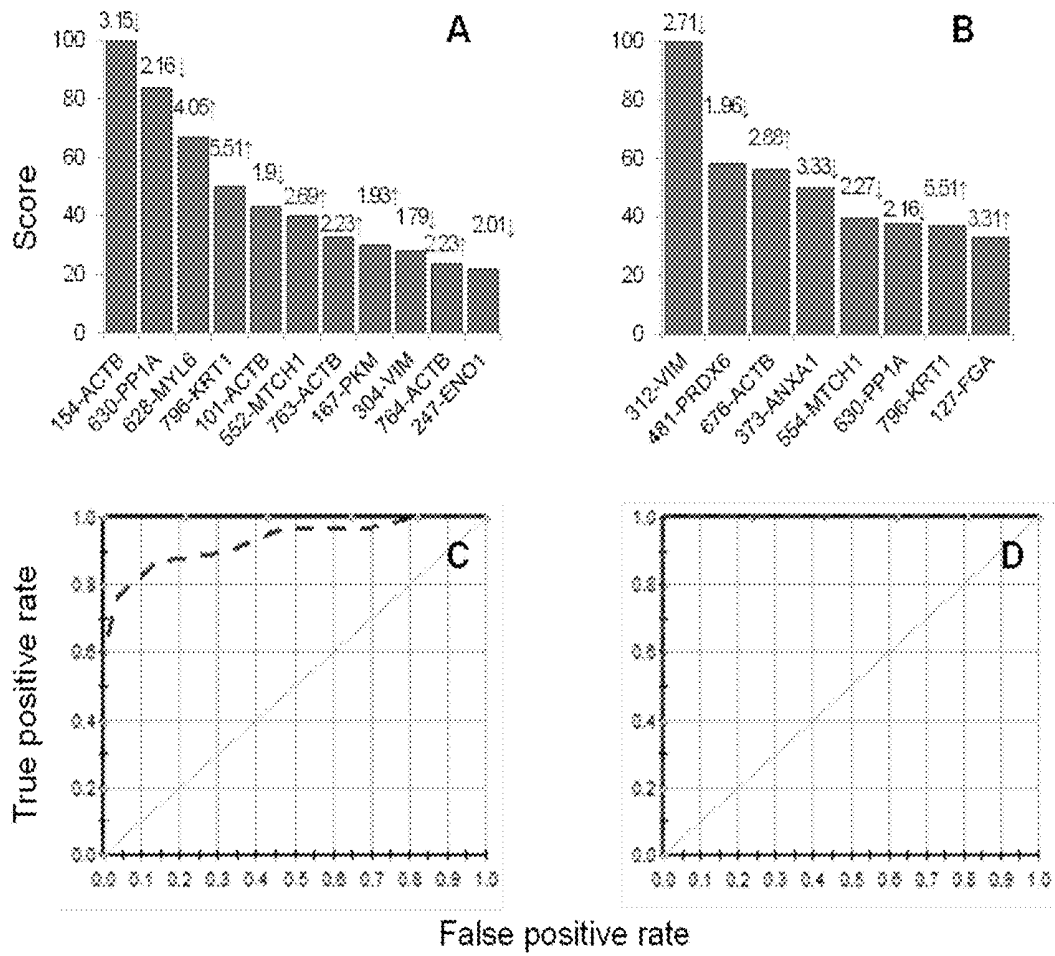


FIG. 16A-16D

BIOMARKERS FOR CHAGAS DISEASE RELATED CARDIOMYOPATHY

STATEMENT REGARDING PRIORITY

This Application claims priority to and is a continuation-in-part of International Application PCT/US2014/022510 filed Mar. 10, 2014, and U.S. Provisional Patent Application No. 61/775,676 filed Mar. 10, 2013, each of which is incorporated herein by reference in its entirety.

STATEMENT REGARDING FEDERALLY FUNDED RESEARCH

This invention was made with government support under HHSN272200800048C and HL094802 awarded by the National Institutes of Health. The United States government has certain rights in the invention.

BACKGROUND

Chagas disease, transmitted by injection of *Trypanosoma cruzi* through the bite of an insect vector, is designated as the most important emerging disease in developed countries, with approximately 16-18 million cases of infection in Latin America with 120 million people (~25% of the population) more at risk of infection (Organization, W. H. (2010) Chagas disease: control and elimination, In *Report of the secretariat. WHO, Geneva*, UNDP/World Bank/WHO). In 30-40% of the infected individuals, the disease may progress to irreversible cardiomyopathy after many years, with infected individuals serving as carriers of the organism and exhibiting considerable morbidity and high risk of mortality (Machado et al. (2012) *Front Biosci (Elite Ed)* 4, 1743-58). Unfortunately, there are no vaccines or safe drugs—benzimidazole and nifurtimox can be used for treatment of acute infection, but have high toxicity in adults and are ineffective in arresting or reversing the progression of the disease—and as a consequence, the NIH and CDC have recognized Chagas disease as a neglected emergency (Bern and Montgomery, (2009) *Clin Infect Dis* 49, e52-54; CDC. (2006) Chagas disease after organ transplantation—Los Angeles, Calif., 2006, *MMWR Morb Mortal Wkly Rep* 55, 798-800; CDC. (2007) Blood donor screening for chagas disease—United States, 2006-2007, *MMWR Morb Mortal Wkly Rep* 56, 141-143).

Thus, there remains a need for additional compositions and methods for identifying subjects harboring Trypanosomes and particularly those subjects at risk of developing cardiomyopathy.

SUMMARY

Blood serves as a useful tissue capable of detecting and responding to the changes induced in the body during the course of *T. cruzi* infection and disease development. The changes in immune response, oxidative stress, and antioxidant imbalance are detectable in peripheral blood of infected mice (Wen et al., (2008) *Microbes Infect*, 10, 1201-09), and, notably, a strong positive correlation was detected for the disease state-specific changes in the heart-versus-blood level of oxidative stress markers and antioxidants (e.g. glutathione peroxidase, glutathione, manganese superoxide dismutase) (Wen et al., (2008) *Microbes Infect*, 10, 1201-09). Distinct plasma protein-nitrosylation profiles have also been documented in acutely- and chronically-infected chagasic animals (Dhiman et al., (2008) *Am J Pathol*, 173, 728-740).

Studies described herein along with documentation of oxidative overload in chagasic humans (Wen et al., (2006) *Free Rad Biol Med*, 41, 270-76; de Oliveira et al., (2007) *Int J Cardiol*, 116, 357-63), support the idea that characterization of plasma proteomes will be useful in identifying the molecular mechanisms that are disturbed during the progression of Chagas disease.

Certain embodiments include assessing the status of a subject by measuring and evaluating the protein levels and/or the levels of protein modification of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more proteins selected from vinculin (SEQ ID NO:1), serum albumin (SEQ ID NO:2), integrin alpha-IIb isoform 3 (SEQ ID NO:3), myeloperoxidase isoform H7 (SEQ ID NO:4), actin (cytoplasmic 2, N-terminal processed) (SEQ ID NO:5), Talin 1 (SEQ ID NO:6), actin (cytoplasmic 1, N-terminal processed) (SEQ ID NO:7), actin (cytoplasmic 1, N-terminal processed) (SEQ ID NO:8), unconventional myosin-IXa (SEQ ID NO:9), peptidyl-prolyl cis-trans isomerase A (SEQ ID NO:10), WD repeat-containing protein 49 (SEQ ID NO:11), Keratin type II cytoskeletal 1 (SEQ ID NO:12), parathyroid hormone 2 receptor (fragment) (SEQ ID NO:13), proteasome subunit beta type-2 (SEQ ID NO:14), ferritin light chain (SEQ ID NO:15), annexin (SEQ ID NO:16), actin (cytoplasmic 1, N-terminal processed) (SEQ ID NO:16), keratin type I cytoskeletal 10 (SEQ ID NO:18), heterogeneous nuclear ribonucleoprotein A1 (Fragment) (SEQ ID NO:19), SH3 domain-binding glutamic acid-rich-like protein 3 (SEQ ID NO:20), Ras-related protein Rap-1b (SEQ ID NO:21), actin (cytoplasmic 1, N-terminal processed) (SEQ ID NO:22), POTE ankyrin domain family member F (SEQ ID NO:23), vimentin (SEQ ID NO:24), protein S100-A11 (SEQ ID NO:25), Isoform 2 of fibrinogen alpha chain (SEQ ID NO:26), tubulin beta chain (SEQ ID NO:27), Myosin regulatory light chain 12B (SEQ ID NO:28), Annexin A3 (SEQ ID NO:29), keratin type I cytoskeletal 10 (SEQ ID NO:30), Actin cytoplasmic 2 N-terminally processed (Fragment) (SEQ ID NO:31), ATP synthase subunit alpha (SEQ ID NO:32) (see table III). The methods further comprising computer implementation of such a method. In certain aspects the subject is diagnosed or at risk of trypanosome infection. In further aspects the subject has a trypanosome infection and is assessed for the presence or absence of indications of cardiomyopathy.

Certain embodiments include methods of assessing a subject having Chagas disease comprising: measuring levels of (i) one or more proteins selected from vimentin, gamma actin, or keratin 10, or (ii) level of cysteinyl-S-nitrosylation (SNO) of one or more of beta actin, annexin A6, ferritin light chain fragment (~0.18 kDa), parathyroid hormone 2 receptor fragment (~20 kDa), or myosin-IXa fragment; wherein elevated levels of the proteins and/or nitrosylation is indicative of risk for developing chagasic cardiomyopathy. Certain protein levels will increase and certain protein levels will decrease as compared to control. SNO modification will either increase or decrease relative to a control. The levels of the markers have been associated with a particular disease state. As SNO modification increases the fluorescence from the modified protein decreases. Likewise, as SNO modification decreases the fluorescence of the lesser-modified protein increases. In certain aspects a SNO modification is associated with cardiomyopathy as is indicated by a negative ratio in the CCM+ group and a positive ratio in the CCM- group. In a further aspect a SNO modification is associated with a non-cardiomyopathic condition in which the CCM- ratio is negative and the CCM+ ratio is positive. Furthermore, an increased or decreased level of a protein can be

associated with CCM+ as is indicated by a positive or negative abundance ratio, respectively.

In certain aspects the level of vimentin is measured. In a further aspect the level of gamma actin is measured. In certain aspects the level of keratin 10 is measured. In certain aspects the levels of vimentin and gamma actin are measured. In certain aspects the level of vimentin and keratin 10 are measured. In certain aspects the level of gamma actin and keratin 10 are measured. In certain aspects the level of vimentin, gamma actin, and keratin 10 are measured. In certain aspects protein levels are determined by western blot analysis, mass spectrometry, or image analysis of two-dimensional gels.

In certain aspects the level of modification of ferritin light chain fragment is measured. In certain aspects the level of modification of annexin A6 is measured. In certain aspects the level of modification of myosin-IXa fragment is measured. In certain aspects the level of modification of ferritin light chain fragment and annexin A6 is measured. In certain aspects the level of modification of ferritin light chain fragment and myosin-IXa fragment is measured. In certain aspects the level of modification of annexin A6 and myosin-IXa fragment is measured. In certain aspects the level of modification of ferritin light chain fragment, annexin A6, and myosin-IXa fragment is measured. In certain aspects the modification level of parathyroid hormone receptor and/or β actin are measured. In certain aspects the level of protein modification is measured by saturation fluorescence labeling.

In certain aspects the protein level and/or SNO modification of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 2, 23, 24, or 25 of the proteins described Table III are measured.

Certain aspects include a computer-implemented method for assessing a subject for trypanosome infection or cardiomyopathy. In certain aspects a computer implemented method comprises the steps of (a) obtaining protein level measurements of one or more of vimentin, gamma actin, or keratin 10, and/or protein modification measurements of one or more of beta actin, annexin A6, ferritin light chain fragment (~18 kDa), parathyroid hormone 2 receptor fragment (~20 kDa), or myosin-IXa fragment, (b) transforming the obtained measurements to a score or ratio, and (c) determining if the measurements indicate the presence of trypanosome infection or the risk of developing or the presence or absence of cardiomyopathy.

Certain aspects include methods of treating a patient at risk of or having initial indication of chagasic cardiomyopathy comprising: administering a treatment for cardiomyopathy to a patient having elevated levels of (i) one or more proteins selected from vimentin, gamma actin, or keratin 10, or (ii); level of cysteinyl-S-nitrosylation (SNO) of one or more of beta actin, annexin A6, ferritin light chain fragment (~18 kDa), parathyroid hormone 2 receptor fragment (~20 kDa), or myosin-IXa fragment.

The treatment of cardiomyopathy includes administration of vasodilators (e.g., prazosin, hydralazine and the like), angiotensin conversion enzyme inhibitors (e.g., captopril and the like) and the like for symptomatic therapy of dilated cardiomyopathy; and administration of β blockers (e.g., propranolol and the like) and Ca antagonists (e.g., verapamil, diltiazem and the like) to treat hypertrophic cardiomyopathy.

Certain embodiments include detecting evidence of chagasic cardiomyopathy in a biological sample, comprising the step of measuring the level or presence of at least one protein selected from the group consisting of gelsolin (GSN), myo-

sin light chain 2 (MYL2), vimentin (VIM), myosin heavy chain 11 (MYH11), vinculin (VCL), and plasminogen (PLG) in the sample. In an undiagnosed subject, the levels of one or more of the proteins can be indicative of *T. cruzi* infection. In a subject already diagnosed with *T. cruzi* infection, the protein levels can be indicative of the severity of disease, e.g., the risk of developing, or the stage of chagasic cardiomyopathy in the subject. Elevated levels of gelsolin (GSN), myosin light chain 2 (MYL2), vimentin (VIM), myosin heavy chain 11 (MYH11), vinculin (VCL), and/or plasminogen (PLG) biomarkers in the samples is indicative of *T. cruzi* infection, Chagas disease, and/or chagasic cardiomyopathy in the subject. The content of U.S. application Ser. No. 13/470,209 filed May 11, 2012 entitled "Diagnostic Methods for Assessing Risk of Chagas Disease and Heart Failure" is incorporated herein by reference in its entirety.

Certain aspects may include assessment of a subject for risk of developing chagasic cardiomyopathy. Levels of biomarkers are measured and these measurements indicate whether a subject is at risk of developing cardiomyopathy. Certain aspects include measuring the levels of VIM, GSN, MYL2, MYH11, VCL, and PLG. In a further aspect, levels of VIM are measured in combination with one or more of GSN, MYL2, MYH11, VCL, or PLG. In a further aspect, levels of GSN are measured in combination with one or more of VIM, MYL2, MYH11, VCL, or PLG. In still a further aspect, levels of MYL2 are measured in combination with one or more of VIM, GSN, MYH11, VCL, or PLG. Certain aspects include measuring levels of MYH11 in combination with one or more of VIM, GSN, MYL2, VCL, or PLG. In further aspects, levels of VCL are measured in combination with one or more of VIM, GSN, MYL2, MYH11, or PLG. In still a further aspect, levels of PLG are measured in combination with one or more of VIM, GSN, MYL2, MYH11, or VCL.

In certain aspects, the methods include treating a subject identified as (a) having *T. cruzi* infection, (b) at risk of developing chagasic cardiomyopathy, or (c) diagnosed with chagasic cardiomyopathy. Treatments can include anti-trypanosome treatments, or preventive or therapeutic treatments for cardiomyopathy, or a combination of both.

Certain aspects include methods for screening blood comprising measuring the levels of one or more of VIM, GSN, MYL2, MYH11, VCL, and PLG proteins. An increased level of one or more of these proteins is indicative of Trypanosome contamination. In certain aspects blood is screened prior to or during banking. In a further aspect, the methods can further comprise conducting confirmatory testing if the levels of one or more of the biomarkers are elevated.

Certain embodiments are directed to serodiagnostic kits for determining whether a subject is infected with *Trypanosoma cruzi* and/or staging the severity of Chagas disease, said kit comprising: (a) an antibody directed against VIM, GSN, MYL2, MYH11, VCL, and/or PLG, wherein said antibody is linked to a reporter molecule; (b) a buffer; and (c) a reagent for detection of the reporter molecule.

Other embodiments of the invention are discussed throughout this application. Any embodiment discussed with respect to one aspect of the invention applies to other aspects of the invention as well and vice versa. Each embodiment described herein is understood to be embodiments of the invention that are applicable to all aspects of the invention. It is contemplated that any embodiment discussed herein can be implemented with respect to any method or composition

of the invention, and vice versa. Furthermore, compositions and kits of the invention can be used to achieve methods of the invention.

The term “antigen” as used herein is defined as a compound, composition, or substance that can stimulate the production of antibodies or a T cell response in an animal, including compositions that are injected or absorbed into an animal. An antigen reacts with the products of specific humoral or cellular immunity, including those induced by heterologous immunogens. The term “antigen” includes all related antigenic epitopes. “Epitope” or “antigenic determinant” refers to a site on an antigen to which B and/or T cells respond. Epitopes can be formed both from contiguous amino acids or noncontiguous amino acids juxtaposed by tertiary folding of a protein.

The term “antibody” as used herein includes immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, i.e., molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen. A naturally occurring antibody (e.g., IgG, IgM, IgD) includes four polypeptide chains, two heavy (H) chains and two light (L) chains interconnected by disulfide bonds. However, it has been shown that the antigen-binding function of an antibody can be performed by fragments of a naturally occurring antibody. Specific, non-limiting examples of binding fragments encompassed within the term antibody include (i) a Fab fragment consisting of the V_L , V_H , C_L and C_{H1} domains; (ii) an F_d fragment consisting of the V_H and C_{H1} domains; (iii) an Fv fragment consisting of the V_L and V_H domains of a single arm of an antibody, (iv) a dAb fragment (Ward et al., Nature 341:544-546, 1989); and (vi) a $F(ab')_2$ fragment. Immunoglobulins and certain variants thereof are known and many have been prepared in recombinant cell culture (e.g., see U.S. Pat. No. 4,745,055; U.S. Pat. No. 4,444,487; WO 88/03565; EP 256,654; EP 120,694; EP 125,023; Falkner et al., Nature 298:286, 1982; Morrison, J. Immunol. 123:793, 1979; Morrison et al., Ann Rev. Immunol 2:239, 1984).

The term “animal” as used herein refers to living multicellular vertebrate organisms, a category that includes, for example, mammals and birds. The term mammal includes both human and non-human mammals. Similarly, the term “subject” includes both human and veterinary subjects. The term mammal includes dogs, cats, cattle, horses, goats, sheep, and other domesticated mammals, as well as non-domesticated mammals. In particular embodiments, the animal is a triatome (the insect vector of *T. cruzi*) host, e.g., a human, opossum, raccoon, armadillo, squirrel, rat, or mouse.

The term “diagnostic” refers to identifying the presence or nature of a pathologic condition. Diagnostic methods differ in their sensitivity and specificity. The “sensitivity” of a diagnostic assay is the percentage of diseased individuals who test positive (percent of true positives). The “specificity” of a diagnostic assay is 1 minus the false positive rate, where the false positive rate is defined as the proportion of those without the disease who test positive. While a particular diagnostic method may not provide a definitive diagnosis of a condition, it suffices if the method provides a positive indication that aids in diagnosis.

“Prognosis” is a probability that a pathologic condition will develop (e.g., result in additional sequelae) or progress (e.g., increase in severity).

The use of the word “a” or “an” when used in conjunction with the term “comprising” in the claims and/or the specification may mean “one,” but it is also consistent with the meaning of “one or more,” “at least one,” and “one or more than one.”

Throughout this application, the term “about” is used to indicate that a value includes the standard deviation of error for the device or method being employed to determine the value.

The use of the term “or” in the claims is used to mean “and/or” unless explicitly indicated to refer to alternatives only or the alternatives are mutually exclusive, although the disclosure supports a definition that refers to only alternatives and “and/or.”

As used in this specification and claim(s), the words “comprising” (and any form of comprising, such as “comprise” and “comprises”), “having” (and any form of having, such as “have” and “has”), “including” (and any form of including, such as “includes” and “include”) or “containing” (and any form of containing, such as “contains” and “contain”) are inclusive or open-ended and do not exclude additional, unrecited elements or method steps.

Other objects, features and advantages of the present invention will become apparent from the following detailed description. It should be understood, however, that the detailed description and the specific examples, while indicating specific embodiments of the invention, are given by way of illustration only, since various changes and modifications within the spirit and scope of the invention will become apparent to those skilled in the art from this detailed description.

DESCRIPTION OF THE DRAWINGS

The following drawings form part of the present specification and are included to further demonstrate certain aspects of the present invention. The invention may be better understood by reference to one or more of these drawings in combination with the detailed description of the specification embodiments presented herein.

FIG. 1. Saturation fluorescence labeling with uncharged cysteine-specific BODIPY-FL-maleimide (BD) dye. Three cases are presented focusing on the degree of cysteine modification reversible by Asc (i.e., SNO). All assume that the protein abundance does not change with the treatment. Case A demonstrates a canonical protein structure with no SNO before treatment with BD, after labeling, and after Asc-treatment and labeling. No change in protein spot fluorescence will be observed unless the protein abundance changes. This is quantified by the ratios of ratios as described in the Methods. Case B demonstrates the partial SNO after treatment and the resultant ratio of ratios upon Asc-treatment and labeling. Here ratios less than 1 are expressed as the negative reciprocal. Case C demonstrates the complete SNO and the ratio of ratios after Asc-reversal. If the protein abundance changes due to the cardiomyopathy, with or without SNO, the ratio of ratios will normalize the values. Taken from ref [Wiktorowicz et al., (2011) *Biochemistry* 50, 5601-5614].

FIG. 2. Variable Importance for MARS model of CCM+. Variable importance was computed for each feature in the MARS model. Y-axis, percent contribution for each analyte.

FIG. 3. ROC analysis. Shown is a Receiver Operating Characteristic (ROC) curve for the predictive model for CCM+. Y-axis, Sensitivity; X-axis, 1-Specificity.

FIG. 4. 2DE images. Shown is a reference gel of 2DE of proteins from the chagasic study subjects. The locations and identities of protein spots that contribute to the prediction of chagasic cardiomyopathy are indicated. SNO=proteins whose SNO modification is discriminatory; AM=proteins whose abundance is discriminatory.

FIG. 5. Box plot of spot 385 identified as an abundance modulated vimentin.

FIG. 6. Box plot of spot 572 identified as an SNO modified ferritin light-chain.

FIG. 7. Box plot of spot 411 identified as an SNO modified myosin fragment.

FIG. 8. Box plot of spot 524 identified as an abundance modulated keratin 10.

FIG. 9. Box plot of spot 627 identified as an SNO modified annexin A6.

FIG. 10. Box plot of spot 563 identified as an abundance modulated gamma actin.

FIG. 11. Probability of inclusion parameters from Stochastic Search Variable Selection model.

FIG. 12. SSVS model differential 2DE spot abundance in chagasic cardiomyopathy. Shown is a box-plot comparison of 2DE spot values between CCM+ and CCM- for spot 506, SNO modified parathyroid hormone receptor.

FIG. 13. SSVS model box-plot comparison of 2DE spot values between CCM+ and CCM- for spot 758, SNO modified beta actin.

FIG. 14. Illustration of computer implementation.

FIG. 15A-15D. MARS analysis of differentially abundant protein spots in C/A (clinically asymptomatic chagasic) subjects.

FIG. 16A-16D. MARS analysis of differentially abundant protein spots in C/S (clinically symptomatic chagasic) subjects.

DESCRIPTION

In 30-40% of trypanosome infected individuals disease may progress to irreversible cardiomyopathy after many years with infected individuals serving as carriers of the organism and exhibiting considerable morbidity and high risk of mortality (Machado et al., (2012) *Front Biosci (Elite Ed)* 4, 1743-58). Unfortunately, there are no vaccines or safe drugs—benznidazole and nifurtimox can be used for treatment of acute infection, but have high toxicity in adults and are ineffective in arresting or reversing the progression of the disease. Accordingly, it is crucial that biomarkers and molecular pathways are identified that could classify the disease state, detect asymptomatic individuals who are at risk of developing chagasic cardiomyopathy, identify new therapies to arrest or prevent the progression of symptomatic clinical disease, and develop tools, methods and kits to assess the efficacy of new therapies.

Distinct cardiac and plasma proteins have been identified as being oxidized/nitrated in acute and chronic chagasic animals and humans (Dhiman et al., (2008) *Am J Pathol* 173, 728-40; Wen and Garg, (2012) *Mol Cell Proteomics* 11, M111.010918. Epub 012011; Wen et al., (2012) *Mol Cell Proteomics* 11, 435-52), and there is a direct correlation between cardiac and peripheral blood level of protein oxidation in chagasic mice (Wen et al., (2008) *Microbes Infect* 10, 1201-09). These observations suggest that pathological processes leading to the development of chagasic cardiomyopathy in patients cause characteristic changes in the concentration/oxidation of proteins in the blood and generate a detectable disease-specific molecular phenotype. The inventors have identified combinations of proteins and oxidatively modified proteins (cysteinylnitrosylated, SNO) that can be used to assess the risk of developing irreversible cardiomyopathy. Certain embodiments include one or more of:

Identifying and/or using a set of proteins whose concentration and/or SNO modifications can be measured in a

patient with or without diagnosed Chagas disease to indicate the presence of trypanosome infection and/or cardiomyopathy. The predictive proteins can include, but are not limited to vimentin, gamma actin, and keratin 10. The predictive SNO proteins include, but are not limited to beta actin, annexin A6, ferritin light chain fragment (~18 kDa), parathyroid hormone 2 receptor fragment (~20 kDa), and a myosin-IXa fragment.

Identifying and/or using a set of proteins whose concentration or SNO modifications can be measured in a patient with Chagas cardiomyopathy that would indicate progression of cardiomyopathy, or the patient's response to treatment.

Formulating a predictive model consisting of weighted combinations of the same measured levels of specific proteins and SNO modified proteins that indicate risk for developing cardiomyopathy.

Clinical Human Cohorts.

The initial phase of one study utilized representative PBMC samples from seropositive chagasic patients that were clinically characterized in Argentina according to published protocols (Wen et al., (2012) *Mol Cell Proteomics* 11, 435-52). In the state of Salta, at the border of Argentina-Bolivia, Chagas disease is endemic. Patients were tested to be seropositive for *T. cruzi* infection, characterized for cardiac function, and grouped as:

CCM- group. The CCM- group included 25 seropositive, asymptomatic subjects with no indication of cardiac involvement (i.e., no echocardiography abnormalities, preserved systolic function (ejection fraction (EF) $\geq 55\%$), no left ventricular dilatations, and negligible-to-minor EKG alterations).

CCM+ group. The CCM+ group included 28 seropositive, symptomatic chagasic patients with a degree of systolic dysfunction (EF: $\leq 40-54\%$) and/or left ventricular dilatation (diastolic diameter ≥ 57 mm).

Classification of Chagas disease was done according to the NYHA Guidelines.

The inventors employ a rigorous blood collection and storage protocol to ensure sample quality. Briefly, heparinized blood (10 ml/subject) is centrifuged at 1000 g, 4° C. for 20 min and the resulting buffy-coat transferred to a new tube containing percoll (1.084 g/L) cushion. After centrifugation as above, PBMCs lying at the PBS-percoll interface are transferred to a new tube, and washed with cold PBS. PBMC pellets are stored at -80° C. for future use.

Saturation Fluorescence Labeling and Cysteinylnitrosylation by Fluorescence (SNOFlu).

After cysteine (cysteic acid) content was determined by amino acid analysis (Model L8800, Hitachi High Technologies America, Pleasanton, Calif.), the proteins obtained from PBMCs of Chagasic patients (+/-cardiomyopathy) by urea/thiourea extraction were split into two equal pools. One pool was processed for quantitative saturation fluorescence labeling with uncharged BODIPY FL-maleimide (BD) at a dye-to-protein thiol ratio of greater than 50:1 ratio. This saturation fluorescence labeling method has yielded high accuracy (>91%) in quantifying blinded protein samples (Pretzer and Wiktorowicz, (2008) *Anal Biochem* 374, 250-262).

The second pool was first treated with 6 mM ascorbic acid (Asc) to remove S-nitrosyl (SNO) groups from cysteine residues. These samples were then dialyzed against the urea/thiourea extraction buffer, after which the proteins were labeled with BD as above.

The BD-labeled proteins were separated using two-dimensional gel electrophoresis (2DE) employing an IPGphor

multiple sample IEF device (Pharmacia, Piscataway, N.J.) in the first dimension, and Protean Plus and Criterion Dodeca cells (Bio-Rad, Hercules, Calif.) in the second dimension (Jamaluddin et al., (2010) *J Virol* 84, 9533-45). Sample aliquots were first loaded onto 11 cm dehydrated precast immobilized pH gradient (IPG) strips (Bio-Rad), and rehydrated overnight. IEF was performed at 20° C. with the following parameters: 50 Volts, 11 h; 250 V, 1 h; 500 V, 1 h; 1000 V, 1 h; 8000 V, 2 h; 8000 V, 6 h. The IPG strips were then be incubated in 4 mL of equilibration buffer (6 M urea, 2% SDS, 50 mM Tris-HCl, pH 8.8, 20% glycerol) containing 10 µl/mL tri-2 (2-carboxyethyl) phosphine (Geno Technology, Inc., St. Louis, Mo.) for 15 minutes at 22° C. with shaking. The samples were incubated in another 4 mL of equilibration Buffer with 25 mg/mL iodoacetamide for 15 min at 22° C. with shaking in order to ensure protein S-alkylation of any residual reduced thiol groups. Electrophoresis was performed at 150 V for 2.25 h, 4° C. with precast 8-16% polyacrylamide gels in Tris-glycine buffer (25 mM Tris-HCl, 192 mM glycine, 0.1% SDS, pH 8.3) (Pretzer and Wiktorowicz, (2008) *Anal Biochem* 374, 250-262).

Protein Fluorescence Staining. After electrophoresis, the gels were directly imaged at 100 µm resolution using the GE Healthcare Typhoon Trio Proteomic Imaging System to quantify BD-labeled proteins (>90% of human proteins contain at least one cysteine (Miseta and Csutora, (2000) *Mol Biol Evol* 17, 1232-39). A gel containing the most common features was selected by Nonlinear SameSpots software (see below) as the reference gel for the entire set of gels. The gel was destained in 20% ethanol/10% acetonitrile, washed with water, and scanned at 485/550 nm (ex/em). The exposure time was adjusted to achieve a value of ~55,000-63,000 pixel intensity (16-bit saturation) from the most intense protein spots on the gel.

Measurement of Relative Spot Intensities.

The 2D gel images were analyzed using Progenesis/SameSpots software (Nonlinear Dynamics, Ltd. Newcastle Upon Tyne, UK). The reference gel was selected according to quality and number of spots. Spots boundaries were established after automated "pixel to pixel" matching with manual adjustment, boundaries were examined to ensure proper distinction, and the gel images were used to obtain the quantitative spot data. This strategy ensures that spot numbers and outlines were identical across all gels in the experiment, eliminating problems with unmatched spots (Dowsey et al., (2010) *Methods Mol Biol* 604, 239-55; 13, 14) as well as ensuring that the greatest number of protein spots and their spot volumes were accurately detected and quantified. Spot volumes were normalized using a software-calculated bias value assuming that the great majority of spot volumes did not change in abundance.

SNOFlo Data Processing.

SNOFlo uses a thiol-reactive fluorescent label to detect free thiols in proteins. The presence of a nitrosyl (NO) group will prevent the labeling of thiols, so that when compared to the same sample for which all NO groups have been removed (Asc+ treatment), SNO labeled proteins will yield spot volumes less than the Asc+ treatment (no NO modification; FIG. 1) (Wiktorowicz et al., (2011) *Biochemistry* 50, 5601-14). However, since one goal was to establish classifiers of chagasic cardiomyopathy, variation in protein intensities (spot volumes) may reflect changes in SNO status, changes in protein abundance, or both. Treatment of half of a patient PBMC extract with Asc removes all NOs, and spot volume ratio within Asc+ treatment, but across patient cardiac status, yields an estimate of the change in protein

abundance, while spot volume ratios within Asc-treatment yields a combined estimate of change in SNO and/or protein abundance. Thus in order to normalize the SNO from abundance changes, the inventors calculate a ratio of ratios of Asc- ratios with Asc+ treatment ratios of each protein spot and a normalized SNO ratio according to the equations as follows:

$$\text{Ratio of ratios} = \frac{\left[\frac{BD_{Asc-}^{Exp}}{BD_{Asc-}^{Ctrl}} \right]}{\left[\frac{BD_{Asc+}^{Exp}}{BD_{Asc+}^{Ctrl}} \right]} = \frac{\Delta[Cys-NO]}{\Delta[\text{protein}]}$$

where BD=normalized BODIPY fluorescence intensity of a protein spot, Asc-=non-Asc treated, Asc+=Asc treated, Exp=CCM+, Ctrl=CCM-.

However, since particular statistical model building software requires single values from each patient within his/her cohort, only the Asc-/Asc+, and Asc+ ratios were used to determine classifiers, as follows:

$$\text{Normalized SNO Ratio} = \frac{BD_{Asc-}}{BD_{Asc+}} = \frac{[Cys-NO]}{[\text{protein}]}$$

to reflect the SNO status of each protein spot, or:

$$\text{Protein Abundance Ratio} = \frac{BD_{Asc+}^{Exp}}{BD_{Asc+}^{Ctrl}} = \Delta[\text{protein}]$$

to reflect the difference in protein abundance CCM+ to CCM-.

Protein Identification.

Selected 2DE spots were picked robotically, trypsin-digested, and peptide masses identified by MALDI TOF/TOF (AB Sciex 5800, Foster City, Calif.). Data were analyzed with the Applied Biosystems software package included 4000 Series Explorer (v. 3.6 RC1) with Oracle Database Schema Version (v. 3.19.0), Data Version (3.80.0) to acquire both MS and MS/MS spectral data. The instrument was operated in positive ion reflectron mode, mass range was 850-3000 Da, and the focus mass was set at 1700 Da. For MS data, 2000-4000 laser shots were acquired and averaged from each sample spot. Automatic external calibration was performed using a peptide mixture with reference masses 904.468, 1296.685, 1570.677, and 2465.199.

Following MALDI MS analysis, MALDI MS/MS was performed on several (5-10) abundant ions from each sample spot. A 1 kV positive ion MS/MS method was used to acquire data under post-source decay (PSD) conditions. The instrument precursor selection window was +/-3 Da. For MS/MS data, 2000 laser shots were acquired and averaged from each sample spot. Automatic external calibration was performed using reference fragment masses 175.120, 480.257, 684.347, 1056.475, and 1441.635 (from precursor mass 1570.700).

Applied Biosystems GPS Explorer™ (v. 3.6) software was used in conjunction with MASCOT to search the respective protein database using both MS and MS/MS spectral data for protein identification. Protein match probabilities were determined using expectation values and/or MASCOT protein scores. MS peak filtering included the following parameters: mass range 800 Da to 4000 Da, minimum S/N filter=10, mass exclusion list tolerance=0.5

Da, and mass exclusion list (for some trypsin and keratin-containing compounds) included masses 842.51, 870.45, 1045.56, 1179.60, 1277.71, 1475.79, and 2211.1. For MS/MS peak filtering, the minimum S/N filter=10 (Wen and Garg, (2012) *Mol Cell Proteomics* 11, M111.010918. Epub 012011; Wen et al., (2012) *Mol Cell Proteomics* 11, 435-52).

For protein identification, the *Homo sapiens* taxonomy was searched in the NCBI database. Other parameters included the following: selecting the enzyme as trypsin; maximum missed cleavages=1; fixed modifications included carbamidomethyl (C) for 2-D gel analyses only; variable modifications included oxidation (M); precursor tolerance was set at 0.2 Da; MS/MS fragment tolerance was set at 0.3 Da; mass=monoisotopic; and peptide charges were only considered as +1 (Wen and Garg, (2012) *Mol Cell Proteomics* 11, M111.010918. Epub 012011; Wen et al., (2012) *Mol Cell Proteomics* 11, 435-52).

Protein identification was performed using a Bayesian algorithm (Zhang and Chait, (2000) *Anal Chem* 72, 2482-89) where matches were indicated by expectation score, an estimate of the number of matches that would be expected in that database if the matches were completely random. In some circumstances, confirmation of the protein identification was performed by LC-MS/MS (Orbitrap Velos, ThermoFinnigan, San Jose, Calif.).

Statistical Analysis.

Statistical comparisons were performed using SPSSv18 (SPSS, Inc., Chicago, Ill.) and R.

Multivariate Adaptive Regression Splines (MARS). Log base 2-transformed differential protein expression data and differential protein SNO data were used for MARS modeling. The MARS model specified 6 possible basis functions. MARS is a non-parametric regression method that uses piecewise linear spline functions (basis functions) as predictors. The basis functions are combinations of independent variables and so this method allows detection of feature interactions and performs well with complex data structures (Friedman and Roosen, (1995) *Stat Methods Med Res* 4, 197-217). MARS uses a two-stage process for constructing the optimal classification model. The first half of the process involves addition of basis functions until a user-specified number of basis functions have been reached. In the second stage, MARS deletes basis functions in order, starting with the basis function that contributes the least to the model until an optimum model is reached. Ten-fold generalized cross-validation was used to avoid over-fitting the classification model (Salford Systems, Inc).

Stochastic Search Variable Selection (SSVS). Stochastic variable search is a procedure that selects promising subsets of predictor variables in the defined design matrix, which is based on embedding the entire regression setup in a hierarchical Bayes normal mixture model, where latent variables are used to specify choices of subsets (George and McCulloch, (1993) *J. American Statistical Association* 88, 881-89). Those subsets with higher probability can be identified by their more frequent appearance in the Gibbs sample. The inventors explored different methods to improve the classification accuracy, having fewer misclassifications while using fewer predictors. The WinBUGS software for Bayesian analysis using Markov Chain Monte Carlo (MCMC) method was used.

Proteomic Analyses.

In one study the chagasic cohort consisted of 53 patients in total (25 CCM-; 28 CCM+) in which each sample was split in two with one treated with ascorbate (to reverse SNO modifications) and the other processed without ascorbate.

After labeling and spot fluorescence quantification, the first treatment reflects the protein concentration, while the second reflects the degree of SNO modification. Both are useful for establishing candidate classifiers for CCM.

Thus 106 2D gels were analyzed, resulting in the detection of 635 protein spots after filtering and manual examination of the gel images. Two separate ratios of each treatment class with respect to the comparison of CCM+ to CCM- patients were calculated as indicated above. Submitted for statistical analyses were the abundance ratio of each spot (Asc+) CCM+:CCM-, and the normalized SNO ratio (Asc-/Asc+) of CCM+ separately from CCM-.

Statistical Analyses.

Multivariate Adaptive Regression Splines (MARS) is a nonparametric, multivariate regression method that can estimate complex nonlinear relationships by a series of spline functions of the predictor variables. Regression splines seek to find thresholds and breaks in relationships between variables and are very well suited for identifying changes in the behavior of individuals or processes over time. As a non-parametric approach, MARS does not make any underlying assumptions about the distribution of the predictor variables of interest. This characteristic is useful in chagasic cardiomyopathy modeling because protein expression values are not normally distributed, as would be required for the application of classical modeling techniques such as logistic regression. The basic concept behind spline models is to model using potentially discrete linear or nonlinear functions of any analyte over differing intervals. The resulting piecewise curve, referred to as a spline, is represented by basis functions within our model. Other studies have shown that MARS is a superior method in the prediction of non-parametric datasets to phenotypes (Brasier et al., (2010) *Clin Transl Sci* 3, 147-57). To reduce over-fitting, the inventors restricted their analysis to models that incorporated one or fewer interaction terms.

The MARS model specified 15 possible basis functions and allowed only 1 interaction term. Ten-fold cross-validation, a more accurate way to measure how efficiently the classifier has learned a concept base using the training set, was used to avoid over-fitting the classification model (Salford Systems, Inc).

The 2D gel electrophoresis data were initially analyzed using Student's t-test, and was performed on two separate classes of data derived from the 635 protein spots that were quantified. The first was performed on the ratio of SNO signal (Asc-) and abundance signal (Asc+); this ratio normalized the SNO signal (Asc-) against the protein abundance indicator (Asc+) for each protein spot. Of the 635 spots detected by 2D gel electrophoresis, 23 had significant p-values (<0.05) for Asc-/Asc+. The second class of data considered only the change in protein abundance (Asc+) between CCM- and CCM+ patients. From this analysis, 13 spots exhibited significant p-values between CCM- and CCM+ patients. Between the two classes of data, the common spots were spot 267, spot 650, and spot 735. The 33 spots in total were used to create a classification model using MARS.

The inventors used the log 2 transform of all the data present in the modeling process, with a possible maximum of 15 basis functions and 1 possible interaction term. This resulted in a model with 6 variables whose relative importance to the model is shown in FIG. 2, where spot 563 (100%) was the most influential and spot 385 the least. This model resulted in 100% accuracy for classifying CCM+/CCM- patients. The distributions of each spot selected in the MARS model are shown in the box plots (FIGS. 5-10).

The MARS model was unable to produce a highly accurate classifier of CCM+. The resultant model was able to accurately predict CCM- status with 100% accuracy, but only 78% accuracy for the CCM+ patients. This resulted in an overall accuracy of 89%. The AUC (area under the curve) for such a model is 0.99 (FIG. 3).

The optimal MARS model is represented by 6 basis functions. The resultant classification model for these 6 basis functions is $Y=1.03427+0.586711*BF2-0.178427*BF5-0.638033*BF10-0.263085*BF11-0.244576*BF12+2.64392*BF14$ (Table I).

The optimal Stochastic Search Variable Selection (SSVS) model with spike and slab priors identified spots **506** and **758** to differentiate CCM+ from CCM- patients. The marginal probability of each spot of being selected is shown in the probability plot (FIG. 11). The distributions of protein expression by disease classification are shown in the box plots (FIGS. 12 and 13). The Gibbs sampler method for SSVS allows for the interrogation of the model space efficiently without fitting all possible models with the inferences not driven by the model assumptions. The Bayesian hierarchical methods to variable selection and classification are complementary approaches of omic data in that the uncertainty in the model choice can be incorporated into the analysis. For analysis of the data with 33 spots, the 25,000 iterations of the MCMC were completed by removing the first 1000 for burn-in and saving every 5th iteration. In the case of a binary outcome, the latent probit model in which posteriors distribution for the latent indicator variables are estimated via MCMC could be used.

The positions of the MARS and the SSVS selected spots are shown in the SameSpots selected reference gel (FIG. 4), with each spot showing its identity and its selection criterion (either abundance or SNO). The protein IDs and other quantitative information are shown in Table II.

Evaluation of the model performance is seen by analysis of the area under the Receiver Operating Characteristic

(ROC) curve (AUC), where sensitivity vs. 1-specificity was plotted. In the ROC analysis, a diagonal line (45 degree slope) starting at zero indicates that the output was a random guess, whereas an ideal classifier with a high true positive rate and low false positive rate will curve positively and strongly towards the upper left quadrant of the plot (Fawcett, (2006) *Pattern Recognition Letters* 27, 861-74). The AUC is equivalent to the probability that two cases, one chosen at random from each group, are correctly ordered by the classifier (Hanley and McNeil, (1982) *Radiology* 143, 29-36). The AUC for the CCM+ model is 0.998.

TABLE I

MARS Basis Functions.			
B_m	Definition	a_m	Variable descriptor
BF2	$(1.07 - \text{Spot } 385)_+$	5.87E-1	Spot 385 (vimentin-abundance)
BF5	$(\text{Spot } 572 - 0.72)_+$	1.78E-1	Spot 572 (ferritin light chain-SNO)
BF10	$(1.09 - \text{Spot } 563)_+$	6.38E-1	Spot 563 (gamma actin-abundance)
BF11	$(\text{Spot } 627 - 0.29)_+$	2.63E-1	Spot 627 (annexin A6-SNO)
BF12	$(\text{Spot } 524 - 0.25)_+$	2.45E-1	Spot 524 (keratin 10-abundance)
BF14	$(0.75 - \text{Spot } 411)_+$	2.64	Spot 411 (myosin fragment-SNO)

Shown are the basis functions (BF) for the MARS model for chagasic cardiomyopathy where, B_m = each individual basis function, a_m = coefficient of the basis function, $(y)_+ = \max(0, y)$. The actual model is: $Y = 1.03427 + 0.586711*BF2 - 0.178427*BF5 - 0.638033*BF10 - 0.263085*BF11 - 0.244576*BF12 + 2.64392*BF14$, where $BF2 = \max(0, 1.07265 - \text{Spot } 385)$, $BF5 = \max(0, \text{Spot } 572 - 0.721195)$, $BF10 = \max(0, 1.9067 - \text{Spot } 563)$, $BF11 = \max(0, \text{Spot } 627 - 0.288306)$, $BF12 = \max(0, \text{Spot } 524 - 0.248617)$, and $BF14 = \max(0, 0.74921 - \text{Spot } 411)$

TABLE II

Spot identities obtained by mass spectrometry. Both abundance and normalized SNO classifiers are provided. t-test values refer to either abundance or SNO ratios, whichever is provided. SSVS denotes spots were selected by Stochastic Search Variables Selection, not t-test. Identities with MS Scores greater than 56 have significance levels of identification greater than 95%.								
No.	Protein name	SwissProt Accession	MW (kDa)	MS Score	Abundance CCM+:CCM-	t test (p)	CCM+ SNO Ratio	CCM- SNO Ratio
1	Vimentin	F5H288	5.72	29	171	1.43	0.006	
2	Ferritin-light chain	PO2792	5.80	18	74		0.023	-1.04
3	γ -Actin	I3L1U9	5.99	18	137	-1.82	0.031	
4	Annexin A6	E5RIU8	5.47	15	103		0.040	-1.18
5	Keratin 10	P13645	9.34	19	286	1.54	0.046	
6	Myosin-IXa fragment		7.98	26	46		0.038	-1.11
7	Parathyroid hormone receptor	H7COB0	8.92	20	42		SSVS	1.36
8	β -Actin	B4E335	5.44	38	624		SSVS	-1.02

TABLE III

Summary of proteins selected.						
SUMMARY OF PROTEINS SELECTED BY p-VALUE AND RATIOS (ABUNDANCE OR RoR)						
No.	Protein name	Accession No.	pI (Gel)	MW (kD)	(Gel)	
1	Vincolin	P18208	7.53	99		
2	Serum albumin (Fragment)	H0YA55	5.97	63		
3	Isoform 3 of Integrin alpha-IIb	P08514-3	4.19	55		
4	Isoform H7 of Myeloperoxidase	P05164-3	0.41	56		
5	Actin, cytoplasmic 2, N-terminally processed	F5H0N0	6.41	41		
6	Talin 1	Q5TCU6	5.18	32		
7	Actin, cytoplasmic 1, N-terminally processed	B4E335	4.88	30		
8	Actin, cytoplasmic 1, N-terminally processed	B4DW52	7.51	26		
9	Unconventional myosin-IXa	H3BMM1	7.98	26		
10	Peptidyl-prolyl cis-trans isomerase A	P62937	8.03	26		
11	WD repeat-containing protein 49	F8WBC8	8.84	23		
12	Keratin, type II cytoskeletal 1	P04264	7.12	20		
13	Parathyroid hormone 2 receptor (Fragment)	H7C0B0	8.92	20		
14	Proteasome subunit beta type-2	P49721	7.95	19		
15	Ferritin light chain	P02792	5.8	18		
16	Annexin	E5RIU8	5.47	15		
17	Actin, cytoplasmic 1, N-terminally processed	G5E9RD	5.12	15		
18	Keratin, type I cytoskeletal 10	P13645	7.71	15		
19	Heterogeneous nuclear ribonucleoprotein A1 (Fragment)	F6W646	7.26	15		
20	SH3 domain-binding glutamic acid-rich-like protein 3	Q9H299	4.32	10		
21	Ras-related protein Rap-1b	B4E335	4.4	0		
22	Actin, cytoplasmic 1, N-terminally processed	B4E335	5.44	38		
23	Actin, cytoplasmic 1, N-terminally processed	B4E335	7.47	78		
24	POTE ankyrin domain family member F	A5A3E0	6.57	41		
25	Vimentin	F5H288	5.72	29		
26	Protein S100-A11	P31949	6.9	10		
27	Isoform 2 of Fibrinogen alpha chain	P02671-2	8.84	41		
28	Tubulin beta chain	Q5JP53	0.33	34		
29	Myosin regulatory light chain 12B	O14950	4.38	17		
30	Annexin A3	P12429	6.09	28		
31	Keratin, type 1 cytoskeletal 10	P13645	9.34	19		
32	Actin, cytoplasmic 2, N-terminally processed (Fragment)	I3L1U9	5.99	18		
33	ATP synthase subunit alpha	ABK092	5.64	16		

No.	MS ID	Abundance	p-Value	p-Value	Selection	
No.	Expectation Value	Ratio	(Asc+ <0.05)	(Asc- <0.05)	Criterion	
1	1.9905E-19	1.32	0.182504	-1.32	0.044584	RoR
2	1.5811E-12	-1.25	0.204533	1.69	0.033111	
3	1.2559E-22	1.17	0.339162	-1.06	0.027258	
4	9.9763E-04	1.75	0.125809	-1.71	0.045972	
5	1.9905E-06	1.30	0.034774	-1.34	0.047502	
6	1.5811E-14	-1.07	0.350146	1.26	0.034137	
7	1.2559E-42	-1.10	0.291819	1.17	0.006024	
8	3.9715E-09	1.13	0.116141	-1.27	0.023729	
9	1.9905E+00	-1.02	0.516115	-1.13	0.037733	
10	7.9245E-07	-1.10	0.195105	1.14	0.021102	
11	1.9905E+00	1.37	0.413441	1.09	0.042012	
12	3.9716E-11	-1.09	0.61982	-1.27	0.012075	
13	5.0000E+00	-1.33	0.051258	1.50	0.033418	
14	5.0000E-04	-1.08	0.532056	-1.23	0.02477	
15	3.1548E-03	1.23	0.08741	-1.15	0.023404	
16	3.9716E-06	1.44	0.150651	-1.38	0.040421	
17	3.9716E-15	1.05	0.915841	-1.19	0.020184	
18	1.5811E+00	-1.00	0.214532	-1.20	0.045743	
19	5.0000E-06	-1.47	0.016761	1.52	0.043125	
20	9.9763E-31	1.29	0.029492	-1.30	0.032468	
21	1.2559E-01	1.23	0.180346	-1.22	0.040693	
22	3.1548E-58	-1.01	0.956162	1.15	0.037653	
23	3.1548E-41	1.50	0.158319	-1.44	0.02411	
24	6.2946E-08	1.39	0.0115	-1.35		Abundance
25	6.2946E-13	1.43	0.00623	-1.41		
26	1.9905E-20	-1.60	0.037919	1.19		
27	3.1548E-01	-1.45	0.035493	1.04		
28	6.2946E-08	-1.20	0.034097	1.19		
29	7.0245E-28	-1.19	0.047581	1.07		
30	9.9753E-51	-1.41	0.027378	1.34		
31	1.9905E-24	1.55	0.046182	-1.35		
32	1.5811E-09	-1.83	0.030027	2.47		
33	2.5050E-05	1.27	0.038451	1.17		

MARS analysis of differentially abundant protein spots in C/A (clinically asymptomatic chagasic) subjects. Input to the model were protein spots that were differentially expressed at $p < 0.001$ in C/A (84 spots, $n=25$) subjects with respect to N/H (normal healthy) controls ($n=30$). 10-fold cross-validation was employed (FIG. 15A and FIG. 15C) and 80% testing/20% training (FIG. 15C and FIG. 15D) approaches to assess the fit of the model for testing dataset. Shown are the protein spots identified with high ranking (score >20) by CV (FIG. 15A) and 80/20 (FIG. 15B) approaches for creating the MARS model for classifying C/A from N/H subjects. Protein spots in FIG. 15A and FIG. 15B are identified as spot #-protein name and fold change (increase \uparrow , decrease \downarrow) are plotted on each bar. The ROC curves show the prediction success of the CV (FIG. 15C) and 80/20 models (FIG. 15D). curves: training data ((AUC/ROC: 1.00), and testing data (AUC/ROC: 0.96 for CV and 0.933 for 80/20).

MARS analysis of differentially abundant protein spots in C/S (clinically symptomatic chagasic) subjects. Input to the model were protein spots that were differentially expressed at $p < 0.001$ in C/S (87 spots, $n=25$) subjects with respect to N/H controls ($n=30$). 10-fold cross-validation was employed (FIG. 16A and FIG. 16C) and 80% testing/20% training (FIG. 16C and FIG. 16D) approaches to assess the fit of the model for testing dataset. Shown are the protein spots identified with high ranking (score >20) by CV (FIG. 16A) and 80/20 (FIG. 16B) approaches for creating the MARS model for classifying C/S subjects from N/H subjects. Protein spots in FIG. 16A and FIG. 16B are identified as spot #-protein name and fold change (increase \uparrow , decrease \downarrow) are plotted on each bar. The ROC curves show the prediction success of the CV (FIG. 16C) and 80/20 models (FIG. 16D). curves: training data ((AUC/ROC: 1.00), and testing data (AUC/ROC: 0.926 for CV and 1.0 for 80/20).

Certain embodiments include biomarkers identified in a previous study. Parasite persistence and oxidative damage in the heart are known to be of pathological significance during Chagas disease (Zacks et al., (2005) *An Acad Bras Cienc*, 77, 695-715; Gupta et al., (2009) *Interdiscip Perspect Infect Dis*, 2009, 190354). Infected rats treated with an anti-parasite drug (BZ) and/or antioxidant (PBN) showed that the beneficial effects of these treatments in controlling parasite- and oxidative stress-induced pathology, respectively (Wen et al., (2006) *Am J Pathol*, 169, 1953-1964; Wen et al., (2010) *J Am Coll Cardiol*, 55, 2499-2508), are reflected in a plasma proteome profile of chagasic rats. In the previous study the inventors identified 92 proteins that were differentially expressed or oxidized in chagasic plasma. Functional analysis allocated a majority of these proteins to inflammation/immunity and lipid metabolism categories, and to molecular pathways associated with cardiovascular dysfunction, e.g., myocardial infarction, hypertrophy, and fibrosis, and pulmonary embolism and hypertension. Some proteins in chagasic rats treated with PBN and/or BZ were allocated to curative pathways (immune regulation and cardiac remodeling). The 2D-GE results were validated by Western blotting. It was demonstrated that the disease-associated increased expression of GSN and VIM, and release of cardiac MYL2 in the plasma of chagasic rats was normalized by PBN/BZ treatment. Increased plasma levels of GSN, MYL2, and VIM were directly correlated with the severity of cardiac disease in human chagasic patients. This is the first study demonstrating that the plasma oxidative and inflammatory response profile and plasma detection of cardiac proteins parallel the pathologic events contributing to Chagas disease development. These findings have utility in

diagnosing disease severity and designing suitable therapy for management of human chagasic patients.

Inflammation/Immune Response.

Ingenuity Pathway Analysis (IPA) is a highly curated and comprehensive software used for the integration of proteins into networks and pathways with biological meaning (Thomas and Bonchev, (2010). *Hum Genomics*, 4, 353-360). Network analysis of the plasma proteome profile of chagasic rats identified four major sub-networks linked to host response to *T. cruzi* infection and disease development (Table V). The maximal numbers of the differentially expressed plasma proteins (19 proteins) in chagasic rats were associated with antigen presentation and inflammatory response category (Table V) and indicators of persistent inflammation, known to be of pathological significance in Chagas disease (Dhiman et al., (2009) *Clinical and Vaccine Immunology*, 16, 660-666; Tanowitz et al., (2009) *Prog Cardiovasc Dis*, 51, 524-539; Junqueira et al., (2010) *Expert Rev Mol Med*, 12, e29). Following functional analysis of the inflammation-associated proteins, 12 proteins (APOA1, APOE, C3, CFB, CFH, FGB, GSN, KRT10, PLG, SCG2, SERPINA1, and SERPINC1) were identified as being involved in immune cell trafficking and cell movement of leukocytes, granulocytes, phagocytes, neutrophils, and dendritic and antigen presenting cells. Some of the differentially expressed proteins in inflammation category were associated with activation (APOE, C3, CFH, GC and PLG), chemotaxis (C3, SCG2, SERPINA1, SERPINC1), and infiltration of leukocytes (APOA1, APOE, C3, PLG, KRT10) and neutrophils (C3, CFB, CFH, PLG). Up regulation of APOE, APOA1, APOH, GC and PLG in chagasic plasma was indicative of activation, binding and accumulation of macrophages in the disease state. Of the 19 differentially expressed inflammation-associated proteins, 11 proteins (APOE, C3, CFB, CFH, GSN, KRT10, SCG2, SERPINA1, SERPINC1, GC, and PLG) were carbonylated in chagasic plasma. PBN treatment prevented the oxidative modification of five of these proteins (i.e., CFB, CFH, SERPINA1, SERPINC1, and PLG). Interestingly, PBN treatment also normalized or regulated the expression of several inflammation-associated proteins, including APOH, APOE, CFH, PLG and SCG2 in acutely infected rats and APOH, GC, GSN and PLG in chronically infected rats; while the expression level of CFB, GSN, C3, and SERPINC1 was partly regulated by PBN in infected rats (Tables IVa-IVb). Other proteins (APOE, C3, KRT3, and SCG2) were exposed to oxidation due to *T. cruzi*-induced, acute oxidative stress, but were normalized in expression and oxidation during the chronic phase.

Treatment of rats with anti-parasite drug (BZ) was not effective in preventing protein carbonylation. These observations indicate that oxidative stress plays an important role in modulating the host immune response against *T. cruzi*. ROS elicit inflammatory cytokines (e.g. TNF- α , IFN- γ , IL-1 α) in cardiomyocytes infected by *T. cruzi* (Gupta et al., (2009) *Free Radic Biol Med*, 47, 1414-21; Ba et al., (2010) *J Biol Chem*, 285, 11596-606). Inflammatory pathology was controlled in chronically infected experimental animals and human patients by enhancing the antioxidant status, which was also beneficial in preserving the cardiac function during Chagas disease (Wen et al., (2006) *Am J Pathol*, 169, 1953-1964; Wen et al., (2010) *J Am Coll Cardiol*, 55, 2499-2508; Ba et al., (2010) *J Biol Chem*, 285, 11596-606; Souza et al., (2010) *Mem Inst Oswaldo Cruz*, 105, 746-751). Recent observations indicate that the mitochondrial release of ROS due to electron transport chain dysfunction and enhanced release of electrons to molecular oxygen is the

primary source of oxidative stress in the heart (Wen and Garg, (2008) *J Bioenerg Biomembr*, 40, 587-598).

Lipid Metabolism.

Seventeen of the differentially expressed proteins in chagasic plasma, i.e., AFM, C4BPA, CACNA1D, DLGAP2, GC, KNG1, MUG1, MYLPF, MY05A, MY05B, PRPH, PZP, RAI14, and SCG2, were allotted to the lipid metabolism/molecular transport/small molecule biochemistry category (Table V) and functionally linked by IPA network analysis to lipid, fatty acid, and carbohydrate metabolism. A majority of the proteins in this category, i.e., ALB, APOA1, APOA4, APOE, APOH, C3, GC, GNAQ, MY05A, PLG, SCD2, SERPINA1, SERPINC1 and VIM, were linked to the synthesis, metabolism, transport, and modification of lipids and fatty acids, and to uptake and release or efflux of lipids, eicosanoids, and cholesterol. PBN/BZ-treated/infected rats exhibited normalization in the expression of 13 of the proteins linked to lipid/fatty acid metabolism (Tables IVa-IVb). These data provide the first indication that lipid/fatty acid metabolism is dysregulated and of pathologic significance in Chagas disease. The observation of increased expression of CEP350 in chagasic rat plasma provides clues to the pathologic mechanism involved in altered lipid/fatty acid metabolism during Chagas disease. CEP350 is a large centrosome-associated protein with a CAP-Gly domain typically found in cytoskeleton-associated proteins (Yan et al., (2006) *Mol Biol Cell*, 17, 634-44; Patel et al., (2005) *J Cell Sci*, 118, 175-86). CEP350 interacts with other centrosomal proteins (e.g. FGFR1) and has been implicated in the mechanisms underlying microtubule anchoring and organization at the centrosome (Yan et al., (2006) *Mol Biol Cell*, 17, 634-44). Interestingly, CEP350 is also shown to alter the activity and sub-cellular compartmentalization of members of the peroxisome proliferator-activated receptors family (PPAR α , PPAR β/δ , and PPAR γ) (Patel et al., (2005) *J Cell Sci*, 118, 175-86) that heterodimerize with retinoid X receptors (RXRs) to function as transcription factors, and play essential roles in the regulation of cell differentiation and lipid/fatty acid metabolism (Qi et al., (2000) *Cell Biochem Biophys*, 32 Spring, 187-204; Sztatmari et al., (2007) *Blood*, 110, 3271-80). Besides CEP350, SERPINS and GPT that were up regulated in chagasic plasma and function in inflammatory response/tissue remodeling and amino acid metabolism, respectively, also belong to the network of proteins regulated by PPARs (Carter and Church, (2009) *PPAR Res*, 2009, 345320; Rakhshandehroo et al., (2010) *PPAR Res*, 2010).

Cardiovascular disease-associated proteins. Twenty-four of the differentially expressed proteins, i.e., AFM, ALB, APOA1, APOA4, APOE, APOH, C3, CFB, CFH, FGB, GC, GNAQ, GSN, HPX, ITIH4, KNG1, MY05A, PLG, SCD2, SCG2, SERPINA1, SERPINC1, SERPINF1, and VIM, were linked to cardiovascular function, skeletal and muscular disorders, and cardiovascular diseases (Table V). Of these, nine proteins (APOA1, APOE, APOH, C3, KNG1, PLG, SCG2, SERPINC1, and SERPINF1) play a functional role in the proliferation of endothelial cells, while several others correlate with angiogenesis (APOE, APOH, PLG, SCG2, SERPINC1, and SERPINF1), thrombosis or thromboembolism (APOE, APOH, CFB, GNAQ, PLG, and SERPINC1), myocardial ischemia and infarction (ALB, C3, FGB, GSN, PLG, APOA1, APOE, PLG, and SERPINC1), and atherosclerosis (APOA1, APOA4, APOE, and PLG) (Diez et al., (2010) *Mol Biosyst*, 6, 289-304). The latter findings indicate that endothelial cell dysfunction plays a role in the progres-

sion of Chagas disease and demonstrate that the plasma proteome profile is a useful indicator of clinical disease status.

Biomarkers of Chagas Disease.

An objective of the studies described below was to identify the diagnostic biomarkers of Chagas disease. Western blot analysis using antibodies specific to GSN, MYL2, and VIM validated the 2D-GE plasma profile of chagasic rats and demonstrated that GSN, MYL2, and VIM are indeed increased in the plasma of chagasic rats. There was a direct correlation in plasma levels of GSN, MYL2, and VIM and disease severity in human chagasic patients. Further, PBN/BZ-mediated control of cardiac pathology and preservation of heart contractile function in chagasic rats (Wen et al., (2006) *Am J Pathol*, 169, 1953-64; Wen et al., (2010) *J Am Coll Cardiol*, 55, 2499-508) was associated with normalized plasma levels of GSN, MYL2, and VIM similar to that noted in normal controls. These findings indicate GSN, MYL2, and VIM can be used as protein biomarkers of Chagas disease.

Pathologic Significance of GSN, MYL2, and VIM in Cardiovascular Diseases.

Besides their importance as diagnostic markers in Chagas disease observed herein, GSN, MYL2, and VIM play a significant role in heart disease. GSN is an actin-binding protein, and a member of the gelsolin/villin superfamily (Silacci et al., (2004) *Cell Mol Life Sci*, 61, 2614-23), located intracellularly (cytosol, mitochondria) and extracellularly (blood, plasma) (Koya et al., (2000) *J Biol Chem*, 275, 15343-49). It is a key regulator of actin filament assembly and disassembly and is involved in maintaining cell structure and motility (Silacci et al., (2004) *Cell Mol Life Sci*, 61, 2614-23). Increased GSN expression is associated with interstitial fibrosis and inflammation (Oikonomou et al., (2009) *Thorax*, 64, 467-75), likely due to the GSN-mediated destabilization of cytoskeleton and increased movement of platelets and immune infiltrate, and GSN^{-/-} mice are shown to develop decreased pulmonary fibrosis and inflammation (Oikonomou et al., (2009) *Thorax*, 64, 467-75). In the heart, GSN catalyzes the disassembly and degradation of myocardial proteins (Yang et al., (2000) *Circulation*, 102, 3046-52), and its increased expression is detected in failing human hearts (Yang et al., (2000) *Circulation*, 102, 3046-52). It has been suggested that GSN interacts with hypoxia inducible factor 1 (HIF1A), a master transcriptional regulator of the cellular and systemic responses to hypoxia, that is known to play an essential role in the pathophysiology of ischemic cardiovascular disease (Richard et al., (2003) *Circulation*, 107, 2227-32).

MYL2 (myosin regulatory light chain 2) is a cardiac-specific protein. MYL2 dimerizes with cardiac myosin beta (or slow) heavy chain, and its phosphorylation by Ca⁺ triggers cardiac contractions. Mutations in MYL2 or abnormalities in MYL2 expression are associated with cardiomyopathy (Richard et al., (2003) *Circulation*, 107, 2227-32), heart failure (Poetter et al., (1996) *Nat Genet*, 13, 63-69), and left ventricular hypertrophy and familial hypertrophy (Flavigny et al., (1998) *J Mol Med*, 76, 208-14; Kabaeva et al., (2002) *Eur J Hum Genet*, 10, 741-48). Expression of MYL2 is altered in chagasic hearts (Cunha-Neto et al., (2005) *Am J Pathol*, 167, 305-13) and isolated cardiomyocytes infected by *T. cruzi* (Goldenberg et al., (2009) *Microbes Infect*, 11, 1140-49), and it is suggested that *T. cruzi*-induced immunoglobulin G autoantibodies and delayed type hypersensitivity to cardiac myosin contribute to disease pathogenesis (Leon and Engman, (2001) *Int J Parasitol*, 31, 555-61; Leon et al., (2004) *Infect Immun*, 72,

3410-17). Certain aspects of the described studies provide the first evidence that the plasma release of MYL2 is linked to disease severity in chagasic patients and indicative of the extent of cardiac muscle injury during Chagas disease development.

VIM is a member of the intermediate filament network, and it is primarily expressed by mesenchymal cells and found in connective tissue. Along with microtubules and actin microfilaments, VIM plays an important role in maintaining cell shape, integrity of the cytoplasm, and stabilizing cytoskeletal interactions (Katsumoto et al., (1990) *Biol Cell*, 68, 139-46). Vimentin is also shown to be localized in the carotid artery and heart valves and serves as a target antigen of peripheral and heart-infiltrating T cells during valvular disease (Fae et al., (2008) *J Autoimmun*, 31, 136-41). Increased detection of vimentin in the heart is indicative of a fibrotic process, as infiltrating fibroblasts replace damaged cardiomyocytes in disease conditions and has been identified by proteomic inventory of myocardial proteins in patients with Chagas disease (Teixeira et al., (2006) *Braz J Med Biol Res*, 39, 1549-62). Results obtained through IPA analysis indicated that VIM modulates NOS2 and is indirectly linked to IL-1 β and TNF- α expression in the disease state.

It is demonstrated herein that depletion of high-abundance plasma proteins enhanced the protein discovery of low-abundance proteins by 2D-GE. Pathological events, i.e., persistent inflammation and oxidative stress, associated with Chagas heart disease, and the beneficial effects of antioxidant and anti-parasite therapies in preserving the cardiac function, were reflected in the plasma protein profile of experimentally infected rodents. These proteomic studies provide the first indication that lipid/fatty acid metabolism is dysregulated and of pathologic significance in Chagas disease. Importantly, protein biomarkers (GSN, MYL2, VIM, MYH11, VCL, and PLG) were identified that have utility in

diagnosing the presence or severity of Chagas disease, and/or identifying the patients at risk of developing clinical symptoms of Chagas disease.

Certain embodiments are directed to methods of detecting Chagas disease in a biological sample, comprising the step of measuring the presence of at least one protein selected from the group consisting of GSN, MYL2, VIM, MYH11, VCL, and PLG in said sample, wherein elevated levels of GSN, MYL2, VIM, MYH11, VCL, and PLG is indicative of Chagas disease in the subject from which the sample was obtained. Generally, the biological sample is a diagnostic sample from a human or non-human animal. Representative samples include but are not limited to a tissue sample, a plasma sample, or a blood sample. Generally, GSN, MYL2, VIM, MYH11, VCL, and PLG may be detected by any assay known to one of ordinary skill in this art. Representative assays include but are not limited to a Western blot assay, an ELISA assay, an immunofluorescence assay, an immunoprecipitation assay, and a radioimmunoassay. Preferably, the assay determines the concentration of GSN, MYL2, VIM, MYH11, VCL, or PLG in said sample to be $\geq 50\%$ greater than normal controls. Normal controls are mammals not having cardiac disease or are not at risk of developing heart failure due to chagasic or other etiologies.

In yet another embodiment of the present invention, there is provided a serodiagnostic kit for determining the presence and/or severity of Chagas disease, said kit comprising: (a) the antibody directed against GSN, MYL2, VIM, MYH11, VCL, and/or PLG, wherein the antibody is linked to a reporter molecule; (b) a buffer; and, (c) a reagent for detection of the reporter molecule. Useful antibodies directed against GSN, MYL2, VIM, MYH11, VCL, and PLG are well known to those with ordinary skill in this art. Representative reporter molecules include but are not limited to luciferase, horseradish peroxidase, P-galactosidase, and fluorescent labels.

TABLE IVa

List of Genes/Proteins Differentially Expressed in Response to <i>T. Cruzi</i> Infection						
Spot#	Gene Name	Protein Name	Accession No.	Putative Biological Function	Putative Cellular Location	
12, 180	KRT1	Keratin, type II	gi/120474989	Oxidative stress response	Membrane	
34	TTC37	KIAA0372 gene product	gi/149058911	Protein binding	N/A	
37, 593	SRPRB	Bal-667	gi/33086638	Iron homeostasis	Extracellular	
49, 673	IGH-1_	Igh-1a protein	gi/299352	Antigen binding	Extracellular	
52, 54, 302	TF	Transferrin	gi/1854476	Transport	Extracellular	
53, 225	SroTP	Serotransferrin	gi/61556986	Proteolysis	Membrane	
72	IDH3A	Isocitrate dehydrogenase 3a	gi/149041700	Metabolism	Mitochondria	
73, 705, 787	ALB	Alpha-1-inhibitor 3	gi/83816939	Inflammatory response	Extracellular	
77	MUG1	Murinoglobulin-1	gi/12831225	Acute-phase response	Extracellular	
88	IGHG-__	g-2a immunoglobulin heavy chain	gi/1220486	Antigen binding	N/A	
94	FGB	Fibrinogen beta chain	gi/124106312	Signal transduction	Membrane	
106	CDK5RAP2	CDK5 regulatory associated protein 2	gi/109476582	tRNA modification	Cytoplasm	
115, 123	SERPINAL1	Alpha-1-antiproteinase	gi/112889	Acute phase response	Extracellular	
149	PUS1	Pseudouridine synthase 1	gi/149063707	tRNA processing	Mitochondria	
153	MYL2	Myosin, light polypeptide 2	gi/149067749	Muscle contraction	Cytosol	
177	AIM	Alpha-1-macroglobulin precursor	gi/21955142	Protein binding	Extracellular	
181	SERPINA3L	Serine protease inhibitor A3L	gi/2507387	Inhibitory protein	Extracellular	
184, 257, 328	CFH	Complement inhibitory factor H	gi/15485713	Immune response	Cytoplasm	
207, 555	CCHL1A1	Calcium channel alpha-1 subunit	gi/1184038	Transport	Membrane	
215	GPT	Glutamic pyruvic transaminase 1	gi/149066073	Gluconeogenesis	Cytoplasm	
266	CEP350	Centrosome-associated protein 350	gi/18027304	Cytoskeleton	Cytoplasm	

TABLE IVa-continued

List of Genes/Proteins Differentially Expressed in Response to <i>T. Cruzi</i> Infection					
Spot#	Gene Name	Protein Name	Accession No.	Putative Biological Function	Putative Cellular Location
299	UMPS	Uridine monophosphate synthetase	gi/149060638	Metabolism	Cytoplasm
315	ITIH4	Inter-alpha-inhibitor H4 heavy chain	gi/126722991	Metabolism	Extracellular
334	ZNF689	Zinc finger, HIT type 6	gi/157818873	Transcription	Nucleus
341	Nmag_2782	Na ⁺ /Ca ²⁺ antiporter	gi/8825638	Transport	Membrane
355, 359	PLG	Plasminogen	gi/16758216	Tissue remodeling	Extracellular
382, 385, 378, 572, 578, 595	CFB	Complement factor B	gill49027999	Immune response	Extracellular
389	GSN	Gelsolin	gi/149038928	Cytoskeleton	Cytosol
430	SCD2	Stearyl-CoA desaturase 2	gi/1763027	Fatty acid synthesis	Membrane
434, 678	COG1	Component of golgi complex 1	gi/149054700	Transport	Membrane
439	C4BPA	C4b-binding protein alpha	gi/2493792	Innate immunity	Extracellular
452	AFM	Afamin, Albumin-binding	gi/60688254	Transport	Extracellular
464	IGH-6	Immunoglobulin heavy chain 6	gi/62201965	Antigen binding	N/A
479	IGHM	Ig mu chain C region	gi/111977	Immune response	Membrane
493	ZFP637	Zinc finger protein 637	gi/201027426	Protein binding	Intracellular
515	CESTIC/ES2	Carboxylesterase	gi/468766	Metabolism	Endoplasmic reticulum
524	ERCC4	DNA repair endonuclease XPF like	gi/109487684	DNA repair	Nucleus
551, 587, 908	C3	Complement C3	gi/158138561	Inflammation	Extracellular
559	HPX	Hemopexin	gi/122065203	Heme scavenging	Extracellular
571	GC	Group specific component	gi/51260133	Vitamin D binding	Extracellular
576, 620	Ac2-248	SERPIN-like protein	gi/32527753	Inflammation response	Extracellular
586, 614	SERPINC1	Serine/cysteine peptidase inhibitor	gi/58865630	Blood clotting	Extracellular
592	DNASE1L1	Deoxyribonuclease 1-like	gi/149029874	DNA catabolism	Endoplasmic reticulum
604	APOH	Beta-2-glycoprotein 1	gi/57528174	Transport	Cell surface
606	GC	Vitamin D binding protein	gi/203927	Transport	Extracellular
627	MAPI	LMW T-kininogen I	gi/205085	Acute-phase response	Extracellular
638	LOC501738	Immune activating receptor	gi/264681503	Receptor activity	N/A
649	SYNE2	Nesprin-2 like	gi/109478368	Cytoskeleton	Nuclear
651	DSTN	Destrin	gi/75991707	Actin binding	Cytoplasm
655	DLGAP2	Disks large-associated protein 2	gi/16758774	Synapse transmission	Membrane
672	SERPINF	Serine/cysteine peptidase inhibitor	gi/29293811	Inhibitory protein	Extracellular
676	rCG33447	Hypothetical	gi/149052919	N/A	N/A
691	APOA4	Apolipoprotein A-IV	gi/114008	Lipid binding	Extracellular
860	KRT10	Keratin, type I	gi/57012436	Protein binding	Intermediate filament
966	Hypothetical	CMRF-35-like molecule-7	gi/109511428	Immunity	Membrane
897	MY05A	Myosin Va	gi/149019170	Myosin complex	Cytoplasm
715	SERPINA1	Proteinase inhibitor-like	gi/930263	Protein binding	Extracellular
724	ALB	Serum albumin	gi/158138568	Transport	Extracellular
728	SYMPK	Symplekin-C	gi/62531221	Protein binding	Nucleus
733	DECR2	2,4-dienoyl-CoA reductase	gi/25282441	Metabolism	Peroxisome
740	PRPH	Peripherin	gi/166063971	Cytoskeleton	Intermediate filament
745	PFKFB1	6-phosphofructo-2-kinase 1	gi/77020248	Metabolism	Cytoplasm
749	MY05B	Myosin-Vb	gi/8393817	Myosin complex	Intracellular
766	SCG2	Secretogranin 2	gi/149016236	Inflammation	Extracellular
779, 909	VIM	Vimentin	gi/149021116	Cell integrity	Cytoplasm
796	Hypothetical p		gi/109468251	N/A	N/A
814	RBM15B	RNA binding motif 15B	gi/109483938	RNA splicing	Nucleoplasm
817	BRPF1	Bromodomain/PHD finger-containing protein 1	gi/109472470	Transcription	Cytoplasm
820, 1081	BFAR	Bifunctional apoptosis regulator	gi/61557021	Apoptosis	Membrane
827	GNAT	Guanine binding protein	gi/84662745	N/A	Cytoplasm
832	PSMB	Proteasome beta-type subunit RN3	gi/9653292	Protein catabolism	Cytoplasm
867	RAI14	Ankyrin	gi/58865464	N/A	Cytoplasm
881	CHD4	Chromodomain helicase DNA binding protein 4	gi/149049419	Transcription	Nucleus
900	rCG25416	Transferrin region	gi/149018747	N/A	N/A
906	APOE	Apolipoprotein E	gi/149056721	Oxidative stress response	Chylomicron
979	rCG25357		gi/149018900	N/A	N/A
992	APOA1	Apolipoprotein A-I	gi/2145143	Transport	Membrane
1019	ZNHIT6	Hypothetical protein FLJ20729	gi/149026162	Protein binding	Pre-snoRNP complex

TABLE IVb

Differential Expression in Response to <i>T. Cruzi</i> Infection										
Spot#	MW (Da)	pI	e-value p < 0.001	RN*	RA*	RAP*	RC*	RCP*	RCB*	RCPB*
12, 180	65059.2	8.04	9.102E-09	4.70	4.03	21.47	9.92	7.22	9.47	11.17
34	68849.3	6.22	0.001	2.29	0.64	0.37	0.31	0.45	0.37	0.25
37, 593	109545.9	8.35	5.319E-08	2.14	5.33	14.38	6.46	6.48	3.21	8.61
49, 673	52500	7.23	0.132	7.89	9.90	19.12	50.91	13.39	3.98	4.48
52, 54, 302	78538.3	6.94	5.55E-08	9.83	5.80	9.80	2.85	14.45	0.60	8.06
53, 225	78512.5	7.14	1.671E-07	6.78	6.20	8.76	2.05	15.12	1.72	5.60
72	30334.3	5.83	6.694E-07	39.31	10.26	18.10	76.03	16.43	83.09	13.00
73, 705, 787	165038.2	5.7	6.561E-09	86.41	19.56	46.94	136.2	38.67	216.9	28.67
77	166589.9	5.68	0.00007856	28.44	16.28	16.3	47.41	8.675	107.7	20.1
88	52242.6	8.15	1.24E-08	2.54	1.45	74.61	38.51	40.49	4.75	17.20
94	54827.9	7.9	0.0008907	0.33	0.51	1.84	1.87	2.55	0.55	0.53
106	208168.7	5.27	0.001	1.47	0.85	1.70	2.22	6.94	2.21	1.67
115, 123	46277.6	5.7	0.272	11.10	6.35	22.27	10.54	10.96	8.36	18.61
149	44463.4	8.1	0.000911	6.34	1.67	0.78	6.50	4.39	1.16	1.17
153	17669.7	4.96	0.00004491	9.21	3.03	27.07	38.86	10.34	2.37	2.66
177	168421.9	6.46	2.312E-10	2.88	1.84	3.71	28.06	1.60	2.77	2.87
181	46419.1	5.48	0.007	1.83	3.57	3.99	17.08	1.90	7.53	3.22
184, 257, 328	144813.9	6.52	0.001	3.69	9.51	4.54	2.46	5.85	6.15	3.32
207, 555	13893.9	6.52	0.0001206	15.79	10.78	13.23	13.97	9.12	11.32	18.65
215	50475.5	6.63	2.201E-08	3.47	1.20	1.73	26.17	1.97	3.23	1.98
266	166809.6	8.63	0.012	0.56	0.22	0.75	0.56	0.54	1.43	1.22
299	33345.2	6.02	0.00001753	2.05	1.45	1.92	0.66	1.17	1.17	2.01
315	103861.8	5.82	0.00001561	1.93	2.95	6.24	7.00	8.23	5.19	3.92
334	53374.8	5.51	4.73E-08	26.07	0.59	0.61	1.00	0.71	1.05	0.45
341	11217.6	8.91	5.217E-06	1.87	1.50	0.59	1.10	1.10	1.44	6.59
355, 359	93213.9	6.79	0.00001998	3.15	4.34	2.99	3.15	2.20	3.29	3.45
382, 385, 378, 572, 578, 595	83735.6	6.05	1.675E-10	5.91	43.78	33.76	30.02	3.29	23.45	5.94
389	86314.2	5.76	6.661E-14	6.51	70.05	37.55	38.06	4.32	44.17	8.39
430	3479.7	9.9	2.661E-09	11.28	40.97	22.40	9.29	8.21	13.65	11.38
434, 678	72098.8	8.06	1.465E-08	29.10	110.5	55.14	34.52	24.63	43.20	30.09
439	64277.8	7.06	9.889E-09	4.21	1.72	4.04	13.64	14.99	1.36	7.56
452	54205.3	5.8	5.923E-09	25.61	13.68	18.92	17.57	10.01	59.65	55.78
464	69059.5	5.69	0.00004813	5.89	7.22	3.89	3.22	6.65	4.66	7.97
479	38189.1	6.72	1.038E-11	2.72	21.09	23.96	10.08	32.56	8.65	14.62
493	31712.4	9.5	6.464E-07	3.75	14.49	9.82	5.45	13.46	17.41	12.88
515	59196.9	5.51	5.223E-07	17.08	3.47	6.87	8.05	7.78	24.22	19.57
524	110025.1	9.2	9.067E-09	120.8	32.57	53.74	55.47	21.96	68.54	30.55
551, 587, 908	187745.9	6.06	1.64E-11	7.046	146.9	88.04	46.76	54.1	32.88	31.97
559	52059.6	7.58	0.167	26.14	16.11	24.39	38.23	27.58	17.91	22.98
571	55079.6	5.65	9.36E-12	37.07	11.96	7.84	74.44	38.63	3.75	24.61
576, 620	67191	6.85	1.098E-07	10.86	14.95	18.08	16.62	16.66	2.38	11.23
586, 614	52714	6.18	3.838E-06	63.42	48.70	50.44	57.02	38.00	132.20	75.38
592	32437	6.31	1.664E-07	21.16	20.04	15.61	12.37	31.55	11.70	17.68
604	39743.2	8.58	6.515E-06	18.54	10.78	22.81	17.48	23.66	67.12	26.76
606	55089.6	5.65	0.006	15.31	5.92	9.60	9.50	5.58	11.27	10.14
627	48757	6.29	1.263E-07	108.9	20.28	30.23	45.81	54.85	44.92	38.20
638	24023.2	9.41	0.00001901	3.11	4.73	4.42	5.82	5.92	4.69	12.14
649	442636.4	5.29	1.843E-08	52.04	10.43	40.69	33.92	37.11	26.48	25.27
651	18806.7	8.19	3.884E-10	23.61	109.0	94.03	176.80	57.85	37.12	51.53
655	111348.9	6.82	6.158E-10	48.96	280.6	240.6	254.70	149.20	151.30	122.60
672	46493.2	6.04	0.00003611	9.02	3.59	7.34	3.45	17.65	23.29	10.52
676	20157.4	9.14	0.00001667	13.09	19.5	14.69	49.61	42.59	24.67	17.95
691	44428.7	5.12	1.996E-06	46.70	42.11	49.99	39.11	16.29	65.41	14.52
860	56698.6	5.1	4.594E-08	6.32	2.94	3.06	3.63	5.79	2.64	20.82
966	9215.8	7.93	3.917E-09	12.66	76.58	53.33	87.53	59.29	49.99	28.90
897	96579.8	9.48	5.875E-06	24.00	9.21	4.82	16.65	31.94	11.65	19.24
715	22867.8	6.06	2.851E-07	6.35	12.36	10.83	24.11	32.20	30.96	12.93
724	70709.9	6.09	5.902E-07	1.19	3.31	1.72	0.46	2.23	2.19	11.17
728	33433.1	4.97	1.601E-11	0.84	1.00	0.76	0.49	1.13	2.21	7.89
733	31614.4	8.51	0.0006324	1.71	1.90	2.24	2.06	2.44	1.67	7.42
740	54063.5	5.32	0.0001771	14.90	5.56	7.81	4.46	7.33	4.02	13.03
745	55301	6.78	3.474E-08	8.56	4.94	4.51	4.17	3.21	2.30	8.93
749	215240.6	6.53	6.828E-10	5.53	9.51	4.71	2.88	1.70	2.46	19.91
766	61578.7	4.69	0.000699	3.94	5.60	3.20	3.16	6.32	3.79	14.46
779, 909	4131.2	9.75	2.984E-09	1.52	6.85	5.45	36.40	6.88	3.08	7.28
796	53156.7	8.32	1.702E-07	10.25	8.42	9.97	7.48	8.33	5.11	11.64
814	96223.1	9.85	4.256E-07	1.65	1.41	0.60	0.63	1.56	3.61	13.27
817	151416.4	8.55	0.024	10.16	21.83	12.14	8.66	29.59	25.15	31.35
820, 1081	53617.2	6.44	0.006	4.77	3.19	4.59	31.17	2.20	13.38	5.61
827	42416.4	5.48	4.658E-09	11.89	15.94	17.91	3.82	17.80	10.78	12.84
832	15426.5	6.82	0.014	2.47	3.16	6.23	1.86	7.55	3.47	8.94
867	106502	5.64	0.0002925	4.34	5.72	2.56	2.86	3.00	2.41	12.07
881	111042	5.43	2.167E-10	11.78	5.61	13.92	17.58	6.68	28.89	8.62
900	66991.6	6.41	9.426E-08	20.46	9.26	25.94	22.29	44.00	7.06	18.89

TABLE IVb-continued

Differential Expression in Response to <i>T. Cruzi</i> Infection										
Spot#	MW (Da)	pI	e-value p < 0.001	RN*	RA*	RAP*	RC*	RCP*	RCB*	RCPB*
906	27354.1	7.93	0.004	43.97	56.73	49.40	26.45	87.74	74.42	57.50
979	3285.6	9.5	2.003E-07	20.05	55.99	59.46	45.31	41.38	31.72	31.72
992	29869.1	5.51	8.784E-07	15.55	41.44	34.51	32.12	57.94	38.11	39.05

N/A: No match available in public information databases,

pI: Isoelectric pH,

MW: molecular weight

*Average Normalized Density $\times 100,000$

TABLE V

IPA network analysis of differentially expressed plasma proteins in Chagasic rats				
ID	Molecules in Network	Score	Focus	
			Molecules	Top Functions
1	Actin, ALB, APOA1, APOA4, APOE, APOH, C3, CFB, CFH, CFHR1, CFP, CHD4, Cytokeratin, DSTN, FGB, Fibrinogen, GSN, HPX, IgG, KRT1, KRT3, KRT4, KRT10, KRT12, KRT13, KRT23, KRT6B, PLG, SERPINF, SERPINF1, SETX, TF, TMPRSS6, TRY6, VIM	41	19	Antigen Presentation, Humoral Immune Response, Inflammatory Response
2	AFM, APP, BRPF3, C4BPA, CACNA1D, COL25A1, DLGAP2, GAB1/2, GC, GRB2, heparin, INSR, KCNMA1, KNG1 (includes EG: 16644), Met dimer, MUG1, MYLPF, MY05A, MY05B, MY05C, PFKFB2, PIK3AP1, PIK3R1, PLA2G2D, PLA2G2E, PRPH, PZP, RAI14, SCG2, SERPINC1, SLC23A1, SNX8, VPS13A, YWHAZ, ZNF32	36	17	Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry
3	ATG4C.BFAR, C10RF25, CASP8, CEBPB, CEP350, CIDEC, CRAT, DSCR3, ESR1, GNAQ, GPT, HNF4A, IDH3A, ITIH4, LGMN, MINA, MYC, PEPD, PPARG, PUS1, PUS3, SCD2, SERPINA1, SLC25A19, SQRDL (includes EG:58472), SRPRB, SYMPK, TMEM176A, TMEM176B, TRUB2, TTC37, UMPS, YME1L1, ZNHIT6	29	14	Cellular Development, Free Radical Scavenging, Molecular Transport

I. Biomarkers

Biomarkers can be used to both define a disease state as well as to provide a means to predict physiological and clinical manifestations of a disease. Three commonly discussed ways in which biomarkers can be used clinically are: (1) to characterize a disease state, i.e. establish a diagnosis, (2) to demonstrate the progression of a disease, and (3) to predict the progression of a disease, i.e. establish a prognosis. Establishing putative biomarkers for such uses typically requires a statistical analysis of relative changes in biomarker expression either cross-sectionally and/or over time (longitudinally). For example, in a state or diagnostic biomarker analysis, levels of one or more biomarkers are measured cross-sectionally, e.g. in patients with disease and in normal control subjects, at one point in time and then related to the clinical status of the groups. Statistically significant differences in biomarker expression can be linked to presence or absence of disease, and would indicate that the biomarkers could subsequently be used to diagnose patients as either having disease or not having disease. In a progression analysis, levels of one or more biomarkers and clinical status are both measured longitudinally. Statistically significant changes over time in both biomarker expression and clinical status would indicate that the biomarkers under study could be used to monitor the progression of the disease. In a prognostic analysis, levels of one or more biomarkers are measured at one point in time and related to

the change in clinical status from that point in time to another subsequent point in time. A statistical relationship between biomarker expression and subsequent change in clinical status would indicate that the biomarkers under study could be used to predict disease progression.

Results from prognostic analyses can also be used for disease staging and for monitoring the effects of drugs. The prediction of variable rates of decline for various groups of patients allows them to be identified as subgroups that are differentiated according to disease severity (i.e. less versus more) or stage (i.e. early versus late). Also, patients treated with a putative disease-modifying therapy may demonstrate an observed rate of decline that does not match the rate of decline predicted by the prognostic analysis. This could be considered evidence of drug or treatment efficacy.

II. Computer Implementation

Embodiments of assays described herein or the analysis thereof may be implemented or executed by one or more computer systems. One such computer system is illustrated in FIG. 12. In various embodiments, computer system may be a server, a mainframe computer system, a workstation, a network computer, a desktop computer, a laptop, or the like. For example, in some cases, the analysis described herein or the like may be implemented as a computer system. Moreover, one or more of servers or devices may include one or more computers or computing devices generally in the form of a computer system. In different embodiments these vari-

ous computer systems may be configured to communicate with each other in any suitable way, such as, for example, via a network.

As illustrated, the computer system includes one or more processors **510** coupled to a system memory **520** via an input/output (I/O) interface **530**. Computer system **500** further includes a network interface **540** coupled to I/O interface **530**, and one or more input/output devices **550**, such as cursor control device **560**, keyboard **570**, and display(s) **580**. In some embodiments, a given entity (e.g., analysis of subjects for trypanosome infection and/or cardiomyopathy) may be implemented using a single instance of computer system **500**, while in other embodiments multiple such systems, or multiple nodes making up computer system **500**, may be configured to host different portions or instances of embodiments. For example, in an embodiment some elements may be implemented via one or more nodes of computer system **500** that are distinct from those nodes implementing other elements (e.g., a first computer system may implement an assessment of a hybrid latent variable assessment or system while another computer system may implement data gathering, scaling, classification etc.).

In various embodiments, computer system **500** may be a single-processor system including one processor **510**, or a multi-processor system including two or more processors **510** (e.g., two, four, eight, or another suitable number). Processors **510** may be any processor capable of executing program instructions. For example, in various embodiments, processors **510** may be general-purpose or embedded processors implementing any of a variety of instruction set architectures (ISAs), such as the x86, POWERPC®, ARM®, SPARC®, or MIPS® ISAs, or any other suitable ISA. In multi-processor systems, each of processors **510** may commonly, but not necessarily, implement the same ISA. Also, in some embodiments, at least one processor **510** may be a graphics-processing unit (GPU) or other dedicated graphics-rendering device.

System memory **520** may be configured to store program instructions and/or data accessible by processor **510**. In various embodiments, system memory **520** may be implemented using any suitable memory technology, such as static random access memory (SRAM), synchronous dynamic RAM (SDRAM), nonvolatile/Flash-type memory, or any other type of memory. As illustrated, program instructions and data implementing certain operations, such as, for example, those described herein, may be stored within system memory **520** as program instructions **525** and data storage **535**, respectively. In other embodiments, program instructions and/or data may be received, sent or stored upon different types of computer-accessible media or on similar media separate from system memory **520** or computer system **500**. Generally speaking, a computer-accessible medium may include any tangible storage media or memory media such as magnetic or optical media—e.g., disk or CD/DVD-ROM coupled to computer system **500** via I/O interface **530**. Program instructions and data stored on a tangible computer-accessible medium in non-transitory form may further be transmitted by transmission media or signals such as electrical, electromagnetic, or digital signals, which may be conveyed via a communication medium such as a network and/or a wireless link, such as may be implemented via network interface **540**.

In an embodiment, I/O interface **530** may be configured to coordinate I/O traffic between processor **510**, system memory **520**, and any peripheral devices in the device, including network interface **540** or other peripheral interfaces, such as input/output devices **550**. In some embodi-

ments, I/O interface **530** may perform any necessary protocol, timing or other data transformations to convert data signals from one component (e.g., system memory **520**) into a format suitable for use by another component (e.g., processor **510**). In some embodiments, I/O interface **530** may include support for devices attached through various types of peripheral buses, such as a variant of the Peripheral Component Interconnect (PCI) bus standard or the Universal Serial Bus (USB) standard, for example. In some embodiments, the function of I/O interface **530** may be split into two or more separate components, such as a north bridge and a south bridge, for example. In addition, in some embodiments some or all of the functionality of I/O interface **530**, such as an interface to system memory **520**, may be incorporated directly into processor **510**.

Network interface **540** may be configured to allow data to be exchanged between computer system **500** and other devices attached to a network, such as other computer systems, or between nodes of computer system **500**. In various embodiments, network interface **540** may support communication via wired or wireless general data networks, such as any suitable type of Ethernet network, for example; via telecommunications/telephony networks such as analog voice networks or digital fiber communications networks; via storage area networks such as Fiber Channel SANs, or via any other suitable type of network and/or protocol.

Input/output devices **550** may, in some embodiments, include one or more display terminals, keyboards, keypads, touch screens, scanning devices, voice or optical recognition devices, or any other devices suitable for entering or retrieving data by one or more computer system **500**. Multiple input/output devices **550** may be present in computer system **500** or may be distributed on various nodes of computer system **500**. In some embodiments, similar input/output devices may be separate from computer system **500** and may interact with one or more nodes of computer system **500** through a wired or wireless connection, such as over network interface **540**.

As shown in FIG. 14, memory **520** may include program instructions **525**, configured to implement certain embodiments described herein, and data storage **535**, comprising various data accessible by program instructions **525**. In an embodiment, program instructions **525** may include software elements of embodiments illustrated herein. For example, program instructions **525** may be implemented in various embodiments using any desired programming language, scripting language, or combination of programming languages and/or scripting languages (e.g., C, C++, C#, JAVA®, JAVASCRIPT®, PERL®, etc). Data storage **535** may include data that may be used in these embodiments. In other embodiments, other or different software elements and data may be included.

A person of ordinary skill in the art will appreciate that computer system **500** is merely illustrative and is not intended to limit the scope of the disclosure described herein. In particular, the computer system and devices may include any combination of hardware or software that can perform the indicated operations. In addition, the operations performed by the illustrated components may, in some embodiments, be performed by fewer components or distributed across additional components. Similarly, in other embodiments, the operations of some of the illustrated components may not be performed and/or other additional operations may be available. Accordingly, systems and methods described herein may be implemented or executed with other computer system configurations.

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 32

<210> SEQ ID NO 1

<211> LENGTH: 1134

<212> TYPE: PRT

<213> ORGANISM: Homo sapien

<400> SEQUENCE: 1

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Met Pro Val Phe His Thr Arg Thr Ile Glu Ser Ile Leu Glu Pro Val
1           5           10           15

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

Asp Gly Lys Ala Ile Pro Asp Leu Thr Ala Pro Val Ala Ala Val Gln
35           40           45

Ala Ala Val Ser Asn Leu Val Arg Val Gly Lys Glu Thr Val Gln Thr
50           55           60

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

Val Glu Asn Ala Cys Thr Lys Leu Val Gln Ala Ala Gln Met Leu Gln
85           90           95

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

Arg Gly Ile Leu Ser Gly Thr Ser Asp Leu Leu Leu Thr Phe Asp Glu
115          120          125

Ala Glu Val Arg Lys Ile Ile Arg Val Cys Lys Gly Ile Leu Glu Tyr
130          135          140

Leu Thr Val Ala Glu Val Val Glu Thr Met Glu Asp Leu Val Thr Tyr
145          150          155          160

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

Glu Arg Gln Gln Glu Leu Thr His Gln Glu His Arg Val Met Leu Val
180          185          190

Asn Ser Met Asn Thr Val Lys Glu Leu Leu Pro Val Leu Ile Ser Ala
195          200          205

Met Lys Ile Phe Val Thr Thr Lys Asn Ser Lys Asn Gln Gly Ile Glu
210          215          220

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

Ile Asn Glu Ile Ile Arg Val Leu Gln Leu Thr Ser Trp Asp Glu Asp
245          250          255

Ala Trp Ala Ser Lys Asp Thr Glu Ala Met Lys Arg Ala Leu Ala Ser
260          265          270

Ile Asp Ser Lys Leu Asn Gln Ala Lys Gly Trp Leu Arg Asp Pro Ser
275          280          285

Ala Ser Pro Gly Asp Ala Gly Glu Gln Ala Ile Arg Gln Ile Leu Asp
290          295          300

Glu Ala Gly Lys Val Gly Glu Leu Cys Ala Gly Lys Glu Arg Arg Glu
305          310          315          320

Ile Leu Gly Thr Cys Lys Met Leu Gly Gln Met Thr Asp Gln Val Ala
325          330          335

Asp Leu Arg Ala Arg Gly Gln Gly Ser Ser Pro Val Ala Met Gln Lys
340          345          350

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

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Asn Ala Ala Arg Lys Leu Glu Ala Met Thr Asn Ser Lys Gln Ser Ile
 370 375 380

Ala Lys Lys Ile Asp Ala Ala Gln Asn Trp Leu Ala Asp Pro Asn Gly
 385 390 395 400

Gly Pro Glu Gly Glu Glu Gln Ile Arg Gly Ala Leu Ala Glu Ala Arg
 405 410 415

Lys Ile Ala Glu Leu Cys Asp Asp Pro Lys Glu Arg Asp Asp Ile Leu
 420 425 430

Arg Ser Leu Gly Glu Ile Ser Ala Leu Thr Ser Lys Leu Ala Asp Leu
 435 440 445

Arg Arg Gln Gly Lys Gly Asp Ser Pro Glu Ala Arg Ala Leu Ala Lys
 450 455 460

Gln Val Ala Thr Ala Leu Gln Asn Leu Gln Thr Lys Thr Asn Arg Ala
 465 470 475 480

Val Ala Asn Ser Arg Pro Ala Lys Ala Ala Val His Leu Glu Gly Lys
 485 490 495

Ile Glu Gln Ala Gln Arg Trp Ile Asp Asn Pro Thr Val Asp Asp Arg
 500 505 510

Gly Val Gly Gln Ala Ala Ile Arg Gly Leu Val Ala Glu Gly His Arg
 515 520 525

Leu Ala Asn Val Met Met Gly Pro Tyr Arg Gln Asp Leu Leu Ala Lys
 530 535 540

Cys Asp Arg Val Asp Gln Leu Thr Ala Gln Leu Ala Asp Leu Ala Ala
 545 550 555 560

Arg Gly Glu Gly Glu Ser Pro Gln Ala Arg Ala Leu Ala Ser Gln Leu
 565 570 575

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

Gln Glu Val Ser Asp Val Phe Ser Asp Thr Thr Thr Pro Ile Lys Leu
 595 600 605

Leu Ala Val Ala Ala Thr Ala Pro Pro Asp Ala Pro Asn Arg Glu Glu
 610 615 620

Val Phe Asp Glu Arg Ala Ala Asn Phe Glu Asn His Ser Gly Lys Leu
 625 630 635 640

Gly Ala Thr Ala Glu Lys Ala Ala Ala Val Gly Thr Ala Asn Lys Ser
 645 650 655

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

Pro Gln Val Val Ser Ala Ala Arg Ile Leu Leu Arg Asn Pro Gly Asn
 675 680 685

Gln Ala Ala Tyr Glu His Phe Glu Thr Met Lys Asn Gln Trp Ile Asp
 690 695 700

Asn Val Glu Lys Met Thr Gly Leu Val Asp Glu Ala Ile Asp Thr Lys
 705 710 715 720

Ser Leu Leu Asp Ala Ser Glu Glu Ala Ile Lys Lys Asp Leu Asp Lys
 725 730 735

Cys Lys Val Ala Met Ala Asn Ile Gln Pro Gln Met Leu Val Ala Gly
 740 745 750

Ala Thr Ser Ile Ala Arg Arg Ala Asn Arg Ile Leu Leu Val Ala Lys
 755 760 765

Arg Glu Val Glu Asn Ser Glu Asp Pro Lys Phe Arg Glu Ala Val Lys
 770 775 780

Ala Ala Ser Asp Glu Leu Ser Lys Thr Ile Ser Pro Met Val Met Asp

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785	790	795	800
Ala Lys Ala Val	Ala Gly Asn Ile	Ser Asp Pro Gly Leu Gln Lys Ser	
	805	810	815
Phe Leu Asp Ser	Gly Tyr Arg Ile	Leu Gly Ala Val Ala Lys Val Arg	
	820	825	830
Glu Ala Phe Gln Pro Gln Glu Pro Asp Phe Pro Pro Pro Pro Pro Asp		840	845
Leu Glu Gln Leu Arg Leu Thr Asp Glu Leu Ala Pro Pro Lys Pro Pro		850	855
			860
Leu Pro Glu Gly Glu Val Pro Pro Pro Arg Pro Pro Pro Pro Glu Glu		870	875
			880
Lys Asp Glu Glu Phe Pro Glu Gln Lys Ala Gly Glu Val Ile Asn Gln		885	890
			895
Pro Met Met Met Ala Ala Arg Gln Leu His Asp Glu Ala Arg Lys Trp		900	905
			910
Ser Ser Lys Pro Gly Ile Pro Ala Ala Glu Val Gly Ile Gly Val Val		915	920
			925
Ala Glu Ala Asp Ala Ala Asp Ala Ala Gly Phe Pro Val Pro Pro Asp		930	935
			940
Met Glu Asp Asp Tyr Glu Pro Glu Leu Leu Leu Met Pro Ser Asn Gln		945	950
			955
Pro Val Asn Gln Pro Ile Leu Ala Ala Ala Gln Ser Leu His Arg Glu		965	970
			975
Ala Thr Lys Trp Ser Ser Lys Gly Asn Asp Ile Ile Ala Ala Ala Lys		980	985
			990
Arg Met Ala Leu Leu Met Ala Glu Met Ser Arg Leu Val Arg Gly Gly		995	1000
			1005
Ser Gly Thr Lys Arg Ala Leu Ile Gln Cys Ala Lys Asp Ile Ala		1010	1015
			1020
Lys Ala Ser Asp Glu Val Thr Arg Leu Ala Lys Glu Val Ala Lys		1025	1030
			1035
Gln Cys Thr Asp Lys Arg Ile Arg Thr Asn Leu Leu Gln Val Cys		1040	1045
			1050
Glu Arg Ile Pro Thr Ile Ser Thr Gln Leu Lys Ile Leu Ser Thr		1055	1060
			1065
Val Lys Ala Thr Met Leu Gly Arg Thr Asn Ile Ser Asp Glu Glu		1070	1075
			1080
Ser Glu Gln Ala Thr Glu Met Leu Val His Asn Ala Gln Asn Leu		1085	1090
			1095
Met Gln Ser Val Lys Glu Thr Val Arg Glu Ala Glu Ala Ala Ser		1100	1105
			1110
Ile Lys Ile Arg Thr Asp Ala Gly Phe Thr Leu Arg Trp Val Arg		1115	1120
			1125
Lys Thr Pro Trp Tyr Gln			
			1130

<210> SEQ ID NO 2

<211> LENGTH: 454

<212> TYPE: PRT

<213> ORGANISM: Homo sapien

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(1)

<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

<400> SEQUENCE: 2

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

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Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys Ala Asp Asp
 420 425 430

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

Gln Ala Ala Leu Gly Leu
 450

<210> SEQ ID NO 3
 <211> LENGTH: 1039
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapien

<400> SEQUENCE: 3

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

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

Asn Leu Asp Pro Val Gln Leu Thr Phe Tyr Ala Gly Pro Asn Gly Ser
 35 40 45

Gln Phe Gly Phe Ser Leu Asp Phe His Lys Asp Ser His Gly Arg Val
 50 55 60

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

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

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

Gln Thr Leu Gln Thr Phe Lys Ala Arg Gln Gly Leu Gly Ala Ser Val
 115 120 125

Val Ser Trp Ser Asp Val Ile Val Ala Cys Ala Pro Trp Gln His Trp
 130 135 140

Asn Val Leu Glu Lys Thr Glu Glu Ala Glu Lys Thr Pro Val Gly Ser
 145 150 155 160

Cys Phe Leu Ala Gln Pro Glu Ser Gly Arg Arg Ala Glu Tyr Ser Pro
 165 170 175

Cys Arg Gly Asn Thr Leu Ser Arg Ile Tyr Val Glu Asn Asp Phe Ser
 180 185 190

Trp Asp Lys Arg Tyr Cys Glu Ala Gly Phe Ser Ser Val Val Thr Gln
 195 200 205

Ala Gly Glu Leu Val Leu Gly Ala Pro Gly Gly Tyr Tyr Phe Leu Gly
 210 215 220

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

Gly Ile Leu Leu Trp His Val Ser Ser Gln Ser Leu Ser Phe Asp Ser
 245 250 255

Ser Asn Pro Glu Tyr Phe Asp Gly Tyr Trp Gly Tyr Ser Val Ala Val
 260 265 270

Gly Glu Phe Asp Gly Asp Leu Asn Thr Thr Glu Tyr Val Val Gly Ala
 275 280 285

Pro Thr Trp Ser Trp Thr Leu Gly Ala Val Glu Ile Leu Asp Ser Tyr
 290 295 300

Tyr Gln Arg Leu His Arg Leu Arg Gly Glu Gln Met Ala Ser Tyr Phe
 305 310 315 320

Gly His Ser Val Ala Val Thr Asp Val Asn Gly Asp Gly Arg His Asp
 325 330 335

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Leu Leu Val Gly Ala Pro Leu Tyr Met Glu Ser Arg Ala Asp Arg Lys
 340 345 350

Leu Ala Glu Val Gly Arg Val Tyr Leu Phe Leu Gln Pro Arg Gly Pro
 355 360 365

His Ala Leu Gly Ala Pro Ser Leu Leu Leu Thr Gly Thr Gln Leu Tyr
 370 375 380

Gly Arg Phe Gly Ser Ala Ile Ala Pro Leu Gly Asp Leu Asp Arg Asp
 385 390 395 400

Gly Tyr Asn Asp Ile Ala Val Ala Ala Pro Tyr Gly Gly Pro Ser Gly
 405 410 415

Arg Gly Gln Val Leu Val Phe Leu Gly Gln Ser Glu Gly Leu Arg Ser
 420 425 430

Arg Pro Ser Gln Val Leu Asp Ser Pro Phe Pro Thr Gly Ser Ala Phe
 435 440 445

Gly Phe Ser Leu Arg Gly Ala Val Asp Ile Asp Asp Asn Gly Tyr Pro
 450 455 460

Asp Leu Ile Val Gly Ala Tyr Gly Ala Asn Gln Val Ala Val Tyr Arg
 465 470 475 480

Ala Gln Pro Val Val Lys Ala Ser Val Gln Leu Leu Val Gln Asp Ser
 485 490 495

Leu Asn Pro Ala Val Lys Ser Cys Val Leu Pro Gln Thr Lys Thr Pro
 500 505 510

Val Ser Cys Phe Asn Ile Gln Met Cys Val Gly Ala Thr Gly His Asn
 515 520 525

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

Lys Pro Arg Gln Gly Arg Arg Val Leu Leu Leu Gly Ser Gln Gln Ala
 545 550 555 560

Gly Thr Thr Leu Asn Leu Asp Leu Gly Gly Lys His Ser Pro Ile Cys
 565 570 575

His Thr Thr Met Ala Phe Leu Arg Asp Glu Ala Asp Phe Arg Asp Lys
 580 585 590

Leu Ser Pro Ile Val Leu Ser Leu Asn Val Ser Leu Pro Pro Thr Glu
 595 600 605

Ala Gly Met Ala Pro Ala Val Val Leu His Gly Asp Thr His Val Gln
 610 615 620

Glu Gln Thr Arg Ile Val Leu Asp Cys Gly Glu Asp Asp Val Cys Val
 625 630 635 640

Pro Gln Leu Gln Leu Thr Ala Ser Val Thr Gly Ser Pro Leu Leu Val
 645 650 655

Gly Ala Asp Asn Val Leu Glu Leu Gln Met Asp Ala Ala Asn Glu Gly
 660 665 670

Glu Gly Ala Tyr Glu Ala Glu Leu Ala Val His Leu Pro Gln Gly Ala
 675 680 685

His Tyr Met Arg Ala Leu Ser Asn Val Glu Gly Phe Glu Arg Leu Ile
 690 695 700

Cys Asn Gln Lys Lys Glu Asn Glu Thr Arg Val Val Leu Cys Glu Leu
 705 710 715 720

Gly Asn Pro Met Lys Lys Asn Ala Gln Ile Gly Ile Ala Met Leu Val
 725 730 735

Ser Val Gly Asn Leu Glu Glu Ala Gly Glu Ser Val Ser Phe Gln Leu
 740 745 750

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

Glu

<210> SEQ ID NO 4
 <211> LENGTH: 745
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapien

<400> SEQUENCE: 4

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

-continued

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

<210> SEQ ID NO 5

<211> LENGTH: 374

<212> TYPE: PRT

<213> ORGANISM: Homo sapien

<400> SEQUENCE: 5

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

-continued

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

<210> SEQ ID NO 6

<211> LENGTH: 2429

<212> TYPE: PRT

<213> ORGANISM: Homo sapien

<400> SEQUENCE: 6

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

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Leu Val Arg Glu Leu Met Glu Glu Lys Lys Glu Glu Ile Thr Gly Thr
 130 135 140

Leu Arg Lys Asp Lys Thr Leu Leu Arg Asp Glu Lys Lys Met Glu Lys
 145 150 155 160

Leu Lys Gln Lys Leu His Thr Asp Asp Glu Leu Asn Trp Leu Asp His
 165 170 175

Gly Arg Thr Leu Arg Glu Gln Gly Val Glu Glu His Glu Thr Leu Leu
 180 185 190

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

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

Asn Gly Ser His Pro Val Ser Phe Asp Lys Ala Cys Glu Phe Ala Gly
 225 230 235 240

Phe Gln Cys Gln Ile Gln Phe Gly Pro His Asn Glu Gln Lys His Lys
 245 250 255

Ala Gly Phe Leu Asp Leu Lys Asp Phe Leu Pro Lys Glu Tyr Val Lys
 260 265 270

Gln Lys Gly Glu Arg Lys Ile Phe Gln Ala His Lys Asn Cys Gly Gln
 275 280 285

Met Ser Glu Ile Glu Ala Lys Val Arg Tyr Val Lys Leu Ala Arg Ser
 290 295 300

Leu Lys Thr Tyr Gly Val Ser Phe Phe Leu Val Lys Glu Lys Met Lys
 305 310 315 320

Gly Lys Asn Lys Leu Val Pro Arg Leu Leu Gly Ile Thr Lys Glu Cys
 325 330 335

Val Met Arg Val Asp Glu Lys Thr Lys Glu Val Ile Gln Glu Trp Asn
 340 345 350

Leu Thr Asn Ile Lys Arg Trp Ala Ala Ser Pro Lys Ser Phe Thr Leu
 355 360 365

Asp Phe Gly Asp Tyr Gln Asp Gly Tyr Tyr Ser Val Gln Thr Thr Glu
 370 375 380

Gly Glu Gln Ile Ala Gln Leu Ile Ala Gly Tyr Ile Asp Ile Ile Leu
 385 390 395 400

Lys Lys Lys Lys Ser Lys Asp His Phe Gly Leu Glu Gly Asp Glu Glu
 405 410 415

Ser Thr Met Leu Glu Asp Ser Val Ser Pro Lys Lys Ser Thr Val Leu
 420 425 430

Gln Gln Gln Tyr Asn Arg Val Gly Lys Val Glu His Gly Ser Val Ala
 435 440 445

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

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

His Arg Gly His Met Pro Pro Leu Thr Ser Ala Gln Gln Ala Leu Thr
 485 490 495

Gly Thr Ile Asn Ser Ser Met Gln Ala Val Gln Ala Ala Gln Ala Thr
 500 505 510

Leu Asp Asp Phe Asp Thr Leu Pro Pro Leu Gly Gln Asp Ala Ala Ser
 515 520 525

Lys Ala Trp Arg Lys Asn Lys Met Asp Glu Ser Lys His Glu Ile His
 530 535 540

-continued

Ser Gln Val Asp Ala Ile Thr Ala Gly Thr Ala Ser Val Val Asn Leu
 545 550 555 560
 Thr Ala Gly Asp Pro Ala Glu Thr Asp Tyr Thr Ala Val Gly Cys Ala
 565 570 575
 Val Thr Thr Ile Ser Ser Asn Leu Thr Glu Met Ser Arg Gly Val Lys
 580 585 590
 Leu Leu Ala Ala Leu Leu Glu Asp Glu Gly Gly Ser Gly Arg Pro Leu
 595 600 605
 Leu Gln Ala Ala Lys Gly Leu Ala Gly Ala Val Ser Glu Leu Leu Arg
 610 615 620
 Ser Ala Gln Pro Ala Ser Ala Glu Pro Arg Gln Asn Leu Leu Gln Ala
 625 630 635 640
 Ala Gly Asn Val Gly Gln Ala Ser Gly Glu Leu Leu Gln Gln Ile Gly
 645 650 655
 Glu Ser Asp Thr Asp Pro His Phe Gln Asp Ala Leu Met Gln Leu Ala
 660 665 670
 Lys Ala Val Ala Ser Ala Ala Ala Leu Val Leu Lys Ala Lys Ser
 675 680 685
 Val Ala Gln Arg Thr Glu Asp Ser Gly Leu Gln Thr Gln Val Ile Ala
 690 695 700
 Ala Ala Thr Gln Cys Ala Leu Ser Thr Ser Gln Leu Val Ala Cys Thr
 705 710 715 720
 Lys Val Val Ala Pro Thr Ile Ser Ser Pro Val Cys Gln Glu Gln Leu
 725 730 735
 Val Glu Ala Gly Arg Leu Val Ala Lys Ala Val Glu Gly Cys Val Ser
 740 745 750
 Ala Ser Gln Ala Ala Thr Glu Asp Gly Gln Leu Leu Arg Gly Val Gly
 755 760 765
 Ala Ala Ala Thr Ala Val Thr Gln Ala Leu Asn Glu Leu Leu Gln His
 770 775 780
 Val Lys Ala His Ala Thr Gly Ala Gly Pro Ala Gly Arg Tyr Asp Gln
 785 790 795 800
 Ala Thr Asp Thr Ile Leu Thr Val Thr Glu Asn Ile Phe Ser Ser Met
 805 810 815
 Gly Asp Ala Gly Glu Met Val Arg Gln Ala Arg Ile Leu Ala Gln Ala
 820 825 830
 Thr Ser Asp Leu Val Asn Ala Ile Lys Ala Asp Ala Glu Gly Glu Ser
 835 840 845
 Asp Leu Glu Asn Ser Arg Lys Leu Leu Ser Ala Ala Lys Ile Leu Ala
 850 855 860
 Asp Ala Thr Ala Lys Met Val Glu Ala Ala Lys Gly Ala Ala Ala His
 865 870 875 880
 Pro Asp Ser Glu Glu Gln Gln Gln Arg Leu Arg Glu Ala Ala Glu Gly
 885 890 895
 Leu Arg Met Ala Thr Asn Ala Ala Ala Gln Asn Ala Ile Lys Lys Lys
 900 905 910
 Leu Val Gln Arg Leu Glu His Ala Ala Lys Gln Ala Ala Ala Ser Ala
 915 920 925
 Thr Gln Thr Ile Ala Ala Ala Gln His Ala Ala Ser Thr Pro Lys Ala
 930 935 940
 Ser Ala Gly Pro Gln Pro Leu Leu Val Gln Ser Cys Lys Ala Val Ala
 945 950 955 960
 Glu Gln Ile Pro Leu Leu Val Gln Gly Val Arg Gly Ser Gln Ala Gln

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965					970					975					
Pro	Asp	Ser	Pro	Ser	Ala	Gln	Leu	Ala	Leu	Ile	Ala	Ala	Ser	Gln	Ser
			980					985					990		
Phe	Leu	Gln	Pro	Gly	Gly	Lys	Met	Val	Ala	Ala	Ala	Lys	Ala	Ser	Val
			995				1000						1005		
Pro	Thr	Ile	Gln	Asp	Gln	Ala	Ser	Ala	Met	Gln	Leu	Ser	Gln	Cys	
	1010					1015					1020				
Ala	Lys	Asn	Leu	Gly	Thr	Ala	Leu	Ala	Glu	Leu	Arg	Thr	Ala	Ala	
	1025					1030					1035				
Gln	Lys	Ala	Gln	Glu	Ala	Cys	Gly	Pro	Leu	Glu	Met	Asp	Ser	Ala	
	1040					1045					1050				
Leu	Ser	Val	Val	Gln	Asn	Leu	Glu	Lys	Asp	Leu	Gln	Glu	Val	Lys	
	1055					1060					1065				
Ala	Ala	Ala	Arg	Asp	Gly	Lys	Leu	Lys	Pro	Leu	Pro	Gly	Glu	Thr	
	1070					1075					1080				
Met	Glu	Lys	Cys	Thr	Gln	Asp	Leu	Gly	Asn	Ser	Thr	Lys	Ala	Val	
	1085					1090					1095				
Ser	Ser	Ala	Ile	Ala	Gln	Leu	Leu	Gly	Glu	Val	Ala	Gln	Gly	Asn	
	1100					1105					1110				
Glu	Asn	Tyr	Ala	Gly	Ile	Ala	Ala	Arg	Asp	Val	Ala	Gly	Gly	Leu	
	1115					1120					1125				
Arg	Ser	Leu	Ala	Gln	Ala	Ala	Arg	Gly	Val	Ala	Ala	Leu	Thr	Ser	
	1130					1135					1140				
Asp	Pro	Ala	Val	Gln	Ala	Ile	Val	Leu	Asp	Thr	Ala	Ser	Asp	Val	
	1145					1150					1155				
Leu	Asp	Lys	Ala	Ser	Ser	Leu	Ile	Glu	Glu	Ala	Lys	Lys	Ala	Ala	
	1160					1165					1170				
Gly	His	Pro	Gly	Asp	Pro	Glu	Ser	Gln	Gln	Arg	Leu	Ala	Gln	Val	
	1175					1180					1185				
Ala	Lys	Ala	Val	Thr	Gln	Ala	Leu	Asn	Arg	Cys	Val	Ser	Cys	Leu	
	1190					1195					1200				
Pro	Gly	Gln	Arg	Asp	Val	Asp	Asn	Ala	Leu	Arg	Ala	Val	Gly	Asp	
	1205					1210					1215				
Ala	Ser	Lys	Arg	Leu	Leu	Ser	Asp	Ser	Leu	Pro	Pro	Ser	Thr	Gly	
	1220					1225					1230				
Thr	Phe	Gln	Glu	Ala	Gln	Ser	Arg	Leu	Asn	Glu	Ala	Ala	Ala	Gly	
	1235					1240					1245				
Leu	Asn	Gln	Ala	Ala	Thr	Glu	Leu	Val	Gln	Ala	Ser	Arg	Gly	Thr	
	1250					1255					1260				
Pro	Gln	Asp	Leu	Ala	Arg	Ala	Ser	Gly	Arg	Phe	Gly	Gln	Asp	Phe	
	1265					1270					1275				
Ser	Thr	Phe	Leu	Glu	Ala	Gly	Val	Glu	Met	Ala	Gly	Gln	Ala	Pro	
	1280					1285					1290				
Ser	Gln	Glu	Asp	Arg	Ala	Gln	Val	Val	Ser	Asn	Leu	Lys	Gly	Ile	
	1295					1300					1305				
Ser	Met	Ser	Ser	Ser	Lys	Leu	Leu	Leu	Ala	Ala	Lys	Ala	Leu	Ser	
	1310					1315					1320				
Thr	Asp	Pro	Ala	Ala	Pro	Asn	Leu	Lys	Ser	Gln	Leu	Ala	Ala	Ala	
	1325					1330					1335				
Ala	Arg	Ala	Val	Thr	Asp	Ser	Ile	Asn	Gln	Leu	Ile	Thr	Met	Cys	
	1340					1345					1350				
Thr	Gln	Gln	Ala	Pro	Gly	Gln	Lys	Glu	Cys	Asp	Asn	Ala	Leu	Arg	
	1355					1360					1365				

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Glu Leu	Glu Thr Val Arg	Glu Leu Leu Glu Asn Pro	Val Gln Pro
1370		1375	1380
Ile Asn	Asp Met Ser Tyr Phe	Gly Cys Leu Asp Ser	Val Met Glu
1385		1390	1395
Asn Ser	Lys Val Leu Gly Glu	Ala Met Thr Gly Ile	Ser Gln Asn
1400		1405	1410
Ala Lys	Asn Gly Asn Leu Pro	Glu Phe Gly Asp Ala	Ile Ser Thr
1415		1420	1425
Ala Ser	Lys Ala Leu Cys Gly	Phe Thr Glu Ala Ala	Ala Gln Ala
1430		1435	1440
Ala Tyr	Leu Val Gly Val Ser	Asp Pro Asn Ser Gln	Ala Gly Gln
1445		1450	1455
Gln Gly	Leu Val Glu Pro Thr	Gln Phe Ala Arg Ala	Asn Gln Ala
1460		1465	1470
Ile Gln	Met Ala Cys Gln Ser	Leu Gly Glu Pro Gly	Cys Thr Gln
1475		1480	1485
Ala Gln	Val Leu Ser Ala Ala	Thr Ile Val Ala Lys	His Thr Ser
1490		1495	1500
Ala Leu	Cys Asn Ser Cys Arg	Leu Ala Ser Ala Arg	Thr Thr Asn
1505		1510	1515
Pro Thr	Ala Lys Arg Gln Phe	Val Gln Ser Ala Lys	Glu Val Ala
1520		1525	1530
Asn Ser	Thr Ala Asn Leu Val	Lys Thr Ile Lys Ala	Leu Asp Gly
1535		1540	1545
Ala Phe	Thr Glu Glu Asn Arg	Ala Gln Cys Arg Ala	Ala Thr Ala
1550		1555	1560
Pro Leu	Leu Glu Ala Val Asp	Asn Leu Ser Ala Phe	Ala Ser Asn
1565		1570	1575
Pro Glu	Phe Ser Ser Ile Pro	Ala Gln Ile Ser Pro	Glu Gly Arg
1580		1585	1590
Ala Ala	Met Glu Pro Ile Val	Ile Ser Ala Lys Thr	Met Leu Glu
1595		1600	1605
Ser Ala	Gly Gly Leu Ile Gln	Thr Ala Arg Ala Leu	Ala Val Asn
1610		1615	1620
Pro Arg	Asp Pro Pro Ser Trp	Ser Val Leu Ala Gly	His Ser Arg
1625		1630	1635
Thr Val	Ser Asp Ser Ile Lys	Lys Leu Ile Thr Ser	Met Arg Asp
1640		1645	1650
Lys Ala	Pro Gly Gln Leu Glu	Cys Glu Thr Ala Ile	Ala Ala Leu
1655		1660	1665
Asn Ser	Cys Leu Arg Asp Leu	Asp Gln Ala Ser Leu	Ala Ala Val
1670		1675	1680
Ser Gln	Gln Leu Ala Pro Leu	Gln Glu Ile Ser His	Leu Ile Glu
1685		1690	1695
Pro Leu	Ala Asn Ala Ala Arg	Ala Glu Ala Ser Gln	Leu Gly His
1700		1705	1710
Lys Val	Ser Gln Met Ala Gln	Tyr Phe Glu Pro Leu	Thr Leu Ala
1715		1720	1725
Ala Val	Gly Ala Ala Ser Lys	Thr Leu Ser His Pro	Gln Gln Met
1730		1735	1740
Ala Leu	Leu Asp Gln Thr Lys	Thr Leu Ala Glu Ser	Ala Leu Gln
1745		1750	1755

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Leu 1760	Tyr	Thr	Ala	Lys	Glu 1765	Ala	Gly	Gly	Asn	Pro 1770	Lys	Leu	Asp	
Glu 1775	Gly	Pro	Met	Gly	Glu 1780	Pro	Glu	Gly	Ser	Phe	Val 1785	Asp	Tyr	Gln
Thr 1790	Thr	Met	Val	Arg	Thr	Ala 1795	Lys	Ala	Ile	Ala	Val 1800	Thr	Val	Gln
Glu 1805	Met	Ile	Gly	Ser	His	Ile 1810	Lys	His	Arg	Val	Gln 1815	Glu	Leu	Gly
His 1820	Gly	Cys	Ala	Ala	Leu	Val 1825	Thr	Lys	Ala	Gly	Ala 1830	Leu	Gln	Cys
Ser 1835	Pro	Ser	Asp	Ala	Tyr	Thr 1840	Lys	Lys	Glu	Leu	Ile 1845	Glu	Cys	Ala
Arg 1850	Arg	Val	Ser	Glu	Lys	Val 1855	Ser	His	Val	Leu	Ala 1860	Ala	Leu	Gln
Ala 1865	Gly	Asn	Arg	Gly	Thr	Gln 1870	Ala	Cys	Ile	Thr	Ala 1875	Ala	Ser	Ala
Val 1880	Ser	Gly	Ile	Ile	Ala	Asp 1885	Leu	Asp	Thr	Thr	Ile 1890	Met	Phe	Ala
Thr 1895	Ala	Gly	Thr	Leu	Asn	Arg 1900	Glu	Gly	Thr	Glu	Thr 1905	Phe	Ala	Asp
His 1910	Arg	Glu	Gly	Ile	Leu	Lys 1915	Thr	Ala	Lys	Val	Leu 1920	Val	Glu	Asp
Thr 1925	Lys	Val	Leu	Val	Gln	Asn 1930	Ala	Ala	Gly	Ser	Gln 1935	Glu	Lys	Leu
Ala 1940	Gln	Ala	Ala	Gln	Ser	Ser 1945	Val	Ala	Thr	Ile	Thr 1950	Arg	Leu	Ala
Asp 1955	Val	Val	Lys	Leu	Gly	Ala 1960	Ala	Ser	Leu	Gly	Ala 1965	Glu	Asp	Pro
Glu 1970	Thr	Gln	Val	Val	Leu	Ile 1975	Asn	Ala	Val	Lys	Asp 1980	Val	Ala	Lys
Ala 1985	Leu	Gly	Asp	Leu	Ile	Ser 1990	Ala	Thr	Lys	Ala	Ala 1995	Ala	Gly	Lys
Val 2000	Gly	Asp	Asp	Pro	Ala	Val 2005	Trp	Gln	Leu	Lys	Asn 2010	Ser	Ala	Lys
Val 2015	Met	Val	Thr	Asn	Val	Thr 2020	Ser	Leu	Leu	Lys	Thr 2025	Val	Lys	Ala
Val 2030	Glu	Asp	Glu	Ala	Thr	Lys 2035	Gly	Thr	Arg	Ala	Leu 2040	Glu	Ala	Thr
Thr 2045	Glu	His	Ile	Arg	Gln	Glu 2050	Leu	Ala	Pro	Pro	Ala 2055	Lys	Thr	Ser
Thr 2060	Pro	Glu	Asp	Phe	Ile	Arg 2065	Met	Thr	Lys	Gly	Ile 2070	Thr	Met	Ala
Thr 2075	Ala	Lys	Ala	Val	Ala	Ala 2080	Gly	Asn	Ser	Cys	Arg 2085	Gln	Glu	Asp
Val 2090	Ile	Ala	Thr	Ala	Asn	Leu 2095	Ser	Arg	Arg	Ala	Ile 2100	Ala	Asp	Met
Leu 2105	Arg	Ala	Cys	Lys	Glu	Ala 2110	Ala	Tyr	His	Pro	Glu 2115	Val	Ala	Pro
Asp 2120	Val	Arg	Leu	Arg	Ala	Leu 2125	His	Tyr	Gly	Arg	Glu 2130	Cys	Ala	Asn
Gly 2135	Tyr	Leu	Glu	Leu	Leu	Asp 2140	His	Val	Leu	Leu	Thr 2145	Leu	Gln	Lys
Pro	Ser	Pro	Glu	Leu	Lys	Gln	Gln	Leu	Thr	Gly	His	Ser	Lys	Arg

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2150	2155	2160
Val Ala Gly Ser Val Thr	Glu Leu Ile Gln Ala Ala	Glu Ala Met
2165	2170	2175
Lys Gly Thr Glu Trp Val	Asp Pro Glu Asp Pro Thr	Val Ile Ala
2180	2185	2190
Glu Asn Glu Leu Leu Gly	Ala Ala Ala Ala Ile Glu	Ala Ala Ala
2195	2200	2205
Lys Lys Leu Glu Gln Leu	Lys Pro Arg Ala Lys Pro	Lys Glu Ala
2210	2215	2220
Asp Glu Ser Leu Asn Phe	Glu Glu Gln Ile Leu Glu	Ala Ala Lys
2225	2230	2235
Ser Ile Ala Ala Ala Thr	Ser Ala Leu Val Lys Ala	Ala Ser Ala
2240	2245	2250
Ala Gln Arg Glu Leu Val	Ala Gln Gly Lys Val Gly	Ala Ile Pro
2255	2260	2265
Ala Asn Ala Leu Asp Asp	Gly Gln Trp Ser Gln Gly	Leu Ile Ser
2270	2275	2280
Ala Ala Arg Met Val Ala	Ala Ala Thr Asn Asn Leu	Cys Glu Ala
2285	2290	2295
Ala Asn Ala Ala Val Gln	Gly His Ala Ser Gln Glu	Lys Leu Ile
2300	2305	2310
Ser Ser Ala Lys Gln Val	Ala Ala Ser Thr Ala Gln	Leu Leu Val
2315	2320	2325
Ala Cys Lys Val Lys Ala	Asp Gln Asp Ser Glu Ala	Met Lys Arg
2330	2335	2340
Leu Gln Ala Ala Gly Asn	Ala Val Lys Arg Ala Ser	Asp Asn Leu
2345	2350	2355
Val Lys Ala Ala Gln Lys	Ala Ala Ala Phe Glu Glu	Gln Glu Asn
2360	2365	2370
Glu Thr Val Val Val Lys	Glu Lys Met Val Gly Gly	Ile Ala Gln
2375	2380	2385
Ile Ile Ala Ala Gln Glu	Glu Met Leu Arg Lys Glu	Arg Glu Leu
2390	2395	2400
Glu Glu Ala Arg Lys Lys	Leu Ala Gln Ile Arg Gln	Gln Gln Tyr
2405	2410	2415
Lys Phe Leu Pro Ser Glu	Leu Arg Asp Glu His	
2420	2425	

<210> SEQ ID NO 7

<211> LENGTH: 351

<212> TYPE: PRT

<213> ORGANISM: Homo sapien

<400> SEQUENCE: 7

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

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Asp Met Glu Lys Ile Trp His His Thr Phe Tyr Asn Glu Leu Arg Val
      85                               90                               95

Ala Pro Glu Glu His Pro Val Leu Leu Thr Glu Ala Pro Leu Asn Pro
      100                               105                               110

Lys Ala Asn Arg Glu Lys Met Thr Gln Ile Met Phe Glu Thr Phe Asn
      115                               120                               125

Thr Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu Ser Leu Tyr Ala
      130                               135                               140

Ser Gly Arg Thr Thr Ala Ile Leu Arg Leu Asp Leu Ala Gly Arg Asp
      145                               150                               155                               160

Leu Thr Asp Tyr Leu Met Lys Ile Leu Thr Glu Arg Gly Tyr Ser Phe
      165                               170                               175

Thr Thr Thr Ala Glu Arg Glu Ile Val Arg Asp Ile Lys Glu Lys Leu
      180                               185                               190

Cys Tyr Val Ala Leu Asp Phe Glu Gln Glu Met Ala Thr Ala Ala Ser
      195                               200                               205

Ser Ser Ser Leu Glu Lys Ser Tyr Glu Leu Pro Asp Gly Gln Val Ile
      210                               215                               220

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

Ser Phe Leu Gly Met Glu Ser Cys Gly Ile His Glu Thr Thr Phe Asn
      245                               250                               255

Ser Ile Met Lys Cys Asp Val Asp Ile Arg Lys Asp Leu Tyr Ala Asn
      260                               265                               270

Thr Val Leu Ser Gly Gly Thr Thr Met Tyr Pro Gly Ile Ala Asp Arg
      275                               280                               285

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

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

Ile Leu Ala Ser Leu Ser Thr Phe Gln Gln Met Trp Ile Ser Lys Gln
      325                               330                               335

Glu Tyr Asp Glu Ser Gly Pro Ser Ile Val His Arg Lys Cys Phe
      340                               345                               350

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<210> SEQ ID NO 8
<211> LENGTH: 467
<212> TYPE: PRT
<213> ORGANISM: Homo sapien

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<400> SEQUENCE: 8

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

Asn Gly Gly Gly Gly Asp Gly Arg Ala Leu Leu Lys Gln Gln Leu Trp
 20      25      30

Ser Phe Pro Gln Gly Arg Gly Arg Ser Gly Ser Leu Thr Arg Thr Gly
 35      40      45

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

Ser Gly Ser Ala Ser Ser Ser Cys Ala Ser Phe Ser Gly Ser Thr Ser
 65      70      75      80

Ser Trp Ser Ala Ala Arg Cys Gln Thr Ala Ser Phe Ala Gly Ser Asp
 85      90      95

Ala Gly Val Arg Gly Val Ser Glu Leu Gly Leu Ala Arg Gly His Thr
 100      105      110

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

<210> SEQ ID NO 9
 <211> LENGTH: 1301
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapien
 <400> SEQUENCE: 9

Met Glu Met Val Gly Phe Leu Pro Lys Thr Arg Arg Gln Ile Phe Ser

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1	5	10	15												
Leu	Leu	Ser	Ala	Ile	Leu	His	Leu	Gly	Asn	Ile	Cys	Tyr	Lys	Lys	Lys
	20							25					30		
Thr	Tyr	Arg	Asp	Asp	Ser	Ile	Asp	Ile	Cys	Asn	Pro	Glu	Val	Leu	Pro
	35						40					45			
Ile	Val	Ser	Glu	Leu	Leu	Glu	Val	Lys	Glu	Glu	Met	Leu	Phe	Glu	Ala
	50					55					60				
Leu	Val	Thr	Arg	Lys	Thr	Val	Thr	Val	Gly	Glu	Lys	Leu	Ile	Leu	Pro
65					70					75					80
Tyr	Lys	Leu	Ala	Glu	Ala	Val	Thr	Val	Arg	Asn	Ser	Met	Ala	Lys	Ser
				85					90					95	
Leu	Tyr	Ser	Ala	Leu	Phe	Asp	Trp	Ile	Val	Phe	Arg	Ile	Asn	His	Ala
			100					105					110		
Leu	Leu	Asn	Ser	Lys	Asp	Leu	Glu	His	Asn	Thr	Lys	Thr	Leu	Ser	Ile
		115					120					125			
Gly	Val	Leu	Asp	Ile	Phe	Gly	Phe	Glu	Asp	Tyr	Glu	Asn	Asn	Ser	Phe
	130					135					140				
Glu	Gln	Phe	Cys	Ile	Asn	Phe	Ala	Asn	Glu	Arg	Leu	Gln	His	Tyr	Phe
145					150					155					160
Asn	Gln	His	Ile	Phe	Lys	Leu	Glu	Gln	Glu	Glu	Tyr	Arg	Thr	Glu	Gly
				165					170					175	
Ile	Ser	Trp	His	Asn	Ile	Asp	Tyr	Ile	Asp	Asn	Thr	Cys	Cys	Ile	Asn
			180					185					190		
Leu	Ile	Ser	Lys	Lys	Pro	Thr	Gly	Leu	Leu	His	Leu	Leu	Asp	Glu	Glu
		195					200					205			
Ser	Asn	Phe	Pro	Gln	Ala	Thr	Asn	Gln	Thr	Leu	Leu	Asp	Lys	Phe	Lys
	210					215					220				
His	Gln	His	Glu	Asp	Asn	Ser	Tyr	Ile	Glu	Phe	Pro	Ala	Val	Met	Glu
225					230					235					240
Pro	Ala	Phe	Ile	Ile	Lys	His	Tyr	Ala	Gly	Lys	Val	Lys	Tyr	Gly	Val
				245					250					255	
Lys	Asp	Phe	Arg	Glu	Lys	Asn	Thr	Asp	His	Met	Arg	Pro	Asp	Ile	Val
			260					265					270		
Ala	Leu	Leu	Arg	Ser	Ser	Lys	Asn	Ala	Phe	Ile	Ser	Gly	Met	Ile	Gly
		275					280					285			
Ile	Asp	Pro	Val	Ala	Val	Phe	Arg	Trp	Ala	Ile	Leu	Arg	Ala	Phe	Phe
	290					295					300				
Arg	Ala	Met	Val	Ala	Phe	Arg	Glu	Ala	Gly	Lys	Arg	Asn	Ile	His	Arg
305					310					315					320
Lys	Thr	Gly	His	Asp	Asp	Thr	Ala	Pro	Cys	Ala	Ile	Leu	Lys	Ser	Met
				325					330					335	
Asp	Ser	Phe	Ser	Phe	Leu	Gln	His	Pro	Val	His	Gln	Arg	Ser	Leu	Glu
		340					345						350		
Ile	Leu	Gln	Arg	Cys	Lys	Glu	Glu	Lys	Tyr	Ser	Lys	Ala	Thr	Asn	Pro
		355					360					365			
Asp	Lys	Leu	Leu	Ser	His	Ile	His	Leu	Glu	Met	Glu	Thr	Arg	Ser	Ile
	370					375						380			
Leu	His	Gln	Gly	Ile	Thr	Arg	Lys	Asn	Pro	Arg	Thr	Pro	Leu	Ser	Asp
385					390					395					400
Leu	Gln	Gly	Met	Asn	Ala	Leu	Asn	Glu	Lys	Asn	Gln	His	Asp	Thr	Phe
				405					410					415	
Asp	Ile	Ala	Trp	Asn	Gly	Arg	Thr	Gly	Ile	Arg	Gln	Ser	Arg	Leu	Ser
			420					425						430	

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Ser Gly Thr Ser Leu Leu Asp Lys Asp Gly Ile Phe Ala Asn Ser Thr
 435 440 445

Ser Ser Lys Leu Leu Glu Arg Ala His Gly Ile Leu Thr Arg Asn Lys
 450 455 460

Asn Phe Lys Ser Lys Pro Ala Leu Pro Lys His Leu Leu Glu Val Asn
 465 470 475 480

Ser Leu Lys His Leu Thr Arg Leu Thr Leu Gln Asp Arg Ile Thr Lys
 485 490 495

Ser Leu Leu His Leu His Lys Lys Lys Lys Pro Pro Ser Ile Ser Ala
 500 505 510

Gln Phe Gln Ala Ser Leu Ser Lys Leu Met Glu Thr Leu Gly Gln Ala
 515 520 525

Glu Pro Tyr Phe Val Lys Cys Ile Arg Ser Asn Ala Glu Lys Leu Pro
 530 535 540

Leu Arg Phe Ser Asp Val Leu Val Leu Arg Gln Leu Arg Tyr Thr Gly
 545 550 555 560

Met Leu Glu Thr Val Arg Ile Arg Gln Ser Gly Tyr Ser Ser Lys Tyr
 565 570 575

Ser Phe Gln Asp Phe Val Ser His Phe His Val Leu Leu Pro Arg Asn
 580 585 590

Ile Ile Pro Ser Lys Phe Asn Ile Gln Asp Phe Phe Arg Lys Ile Asn
 595 600 605

Leu Asn Pro Asp Asn Tyr Gln Val Gly Lys Thr Met Val Phe Leu Lys
 610 615 620

Glu Gln Glu Arg Gln His Leu Gln Asp Leu Leu His Gln Glu Val Leu
 625 630 635 640

Arg Arg Ile Ile Leu Leu Gln Arg Trp Phe Arg Val Leu Leu Cys Arg
 645 650 655

Gln His Phe Leu His Leu Arg Gln Ala Ser Val Ile Ile Gln Arg Phe
 660 665 670

Trp Arg Asn Tyr Leu Asn Gln Lys Gln Val Arg Asp Ala Ala Val Gln
 675 680 685

Lys Asp Ala Phe Val Met Ala Ser Ala Ala Ala Leu Leu Gln Ala Ser
 690 695 700

Trp Arg Ala His Leu Glu Arg Gln Arg Tyr Leu Glu Leu Arg Ala Ala
 705 710 715 720

Ala Ile Val Ile Gln Gln Lys Trp Arg Asp Tyr Tyr Arg Arg Arg His
 725 730 735

Met Ala Ala Ile Cys Ile Gln Ala Arg Trp Lys Ala Tyr Arg Glu Ser
 740 745 750

Lys Arg Tyr Gln Glu Gln Arg Lys Lys Ile Ile Leu Leu Gln Ser Thr
 755 760 765

Cys Arg Gly Phe Arg Ala Arg Gln Arg Phe Lys Ala Leu Lys Glu Gln
 770 775 780

Arg Leu Arg Glu Thr Lys Pro Glu Val Gly Leu Val Asn Ile Lys Gly
 785 790 795 800

Tyr Gly Ser Leu Glu Ile Gln Gly Ser Asp Pro Ser Gly Trp Glu Asp
 805 810 815

Cys Ser Phe Asp Asn Arg Ile Lys Ala Ile Glu Glu Cys Lys Ser Val
 820 825 830

Ile Glu Ser Asn Arg Ile Ser Arg Glu Ser Ser Val Asp Cys Leu Lys
 835 840 845

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Glu Ser Pro Asn Lys Gln Gln Glu Arg Ala Gln Ser Gln Ser Gly Val
 850 855 860

Asp Leu Gln Glu Asp Val Leu Val Arg Glu Arg Pro Arg Ser Leu Glu
 865 870 875 880

Asp Leu His Gln Lys Lys Val Gly Arg Ala Lys Arg Glu Ser Arg Arg
 885 890 895

Met Arg Glu Leu Glu Gln Ala Ile Phe Ser Leu Glu Leu Leu Lys Val
 900 905 910

Arg Ser Leu Gly Gly Ile Ser Pro Ser Glu Asp Arg Arg Trp Ser Thr
 915 920 925

Glu Leu Val Pro Glu Gly Leu Gln Ser Pro Arg Gly Thr Pro Asp Ser
 930 935 940

Glu Ser Ser Gln Gly Ser Leu Glu Leu Leu Ser Tyr Glu Glu Ser Gln
 945 950 955 960

Lys Ser Lys Leu Glu Ser Val Ile Ser Asp Glu Gly Asp Leu Gln Phe
 965 970 975

Pro Ser Pro Lys Ile Ser Ser Ser Pro Lys Phe Asp Ser Arg Asp Asn
 980 985 990

Ala Leu Ser Ala Ser Asn Glu Thr Ser Ser Ala Glu His Leu Lys Asp
 995 1000 1005

Gly Thr Met Lys Glu Met Val Val Cys Ser Ser Glu Ser Ile Thr
 1010 1015 1020

Cys Lys Pro Gln Leu Lys Asp Ser Phe Ile Ser Asn Ser Leu Pro
 1025 1030 1035

Thr Phe Phe Tyr Ile Pro Gln Gln Asp Pro Leu Lys Thr Asn Ser
 1040 1045 1050

Gln Leu Asp Thr Ser Ile Gln Arg Asn Lys Leu Leu Glu Asn Glu
 1055 1060 1065

Asp Thr Ala Gly Glu Ala Leu Thr Leu Asp Ile Asn Arg Glu Thr
 1070 1075 1080

Arg Arg Tyr His Cys Ser Gly Lys Asp Gln Ile Val Pro Ser Leu
 1085 1090 1095

Asn Thr Glu Ser Ser Asn Pro Val Leu Lys Lys Leu Glu Lys Leu
 1100 1105 1110

Asn Thr Glu Lys Glu Glu Arg Gln Lys Gln Leu Gln Gln Gln Asn
 1115 1120 1125

Glu Lys Glu Met Met Glu Gln Ile Arg Gln Gln Thr Asp Ile Leu
 1130 1135 1140

Glu Lys Glu Arg Lys Ala Phe Lys Thr Ile Glu Lys Pro Arg Ile
 1145 1150 1155

Gly Glu Cys Leu Val Ala Pro Ser Ser Tyr Gln Ser Lys Gln Arg
 1160 1165 1170

Val Glu Arg Pro Ser Ser Leu Leu Ser Leu Asn Thr Ser Asn Lys
 1175 1180 1185

Gly Glu Leu Asn Val Leu Gly Ser Leu Ser Leu Lys Asp Ala Ala
 1190 1195 1200

Leu Ala Gln Lys Asp Ser Ser Ser Ala His Leu Pro Pro Lys Asp
 1205 1210 1215

Arg Pro Val Thr Val Phe Phe Glu Arg Lys Gly Ser Pro Cys Gln
 1220 1225 1230

Ser Ser Thr Val Lys Glu Leu Ser Lys Thr Asp Arg Met Gly Thr
 1235 1240 1245

Gln Leu Asn Val Ala Cys Lys Leu Ser Asn Asn Arg Ile Ser Lys

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

<210> SEQ ID NO 13

<211> LENGTH: 53

<212> TYPE: PRT

<213> ORGANISM: Homo sapien

<400> SEQUENCE: 13

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

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<210> SEQ ID NO 14
 <211> LENGTH: 201
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapien

<400> SEQUENCE: 14

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

<210> SEQ ID NO 15
 <211> LENGTH: 175
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapien

<400> SEQUENCE: 15

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

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Phe Leu Glu Thr His Phe Leu Asp Glu Glu Val Lys Leu Ile Lys Lys
 130 135 140

Met Gly Asp His Leu Thr Asn Leu His Arg Leu Gly Gly Pro Glu Ala
 145 150 155 160

Gly Leu Gly Glu Tyr Leu Phe Glu Arg Leu Thr Leu Lys His Asp
 165 170 175

<210> SEQ ID NO 16
 <211> LENGTH: 95
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapien

<400> SEQUENCE: 16

Met Ala Lys Pro Ala Gln Gly Ala Lys Tyr Arg Gly Ser Ile His Asp
 1 5 10 15

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

Met Lys Gly Phe Gly Ser Asp Lys Glu Ala Ile Leu Asp Ile Ile Thr
 35 40 45

Ser Arg Ser Asn Arg Gln Arg Gln Glu Val Cys Gln Ser Tyr Lys Ser
 50 55 60

Leu Tyr Gly Lys Asp Leu Ile Ala Asp Leu Lys Tyr Glu Leu Thr Gly
 65 70 75 80

Lys Phe Glu Arg Leu Ile Val Gly Gly Leu Ser Asp Val Gly Thr
 85 90 95

<210> SEQ ID NO 17
 <211> LENGTH: 125
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapien

<400> SEQUENCE: 17

Met Asp Asp Asp Ile Ala Ala Leu Val Val Asp Asn Gly Ser Gly Met
 1 5 10 15

Cys Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val Phe Pro
 20 25 30

Ser Ile Val Gly Arg Pro Arg His Gln Gly Val Met Val Gly Met Gly
 35 40 45

Gln Lys Asp Ser Tyr Val Gly Asp Glu Ala Gln Ser Lys Arg Gly Ile
 50 55 60

Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Val Thr Asn Trp Asp
 65 70 75 80

Asp Met Glu Lys Ile Trp His His Thr Phe Tyr Asn Glu Leu Arg Val
 85 90 95

Ala Pro Glu Glu His Pro Val Leu Leu Thr Glu Ala Pro Leu Asn Pro
 100 105 110

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

<210> SEQ ID NO 18
 <211> LENGTH: 584
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapien

<400> SEQUENCE: 18

Met Ser Val Arg Tyr Ser Ser Ser Lys His Tyr Ser Ser Ser Arg Ser
 1 5 10 15

Gly Gly Gly Gly Gly Gly Gly Gly Cys Gly Gly Gly Gly Val Ser

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20				25				30							
Ser	Leu	Arg	Ile	Ser	Ser	Ser	Lys	Gly	Ser	Leu	Gly	Gly	Gly	Phe	Ser
		35					40					45			
Ser	Gly	Gly	Phe	Ser	Gly	Gly	Ser	Phe	Ser	Arg	Gly	Ser	Ser	Gly	Gly
	50				55						60				
Gly	Cys	Phe	Gly	Gly	Ser	Ser	Gly	Gly	Tyr	Gly	Gly	Leu	Gly	Gly	Phe
65					70					75					80
Gly	Gly	Gly	Ser	Phe	Arg	Gly	Ser	Tyr	Gly	Ser	Ser	Ser	Phe	Gly	Gly
				85					90					95	
Ser	Tyr	Gly	Gly	Ile	Phe	Gly	Gly	Gly	Ser	Phe	Gly	Gly	Gly	Ser	Phe
				100					105					110	
Gly	Gly	Gly	Ser	Phe	Gly	Gly	Gly	Gly	Phe	Gly	Gly	Gly	Gly	Phe	Gly
				115					120					125	
Gly	Gly	Phe	Gly	Gly	Gly	Phe	Gly	Gly	Asp	Gly	Gly	Leu	Leu	Ser	Gly
	130					135					140				
Asn	Glu	Lys	Val	Thr	Met	Gln	Asn	Leu	Asn	Asp	Arg	Leu	Ala	Ser	Tyr
145					150						155				160
Leu	Asp	Lys	Val	Arg	Ala	Leu	Glu	Glu	Ser	Asn	Tyr	Glu	Leu	Glu	Gly
				165						170				175	
Lys	Ile	Lys	Glu	Trp	Tyr	Glu	Lys	His	Gly	Asn	Ser	His	Gln	Gly	Glu
				180					185				190		
Pro	Arg	Asp	Tyr	Ser	Lys	Tyr	Tyr	Lys	Thr	Ile	Asp	Asp	Leu	Lys	Asn
		195				200						205			
Gln	Ile	Leu	Asn	Leu	Thr	Thr	Asp	Asn	Ala	Asn	Ile	Leu	Leu	Gln	Ile
	210					215					220				
Asp	Asn	Ala	Arg	Leu	Ala	Ala	Asp	Asp	Phe	Arg	Leu	Lys	Tyr	Glu	Asn
225					230					235					240
Glu	Val	Ala	Leu	Arg	Gln	Ser	Val	Glu	Ala	Asp	Ile	Asn	Gly	Leu	Arg
				245					250					255	
Arg	Val	Leu	Asp	Glu	Leu	Thr	Leu	Thr	Lys	Ala	Asp	Leu	Glu	Met	Gln
				260					265					270	
Ile	Glu	Ser	Leu	Thr	Glu	Glu	Leu	Ala	Tyr	Leu	Lys	Lys	Asn	His	Glu
		275					280					285			
Glu	Glu	Met	Lys	Asp	Leu	Arg	Asn	Val	Ser	Thr	Gly	Asp	Val	Asn	Val
	290					295					300				
Glu	Met	Asn	Ala	Ala	Pro	Gly	Val	Asp	Leu	Thr	Gln	Leu	Leu	Asn	Asn
305					310					315					320
Met	Arg	Ser	Gln	Tyr	Glu	Gln	Leu	Ala	Glu	Gln	Asn	Arg	Lys	Asp	Ala
				325					330					335	
Glu	Ala	Trp	Phe	Asn	Glu	Lys	Ser	Lys	Glu	Leu	Thr	Thr	Glu	Ile	Asp
				340					345				350		
Asn	Asn	Ile	Glu	Gln	Ile	Ser	Ser	Tyr	Lys	Ser	Glu	Ile	Thr	Glu	Leu
		355				360						365			
Arg	Arg	Asn	Val	Gln	Ala	Leu	Glu	Ile	Glu	Leu	Gln	Ser	Gln	Leu	Ala
		370				375					380				
Leu	Lys	Gln	Ser	Leu	Glu	Ala	Ser	Leu	Ala	Glu	Thr	Glu	Gly	Arg	Tyr
385					390					395					400
Cys	Val	Gln	Leu	Ser	Gln	Ile	Gln	Ala	Gln	Ile	Ser	Ala	Leu	Glu	Glu
				405					410					415	
Gln	Leu	Gln	Gln	Ile	Arg	Ala	Glu	Thr	Glu	Cys	Gln	Asn	Thr	Glu	Tyr
				420					425				430		
Gln	Gln	Leu	Leu	Asp	Ile	Lys	Ile	Arg	Leu	Glu	Asn	Glu	Ile	Gln	Thr
		435					440							445	

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Tyr Arg Ser Leu Leu Glu Gly Glu Gly Ser Ser Gly Gly Gly Gly Arg
 450 455 460
 Gly Gly Gly Ser Phe Gly Gly Gly Tyr Gly Gly Gly Ser Ser Gly Gly
 465 470 475 480
 Gly Ser Ser Gly Gly Gly His Gly Gly Gly His Gly Gly Ser Ser Gly
 485 490 495
 Gly Gly Tyr Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly
 500 505 510
 Tyr Gly Gly Gly Ser Ser Ser Gly Gly His Gly Gly Ser Ser Ser Gly
 515 520 525
 Gly Tyr Gly Gly Gly Ser Ser Gly Gly Gly Gly Gly Tyr Gly Gly
 530 535 540
 Gly Ser Ser Gly Gly Gly Ser Ser Ser Gly Gly Gly Tyr Gly Gly Gly
 545 550 555 560
 Ser Ser Ser Gly Gly His Lys Ser Ser Ser Ser Gly Ser Val Gly Glu
 565 570 575
 Ser Ser Ser Lys Gly Pro Arg Tyr
 580

<210> SEQ ID NO 19
 <211> LENGTH: 156
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapien

<400> SEQUENCE: 19

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

<210> SEQ ID NO 20
 <211> LENGTH: 93
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapien

<400> SEQUENCE: 20

Met Ser Gly Leu Arg Val Tyr Ser Thr Ser Val Thr Gly Ser Arg Glu
 1 5 10 15
 Ile Lys Ser Gln Gln Ser Glu Val Thr Arg Ile Leu Asp Gly Lys Arg
 20 25 30

-continued

Ile Gln Tyr Gln Leu Val Asp Ile Ser Gln Asp Asn Ala Leu Arg Asp
 35 40 45
 Glu Met Arg Ala Leu Ala Gly Asn Pro Lys Ala Thr Pro Pro Gln Ile
 50 55 60
 Val Asn Gly Asp Gln Tyr Cys Gly Asp Tyr Glu Leu Phe Val Glu Ala
 65 70 75 80
 Val Glu Gln Asn Thr Leu Gln Glu Phe Leu Lys Leu Ala
 85 90

<210> SEQ ID NO 21
 <211> LENGTH: 184
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapien

<400> SEQUENCE: 21

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

<210> SEQ ID NO 22
 <211> LENGTH: 375
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapien

<400> SEQUENCE: 22

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

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

<210> SEQ ID NO 23

<211> LENGTH: 1075

<212> TYPE: PRT

<213> ORGANISM: Homo sapien

<400> SEQUENCE: 23

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

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65	70	75	80
Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn	85	90	95
Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser	100	105	110
Ser Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe	115	120	125
Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His	130	135	140
Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met	145	150	160
Leu Arg Asp Thr Asp Val Asn Lys Gln Asp Lys Gln Lys Arg Thr Ala	165	170	175
Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu	180	185	190
Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr	195	200	205
Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met	210	215	220
Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn	225	230	240
Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys	245	250	255
Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly	260	265	270
Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val	275	280	285
Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr	290	295	300
Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile	305	310	320
Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu	325	330	335
Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His His Val	340	345	350
Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile	355	360	365
Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu	370	375	380
Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser Gln Pro Glu Lys	385	390	400
Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Val Glu	405	410	415
Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly Leu Leu Glu Asn	420	425	430
Leu Thr Asn Gly Val Thr Ala Gly Asn Gly Asp Asn Gly Leu Ile Pro	435	440	445
Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe Pro Asp Asn Glu	450	455	460
Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Leu Ser Asp Tyr Lys Glu	465	470	475
Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp	485	490	495

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Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu Lys Gly Ser Glu
 500 505 510

Asn Gly Gln Pro Glu Lys Arg Ser Gln Glu Pro Glu Ile Asn Lys Asp
 515 520 525

Gly Asp Arg Glu Leu Glu Asn Phe Met Ala Ile Glu Glu Met Lys Lys
 530 535 540

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

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

Thr Pro Glu Ser Gln Gln Phe Pro Asp Thr Glu Asn Glu Glu Tyr His
 580 585 590

Ser Asp Glu Gln Asn Asp Thr Gln Lys Gln Phe Cys Glu Glu Gln Asn
 595 600 605

Thr Gly Ile Leu His Asp Glu Ile Leu Ile His Glu Glu Lys Gln Ile
 610 615 620

Glu Val Val Glu Lys Met Asn Ser Glu Leu Ser Leu Ser Cys Lys Lys
 625 630 635 640

Glu Lys Asp Ile Leu His Glu Asn Ser Thr Leu Arg Glu Glu Ile Ala
 645 650 655

Met Leu Arg Leu Glu Leu Asp Thr Met Lys His Gln Ser Gln Leu Arg
 660 665 670

Glu Lys Lys Tyr Leu Glu Asp Ile Glu Ser Val Lys Lys Arg Asn Asp
 675 680 685

Asn Leu Leu Lys Ala Leu Gln Leu Asn Glu Leu Thr Met Asp Asp Asp
 690 695 700

Thr Ala Val Leu Val Ile Asp Asn Gly Ser Gly Met Cys Lys Ala Gly
 705 710 715 720

Phe Ala Gly Asp Asp Ala Pro Arg Ala Val Phe Pro Ser Ile Val Gly
 725 730 735

Arg Pro Arg Gln Gln Gly Met Met Gly Gly Met His Gln Lys Glu Ser
 740 745 750

Tyr Val Gly Lys Glu Ala Gln Ser Lys Arg Gly Ile Leu Thr Leu Lys
 755 760 765

Tyr Pro Met Glu His Gly Ile Ile Thr Asn Trp Asp Asp Met Glu Lys
 770 775 780

Ile Trp His His Thr Phe Tyr Asn Glu Leu Arg Val Ala Pro Glu Glu
 785 790 795 800

His Pro Val Leu Leu Thr Glu Ala Thr Leu Asn Pro Lys Ala Asn Arg
 805 810 815

Glu Lys Met Thr Gln Ile Met Phe Glu Thr Phe Asn Thr Pro Ala Met
 820 825 830

Tyr Val Ala Ile Gln Ala Val Leu Ser Leu Tyr Thr Ser Gly Arg Thr
 835 840 845

Thr Gly Ile Val Met Asp Ser Gly Asp Gly Val Thr His Thr Val Pro
 850 855 860

Ile Tyr Glu Gly Asn Ala Leu Pro His Ala Thr Leu Arg Leu Asp Leu
 865 870 875 880

Ala Gly Arg Glu Leu Pro Asp Tyr Leu Met Lys Ile Leu Thr Glu His
 885 890 895

Gly Tyr Arg Phe Thr Thr Met Ala Glu Arg Glu Ile Val Arg Asp Ile
 900 905 910

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Lys Glu Lys Leu Cys Tyr Val Ala Leu Asp Phe Glu Gln Glu Met Ala
 915 920 925

 Thr Val Ala Ser Ser Ser Ser Leu Glu Lys Ser Tyr Glu Leu Pro Asp
 930 935 940

 Gly Gln Val Ile Thr Ile Gly Asn Glu Arg Phe Arg Cys Pro Glu Ala
 945 950 955 960

 Leu Phe Gln Pro Cys Phe Leu Gly Met Glu Ser Cys Gly Ile His Glu
 965 970 975

 Thr Thr Phe Asn Ser Ile Met Lys Ser Asp Val Asp Ile Arg Lys Asp
 980 985 990

 Leu Tyr Thr Asn Thr Val Leu Ser Gly Gly Thr Thr Met Tyr Pro Gly
 995 1000 1005

 Met Ala His Arg Met Gln Lys Glu Ile Ala Ala Leu Ala Pro Ser
 1010 1015 1020

 Met Met Lys Ile Arg Ile Ile Ala Pro Pro Lys Arg Lys Tyr Ser
 1025 1030 1035

 Val Trp Val Gly Gly Ser Ile Leu Ala Ser Leu Ser Thr Phe Gln
 1040 1045 1050

 Gln Met Trp Ile Ser Lys Gln Glu Tyr Asp Glu Ser Gly Pro Ser
 1055 1060 1065

 Ile Val His Arg Lys Cys Leu
 1070 1075

<210> SEQ ID NO 24
 <211> LENGTH: 111
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapien

<400> SEQUENCE: 24

Met Phe Gly Gly Pro Gly Thr Gly Ser Arg Pro Ser Ser Thr Arg Ser
 1 5 10 15

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

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

 Val Thr Arg Ser Ser Ala Val Arg Leu Arg Ser Ser Val Pro Gly Val
 50 55 60

 Arg Leu Leu Gln Asp Ser Val Asp Phe Ser Leu Ala Asp Ala Ile Asn
 65 70 75 80

 Thr Glu Phe Lys Asn Thr Arg Thr Asn Glu Lys Val Glu Leu Gln Glu
 85 90 95

 Leu Asn Asp Arg Phe Ala Asn Tyr Ile Asp Lys Val Arg Phe Leu
 100 105 110

<210> SEQ ID NO 25
 <211> LENGTH: 105
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapien

<400> SEQUENCE: 25

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

 Leu Ile Ala Val Phe Gln Lys Tyr Ala Gly Lys Asp Gly Tyr Asn Tyr
 20 25 30

 Thr Leu Ser Lys Thr Glu Phe Leu Ser Phe Met Asn Thr Glu Leu Ala
 35 40 45

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Ala Phe Thr Lys Asn Gln Lys Asp Pro Gly Val Leu Asp Arg Met Met
50 55 60

Lys Lys Leu Asp Thr Asn Ser Asp Gly Gln Leu Asp Phe Ser Glu Phe
65 70 75 80

Leu Asn Leu Ile Gly Gly Leu Ala Met Ala Cys His Asp Ser Phe Leu
85 90 95

Lys Ala Val Pro Ser Gln Lys Arg Thr
100 105

<210> SEQ ID NO 26
 <211> LENGTH: 866
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapien

<400> SEQUENCE: 26

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

Ala Trp Thr Ala Asp Ser Gly Glu Gly Asp Phe Leu Ala Glu Gly Gly
20 25 30

Gly Val Arg Gly Pro Arg Val Val Glu Arg His Gln Ser Ala Cys Lys
35 40 45

Asp Ser Asp Trp Pro Phe Cys Ser Asp Glu Asp Trp Asn Tyr Lys Cys
50 55 60

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

Phe Thr Asn Arg Ile Asn Lys Leu Lys Asn Ser Leu Phe Glu Tyr Gln
85 90 95

Lys Asn Asn Lys Asp Ser His Ser Leu Thr Thr Asn Ile Met Glu Ile
100 105 110

Leu Arg Gly Asp Phe Ser Ser Ala Asn Asn Arg Asp Asn Thr Tyr Asn
115 120 125

Arg Val Ser Glu Asp Leu Arg Ser Arg Ile Glu Val Leu Lys Arg Lys
130 135 140

Val Ile Glu Lys Val Gln His Ile Gln Leu Leu Gln Lys Asn Val Arg
145 150 155 160

Ala Gln Leu Val Asp Met Lys Arg Leu Glu Val Asp Ile Asp Ile Lys
165 170 175

Ile Arg Ser Cys Arg Gly Ser Cys Ser Arg Ala Leu Ala Arg Glu Val
180 185 190

Asp Leu Lys Asp Tyr Glu Asp Gln Gln Lys Gln Leu Glu Gln Val Ile
195 200 205

Ala Lys Asp Leu Leu Pro Ser Arg Asp Arg Gln His Leu Pro Leu Ile
210 215 220

Lys Met Lys Pro Val Pro Asp Leu Val Pro Gly Asn Phe Lys Ser Gln
225 230 235 240

Leu Gln Lys Val Pro Pro Glu Trp Lys Ala Leu Thr Asp Met Pro Gln
245 250 255

Met Arg Met Glu Leu Glu Arg Pro Gly Gly Asn Glu Ile Thr Arg Gly
260 265 270

Gly Ser Thr Ser Tyr Gly Thr Gly Ser Glu Thr Glu Ser Pro Arg Asn
275 280 285

Pro Ser Ser Ala Gly Ser Trp Asn Ser Gly Ser Ser Gly Pro Gly Ser
290 295 300

Thr Gly Asn Arg Asn Pro Gly Ser Ser Gly Thr Gly Gly Thr Ala Thr
305 310 315 320

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

<210> SEQ ID NO 27
 <211> LENGTH: 426
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapien

<400> SEQUENCE: 27

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

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<210> SEQ ID NO 29
<211> LENGTH: 323
<212> TYPE: PRT
<213> ORGANISM: Homo sapien

<400> SEQUENCE: 29

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

Gly Asp Asp

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<210> SEQ ID NO 30
<211> LENGTH: 584
<212> TYPE: PRT
<213> ORGANISM: Homo sapien

<400> SEQUENCE: 30

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Met Ser Val Arg Tyr Ser Ser Ser Lys His Tyr Ser Ser Ser Arg Ser
1           5           10           15

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Gly Gly Gly Gly Gly Gly Gly Gly Cys Gly Gly Gly Gly Gly Val Ser
 20 25 30

Ser Leu Arg Ile Ser Ser Ser Lys Gly Ser Leu Gly Gly Gly Phe Ser
 35 40 45

Ser Gly Gly Phe Ser Gly Gly Ser Phe Ser Arg Gly Ser Ser Gly Gly
 50 55 60

Gly Cys Phe Gly Gly Ser Ser Gly Gly Tyr Gly Gly Leu Gly Gly Phe
 65 70 75 80

Gly Gly Gly Ser Phe Arg Gly Ser Tyr Gly Ser Ser Ser Phe Gly Gly
 85 90 95

Ser Tyr Gly Gly Ile Phe Gly Gly Gly Ser Phe Gly Gly Gly Ser Phe
 100 105 110

Gly Gly Gly Ser Phe Gly Gly Gly Gly Phe Gly Gly Gly Gly Phe Gly
 115 120 125

Gly Gly Phe Gly Gly Gly Phe Gly Gly Asp Gly Gly Leu Leu Ser Gly
 130 135 140

Asn Glu Lys Val Thr Met Gln Asn Leu Asn Asp Arg Leu Ala Ser Tyr
 145 150 155 160

Leu Asp Lys Val Arg Ala Leu Glu Glu Ser Asn Tyr Glu Leu Glu Gly
 165 170 175

Lys Ile Lys Glu Trp Tyr Glu Lys His Gly Asn Ser His Gln Gly Glu
 180 185 190

Pro Arg Asp Tyr Ser Lys Tyr Tyr Lys Thr Ile Asp Asp Leu Lys Asn
 195 200 205

Gln Ile Leu Asn Leu Thr Thr Asp Asn Ala Asn Ile Leu Leu Gln Ile
 210 215 220

Asp Asn Ala Arg Leu Ala Ala Asp Asp Phe Arg Leu Lys Tyr Glu Asn
 225 230 235 240

Glu Val Ala Leu Arg Gln Ser Val Glu Ala Asp Ile Asn Gly Leu Arg
 245 250 255

Arg Val Leu Asp Glu Leu Thr Leu Thr Lys Ala Asp Leu Glu Met Gln
 260 265 270

Ile Glu Ser Leu Thr Glu Glu Leu Ala Tyr Leu Lys Lys Asn His Glu
 275 280 285

Glu Glu Met Lys Asp Leu Arg Asn Val Ser Thr Gly Asp Val Asn Val
 290 295 300

Glu Met Asn Ala Ala Pro Gly Val Asp Leu Thr Gln Leu Leu Asn Asn
 305 310 315 320

Met Arg Ser Gln Tyr Glu Gln Leu Ala Glu Gln Asn Arg Lys Asp Ala
 325 330 335

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

Asn Asn Ile Glu Gln Ile Ser Ser Tyr Lys Ser Glu Ile Thr Glu Leu
 355 360 365

Arg Arg Asn Val Gln Ala Leu Glu Ile Glu Leu Gln Ser Gln Leu Ala
 370 375 380

Leu Lys Gln Ser Leu Glu Ala Ser Leu Ala Glu Thr Glu Gly Arg Tyr
 385 390 395 400

Cys Val Gln Leu Ser Gln Ile Gln Ala Gln Ile Ser Ala Leu Glu Glu
 405 410 415

Gln Leu Gln Gln Ile Arg Ala Glu Thr Glu Cys Gln Asn Thr Glu Tyr
 420 425 430

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Gln Gln Leu Leu Asp Ile Lys Ile Arg Leu Glu Asn Glu Ile Gln Thr
 435 440 445

Tyr Arg Ser Leu Leu Glu Gly Glu Gly Ser Ser Gly Gly Gly Gly Arg
 450 455 460

Gly Gly Gly Ser Phe Gly Gly Gly Tyr Gly Gly Gly Ser Ser Gly Gly
 465 470 475 480

Gly Ser Ser Gly Gly Gly His Gly Gly Gly His Gly Gly Ser Ser Gly
 485 490 495

Gly Gly Tyr Gly Gly Gly Ser Ser Gly Gly Gly Ser Ser Gly Gly Gly
 500 505 510

Tyr Gly Gly Gly Ser Ser Ser Gly Gly His Gly Gly Ser Ser Ser Gly
 515 520 525

Gly Tyr Gly Gly Gly Ser Ser Gly Gly Gly Gly Gly Gly Tyr Gly Gly
 530 535 540

Gly Ser Ser Gly Gly Gly Ser Ser Ser Gly Gly Gly Tyr Gly Gly Gly
 545 550 555 560

Ser Ser Ser Gly Gly His Lys Ser Ser Ser Ser Gly Ser Val Gly Glu
 565 570 575

Ser Ser Ser Lys Gly Pro Arg Tyr
 580

<210> SEQ ID NO 31
 <211> LENGTH: 214
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapien

<400> SEQUENCE: 31

Met Glu Glu Glu Ile Ala Ala Leu Val Ile Asp Asn Gly Ser Gly Met
 1 5 10 15

Cys Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val Phe Pro
 20 25 30

Ser Ile Val Gly Arg Pro Arg His Gln Gly Val Met Val Gly Met Gly
 35 40 45

Gln Lys Asp Ser Tyr Val Gly Asp Glu Ala Gln Ser Lys Arg Gly Ile
 50 55 60

Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile Val Thr Asn Trp Asp
 65 70 75 80

Asp Met Glu Lys Ile Trp His His Thr Phe Tyr Asn Glu Leu Arg Val
 85 90 95

Ala Pro Glu Glu His Pro Val Leu Leu Thr Glu Ala Pro Leu Asn Pro
 100 105 110

Lys Ala Asn Arg Glu Lys Met Thr Gln Ile Met Phe Glu Thr Phe Asn
 115 120 125

Thr Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu Ser Leu Tyr Ala
 130 135 140

Ser Gly Arg Thr Thr Gly Ile Val Met Asp Ser Gly Asp Gly Val Thr
 145 150 155 160

His Thr Val Pro Ile Tyr Glu Gly Tyr Ala Leu Pro His Ala Ile Leu
 165 170 175

Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr Asp Tyr Leu Met Lys Ile
 180 185 190

Leu Thr Glu Arg Gly Tyr Ser Phe Thr Thr Thr Ala Glu Arg Glu Ile
 195 200 205

Val Arg Asp Ile Lys Glu
 210

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<210> SEQ ID NO 32
<211> LENGTH: 553
<212> TYPE: PRT
<213> ORGANISM: Homo sapien

<400> SEQUENCE: 32

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

Arg Ala Gly Leu Val Ser Arg Asn Ala Leu Gly Ser Ser Phe Ile Ala
20                               25                               30

Ala Arg Asn Phe His Ala Ser Asn Thr His Leu Gln Lys Thr Gly Thr
35                               40                               45

Ala Glu Met Ser Ser Ile Leu Glu Glu Arg Ile Leu Gly Ala Asp Thr
50                               55                               60

Ser Val Asp Leu Glu Glu Thr Gly Arg Val Leu Ser Ile Gly Asp Gly
65                               70                               75                               80

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

Glu Phe Ser Ser Gly Leu Lys Gly Met Ser Leu Asn Leu Glu Pro Asp
100                              105                              110

Asn Val Gly Val Val Val Phe Gly Asn Asp Lys Leu Ile Lys Glu Gly
115                              120                              125

Asp Ile Val Lys Arg Thr Gly Ala Ile Val Asp Val Pro Val Gly Glu
130                              135                              140

Glu Leu Leu Gly Arg Val Val Asp Ala Leu Gly Asn Ala Ile Asp Gly
145                              150                              155                              160

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

Pro Gly Ile Ile Pro Arg Ile Ser Val Arg Glu Pro Met Gln Thr Gly
180                              185                              190

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

Leu Ile Ile Gly Asp Arg Gln Thr Gly Lys Thr Ser Ile Ala Ile Asp
210                              215                              220

Thr Ile Ile Asn Gln Lys Arg Phe Asn Asp Gly Ser Asp Glu Lys Lys
225                              230                              235                              240

Lys Leu Tyr Cys Ile Tyr Val Ala Ile Gly Gln Lys Arg Ser Thr Val
245                              250                              255

Ala Gln Leu Val Lys Arg Leu Thr Asp Ala Asp Ala Met Lys Tyr Thr
260                              265                              270

Ile Val Val Ser Ala Thr Ala Ser Asp Ala Ala Pro Leu Gln Tyr Leu
275                              280                              285

Ala Pro Tyr Ser Gly Cys Ser Met Gly Glu Tyr Phe Arg Asp Asn Gly
290                              295                              300

Lys His Ala Leu Ile Ile Tyr Asp Asp Leu Ser Lys Gln Ala Val Ala
305                              310                              315                              320

Tyr Arg Gln Met Ser Leu Leu Leu Arg Arg Pro Pro Gly Arg Glu Ala
325                              330                              335

Tyr Pro Gly Asp Val Phe Tyr Leu His Ser Arg Leu Leu Glu Arg Ala
340                              345                              350

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

Val Ile Glu Thr Gln Ala Gly Asp Val Ser Ala Tyr Ile Pro Thr Asn

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专利名称(译)	与chagas疾病相关的心肌病的生物标志物		
公开(公告)号	US9696323	公开(公告)日	2017-07-04
申请号	US14/850113	申请日	2015-09-10
申请(专利权)人(译)	德州大学系统的校董会		
当前申请(专利权)人(译)	德州大学系统的校董会		
[标]发明人	BRASIER ALLAN WIKTOROWICZ JOHN E JU HYUNSU GARG NISHA JAIN		
发明人	BRASIER, ALLAN WIKTOROWICZ, JOHN E. JU, HYUNSU GARG, NISHA JAIN		
IPC分类号	G01N33/53 G01N33/68 G01N33/569		
CPC分类号	G01N33/6896 G01N33/56905 G01N2800/28		
优先权	61/775676 2013-03-10 US		
其他公开文献	US20150377911A1		
外部链接	Espacenet USPTO		

摘要(译)

某些实施方案包括用于评估具有锥虫感染的受试者是否存在心肌病适应症的方法。

