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(54) **MARKERS FOR RENAL DISEASE**

MARKER FÜR NIERENERKRANKUNG

MARQUEURS DE NÉPHROPATHIES

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(56) References cited:
WO-A1-2004/002518 **WO-A2-2011/079280**
US-A1- 2007 087 448

- **QIAN ZHANG ET AL: "Identification of novel serum biomarkers in child nephroblastoma using proteomics technology", MOLECULAR BIOLOGY REPORTS ; AN INTERNATIONAL JOURNAL ON MOLECULAR AND CELLULAR BIOLOGY, KLUWER ACADEMIC PUBLISHERS, DO, vol. 38, no. 1, 6 April 2010 (2010-04-06), pages 631-638, XP019866460, ISSN: 1573-4978, DOI: DOI:10.1007/S11033-010-0149-4**
- **OLGA GURSKY ET AL: "Thermodynamic Analysis of Human Plasma Apolipoprotein C-1: High-Temperature Unfolding and Low-Temperature Oligomer Dissociation +", BIOCHEMISTRY, vol. 37, no. 5, 1 February 1998 (1998-02-01), pages 1283-1291, XP55003215, ISSN: 0006-2960, DOI: 10.1021/bi971801q**
- **FRANK DIETERLE ET AL: "Urinary clusterin, cystatin C, [beta]2-microglobulin and total protein as markers to detect drug-induced kidney injury", NATURE BIOTECHNOLOGY, vol. 28, no. 5, 1 May 2010 (2010-05-01), pages 463-469, XP55003106, ISSN: 1087-0156, DOI: 10.1038/nbt.1622**
- **PUPPIONE D L ET AL: "Mass spectral analysis of the apolipoproteins on dog (Canis lupus familiaris) high density lipoproteins. Detection of apolipoprotein A-II", COMPARATIVE BIOCHEMISTRY AND PHYSIOLOGY. PART D: GENOMICS ANDPROTEOMICS, ELSEVIER, AMSTERDAM, NL, vol. 3, no. 4, 1 December 2008 (2008-12-01), pages 290-296, XP025587941, ISSN: 1744-117X, DOI: 10.1016/J.CBD.2008.08.002 [retrieved on 2008-09-07]**

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- DATABASE GENESEQ [Online] 03 February 2011 'Human organ specific protein related amino acid sequence SEQ:32987.' Retrieved from EBI, accession no. GSP:AUN31646 Database accession no. AUN31646
- 'Human organ specific protein related amino acid sequence SEQ:32987' XP007923070
- ANDREW S. LEVEY ET AL: 'The definition, classification, and prognosis of chronic kidney disease: a KDIGO Controversies Conference report' KIDNEY INTERNATIONAL vol. 80, no. 1, 01 July 2011, LONDON, GB, pages 17 - 28, XP055245390 DOI: 10.1038/ki.2010.483 ISSN: 0085-2538
- M.B. NABITY ET AL: 'Urinary Biomarkers of Renal Disease in Dogs with X-Linked Hereditary Nephropathy' JOURNAL OF VETERINARY INTERNAL MEDICINE vol. 26, no. 2, 22 March 2012, US, pages 282 - 293, XP055245407 DOI: 10.1111/j.1939-1676.2012.00891.x ISSN: 0891-6640
- MARY B. NABITY ET AL: 'Day-to-Day Variation of the Urine Protein: Creatinine Ratio in Female Dogs with Stable Glomerular Proteinuria Caused by X-Linked Hereditary Nephropathy' JOURNAL OF VETERINARY INTERNAL MEDICINE vol. 21, no. 3, 01 May 2007, US, pages 425 - 430, XP055245410 DOI: 10.1111/j.1939-1676.2007.tb02985.x ISSN: 0891-6640

Description

[0001] Renal disease is associated with increased water consumption, frequent urination, diminished appetite, weight loss and muscle atrophy. Generally, by the time clinical symptoms of renal disease develop, irreparable kidney damage has occurred. Early detection permits earlier treatment and in turn slows disease progression. Current treatment includes dialysis and a diet low in phosphorous and protein. Unfortunately, no cure for chronic renal disease exists and kidney failure will eventually occur. Therefore, early detection is crucial for improved life span and quality of life.

[0002] In mammals, renal disease progression is divided into five levels. Current methods for detecting canine renal disease include kidney ultrasound, biopsy, or measurement of urine protein/creatinine levels. Biopsy is invasive and creatinine measurement is not accurate until stage three of renal failure, which is after significant tissue damage has occurred. Methods for detecting canine renal disease at earlier stages are needed in the art as such methods would inhibit disease progression.

WO 2001/079280 relates to the identification of combinations of novel biomarkers for diagnosing and monitoring renal diseases in a canine. Puppione et al. (Comparative Biochemistry and Physiology, Part D 3 (2008) 290-296) discloses the detection of apolipoprotein A-II in dogs via mass spectral analyses of canine high density lipoproteins. US 2007/0087448 A1 describes the use of protein profile analysis to diagnose the progression of *inter alia* renal disease.

The present invention relates to a method for diagnosing stage 1 to 5 of renal disease, the method comprising:

(a) determining the amount of at least one polypeptide in a canine patient sample, wherein said polypeptide(s) comprise one or more of SEQ ID NO: 1, SEQ ID NO: 2, and SEQ ID NO: 3, and

(b) comparing the amount of said at least one polypeptide in the canine patient sample to a control sample, wherein increased levels of said polypeptide in the canine patient sample versus the control sample is an indication of renal disease.

The present invention relates to a method as outlined above, wherein the polypeptide comprises SEQ ID NO: 1.

The present invention relates to a method as outlined above, wherein determining the amount of the polypeptide is performed by immunoassay.

The present invention relates to a method as outlined above, wherein the renal disease is glomerular or tubular.

The present invention relates to a method as outlined above, wherein the patient sample is blood, serum, plasma or urine.

[0003] These and other objects and features of this invention will be better understood from the following detailed description taken in conjunction with the drawings wherein:

Figure 1 is a graph representing LC/MS measurement of inosine levels between high creatinine and control (low creatinine) dogs.

Figure 2 is a graph representing inosine, NGAL, and creatinine levels over time in an induced canine model of renal disease. Units of measurement include: Inosine in μg/deciliter; Creatinine in mg/centiliter; and NGAL in ng/ml.

Figure 3 is a series of graphs representing relative concentrations of apolipoprotein C1 (Figure 3A), kininogen (Figure 3B), and Inter-Alpha Inhibitor H4 (ITIH4) (Figure 3C) levels over time in an induced model of canine model of renal disease.

[0004] This invention is more particularly described below and the Examples set forth herein are intended as illustrative only, as numerous modifications and variations therein will be apparent to those skilled in the art. As used in the description herein and throughout the claims that follow, the meaning of "a", "an", and "the" includes plural reference unless the context clearly dictates otherwise. The terms used in the specification generally have their ordinary meanings in the art, within the context of the invention, and in the specific context where each term is used. Some terms have been more specifically defined below to provide additional guidance to the practitioner regarding the description of the invention.

[0005] As used herein, a "patient" or "subject" to be treated by the disclosed methods can mean either a human or non-human animal but in certain particular embodiments is a human feline, or canine.

[0006] The term "patient sample" as used herein includes but is not limited to a blood, serum, plasma, or urine sample obtained from a patient.

[0007] The term "control sample" as used herein can mean a sample obtained from a non-diseased individual or population, more particularly an individual or population that does not suffer from renal disease.

[0008] The term "polypeptides" can refer to one or more of one type of polypeptide (a set of polypeptides). "Polypeptides" can also refer to mixtures of two or more different types of polypeptides (*i.e.*, a mixture of polypeptides that includes but is not limited to full-length protein, truncated protein, or protein fragments). The terms "polypeptides" or "polypeptide" can each also mean "one or more polypeptides."

[0009] The term "full-length" as used herein refers to a protein comprising its natural amino acid sequence as expressed *in vivo*, or variants thereof. The term "truncated" refers to a protein that is lacks amino acids from the N- or C- terminal ends of the protein. The term "peptide fragment" refers to a partial amino acid sequence from a larger protein. In particular, a peptide fragment can be 10, 20, 30, 40, or 50 amino acids in length.

As disclosed herein, the polypeptides comprise one or a plurality of proteins that have altered expression (e.g., either increased or decreased) in patients with renal disease. In some cases, the proteins are found in blood, serum, plasma, or urine. The relative levels of specific polypeptides can indicate progression of renal failure and disease severity.

It is an advantage that altered or increased expression of the polypeptides provided herein can be readily detected using methods well known to the skilled worker.

The invention provides methods for identifying renal disease in dogs. In certain embodiments, the invention provides methods for providing a diagnosis for a renal patient according to claim 1. As disclosed herein, identifying the polypeptides in patient samples can be an independent predictor of kidney disease or an identifier of disease stage (stages 1-5). This advantageously permits diagnosis and identification of kidney disease stage prior to stage three and is not limited by patient age or body mass.

For the purposes of this invention, the term "immunological reagents" is intended to encompass antisera and antibodies, particularly monoclonal antibodies, as well as fragments thereof (including F(ab), $F(ab)_2$, F(ab)' and F_v fragments). Also included in the definition of immunological reagent are chimeric antibodies, humanized antibodies, and recombinantly-produced antibodies and fragments thereof. Immunological methods used in conjunction with the reagents described herein include direct and indirect (*for example,* sandwich-type) labeling techniques, immunoaffinity columns, immunomagnetic beads, fluorescence activated cell sorting (FACS), enzyme-linked immunosorbent assays (ELISA), radioimmune assay (RIA), as well as peroxidase labeled secondary antibodies that detect the primary antibody.

The immunological reagents are preferably detectably-labeled, most preferably using fluorescent labels that have excitation and emission wavelengths adapted for detection using commercially-available instruments such as and most preferably fluorescence activated cell sorters. Examples of fluorescent labels useful in the practice of the invention include phycoerythrin (PE), fluorescein isothiocyanate (FITC), rhodamine (RH), Texas Red (TX), Cy3, Hoechst 33258, and 4',6-diamidino-2-phenylindole (DAPI). Such labels can be conjugated to immunological reagents, such as antibodies and most preferably monoclonal antibodies using standard techniques (Maino et al., 1995, Cytometry 20: 127-133).

Antibodies are antibody molecules that specifically bind to polypeptides as provided in Table 1, variant polypeptides, or fragments thereof. An antibody can be specific for polypeptide fragments of apolipoprotein C-I, apolipoprotein C-II, fibrinogen alpha chain, or fibrinogen A-alpha chain, for example, an antibody specific for one or a plurality of SEQ ID NOS: 3, 7, 13, or 20. An antibody preferably recognizes multiple protein products. For example an antibody specific to SEQ ID NO: 3 recognizes multiple peptide fragment of apolipoprotein C-I, including SEQ ID NOS: 1 - 2, as well as full-length protein. One of skill in the art can easily determine if an antibody is specific for a polypeptide of Table 1 using assays described herein. An antibody can be a polyclonal antibody, a monoclonal antibody, a single chain antibody (scFv), or an antigen binding fragment of an antibody. Antigen-binding fragments of antibodies are a portion of an intact antibody comprising the antigen binding site or variable region of an intact antibody, wherein the portion is free of the constant heavy chain domains of the Fc region of the intact antibody. Examples of antigen binding antibody fragments include Fab, Fab', Fab'-SH, $F(ab')_2$ and F_v fragments.

[0010] An antibody can be any antibody class, including for example, IgG, IgM, IgA, ID and IgE. An antibody or fragment thereof binds to an epitope of a polypeptide. An antibody can be made *in vivo* in suitable laboratory animals or *in vitro* using recombinant DNA techniques. Means for preparing and characterizing antibodies are well know in the art. *See*, *e.g.*, Dean, Methods Mol. Biol. 80:23-37 (1998); Dean, Methods Mol. Biol. 32:361-79 (1994); Baileg, Methods Mol. Biol. 32:381-88 (1994); Gullick, Methods Mol. Biol. 32:389-99 (1994); Drenckhahn et al. Methods Cell. Biol. 37:7-56 (1993); Morrison, Ann. Rev. Immunol. 10:239-65 (1992); Wright et al. Crit. Rev. Immunol. 12:125-68 (1992). For example, polyclonal antibodies can be produced by administering a polypeptide to an animal, such as a human or other primate, mouse, rat, rabbit, guinea pig, goat, pig, dog, cow, sheep, donkey, or horse. Serum from the immunized animal is collected and the antibodies are purified from the plasma by, for example, precipitation with ammonium sulfate, followed by chromatography, such as affinity chromatography. Techniques for producing and processing polyclonal antibodies are known in the art.

[0011] "Specifically binds," "specifically bind," or "specific for" means that a first antigen, *e.g.*, a polypeptide of Table 1, recognizes and binds to an antibody with greater affinity than to other, non-specific molecules. "Specifically binds," "specifically bind" or "specific for" also means a first antibody, *e.g.*, an antibody raised against SEQ ID NOS:1-59, recognizes and binds to SEQ ID NOS:1-59, with greater affinity than to other non-specific molecules. A non-specific molecule is an antigen that shares no common epitope with the first antigen. Specific binding can be tested using, for example, an enzyme-linked immunosorbant assay (ELISA), a radioimmunoassay (RIA), or a western blot assay using methodology well known in the art.

[0012] The phrase "competes for binding" as used herein refers to an antibody that has a binding affinity for a particular polypeptide sequence or antigen such that when present, it will bind preferentially and specifically to the peptide sequence/antigen over other non-specific molecules. Again, a non-specific molecule is an antigen that shares no common epitope with the first antigen.

[0013] Antibodies include antibodies and antigen binding fragments thereof that (a) compete with a reference antibody for binding to SEQ ID NOS: 1-59 or antigen binding fragments thereof; (b) binds to the same epitope of SEQ ID NOS: 1-59 or antigen binding fragments thereof as a reference antibody; (c) binds to SEQ ID NOS: 1-59 or antigen binding fragments thereof with substantially the same K_d as a reference antibody; and/or (d) binds to SEQ ID NOS: 1-59 or fragments thereof with substantially the same off rate as a reference antibody, wherein the reference antibody is an antibody or antigen-binding fragment thereof that specifically binds to a polypeptide of SEQ ID NOS: 1-59 or antigen binding fragments thereof with a binding affinity K_a of 10^7 l/mol or more.
The affinity of a molecule X for its partner Y can be represented by a dissociation constant (Kd). The equilibrium dissocation constant (Kd) is calculated at the ration of k_{off}/k_{on}. *See* Chen, Y. et al., 1999, J. Mol. Biol. 293: 865-881. A variety of methods are known in the art for measuring affinity constants, which can be used for purposes of the present invention. The reference antibody can be an antibody or antigen-binding fragment thereof that has a binding affinity to a polypeptide of SEQ ID NOS: 1-59 with a particular K_{on} rate/association rate or K_{off} rate. The antibodies specifically bind with a K_{on} of 6 x 10^5 $M^{-1}s^{-1}$ or better; antibodies specifically bind with a K_{off} rate of 5 x 10^{-6} s^{-1} or better; or antibodies specifically bind with a binding affinity of 500 pM, 400 pM, 300 pM, 200 pM, 100 pM, 50 pM, 40 pM, 30 pM, 20 pM or better.
Additionally, monoclonal antibodies directed against epitopes present on a polypeptide can also be readily produced. For example, normal B cells from a mammal, such as a mouse, which was immunized with a polypeptide can be fused with, for example, HAT-sensitive mouse myeloma cells to produce hybridomas. Hybridomas producing polypeptide-specific antibodies can be identified using RIA or ELISA and isolated by cloning in semi-solid agar or by limiting dilution. Clones producing specific antibodies are isolated by another round of screening. Monoclonal antibodies can be screened for specificity using standard techniques, for example, by binding a polypeptide of the invention to a microtiter plate and measuring binding of the monoclonal antibody by an ELISA assay. Techniques for producing and processing monoclonal antibodies are known in the art. *See e.g.*, Kohler & Milstein, Nature, 256:495 (1975). Particular isotypes of a monoclonal antibody can be prepared directly, by selecting from the initial fusion, or prepared secondarily, from a parental hybridoma secreting a monoclonal antibody of a different isotype by using a sib selection technique to isolate class-switch variants. *See* Steplewski et al., P.N.A.S. U.S.A. 82:8653 1985; Spria et al., J. Immunolog. Meth. 74:307, 1984. Monoclonal antibodies can also be recombinant monoclonal antibodies. *See, e.g.*, U.S. Patent No. 4,474,893; U.S. Patent No. 4,816,567. Antibodies can also be chemically constructed. *See*, *e.g.*, U.S. Patent No. 4,676,980.

[0014] Antibodies can be chimeric (*see*, *e.g.*, U.S. Patent No. 5,482,856), humanized (*see*, *e.g.*, Jones et al., Nature 321:522 (1986); Reichmann et al., Nature 332:323 (1988); Presta, Curr. Op. Struct. Biol. 2:593 (1992)), caninized, canine, or human antibodies. Human antibodies can be made by, for example, direct immortilization, phage display, transgenic mice, or a Trimera methodology, *see e.g.*, Reisener et al., Trends Biotechnol. 16:242-246 (1998).

[0015] Antibodies that specifically bind SEQ ID NOS: 1-59 are particularly useful for detecting the presence of polypeptide fragments specific for renal disease present in a sample, such as a serum, blood, plasma, cell, tissue, or urine sample from an animal. An immunoassay for can utilize one antibody or several antibodies. An immunoassay can use, for example, a monoclonal antibody specific for one epitope, a combination of monoclonal antibodies specific for epitopes of one polypeptide, monoclonal antibodies specific for epitopes of different polypeptides, polyclonal antibodies specific for the same antigen, polyclonal antibodies specific for different antigens, or a combination of monoclonal and polyclonal antibodies. Immunoassay protocols can be based upon, for example, competition, direct reaction, or sandwich type assays using, for example, labeled antibody. Antibodies can be labeled with any type of label known in the art, including, for example, fluorescent, chemiluminescent, radioactive, enzyme, colloidal metal, radioisotope and bioluminescent labels.

[0016] Antibodies or antigen-binding fragments thereof can be bound to a support and used to detect the presence of proteins differential produced in renal disease. Supports include, for example, glass, polystyrene, polypropylene, polyethylene, dextran, nylon, amylases, natural and modified celluloses, polyacrylamides, agaroses and magletite.

[0017] Antibodies can further be used to isolate polypeptides by immunoaffinity columns. The antibodies can be affixed to a solid support by, for example, absorption or by covalent linkage so that the antibodies retain their immunoselective activity. Optionally, spacer groups can be included so that the antigen binding site of the antibody remains accessible. The immobilized antibodies can then be used to bind the polypeptides of Table 1 from a biological sample, including but not limited to saliva, serum, blood, and urine.

[0018] Antibodies can also be used in immunolocalization studies to analyze the presence and distribution of a polypeptide of the invention during various cellular events or physiological conditions. Antibodies can also be used to identify molecules involved in passive immunization and to identify molecules involved in the biosynthesis of non-protein antigens. Identification of such molecules can be useful in vaccine development. Antibodies including, for example, monoclonal antibodies and single chain antibodies, can be used to monitor the course of amelioration of a kidney disease. By measuring the increase or decrease of antibodies specific for the polypeptides of Table 1 in a test sample from an animal, it can be determined whether a particular therapeutic regiment aimed at ameliorating the disorder is effective. Antibodies can be detected and/or quantified using for example, direct binding assays such as RIA, ELISA, or Western blot assays.

[0019] The methods can be used to detect polypeptide fragments of Table 1 or full-length proteins containing an amino acid sequence provided in Table 1, wherein antibodies or antigen-binding antibody fragments are specific for SEQ ID NOS : 1-59. A biological sample can include, for example, sera, blood, cells, plasma, saliva, or urine from a mammal such as a dog, cat or human. The test sample can be untreated, precipitated, fractionated, separated, diluted, concentrated, or purified.

Methods described herein comprise contacting a test sample with one or a plurality of antibodies specific to SEQ ID NOS: 1-59 under conditions that allow polypeptide/antibody complexes, *i.e.*, immunocomplexes, to form. That is, antibodies specifically bind to one or a plurality of polypetides of SEQ ID NOS: 1-59 located in the sample. One of skill in the art is familiar with assays and conditions that are used to detect antibody/polypeptide complex binding. The formation of a complex between polypeptides and antibodies in the sample is detected. The formation of antibody/polypeptide complexes is an indication that polypeptides are present in the patient sample.

Antibodies can be used in a method of the diagnosis of renal disease by obtaining a test sample from, *e.g.*, a human, cat or dog suspected of suffering from renal disease. The test sample is contacted with antibodies under conditions enabling the formation of antibody-antigen complexes (*i.e.*, immunocomplexes). One of skill in the art is aware of conditions that enable and are appropriate for formation of antigen/antibody complexes. The amount of antibody-antigen complexes can be determined by methodology known in the art.

Methods comprise diagnosing renal disease in a patient by identifying the differential expression of the polypeptides of Table 1 in a patient sample as compared to control. These methods include the diagnosis or identification of disease stage (*e.g.*, stages 1-5). In one aspect, methods can be performed at multiple time points to evaluate disease progression or treatment efficacy. The methods may be performed at diagnosis and then at specific time points posttreatment wherein a specific therapy should result in a reduction or amelioration of disease progression.

Alternatively, the methods are used to assess the efficacy of a composition or treatment regime (whether a composition or diet) for the amelioration of renal disease progression. Similarly, the methods can be used for assessing a composition or treatment regimens activity on patient levels of the polypeptides of Table 1.

Differential levels of antibody-complexes present in patient samples versus control samples provides an indicator for renal disease. An antibody may be specific for one or plurality of the polypeptides provided in Table 1. An antibody can be contacted with a test sample. Antibodies specific to the polypeptides present in a test sample will form antigen-antibody complexes under suitable conditions. The amount of antibody-antigen complexes can be determined by methods known in the art.

Renal disease can be detected in a subject. A biological sample is obtained from the subject. One or more antibodies specific to the polypeptides comprising SEQ ID NOS: 1-59 or other polypeptides are contacted with the biological sample under conditions that allow polypeptide/antibody complexes to form. The polypeptide/antibody complexes are detected. The detection of the polypeptide/antibody complexes at differential levels as compared to controls is an indication that the mammal has renal disease.

The polypeptide/antibody complex may be detected when an indicator reagent, such as an enzyme conjugate, which is bound to the antibody, catalyzes a detectable reaction. Optionally, an indicator reagent comprising a signal generating compound can be applied to the polypeptide/antibody complex under conditions that allow formation of a polypeptide/antibody/indicator complex. The polypeptide/antibody/indicator complex is detected. Optionally, the polypeptide or antibody can be labeled with an indicator reagent prior to the formation of a polypeptide/antibody complex. The method can optionally comprise a positive or negative control.

One or more antibodies may be attached to a solid phase or substrate. A test sample potentially comprising a protein comprising a polypeptide is added to the substrate. One or more antibodies that specifically bind polypeptides are added. The antibodies can be the same antibodies used on the solid phase or can be from a different source or species and can be linked to an indicator reagent, such as an enzyme conjugate. Wash steps can be performed prior to each addition. A chromophore or enzyme substrate is added and color is allowed to develop. The color reaction is stopped and the color can be quantified using, for example, a spectrophotometer.

One or more antibodies may be attached to a solid phase or substrate. A test sample potentially containing a protein comprising a polypeptide is added to the substrate. Second anti-species antibodies that specifically bind polypeptides are added. These second antibodies are from a different species than the solid phase antibodies. Third anti-species antibodies are added that specifically bind the second antibodies and that do not specifically bind the solid phase antibodies are added. The third antibodies can comprise and indicator reagent such as an enzyme conjugate. Wash steps can be performed prior to each addition. A chromophore or enzyme substrate is added and color is allowed to develop. The color reaction is stopped and the color can be quantified using, for example, a spectrophotometer.

One or more capture antibodies can specifically bind to one or more epitopes of a polypeptide. The capture antibody or antibodies would be used to immobilize one or a plurality of polypeptide of SEQ ID NOS : 1 - 59 to, for example a solid support. One or more detection antibodies can specifically bind to the same one or more epitopes or different one or more epitopes of the polypeptides. The detection antibody can be used to detect or visualize the immobilization of the polypeptide to a solid support. This is advantageous because it is more specific and more sensitive than assays using only one antibody for both capture and detection functions.

Assays include, but are not limited to those based on competition, direct reaction or sandwich-type assays, including, but not limited to enzyme linked immunosorbent assay (ELISA), western blot, IFA, radioimmunoassay (RIA), hemagglutination (HA), fluorescence polarization immunoassay (FPIA), and microtiter plate assays (any assay done in one or more wells of a microtiter plate). One assay comprises a reversible flow chromatographic binding assay, for example a SNAP® assay. See e.g., U.S. Pat. No. 5,726,010.
Assays can use solid phases or substrates or can be performed by immunoprecipitation or any other methods that do not utilize solid phases. Where a solid phase or substrate is used, one or more polypeptides are directly or indirectly attached to a solid support or a substrate such as a microtiter well, magnetic bead, nonmagnetic bead, column, matrix, membrane, fibrous mat composed of synthetic or natural fibers (*e.g.*, glass or cellulose-based materials or thermoplastic polymers, such as, polyethylene, polypropylene, or polyester), sintered structure composed of particulate materials (*e.g.*, glass or various thermoplastic polymers), or cast membrane film composed of nitrocellulose, nylon, polysulfone or the like (generally synthetic in nature). A substrate may be sintered, fine particles of polyethylene, commonly known as porous polyethylene, for example, 10-15 micron porous polyethylene from Chromex Corporation (Albuquerque, NM). All of these substrate materials can be used in suitable shapes, such as films, sheets, or plates, or they may be coated onto or bonded or laminated to appropriate inert carriers, such as paper, glass, plastic films, or fabrics. Suitable methods for immobilizing antibodies on solid phases include ionic, hydrophobic, covalent interactions and the like.

[0020] In one type of assay format, one or more antibodies can be coated on a solid phase or substrate, A test sample suspected of containing polypeptides of Table 1 or fragments thereof is incubated with an indicator reagent comprising a signal generating compound conjugated to an antibodies or antibody fragments specific for said polypeptides for a time and under conditions sufficient to form antigen/antibody complexes of either antibodies of the solid phase to the test sample polypeptides or the indicator reagent compound conjugated to an antibody specific for the polypeptides. The binding of the indicator reagent conjugated to anti-polypeptide antibodies to the solid phase can be quantitatively measured. A measurable alteration in the signal compared to the signal generated from a control sample indicates the presence of polypeptides (SEQ ID NOS : 1 - 59). This type of assay can quantitate the amount of polypeptide in a test sample.

[0021] In another type of assay format, one or more antibodies are coated onto a support or substrate. An antibody is conjugated to an indicator reagent and added to a test sample. This mixture is applied to the support or substrate. If polypeptides are present in the test sample, they will bind the one or more antibodies conjugated to an indicator reagent and to the one or more antibodies immobilized on the support. The polypeptide/antibody/indicator complex can then be detected. This type of assay can quantitate the amount of polypeptide in a test sample.

[0022] In another type of assay format, one or more antibodies are coated onto a support or substrate. The test sample is applied to the support or substrate and incubated. Unbound components from the sample are washed away by washing the solid support with a wash solution. If the polypeptides of Table 1 are present in the test sample, they will bind to the antibody coated on the solid phase. This polypeptide/antibody complex can be detected using a second species-specific antibody that is conjugated to an indicator reagent. The polypeptide/antibody/anti-species antibody indicator complex can then be detected. This type of assay can quantitate the amount of polypeptides in a test sample.

[0023] The formation of a polypeptide/antibody complex or a polypeptide/antibody/indicator complex can be detected by, for example, radiometric, colorimetric, fluorometric, size-separation, or precipitation methods. Optionally, detection of a polypeptide/antibody complex is by the addition of a secondary antibody that is coupled to an indicator reagent comprising a signal generating compound. Indicator reagents comprising signal generating compounds (labels) associated with a polypeptide/antibody complex can be detected using the methods described above and include chromogenic agents, catalysts such as enzyme conjugates fluorescent compounds such as fluorescein and rhodamine, chemiluminescent compounds such as dioxetanes, acridiniums, phenanthridiniums, ruthenium, and luminol, radioactive elements, direct visual labels, as well as cofactors, inhibitors, magnetic particles, and the like. Examples of enzyme conjugates include alkaline phosphatase, horseradish peroxidase, beta-galactosidase, and the like. The selection of a particular label is not critical, but it will be capable of producing a signal either by itself or in conjunction with one or more additional substances.

[0024] Formation of the complex at differential levels as compared to control is indicative of the presence of renal disease. Therefore, the methods of the invention can be used to diagnose kidney disease in an animal.

[0025] The phrase "determining the amounts" as used herein refers to measuring or identifying the levels of one or a plurality polypeptides in a patient sample. In a particular embodiment, the identification of a specific epitope in polypeptides of multiple lengths including full-length protein, truncated protein, and protein fragments is provided. This can be accomplished by methodology well known in the art for the detection of polypeptides including using antibodies including, for example enzyme-linked immunosorbant assay (ELISA), a radioimmunoassay (RIA), or a western blot assay, or immunohistochemistry. Alternatively polypeptides, SEQ ID NOS: 1-59, can be determined by mass spectrometry or similar methods known by one of skill in the art. Determining the amount of polypeptide present in a patient sample is accomplished by such in vitro analysis and experimental manipulation. The amount of polypeptide present cannot be assessed by mere inspection.

Alternatively, elevated or reduced levels of one or a plurality of polypeptide transcripts of Table 1 present in a patient sample are detected by a process of hybridizing a nucleic acid probe that selectively hybridizes to the polypeptides. Conditions are utilized that permit high stringency hybridization between the nucleic acid probe, which is used as a detection means, and the polypeptide transcripts, wherein a level of nucleic acid complex formation and detection is indicative of the level of transcript in a sample. The enhanced or reduced level of polypeptide is indicative of renal disease. Methods for producing nucleic acid probes specific to the polypeptide transcripts are well known in the art.

The methods can also indicate the amount or quantity of polypeptides of Table 1 or full-length proteins comprising a polypeptide sequence of Table 1 in a test sample. In a particular embodiment, the amount or quantity of certain polypeptides provides an indicator of disease stage (*i.e.*, stages 1-5), disease progression, and/or a prognostic indicator. With many indicator reagents, such as enzyme conjugates, the amount of polypeptide present is proportional to the signal generated. Depending upon the type of test sample, it can be diluted with a suitable buffer reagent, concentrated, or contacted with a solid phase without any manipulation. For example, it usually is preferred to test serum or plasma samples that previously have been diluted, or concentrated specimens such as urine, in order to determine the presence and/or amount of polypeptide present.

[0026] Polypeptides and assays can be combined with other polypeptides or assays to detect the presence of renal disease. For example, polypeptides and assays can be combined with reagents that creatinine or general protein levels.

[0027] The fact that polypeptides SEQ ID NOS:1-59 are smaller than the full length proteins is important because smaller polypeptides can have greater specificity and/or sensitivity than full length polypeptides assays. These smaller polypeptides can be less expensive to manufacture, and may be obtained at greater purity than the full length polypeptide. Additionally, the smaller fragments and the levels of smaller fragements present in a sample are indicative of disease state. The differential expression of fragmented proteins is a marker for renal disease.

Variant polypeptides are at least about 80%, or about 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% identical to the polypeptide sequences shown in SEQ ID NOS: 1-59. For example, a variant polypeptide of SEQ ID NOS: 1-59 can be about at least 97%, 94%, 90%, 87%, 84%, or 81% identical to SEQ ID NOS: 1-59. Variant polypeptides have one or more conservative amino acid variations or other minor modifications and retain biological activity, *i.e.*, are biologically functional equivalents. A biologically active equivalent has substantially equivalent function when compared to the corresponding wild-type polypeptide. A polypeptide may have about 1, 2, 3, 4, 5, 10, 20 or less conservative amino acid substitutions.

Percent sequence identity has an art recognized meaning and there are a number of methods to measure identity between two polypeptide or polynucleotide sequences. See, *e.g.*, Lesk, Ed., Computational Molecular Biology, Oxford University Press, New York, (1988); Smith, Ed., Biocomputing: Informatics And Genome Projects, Academic Press, New York, (1993); Griffin & Griffin, Eds., Computer Analysis Of Sequence Data, Part I, Humana Press, New Jersey, (1994); von Heinje, Sequence Analysis In Molecular Biology, Academic Press, (1987); and Gribskov & Devereux, Eds., Sequence Analysis Primer, M Stockton Press, New York, (1991). Methods for aligning polynucleotides or polypeptides are codified in computer programs, including the GCG program package (Devereux et al., Nuc. Acids Res. 12:387 (1984)), BLASTP, BLASTN, FASTA (Atschul et al., J. Molec. Biol. 215:403 (1990)), and Bestfit program (Wisconsin Sequence Analysis Package, Version 8 for Unix, GeneticsComputer Group, University Research Park, 575 Science Drive, Madison, WI 53711) which uses the local homology algorithm of Smith and Waterman (Adv. App. Math., 2:482-489 (1981)). For example, the computer program ALIGN which employs the FASTA algorithm can be used, with an affine gap search with a gap open penalty of -12 and a gap extension penalty of -2.

[0028] When using any of the sequence alignment programs to determine whether a particular sequence is, for instance, about 95% identical to a reference sequence, the parameters are set such that the percentage of identity is calculated over the full length of the reference polynucleotide and that gaps in identity of up to 5% of the total number of nucleotides in the reference polynucleotide are allowed.

[0029] Variant polypeptides can generally be identified by modifying one of the polypeptide sequences of the invention, and evaluating the properties of the modified polypeptide to determine if it is a biological equivalent. A variant is a biological equivalent if it reacts substantially the same as a polypeptide of the invention in an assay such as an immunohistochemical assay, an enzyme-linked immunosorbent Assay (ELISA), a radioimmunoassay (RIA), immunoenzyme assay or a western blot assay, *e.g.* has 90-110% of the activity of the original polypeptide. In one embodiment, the assay is a competition assay wherein the biologically equivalent polypeptide is capable of reducing binding of the polypeptide of the invention to a corresponding reactive antigen or antibody by about 80, 95, 99, or 100%. An antibody that specifically binds a corresponding wild-type polypeptide also specifically binds the variant polypeptide.

[0030] A conservative substitution is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydropathic nature of the polypeptide to be substantially unchanged. In general, the following groups of amino acids represent conservative changes: (1) ala, pro, gly, glu, asp, gin, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his.

A polypeptide can further comprise a signal (or leader) sequence that co-translationally or post-translationally directs transfer of the protein. The polypeptide can also comprise a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (*e.g.*, poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide can be conjugated to an immunoglobulin Fc region or bovine serum albumin.

A polypeptide can be covalently or non-covalently linked to an amino acid sequence to which the polypeptide is not normally associated with in nature, *i.e.*, a heterologous amino acid sequence. A heterologous amino acid sequence can be from a different organism, a synthetic sequence, or a sequence not usually located at the carboxy or amino terminus of a polypeptide. Additionally, a polypeptide can be covalently or non-covalently linked to compounds or molecules other than amino acids, such as indicator reagents. A polypeptide can be covalently or non-covalently linked to an amino acid spacer, an amino acid linker, a signal sequence, a stop transfer sequence, a transmembrane domain, a protein purification ligand, or a combination thereof. A polypeptide can also be linked to a moiety (*i.e.*, a functional group that can be a polypeptide or other compound) that enhances an immune response (*e.g.*, cytokines such as IL-2), a moiety that facilitates purification (*e.g.*, affinity tags such as a six-histidine tag, trpE, glutathione, maltose binding protein), or a moiety that facilitates polypeptide stability (*e.g.*, polyethylene glycol; amino terminus protecting groups such as acetyl, propyl, succinyl, benzyl, benzyloxycarbonyl or t- butyloxycarbonyl; carboxyl terminus protecting groups such as amide, methylamide, and ethylamide). A protein purification ligand can be one or more C amino acid residues at, for example, the amino terminus or carboxy terminus or both termini of a polypeptide. An amino acid spacer is a sequence of amino acids that are not associated with a polypeptide in nature. An amino acid spacer can comprise about 1, 5, 10, 20, 100, or 1,000 amino acids.

[0031] If desired, a polypeptide can be part of a fusion protein, which contains other amino acid sequences, such as amino acid linkers, amino acid spacers, signal sequences, TMR stop transfer sequences, transmembrane domains, as well as ligands useful in protein purification, such as glutathione-S-transferase, histidine tag, and *Staphylococcal* protein A. More than one polypeptide can be present in a fusion protein. A polypeptide can be operably linked to proteins of a different organism or to form fusion proteins. A fusion protein can comprise one or more of polypeptides fragments thereof, or combinations thereof. A fusion protein does not occur in nature. The term "operably linked" means that the polypeptide and the other polypeptides are fused in-frame to each other either to the N-terminus or C-terminus of the polypeptide.

[0032] Polypeptides can be in a multimeric form. That is, a polypeptide can comprise one or more copies of a polypeptide or a combination thereof. A multimeric polypeptide can be a multiple antigen peptide (MAP). *See e.g.*, Tam, J. Immunol. Methods, 196:17-32 (1996).

[0033] Polypeptides can comprise an antigen that is recognized by an antibody specific for the polypeptides of SEQ ID NOS: 1-59. The antigen can comprise one or more epitopes (*i.e.*, antigenic determinants). An epitope can be a linear epitope, sequential epitope or a conformational epitope. Epitopes within a polypeptide of the invention can be identified by several methods. *See, e.g.*, U.S. Patent No. 4,554,101; Jameson & Wolf, CABIOS 4:181-186 (1988). For example, a polypeptide can be isolated and screened. A series of short peptides, which together span an entire polypeptide sequence, can be prepared by proteolytic cleavage. By starting with, for example, 30-mer polypeptide fragments (or smaller fragments), each fragment can be tested for the presence of epitopes recognized in an ELISA. For example, in an ELISA assay, a polypeptide, such as a 30-mer polypeptide fragment, is attached to a solid support, such as the wells of a plastic multi-well plate. A population of antibodies are labeled, added to the solid support and allowed to bind to the unlabeled antigen, under conditions where non-specific absorption is blocked, and any unbound antibody and other proteins are washed away. Antibody binding is detected by, for example, a reaction that converts a colorless substrate into a colored reaction product. Progressively smaller and overlapping fragments can then be tested from an identified 30-mer to map the epitope of interest.

[0034] A polypeptide can be produced recombinantly. A polynucleotide encoding a polypeptide can be introduced into a recombinant expression vector, which can be expressed in a suitable expression host cell system using techniques well known in the art. A variety of bacterial, yeast, plant, mammalian, and insect expression systems are available in the art and any such expression system can be used. Optionally, a polynucleotide encoding a polypeptide can be translated in a cell-free translation system. A polypeptide can also be chemically synthesized or obtained from patient samples or cells.

[0035] An immunogenic polypeptide an comprise an amino acid sequence shown in SEQ ID NOS:1-59 or fragments thereof. An immunogenic polypeptide can elicit antibodies or other immune responses (*e.g.*, T-cell responses of the immune system) that recognize epitopes of a polypeptide having SEQ ID NOS:1-59. An immunogenic polypeptide can also be a fragment of a polypeptide that has an amino acid sequence shown in SEQ ID NOS:1-6. An immunogenic polypeptide fragment can be about 10, 15, 20, 25, 30, 40, 50 or more amino acids in length. An immunogenic polypeptide fragment can be about 50, 40, 30, 20, 15, 10 or less amino acids in length.

[0036] The invention illustratively described herein suitably can be practiced in the absence of any element or elements, limitation or limitations that are not specifically disclosed herein.

Examples

[0037] The Examples that follow are illustrative of specific embodiments of the invention, and various uses thereof. They set forth for explanatory purposes only, and are not to be taken as limiting the invention.

Example 1

Identification and Purification of Blood Samples

[0038] Patient blood samples were collected from dogs. The dogs were members of a single family maintained at Texas A & M University since 1997. More specifically, this family is a colony of heterozygous (carrier) females with X-linked hereditary nephropathy (XLHN). XLHN is caused by a mutation in the gene *COL4A5* which in the female dogs causes a mosaic expression of type IV collagen peptides and onset of glomerular proteinuria between 3 and 6 months of age. Nabity et al., J Vet Intern Med 2007; 21 :425-430. Control versus experimental (diseased) was selected wherein controls were healthy dogs and the experimental or diseased group were dogs exhibiting elevated creatinine levels.

[0039] The following procedure was utilized for the preparation of patient samples for experimental analysis. Utilizing a 0.5 mL protein LoBind eppendorf tube, 110uL of serum was precipitated by addition of 200uL N,N-dimethylacetamide, which was followed by vortexing for 10 seconds, and incubating the sample at room temperature for 30 minutes. Resulting precipitate was pelleted by centrifugation at 13000 rpm for 30 minutes at 10°C. Supernatant was decanted into a borosilicate culture tube containing 5.0 mL of 0.1% formic acid in water and mixed to homogeneity.

[0040] The diluted extract was then further fractionated using a Caliper Life Science Rapid trace automated solid phase extraction apparatus as follows: 1mL (30mg) Waters OASIS® HLB solid phase extraction cartridges were conditioned at 0.5 mL/sec first with 1.0 mL 0.1 % formic acid in water followed by 1.0 mL 0.1% formic acid in acetonitrile and finally with 2.0 mL 0.1% formic acid in water. Samples were loaded at a flow rate of 0.015 mL/sec then washed with 1.25 mL of 0.1% formic acid in water at a flow rate of 0.015 mL/sec. 1.25 mL fractions were then collected into borosilicate glass tubes containing 5μL of 20mg/mL N-nonyl-β-glucopyranoside in water. Fractions were eluted consecutively and collected separately using first 0.1% formic acid in 35% acetonitrile/water and next 0.1% formic acid in 65% acetonitrile/water at a flow rate of 0.015 mL/sec. The canula and solvent transfer lines were purged and cleaned between runs with 3.0 mL of 0.1% formic acid in acetonitrile then 3.0 mL of 0.1% formic acid in water at a flow rate of 0.5 mL/sec.

[0041] Fractions were split in half and evaporated to dried state at room temperature using a Savant Speed Vac Concentrator Model SVC-100H. The dried samples were then separated into two batches and stored at -80° C. For analysis, the samples were reconstituted in 60 μL 0.1% formic acid in either 5% (35% fraction) or 35% (65% fraction) acetonitrile and analyzed by liquid chromatography/mass spectrometry (LC/MS).

Example 2

Identification of Polypeptides in Diseased Dogs by Liquid Chromatography/Mass Spectrometry

[0042] Experimental and control samples were subjected to liquid chromatography/mass spectrometry (LC/MS) for the identification of differentially produced polypeptides by mass. The identified polypeptide masses were then annotated to determine the corresponding protein name by performing a peptide ID search of existing databases. A unique databases for peptide annotation was created from NCBI, Swissprot, Uniprot.

[0043] The resulting data provided the polypeptides provided in Table 1. SEQ ID NOS: 1-59 are the polypeptides that were differentially produced in dogs with renal disease. Therefore, these polypeptides provide unique biomarkers for the detection renal disease in dogs.

Table 1: Polypeptides differentially produced in dogs with renal disease.

Accession	No. Peptides	No. AAs	MW [kDa]	Description		Expression Levels
P56595	3	88	9.7	Apolipoprotein C-I OS=Canis familiaris GN=APOC1 PE=2 SV=1-[APOC1_CANFA]		Increased
	Sequence	**m/z [Da]**	**MH+ [Da]**	**RT [min]**		
	AGEISSTFERIPDKLKEFGNT LEDKA (SEQ. ID NO: 1)	965.83238	2895.48259	27.98		
	EISSTFERIPDKLKEFGNTLE DKA (SEQ. ID NO: 2)	923.14789	2767.42910	27.41		
	DKLKEFGNTLEDKA (SEQ. ID NO: 3)	536.61725	1607.83719	20.36		
Q28243	4	443	45.9	Fibrinogen A-alpha-chain (Fragment) OS=Canis familiaris PE=4 SV=1-[Q28243_CANFA]		Decreased
	Sequence	**m/z [Da]**	**MH+ [Da]**	**RT [min]**		
	IMGSDSDIFTNIGTPEFPSSG KTSSHSKQFVTSSTT (SEQ. ID NO: 4)	945.45618	3778.80288	26.50		
	THIMGSDSDIFTNIGTPEFPS SGKTSSH (SEQ. ID NO: 5)	738.34826	2950.37119	26.38		
	THIMGSDSDIFTNIGTPEFPS SGKTSSHS (SEQ. ID NO: 6)	1013.1373 3	3037.39743	26.25		
	IMGSDSDIFTNIGTPEFPSSG KTSSHS (SEQ. ID NO: 7)	933.76956	2799.29412	27.29		
P12278	6	101	11.2	Apolipoprotein C-II OS=Canis familiaris GN=APOC2 PE=2 SV=1 - [APOC2_CANFA]		Increased
	Sequence	**m/z [Da]**	**MH+ [Da]**	**RT [min]**		
	AHESQQDETTSSALLTQMQ ESLYSYWGTARSAAEDL (SEQ. ID NO: 8)	1335.6136 5	4004.82639	35.25		
	AHESQQDETTSSALLTQMQ ESL (SEQ. ID NO: 9)	1217.5585 9	2434.10991	28.22		

(continued)

	Sequence	m/z [Da]	MH+ [Da]	RT [min]		
	AHESQQDETTSSALLTQMQ ESLYSYWGTA (SEQ. ID NO: 10)	1088.1586 9	3262.46152	33.89		
	AHESQQDETTSSALLTQMQ ESL (SEQ. ID NO: 11)	812.04224	2434.11216	28.24		
	AHESQQDETTSSALLTQMQ ESLYSYWGTA (SEQ. ID NO: 12)	1631.7337 6	3262.46025	33.91		
	AHESQQDETTSSALL (SEQ. ID NO: 13)	808.87756	1616.74785	20.77		
P68213	7	28	3.0	Fibrinogen alpha chain (Fragment) OS=Canis familiaris GN=FGA PE=1 SV=1-[FIBA CANFA]		Decreased
	Sequence	**m/z [Da]**	**MH+ [Da]**	**RT [min]**		
	NSKEGEFIAEGGGV (SEQ. ID NO: 14)	697.33575	1393.66423	21.26		
	SKEGEFIAEGGGV (SEQ. ID NO: 15)	640.31421	1279.62114	21.32		
	TNSKEGEFIAEGGGV (SEQ. ID NO: 16)	747.85939	1494.71151	21.25		
	KEGEFIAEGGGV (SEQ. ID NO: 17)	596.79858	1192.58989	21.20		
	EGEFIAEGGGV (SEQ. ID NO: 18)	1064.4936 2	1064.49362	22.99		
	GEFIAEGGGV (SEQ. ID NO: 19)	935.44861	935.44861	22.73		
	FIAEGGGV (SEQ. ID NO: 20)	749.38739	749.38739	20.88		
XP_53583 6	4	653	73.1	Kininogen		Decreased

(continued)

	Sequence	Charge	m/z [Da]	MH+ [Da]	RT [min]	
	HGGQRELDFDLEHQ (SEQ. ID NO: 21)	3	560.93286	1680.78403	20.94	
	DEEWDSGKEQGPTHGHG (SEQ. ID NO: 22)	3	622.59778	1865.77878	15.61	
	ELDFDLEHQ (SEQ. ID NO: 23)	2	573.26135	1145.51543	24.10	
	DCDYKESTQAATGEC (SEQ. ID NO: 24)	3	540.87445	1620.60880	26.40	
XP_84876 5 & XP_84367 2	4	958	105.0	Inter-Alpha Inhibitor H4 (ITIH4)		Differentially expressed
	Sequence	**Charge**	**m/z [Da]**	**MH+ [Da]**	**RT [min]**	
	GSEIVVVGKLRDQSPDVLSA KV (SEQ. ID NO: 25)	3	766.10455	2296.29911	24.87	
	PRDWKPLLVPASPENVD (SEQ. ID NO: 26)	3	645.01086	1933.01804	18.72	
	ETLFSMMPGLNMTMDKTGL LL (SEQ. ID NO: 27)	2	1172.08431	2343.16135	34.46	
	AETVQ (SEQ. ID NO: 28)	1	547.27649	547.27649	20.09	
XP_54513 0	66.23	3	77	8.8	CysA	Differentially expressed
	Sequence	**Charge**	**m/z [Da]**	**MH+ [Da]**	**RT [min]**	
	VGDNSYIHLKIFKGLP (SEQ. ID NO: 29)	3	601.00467	1800.99945	26.31	
	LTLTGYQTDKSKDDELTG (SEQ. ID NO: 30)	3	662.33471	1984.98957	18.10	
	KPQLEEKTNETYQEFEA (SEQ. ID NO: 31)	3	695.32800	2083.96946	19.15	
XP_53560 1	75.32	7	77	9.0	CysB	Decreased

(continued)

	Sequence	Charge	m/z [Da]	MH+ [Da]	RT [min]	
	YQTNKAKHDELAYF (SEQ. ID NO: 32)	3	576.61572	1727.83261	21.46	
	QTNKAKHDELAYF (SEQ. ID NO: 33)	3	522.26111	1564.76877	20.82	
	ENKPLALSSYQTNK (SEQ. ID NO: 34)	2	796.91620	1592.82513	27.77	
	QVVAGTPY (SEQ. ID NO: 35)	1	834.43532	834.43532	31.89	
	EERENKKYTTFK (SEQ. ID NO: 36)	2	786.90753	1572.80779	31.24	
	YFIKVQVDDDEFVHLR (SEQ. ID NO: 37)	3	675.00958	2023.01419	23.40	
	VVAGTPYFIKVQVDDD (SEQ. ID NO: 38)	3	589.30709	1765.90671	19.41	
NP_00101 3443	43.66	21	568	57.6	Keratin Type I Cytoskeletal 10	Differentially expressed
	Sequence	**Charge**	**m/z [Da]**	**MH+ [Da]**	**RT [min]**	
	MQNLNDRLAS (SEQ. ID NO: 39)	2	581.28491	1161.56255	20.90	
	FGGGYGGVSFGGGSFGGG SFGG (SEQ. ID NO: 40)	3	624.60724	1871.80716	19.91	
	SFGGGYGGVSFG (SEQ. ID NO: 41)	2	546.24731	1091.48735	25.33	
	FSRGSSGGGCFGGSSGGY GGLGG (SEQ. ID NO: 42)	3	656.61829	1967.84031	28.01	
	EEQLQ (SEQ. ID NO: 43)	1	646.30862	646.30862	15.60	
	QNRKDAEAWFNEKSK (SEQ. ID NO: 44)	3	617.64661	1850.92527	19.80	
	PRDYSKYYQTIEDLKNQI (SEQ. ID NO: 45)	3	758.71680	2274.13584	26.49	

(continued)

	Sequence	Charge	m/z [Da]	MH+ [Da]	RT [min]	
	KDAEAWFNEKSKEL (SEQ. ID NO: 46)	3	565.61548	1694.83188	19.42	
	KYENEVALRQSVEA (SEQ. ID NO: 47)	3	545.94529	1635.82131	19.39	
	KSKELTTEINSNIEQM (SEQ. ID NO: 48)	3	622.31818	1864.93998	19.60	
	LQIDN (SEQ. ID NO: 49)	1	602.31784	602.31784	16.07	
	SIGGGFSSGG (SEQ. ID NO: 50)	1	825.37653	825.37653	34.30	
	FGGGGFSGGSFGGYGGGY GGDGGLL (SEQ. ID NO: 51)	3	719.64934	2156.93346	23.14	
	LENEIQTYRSLLEGEG (SEQ. ID NO: 52)	3	617.64661	1850.92527	19.80	
	GSIGGGFSSG (SEQ. ID NO: 53j	1	825.37653	825.37653	34.30	
	EDLKNQILNLTTDN (SEQ. ID NO: 54)	2	815.92169	1630.83611	26.45	
	GGGGYGGGSSGGGGSHGG SSGG (SEQ. ID NO: 55)	3	537.21368	1609.62650	19.61	
	GRYCVQLSQIQAQISS (SEQ. ID NO: 56)	2	890.94928	1780.89128	20.25	
	RVLDELTLT (SEQ. ID NO: 57)	1	1059.60266	1059.60266	33.79	
	RLASYLDKVRALEESNY (SEQ. ID NO: 58)	2	1014.02356	2027.03984	37.86	
	GGGYGGDGGLLSGNEKV (SEQ. ID NO: 59)	2	768.86627	1536.72527	22.51	

[0044] Although methods for performing LC/MS are well known in the art, the specific liquid chromatography/ mass spectrometry methods utilized for the present study are provided below:

Liquid Chromatography Parameters

[0045] Solvent A: 0.1 % Formic acid in water; Solvent B: 0.1 % Formic acid in acetonitrile; Column: Acquity UPLC BEH130 C18 1.7μM 2.1id x 150mm length; Guard Column: vanguard BEH 300 C_{18} 1.7uM; Injection volume: 25μL; Tray temp: 10°C; Column oven temp: 45°C; MS run time: 60 minutes; Divert valve: none

Table 2: Gradient for 35% fraction

No	Time	A%	B%	C%	D%	μL/min
1	0	100	0	0	0	300
2	5	100	0	0	0	300
3	45	50	50	0	0	300
4	46	100	0	0	0	300
5	60	100	0	0	0	300

Table 3: Gradient for 65% fraction

No	Time	A%	B%	C%	D%	μL/min
1	0	70	30	0	0	300
2	5	70	30	0	0	300
3	45	25	75	0	0	300
4	46	70	30	0	0	300
5	60	70	30	0	0	300

Mass Spectrometry Parameters and Methods

MS scan event 1: FTMS; resolution 30000; scan range 500.0-2000.0 MS scan event 2-6: ITMS + c norm Dep MS/MS 1st, 2nd, 3rd most intense ion from scan 1 for differential expression and from list for targeted identification

Activation Type: CID
Min Signal Required: 500
Isolation Width: 1.5
Normalized Coll. Energy: 35.0
Default Charge State: 2
Activation Q: 0.250
Activation Time: 30.000
CV = 0.0V

Data Dependent Settings for differential expression:

Use separate polarity settings disabled
Parent Mass List: none
Reject Mass List: none
Neutral loss Mass List: none
Product Mass List: none
Neutral loss in top: 3
Product in top: 3
Most intense if no parent masses found not enabled
Add/subtract mass not enabled
FT master scan preview mode enabled

(continued)

<u>Data Dependent Settings for differential expression:</u> Charge state screening enabled Monoisotopic precursor selection enabled Non-peptide monoisotopic recognition not enabled Charge state rejection enabled Unassigned charge states: rejected Charge state 1: not rejected Charge state 2: not rejected Charge state 3: not rejected Charge state 4+: not rejected
<u>Data Dependent Settings for targeted identification:</u> Use separate polarity settings disabled Reject Mass List: none Neutral loss Mass List: none Product Mass List: none Neutral loss in top: 3 Product in top: 3 Most intense if no parent masses found not enabled Add/subtract mass not enabled FT master scan preview mode enabled Charge state screening enabled Monoisotopic precursor selection enabled Non-peptide monoisotopic recognition not enabled Charge state rejection enabled Unassigned charge states: rejected Charge state 1: not rejected Charge state 2: not rejected Charge state 3 : not rejected Charge state 4+: not rejected
<u>Global Data Dependent Settings"</u> Use global parent and reject mass lists not enabled for differential expression and enabled for targeted identification Exclude parent mass from data dependent selection not enabled
Exclusion mass width relative to mass Exclusion mass width relative to low (ppm): 20.00 Exclusion mass width relative to high (ppm): 20.00 Parent mass width relative to mass Parent mass width low (ppm): 10.00 Parent mass width high (ppm): 10.00 Reject mass width relative to mass Reject mass width low (ppm): 20.00 Reject mass width high (ppm): 20.00 Zoom/UltraZoom scan mass width by mass Zoom/UltraZoom scan mass low: 5.00 Zoom/UltraZoom scan mass high: 5.00 FT SIM scan mass width low: 5.00 FT SIM scan mass width high: 5.00 Neutral Loss candidates processed by decreasing intensity Neutral loss mass width by mass Neutral Loss mass width low: 0.50000

(continued)

Global Data Dependent Settings" Neutral Loss mass width high: 0.50000 Product candidates processed by decreasing intensity Product mass width by mass Product mass width low: 0.50000 Product mass width high: 0.50000 MS mass range: 0.00-1000000.00 Use m/z values as masses not enabled Analog UV data dep. Not enabled Dynamic exclusion enabled Repeat Count: 2 Repeat Duration: 30.00 Exclusion List Size: 500 Exclusion Duration: 60.00 Exclusion mass width relative to mass Exclusion mass width low (ppm): 20.00 Exclusion mass width high (ppm): 20.00 Isotopic data dependence not enabled Mass Tags data dependence not enabled Custom Data Dependent Settings not enabled
MS Tune File Values Source Type: ESI Capillary Temp (°C): 250.00 Sheath gas Flow: 24.00 Aux Gas Flow: 13.00 Sweep Gas Flow: 0 Ion Trap MSn AGC Target: 10000 FTMS Injection waveforms: off FTMS AGC Target: 500000 Source voltage (kV): 4.50
Source current (μA): 100.00 Capillary Voltage (V): 68.28 Tube Lens (V): 130.00 Skimmer Offset (V): 0.00 Multipole RF Amplifier (Vp-p): 550.00 Multipole 00 offset (V): -1.60 Lens 0 Voltage (V): -2.70 Multipole 0 offset (V): -5.80 Lens 1 Voltage (V): -11.00 Gate Lens offset (V): -60.00 Multipole 1 offset (V): -10.50 Front Lens (V): -5.18 FTMS full microscans: 1 FTMS full Max Ion Time (ms): 500 Ion Trap MSn Micro Scans: 3 Ion Trap MSn Max Ion Time: 100

[0046] The mass spec data from the above analysis were analyzed for differential expression of the peptides using SIEVE 1.3 software with the following parameters:

Table 4: SIEVE Parameters

Alignment Parameters	
AlignmentBypass	False
CorrelationBinWidth	1
RT LimitsForAlignment	True
TileIncrement	150
TileMaximum	300
TileSize	300
Tile Threshold	0.6
Analysis Definition	
Experiment Target	PROTEOMICS
Experiment Type	AVSB
Frame Parameters	
AvgChargeProcessor	False
ControlGroup	c
FrameIDCriteria	ORDER BY PVALUE ASC
FrameSeedFile	
KMClusters	10
MS2CorrProcessor	False
MZStart	500
MZStop	2000
MZWidth	0.01
ProcessorModules	PCA V1.0:ROC V1.0
RTStart	0
RTStop	59.98
RTWidth	1.5
UseTICNormalizedRatios	False

Table 5: Global Parent mass 35% fraction for targeted identification:

m/z	start time (min)	End time (min)
500.837	20.8	21.4
511.557	20.8	21.4
516.216	20.8	21.4
529.195	20.8	21.4
534.519	20.8	21.4
540.878	23.4	24.0
549.959	44.1	44.7
554.519	22.1	22.7
586.686	23.3	23.9
588.915	20.8	21.4
590.986	44.1	44.7
596.798	20.7	21.3
630.336	26.0	26.6
632.392	37.0	37.6
640.314	20.8	21.4
646.067	17.9	18.5
661.491	35.0	35.6
662.294	27.1	27.7
666.330	37.3	37.9
666.770	20.8	21.4
697.336	20.7	21.3
697.837	20.7	21.3
714.396	27.1	27.7
722.599	20.7	21.3
732.085	20.7	21.3
736.079	20.7	21.3
745.375	28.8	29.4
747.859	20.7	21.3
748.299	20.8	21.4
746.279	22.5	23.1
758.347	20.8	21.4
761.089	20.8	21.4
762.952	33.1	33.7
766.832	20.8	21.4
770.824	20.8	21.4
774.316	20.8	21.4
785.495	37.0	37.6
792.484	37.0	37.6
798.662	27.1	27.7
815.324	23.7	24.3
815.292	22.0	22.6
831.276	22.0	22.6
845.270	27.1	27.7
857.071	27.1	27.7
883.346	36.5	37.1
888.005	20.8	21.4
908.015	20.8	21.4
926.783	21.2	21.8
929.445	20.7	21.3
946.081	37.0	37.6
963.128	20.7	21.3
972.536	37.0	37.6
980.768	20.7	21.3
996.811	20.7	21.3
999.409	20.7	21.3
1014.449	20.8	21.4
1017.377	39.7	40.3
1017.250	39.6	40.2
1034.163	36.5	37.1
1061.032	38.0	38.6
1071.011	20.7	21.3
1073.287	38.3	38.9
1074.429	43.6	44.2
1075.546	43.0	43.6
1078.177	40.3	40.9
1083.736	22.1	22.7
1089.401	38.0	38.6
1096.026	20.7	21.3
1101.960	43.0	43.6
1104.411	37.4	38.0
1109.504	20.7	21.3
1117.566	42.9	43.5
1141.310	40.2	40.8
1140.059	40.2	40.8
1162.715	39.6	40.2
1162.285	39.6	40.2
1175.385	42.8	43.4
1175.963	20.7	21.3
1182.040	36.5	37.1
1185.065	38.6	39.2
1184.315	38.7	39.3
1184.044	36.5	37.1
1186.945	20.7	21.3
1189.456	36.5	37.1
1197.564	38.3	38.9
1201.052	38.0	38.6
1205.551	27.1	27.7
1221.832	38.1	38.7
1221.330	38.0	38.6
1221.956	38.1	38.7
1221.203	38.0	38.6
1229.059	41.7	42.3
1229.337	43.0	43.6
1234.050	43.3	43.9
1234.184	43.2	43.8
1237.197	38.1	38.7
1239.714	38.3	38.9

1239.903	40.3	40.9	1405.390	37.0	37.6
1239.906	22.0	22.6	1412.808	42.9	43.5
1239.336	39.3	39.9	1416.957	38.2	38.8
1241.893	22.0	22.6	1417.242	38.2	38.8
1245.780	42.9	43.5	1416.813	38.2	38.8
1244.893	41.7	42.3	1415.521	38.3	38.9
1244.821	38.2	38.8	1416.365	38.2	38.8
1252.485	42.9	43.5	1423.711	43.0	43.6
1253.180	38.0	38.6	1432.054	43.1	43.7
1262.757	41.7	42.3	1434.534	38.3	38.9
1269.226	43.0	43.6	1444.691	20.7	21.3
1268.942	42.9	43.5	1461.219	39.3	39.9
1271.795	41.7	42.3	1466.392	38.3	38.9
1271.940	41.7	42.3	1480.934	43.0	43.6
1272.223	41.7	42.3	1480.763	42.9	43.5
1271.511	41.7	42.3	1483.434	41.5	42.1
1271.366	41.5	42.1	1483.261	41.5	42.1
1271.653	43.6	44.2	1483.594	43.1	43.7
1271.939	42.9	43.5	1483.096	41.5	42.1
1271.663	43.0	43.6	1488.084	41.5	42.1
1279.356	41.7	42.3	1488.253	41.5	42.1
1279.640	41.7	42.3	1492.580	41.8	42.4
1280.487	43.1	43.7	1492.738	43.1	43.7
1282.341	42.9	43.5	1494.710	20.7	21.3
1282.623	42.9	43.5	1493.188	41.4	42.0
1283.501	41.7	42.3	1501.262	43.1	43.7
1283.215	41.7	42.3	1501.243	42.8	43.4
1287.661	42.8	43.4	1504.607	41.4	42.0
1287.380	42.8	43.4	1519.408	40.2	40.8
1287.671	42.9	43.5	1519.963	42.8	43.4
1289.949	41.4	42.0	1533.454	41.4	42.0
1290.093	41.4	42.0	1550.589	42.9	43.5
1290.231	41.4	42.0	1567.262	43.0	43.6
1295.514	42.8	43.4	1566.964	43.2	43.8
1302.780	40.2	40.8	1616.809	42.8	43.4
1313.671	42.8	43.4	1625.276	38.1	38.7
1326.085	42.9	43.5	1682.802	41.4	42.0
1329.279	41.4	42.0	1708.700	35.2	35.8
1340.257	42.8	43.4	1715.693	43.0	43.6
1353.504	38.6	39.2	1719.490	42.8	43.4
1353.226	38.0	38.6	1720.363	43.1	43.7
1354.345	38.0	38.6	1720.076	41.7	42.3
1355.998	39.6	40.2	1735.925	42.9	43.5
1361.344	38.6	39.2	1735.448	42.9	43.5
1378.833	43.0	43.6	1742.423	42.8	43.4
1393.662	20.7	21.3	1742.691	39.3	39.9
1395.947	38.0	38.6	1749.090	42.8	43.4
1395.808	38.1	38.7	1755.091	42.9	43.5
1396.095	38.0	38.6	1766.811	43.0	43.6
1396.238	38.1	38.7	1769.294	42.9	43.5
1403.093	38.1	38.7	1775.798	43.0	43.6

1802.490	42.8	43.4	1144.899	5.0	60.0
1808.484	42.9	43.5	1205.104	5.0	60.0
1822.120	41.4	42.0	1526.197	5.0	60.0
1893.263	5.0	60.0	1430.872	5.0	60.0
1796.466	5.0	60.0	1907.494	5.0	60.0
1596.971	5.0	60.0	1760.841	5.0	60.0
1368.976	5.0	60.0	1977.132	5.0	60.0
1150.101	5.0	60.0	1757.527	5.0	60.0
1635.848	5.0	60.0	1581.907	5.0	60.0
1338.604	5.0	60.0	1438.189	5.0	60.0
921.201	5.0	60.0	1054.941	5.0	60.0
775.405	5.0	60.0	879.285	5.0	60.0
1618.973	5.0	60.0	659.716	5.0	60.0
1324.797	5.0	60.0	1897.745	5.0	60.0
1121.137	5.0	60.0	1660.653	5.0	60.0
911.113	5.0	60.0	1022.328	5.0	60.0
809.990	5.0	60.0	633.253	5.0	60.0
1529.751	5.0	60.0	1831.242	5.0	60.0
1384.157	5.0	60.0	1664.857	5.0	60.0
1263.883	5.0	60.0	1526.203	5.0	60.0
1211.263	5.0	60.0	1408.880	5.0	60.0
1162.853	5.0	60.0	1308.318	5.0	60.0
1247.480	5.0	60.0	796.762	5.0	60.0
1366.192	5.0	60.0	733.101	5.0	60.0
1510.899	5.0	60.0	1991.952	5.0	60.0
1950.616	5.0	60.0	1770.739	5.0	60.0
1540.172	5.0	60.0	1593.766	5.0	60.0
1170.773	5.0	60.0	1448.969	5.0	60.0
1090.293	5.0	60.0	1328.306	5.0	60.0
1185.014	5.0	60.0	1226.206	5.0	60.0
1362.615	5.0	60.0	1138.692	5.0	60.0
1542.070	5.0	60.0	1062.846	5.0	60.0
1445.754	5.0	60.0	996.481	5.0	60.0
1360.769	5.0	60.0	937.924	5.0	60.0
1285.227	5.0	60.0	885.873	5.0	60.0
1217.636	5.0	60.0	839.301	5.0	60.0
1156.805	5.0	60.0	797.909	5.0	60.0
1101.767	5.0	60.0	759.464	5.0	60.0
1051.732	5.0	60.0	724.988	5.0	60.0
1006.048	5.0	60.0	693.511	5.0	60.0
964.172	5.0	60.0	664.657	5.0	60.0
14138.386	5.0	60.0	638.111	5.0	60.0
1768.180	5.0	60.0	1427.610	5.0	60.0
1286.224	5.0	60.0	1223.810	5.0	60.0
1088.498	5.0	60.0	1070.959	5.0	60.0
943.499	5.0	60.0	856.969	5.0	60.0
884.593	5.0	60.0	779.154	5.0	60.0
786.924	5.0	60.0	782.314	5.0	60.0
745.080	5.0	60.0	626.056	5.0	60.0
954.251	5.0	60.0	1042.755	5.0	60.0
1040.909	5.0	60.0	1037.510	5.0	60.0

692.009	5.0	60.0
519.259	5.0	60.0
1291.643	5.0	60.0
861.431	5.0	60.0
646.325	5.0	60.0
1480.558	5.0	60.0
905.177	5.0	60.0
857.589	5.0	60.0
1394.901	5.0	60.0
761.313	5.0	60.0
1104.010	5.0	60.0
631.727	5.0	60.0
883.410	5.0	60.0
1768.860	5.0	60.0
708.148	5.0	60.0
590.291	5.0	60.0
785.635	5.0	60.0
845.991	5.0	60.0
916.407	5.0	60.0
999.625	5.0	60.0
1221.540	5.0	60.0
1831.806	5.0	60.0
1615.749	5.0	60.0
1243.116	5.0	60.0
1077.502	5.0	60.0
950.855	5.0	60.0
850.871	5.0	60.0
1177.032	5.0	60.0
969.498	5.0	60.0
1098.630	5.0	60.0
1862.260	5.0	60.0
1676.135	5.0	60.0
1289.567	5.0	60.0
1117.759	5.0	60.0
882.653	5.0	60.0
1480.757	5.0	60.0
1253.103	5.0	60.0
1018.335	5.0	60.0
905.299	5.0	60.0
1472.097	5.0	60.0
1104.325	5.0	60.0
1766.315	5.0	60.0
883.661	5.0	60.0
679.972	5.0	60.0
589.443	5.0	60.0
1809.590	5.0	60.0
1357.444	5.0	60.0
1086.157	5.0	60.0
958.492	5.0	60.0
857.704	5.0	60.0
1286.224	5.0	60.0

1768.180	5.0	60.0
1571.827	5.0	60.0
1414.745	5.0	60.0
1179.883	5.0	60.0

Table 6

MZ	Start Time	End Time
747.8585	20.963	21.963
748.3594	20.963	21.963
1494.711	20.973	21.973
1393.662	20.925	21.925
997.1431	20.963	21.963
1091.809	43.558	44.558
758.9495	23.687	24.687
963.4607	20.963	21.963
996.8089	20.963	21.963
529.4085	20.079	21.079
963.1265	20.963	21.963
1495.694	21.586	22.586
939.1018	37.446	38.446
785.4966	37.446	38.446
1279.621	20.973	21.973
938.6002	37.446	38.446
632.3923	37.449	38.449
692.862	27.718	28.718
1245.308	37.446	38.446
713.5975	24.835	25.835
766.8335	20.973	21.973
1118.573	18.91	19.91
1356.332	40.142	41.142
713.2632	24.862	25.862
632.8939	37.449	38.449
767.3351	20.973	21.973
1245.354	45.921	46.921
1092.202	37.164	38.164
1091.703	37.446	38.446
576.0089	45.797	46.797
774.3157	20.963	21.963
1398.409	37.446	38.446
1082.377	29.745	30.745
1082.521	29.72	30.72
747.7883	28.871	29.871
747.5877	28.871	29.871
1017.626	40.143	41.143
856.5498	27.091	28.091
1082.234	29.745	30.745
923.815	27.718	28.718
514.3178	45.805	46.805
670.3671	22.036	23.036
1185.613	29.438	30.438
534.9825	45.819	46.819

(continued)

MZ	Start Time	End Time
520.341	45.691	46.691
747.9889	28.871	29.871
886.6	30.939	31.939
1262.604	29.769	30.769
723.3659	32.732	33.732
994.2356	45.096	46.096

Table 7: Global Parent Masses 65% fraction for targeted identification

m/z	Start time (min)	End time (min)
1222.77185	18.898	19.498
1222.62903	18.898	19.498
1222.91467	18.898	19.498
1222.48633	18.898	19.498
1222.34363	18.898	19.498
535.41309	44.458	45.058
549.31537	35.307	35.907
1240.9231	18.895	19.495
1241.21008	18.895	19.495
522.59802	47.752	48.352
500.20343	24.938	25.538
557.44525	34.845	35.445
700.55261	44.458	45.058
502.29593	31.133	31.733
576.00928	20.109	20.709
1229.77344	19.099	19.699
1227.05896	21.087	21.687
666.32935	12.86	13.46
555.42859	44.458	45.058
919.62494	10.837	11.437
1086.43494	18.895	19.495
500.20352	24.16	24.76
785.54749	44.458	45.058
1240.49377	18.893	19.493
656.32324	35.678	36.278
576.00928	20.962	21.562
1044.64368	33.755	34.355
565.43127	34.845	35.445
534.98254	20.109	20.709
689.45453	33.647	34.247
522.59821	46.986	47.586
552.97772	35.36	35.96
1160.28918	18.176	18.776
535.41296	40.034	40.634
514.31842	22.557	23.157
1092.1864	19.016	19.616
1226.62988	21.087	21.687
1245.21155	21.073	21.673
538.27802	31.183	31.783
595.95276	20.109	20.709
770.53705	35.665	36.265
514.13129	22.572	23.172
533.19391	45.359	45.959
503.29941	31.133	31.733
1035.65649	33.8	34.4
1228.77197	19.099	19.699
865.69196	44.492	45.092
552.64246	35.36	35.96
621.2735	35.307	35.907
639.38116	12.36	12.96
795.98547	12.411	13.011
788.02655	34.697	35.297
816.57715	46.757	47.357
1245.06909	21.073	21.673
590.78833	35.36	35.96
522.59857	46.026	46.626
1089.55884	16.803	17.403
785.59174	41.855	42.455
656.03418	44.963	45.563
1245.64099	21.073	21.673
734.5838	41.312	41.912
527.42432	44.458	45.058
816.57703	45.912	46.512
564.90961	44.767	45.367
1160.14612	18.176	18.776
787.98962	33.811	34.411
1530.9856	33.8	34.4
834.60272	45.536	46.136
1013.6778	47.807	48.407
927.50275	24.16	24.76
770.53809	41.117	41.717
672.8623	20.478	21.078
1236.03796	18.898	19.498
827.44568	17.482	18.082
1021.62933	31.226	31.826
612.2973	35.687	36.287
818.59338	40.929	41.529
763.073	44.933	45.533
884.26294	15.568	16.168
784.58783	34.201	34.801
647.50586	43.805	44.405
816.57739	42.456	43.056
816.57806	44.856	45.456
589.98645	20.109	20.709
678.38123	29.773	30.373
574.37909	36.07	36.67
590.789	33.644	34.244

550.38953	39.608	40.208	1089.43811	21.069	21.669
1234.76331	21.088	21.688	834.58734	44.106	44.706
747.63464	45.81	46.41	548.95966	20.109	20.709
684.06628	43.942	44.542	811.67133	44.9	45.5
834.60327	43.684	44.284	977.78485	43.805	44.405
1226.48657	21.087	21.687	984.71124	45.034	45.634
537.77429	31.183	31.783	816.57745	39.918	40.518
726.76282	35.307	35.907	541.35706	37.363	37.963
575.44519	44.421	45.021	1242.32043	21.087	21.687
856.57281	44.856	45.456	1296.89185	18.895	19.495
818.56958	41.989	42.589	816.57672	41.217	41.817
818.59167	37.061	37.661	834.60321	42.206	42.806
780.55658	44.856	45.456	800.58289	36.618	37.218
783.59045	45.191	45.791	1057.11133	31.226	31.826
806.57233	36.618	37.218	841.43475	46.467	47.067
547.08124	12.898	13.498	1090.30103	18.898	19.498
1255.62939	19.003	19.603	1076.55383	19.11	19.71
1101.73071	47.659	48.259	516.23901	44.751	45.351
616.12958	24.863	25.463	699.44244	34.996	35.596
942.46729	24.16	24.76	1082.91907	19.11	19.71
1065.6875	33.644	34.244	816.57849	36.279	36.879
564.9295	35.766	36.366	1073.30225	21.087	21.687
1096.42273	16.828	17.428	836.44843	35.316	35.916
816.57843	43.658	44.258	928.77789	43.805	44.405
747.63562	42.131	42.731	500.30814	33.647	34.247
606.30951	33.644	34.244	1096.2981	16.79	17.39
809.47382	43.611	44.211	1252.44897	19.099	19.699
1255.79785	12.391	12.991	800.5827	37.369	37.969
868.50171	39.152	39.752	797.4433	31.183	31.783
1234.90649	21.088	21.688	780.55627	41.566	42.166
789.95789	31.226	31.826	997.70264	47.786	48.386
576.27594	35.36	35.96	1207.7627	18.983	19.583
799.41437	15.568	16.168	847.11377	44.569	45.169
528.29279	35.166	35.766	1512.69934	18.898	19.498
842.56836	45.191	45.791	1856.21155	12.469	13.069
1081.91406	18.898	19.498	1250.02783	19.099	19.699
1865.21143	12.45	13.05	1095.60803	33.811	34.411
536.73425	10.897	11.497	658.4317	36.611	37.211
800.58289	44.856	45.456	1098.92664	19.016	19.616
1761.11316	33.8	34.4	972.04376	11.007	11.607
1234.33362	21.088	21.688	571.61591	31.37	31.97
523.28363	46.596	47.196	561.2981	31.327	31.927
692.56415	44.492	45.092	591.93182	39.863	40.463
856.57227	44.038	44.638	800.58289	39.551	40.151
682.36548	42.931	43.531	1309.29358	31.226	31.826
584.9256	45.702	46.302	817.58173	41.855	42.455
508.58325	47.575	48.175	650.42218	31.629	32.229
549.30127	31.216	31.816	591.38416	35.266	35.866
547.81464	35.36	35.96	550.34637	36.076	36.676
640.4176	34.467	35.067	507.32535	32.394	32.994
874.50842	12.645	13.245	1242.32202	19.128	19.728

1452.40747	16.828	17.428	968.62842	39.552	40.152
640.44788	36.711	37.311	863.56744	43.589	44.189
1296.60388	18.899	19.499	1439.88672	21.088	21.688
574.38922	39.095	39.695	809.54089	40.947	41.547
1127.66003	35.36	35.96	1234.05066	21.049	21.649
549.04468	10.94	11.54	1080.41943	19.099	19.699
1288.52576	20.914	21.514	1259.47473	20.829	21.429
1452.41113	21.087	21.687	1251.28943	12.43	13.03
943.24799	33.642	34.242	1874.19434	12.428	13.028
1244.78503	21.069	21.669	1098.1825	12.403	13.003
1236.81531	12.778	13.378	678.40588	35.36	35.96
656.0343	43.815	44.415	1080.2937	21.09	21.69
552.31799	33.644	34.244	1163.60168	31.331	31.931
533.19354	44.604	45.204	1081.90649	21.003	21.603
800.58374	38.715	39.315	1303.35498	20.914	21.514
800.58313	41.099	41.699	730.01355	37.502	38.102
1105.16418	19.016	19.616	540.86346	41.855	42.455
1080.5448	19.042	19.642	627.93677	39.175	39.775
1234.19116	21.088	21.688	1226.34363	21.087	21.687
834.58575	37.992	38.592	754.50586	44.569	45.169
722.05969	44.8	45.4	820.47766	35.368	35.968
1537.02759	33.8	34.4	1440.05261	21.087	21.687
542.90161	44.569	45.169	763.05652	39.17	39.77
1441.04272	18.895	19.495	965.57751	35.3	35.9
1057.70325	34.656	35.256	956.92969	18.895	19.495
575.38568	44.131	44.731	549.7619	33.862	34.462
528.40558	36.809	37.409	1039.28918	32.404	33.004
694.05194	43.783	44.383	1027.18225	38.565	39.165
591.98376	21.656	22.256	540.86285	40.956	41.556
780.55603	42.334	42.934	1220.05237	18.899	19.499
832.57202	40.929	41.529	646.42871	33.65	34.25
708.03638	44.492	45.092	1864.20129	12.391	12.991
743.07135	41.312	41.912	1279.36121	18.902	19.502
731.60846	42.622	43.222	1501.39685	18.898	19.498
1350.76477	38.534	39.134	1238.34937	20.516	21.116
548.95728	33.799	34.399	1252.34387	20.983	21.583
816.57764	35.123	35.723	1425.90979	33.836	34.436
1080.66956	21.088	21.688	1087.41003	19.128	19.728
1063.85815	20.109	20.709	1356.00232	16.785	17.385
742.09894	35.339	35.939	804.55017	40.49	41.09
527.31049	33.782	34.382	1611.92188	31.276	31.876
585.40204	33.044	33.644	650.42383	33.647	34.247
859.44659	35.307	35.907	1238.32214	17.718	18.318
1080.41858	21.09	21.69	795.48767	35.162	35.762
818.59222	34.562	35.162	868.92645	31.353	31.953
1370.99316	44.806	45.406	1664.72192	12.411	13.011
1089.53223	19.11	19.71	1260.61768	21.069	21.669
1431.85144	12.411	13.011	1159.58667	46.467	47.067
695.89008	20.593	21.193	741.53467	37.131	37.731
591.42761	41.789	42.389	1266.21619	18.902	19.502
504.75061	31.022	31.622	1275.7948	33.733	34.333

1245.63	20.983	21.583
696.51019	44.963	45.563
1089.3103	21.087	21.687
704.9386	43.649	44.249
1178.38953	35.3	35.9
811.95068	10.634	11.234
751.05286	44.8	45.4
936.49298	31.271	31.871
737.05133	44.458	45.058
939.39587	24.473	25.073
1027.66821	33.8	34.4
714.42725	39.557	40.157
780.98224	35.166	35.766
834.58661	41.639	42.239
571.37	39.418	40.018

Table 8:

MZ	Start Time	End Time
502.2947	30.953	31.953
576.0092	17.85	18.85
1035.655	33.622	34.622
1021.629	31.026	32.026
787.9893	33.601	34.601
534.9822	17.85	18.85
1530.986	33.601	34.601
666.3301	12.673	13.673
789.9586	31.016	32.016
1027.67	33.601	34.601
1309.292	31.026	32.026
595.9525	17.85	18.85
780.982	35.033	36.033

[0047] Proteome Discoverer 1.1 was used to identify the differentially expressed peptides with the work flow as follows:

Table 9:

Input Data	
1. General Settings	
Precursor Selection Use MS1 Precursor	
2. Spectrum Properties Filter	
Lower RT Limit	5
Upper RT Limit	84
Lowest Charge State	1
Highest Charge State	4
Min. Precursor Mass	100 D a
Max. Precursor Mass	9000 D a
Total Intensity Threshold	0
Minimum Peak Count	1

(continued)

Input Data	
3. Scan Event Filters	
Mass Analyzer	Is ITMS; FTMS
MS Order	Is MS2
Activation Type	Is CID
Scan Type	Is Full
Ionization Source	Is ESI
Polarity Mode	Is +
3. Peak Filters	
S/N Threshold	0
4. Replacement for Unrecognized Properties	
Unrecognized Charge Re	1;2;3;4
Unrecognized Mass Anal	ITMS
Unrecognized MS Order	MS2
Unrecognized Activation	CID
Unrecognized Polarity	+
1. Spectrum Match Criteria	
Precursor Mass Criterion	Same Measured M
Presursor Mass Tolerance	7 ppm
Max. RT Difference [min]	1.5
Allow Mass Analyzer Mis	False
Allow MS Order Mismatch	False
1. Thresholds	
S/N Threshold	0
1. Filter Settings	
Mass Analyzer	Is ITMS; FTMS
MS Order	Is MS1; MS2
Activation Type	Is CID
Scan Type	Is Full
Ionization Source	Is ESI
Polarity Mode	Is +
1. Spectrum Properties	
Lowest Charge State	1
Highest Charge State	4
Min. Precursor Mass	100 D a
Max. Precursor Mass	9000 D a

(continued)

Input Data	
2. Thresholds	
Total Intensity Threshold	0
Minimum Peak Count	1

Table 10:

1. Input Data	
Protein Database	Maha.fasta
Enzyme Name	No-Enzyme [No
Maximum Missed Cleavage	0
2. Decoy Database Search	
Search Against Decoy D	False
Target FDR (Strict)	0.01
Target FDR (Relaxed)	0.05
3. Tolerances	
Precursor Mass Tolerance	7 ppm
Fragment Mass Tolerance	0.8 D a
Use Average Precursor	False
Use Average Fragment	False
4. Ion Series	
Use Neutral Loss a Ions	True
Use Neutral Loss b Ions	True
Use Neutral Loss y Ions	True
Weight of a Ions	0
Weight of b Ions	1
Weight of c Ions	0
Weight of x Ions	0
Weight of y Ions	1
Weight of z Ions	0
5. Dynamic Modifications	
N-Terminal Modification	None
C-Terminal Modification	None
1. Dynamic Modification	None
2. Dynamic Modification	None
3. Dynamic Modification	None
4. Dynamic Modification	None
5. Dynamic Modification	None
6. Dynamic Modification	None

(continued)

6. Static Modifications	
Peptide N-Terminus	None
Peptide C-Terminus	None

[0048] The database for peptide annotation was created from NCBI, Swissprot, and Uniprot. The resulting annotated proteins are provided above in Table 1.

Example 3

Inosine Concentrations in Dogs with Renal Disease

[0049] Dog serum was obtained from field samples submitted to IDEXX Reference Laboratories. Dogs were of various breeds and ages. 25 samples with < 1.8 mg/dL serum creatinine were assigned to a low creatinine group, and 25 samples with >1.8 mg/dL serum creatinine were assigned to a high creatinine group. Again, high creatinine is associated with renal disease, therefore inosine levels were assessed to determine whether inosine could be a biomarker for reduced kidney function.

[0050] Serum samples from a high creatinine and normal creatinine canine populations were analyzed on LC/MS and differentially produced mass features were indentified by informatics as previously described. LC/MS was run for each sample (i.e., dog) individually. SIEVE software (Thermo Scientific, Waltham, Massachusetts) was used for statistical analysis of the LC/MS data. Raw LC/MS data files were loaded into SIEVE, and peaks were identified. Statistical analysis was performed to compare peaks in low creatinine and high creatinine samples. A differential peak corresponding to inosine was identified. Serum inosine was found to be depleted in 13 out of the 25 dogs with high serum creatinine. The ion intensity for inosine (as measured by LC/MS) is shown in Figure 1, where "Renal" represents the 13 dogs with high creatinine and inosine depletion, and "Control" represents all 25 dogs with low serum creatinine.

[0051] A protocol utilized for initial LC/MS analysis as shown in Figure 1 follows below: Plasma extraction was performed in a 0.5 mL protein LoBind eppendorf tube. 110uL of canine serum was precipitated by addition of 200uL acetonitrile. After vortexing for 10 seconds, and leaving the sample at room temperature for 30 minutes, the precipitate was pelleted by centrifugation at 13,000 rpm for 30 minutes at room temperature using a benchtop centrifuge. The supernatant was then analyzed by LC/MS. SIEVE and R were used to identify molecules present at differential levels (p-value <0.05).

[0052] LC method was performed with Solvent A: 0.1% Formic acid in water and Solvent B:
0.1% Formic acid in acetonitrile:

No	Time	A%	B%	C%	D%	μL/min
1	0	100	0	0	0	300
2	5	100	0	0	0	300
3	23	65	35	0	0	300
4	26	65	35	0	0	300
5	44	5	95	0	0	300
6	46	5	95	0	0	300
7	46.5	100	0	0	0	300
8	60	100	0	0	0	300

Column: Acquity UPLC BEH130 C18 1.7μM 2.1id x 150mm length
Guard Column: vanguard BEH 300 C_{18} 1.7uM
Injection volume: 25μL
Tray temp: 10°C
Column oven temp: 45°C
MS run time: 60 minutes
Divert valve:

To waste 0-5
To source 5-55
To waste 55-60

[0053] Mass Spectrometry method was performed according to the following parameters:

MS scan event 1: FTMS; resolution 30000; scan range 100.0-500.0
MS scan event 2: FTMS; resolution 30000; scan range 500.0-2000.0

MS Tune File Values
Source Type: ESI
Capillary Temp (°C): 250.00
Sheath gas Flow: 24.00
Aux Gas Flow: 13.00
Sweep Gas Flow: 0
Ion Trap MSn AGC Target: 10000
FTMS Injection waveforms: off
FTMS AGC Target: 500000
Source voltage (kV): 4.50
Source current (μA): 100.00
Capillary Voltage (V): 68.28
Tube Lens (V): 130.00
Skimmer Offset (V): 0.00
Multipole RF Amplifier (Vp-p): 550.00
Multipole 00 offset (V): -1.60
Lens 0 Voltage (V): -2.70
Multipole 0 offset (V): -5.80
Lens 1 Voltage.(V): -11.00
Gate Lens offset (V): -60.00
Multipole 1 offset (V): -10.50
Front Lens (V): -5.18
FTMS full microscans: 1
FTMS full Max Ion Time (ms): 500
Ion Trap MSn Micro Scans: 3
Ion Trap MSn Max Ion Time: 100

To verify inosine as a biomarker for kidney disease, a complementary study was performed on dogs with X- linked hereditary nephropathy (XLHN). XLHN is caused by a mutation in the gene *COL4A5* (see Example 1 for details). These XLHN dogs provided a model of kidney disease that begins as glomerular defect and progresses to tubular failure. Serum and urine samples from four male dog puppies with XLHN (Table 11) were collected at pre-disease, mid-stage, and end-stage disease and analyzed for inosine as described in the Renal LC/MS

Assay provided below.

<u>LC/ MS Mobile Phases Prep.</u>

[0054]

1. Mobile Phase A: to 1 liter of water add 1ml acetic acid. Mix well.
2. Mobile Phase B: to 1 liter of Acetonitrile add 1ml of acetic acid. Mix well.

<u>Internal STD (IS solution) prep</u>

[0055]

1. Weigh 5mg deuterated creatinine and 6-Chloropurine riboside into a 20ml vial.
2. Add 5 ml of water to dilute. (1mg/ml solution).
3. Transfer 5ml of # 2 into a 21 flask and add 21 of water to the mark (2.5ug/ml solution).

4. Use # 3 as internal STD spiking solution.

STD Curve Prep

[0056]

1. Weigh 10mg creatinine and 10mg inosine into a 2ml vial and add 10ml of Water to dissolve (1mg/ml solution).
2. Weigh 345mg of Bovine Serum albumin (BSA) into 5ml of phosphate buffer saline solution. Mix well. Scale up or down as needed (PBS-BSA Solution).
3. Transfer 5ul of 1mg/ml solution into 990ul of PBS-BSA solution (5ug/ml STD point1)
4. Make 11 1/1 serial dilutions of # 3 for STD points , 2, 3, 4, 5, 6, 7, 8,9,10,11 and a blank.

Sample Prep

[0057]

1. Thaw serum samples.
2. Vortex samples for 10secs then centrifuge at 3000xg at room temperature for 10min.
3. Transfer 50ul of samples and STD curve points into microfuge tubes or 96well plate.
4. Add 50ul of IS solution into each sample.
5. Add 100ul of Acetonitrile.
6. Vortex to mix.
7. Sonicate for 20min in water bath.
8. Centrifuge at 3000xg for 20min at 25 degrees c.
9. Filter supernatant into amber vials/96well plates using 0.4micron nylon filters.
10. Analyze samples by LC/MS.

LC/MS METHOD

HPLC Parameters

[0058]

Column	50x4.6 XBridge Amide, 3.5um column
Flow	1ml/min

Gradient

Step	total time	flow rate (ul/ml)	A%	B%
0	0.1	1000	20	80
1	5.0	1000	100	0
2.	8.00	1000	100	0
3.	8.10	1000	20	80
4.	14.00	1000	20	80
Time		14 min		
Temperature		ambient		

MS Parameters

Scan Type:	MRM
Polarity:	Positive
Scan Mode:	N/A
Ion Source:	Turbo Spray
Resolution Q1:	Unit
Resolution Q3:	Unit

(continued)

Intensity Thres.:	0.00cps
Settling time:	0.000msec
MR pause:	5.000msec
MCA:	No
Step size:	0.00 amu

Inosine

Q1 Mass (amu)	Q3 Mass (amu)	Dwell (msec)	Parameters	Value
269.1	137.1	150.00	DP	30
			EP	7
			CEP	8
			CE	17
			CXP	3

CREATININE

Q1 Mass (amu)	Q3 Mass (amu)	Dwell (msec)	Parameters	Value
114.20	44.2	150.00	DP	20
			EP	6.30
			CEP	8.34
			CE	35
			CXP	4

DEUTERATED CREATININE

Q1 Mass (amu)	Q3 Mass (amu)	Dwell (msec)	Parameters	Value
117.20	47.2	150.00	DP	20
			EP	6.30
			CEP	8.47
			CE	35
			CXP	4

6-CHLOROPURINE RIBOSIDE

Q1 Mass (amu)	Q3 Mass (amu)	Dwell (msec)	Parameters	Value
285.29	153.2	150.00	DP	30
			EP	7
			CEP	8
			CE	17
			CXP	3

[0059] The inosine concentrations identified as a result of the above analysis are shown in Table 11, where serum inosine and urine inosine are shown in ug/dL, and creatinine is shown in mg/dL. A significant decrease in inosine is reflected in each animal over time as kidney disease progresses. These data confirm the role of inosine as a biomarker for kidney disease and tubular failure.

Table 11: Inosine Levels in Dogs with XLHN

Animal ID	DAY	Serum Inosine	Urine Inosine	Serum Creatinine
RASCAL	0	217.03	182.16	0.34
	84	188.54	44.30	1.88
	119	37.10	25.99	3.02
SANTANA	0	288.08	167.91	0.41

(continued)

Animal ID	DAY	Serum Inosine	Urine Inosine	Serum Creatinine
	56	241.82	48.45	1.17
	99	85.80	33.92	6.47
STEEL	0	174.74	556.90	0.35
	87	128.38	N/D	1.84
	147	11.25	199.25	4.01
XELLUS	0	115.96	2335.26	0.74
	91	59.87	N/D	1.88
	129	40.61	1640.90	4.05

Example 4

Renal Disease Progression in XLHN

[0060] Patient blood samples were collected from heterozygous female XLHN dogs as described in Example 1. The samples were prepared as described in Example 1 with the exception that all fractions were eluted in 0.1% formic acid in 35% acetonitrile/water, and that the samples were reconstituted in 0.1% formic acid in 3.5% acetonitrile/water.

[0061] The samples were then subjected to LC/MS as described in Example 2 above, except that the tray temperature was 10 degrees Celsius and the MS run time was 60 minutes. Table 12 shows the results of LC/MS measurements of five peptides (SEQ ID NO:1 (Apolipoprotein C1); SEQ ID NO:31 (Cystatin A); SEQ ID NO:18 (Fibrinogen α chain); SEQ ID NO:25 (Inter-Alpha Inhibitor H4 (ITIH4)); SEQ ID NO:23 (Kininogen) over time, in four heterozygous female XLHN dogs. In Table 12, "NF" is an abbreviation for "not found" (i.e. below the limit of detection), while "ND" is an abbreviation for "not determined". As the kidney disease progressed, ApoC 1 and Inter-Alpha Inhibitor H4 (ITIH4) levels increased, while Fibrinogen alpha levels decreased. Kininogen levels were higher in the XLHN dogs than in the control dogs. Cystatin A levels were higher in at least three out of the four XLHN dogs as compared to the control dogs.

Table 12: Peptide Levels During Renal Disease Progression

Animal ID	Age	Apolipoprotein C1 AA-26 (SEQ ID NO:1)	Cystatin A KA-17 (SEQ ID NO:31)	Fibrinogen α chain EV-11 (SEQ ID NO:18)	Inter-Alpha Inhibitor H4 (ITIH4) GV-22 (SEQ ID NO:25)	Kininogen EQ-9 (SEQ ID NO:23)	Serum Creatinine (mg/dl)
CONTROL 1	3-4 months Old	NF	NF	4386.5	5.9	NF	ND
CONTROL 2	3-4 months Old	20.6	NF	3881.7	2.2	NF	ND
CONTROL 3	3-4 months Old	17.7	NF	2344.1	3.6	NF	ND
CONTROL 4	3-4 months Old	22.3	NF	3741.2	4.3	NF	ND
RASCAL	0	114.4	5.2	6712.9	26.2	42.8	0.34
RASCAL	84	321.6	NF	6819.3	92.3	66.5	1.88
RASCAL	119	247.1	2.7	3741.2	108.1	19.4	3.02
XELLUS	0	122.8	NF	4233.3	58.6	10.7	0.74
XELLUS	91	145.8	NF	3144.7	53.0	1.2	1.88
XELLUS	129	218.6	NF	2595.7	99.0	16.4	4.05
SANTANA	0	152.6	9.8	9439.1	62.2	26.7	0.41
SANTANA	56	149.7	30.9	8811.6	76.6	31.0	1.17
SANTANA	99	202.4	28.2	7140.7	110.9	17.6	6.46
STEEL	0	110.9	5.9	12354.8	58.4	21.3	0.35

(continued)

Animal ID	Age	Apolipoprotein C1 AA-26 (SEQ ID NO:1)	Cystatin A KA-17 (SEQ ID NO:31)	Fibrinogen α chain EV-11 (SEQ ID NO:18)	Inter-Alpha Inhibitor H4 (ITIH4) GV-22 (SEQ ID NO:25)	Kininogen EQ-9 (SEQ ID NO:23)	Serum Creatinine (mg/dl)
STEEL	87	210.9	12.6	8246.6	85.0	38.3	1.84
STEEL	147	305.3	NF	6628.9	71.4	21.5	4.01

Example 5

Renal-Failure Induced Canine Model

[0062] Dogs of mixed breeds and sizes were injected with dichromate, inducing acute renal failure, specifically due to tubular injury. *See* Ruegg et al., Toxicol Appl Pharmacol. 1987, 90(2):261-7; Pedraza-Chaverri et al., BMC Nephrology 2005, 6:4; Chiusolo et al., Toxicol Pathol. 2010, 38:338-45. Specifically, dogs were injected with 0.2 mL/kg of potassium dichromate (5 mg/ml). Serum was prepared from blood samples collected at various time points. NGAL (neutrophil gelatinase-associated lipocalin) was assayed with the Dog NGAL ELISA Kit (BioPorto Diagnostics, Gentofte, Denmark) according to the manufacturer's instructions. Inosine concentrations were measured in serum derived from blood samples taken at various times after injection of dichromate. Inosine and creatinine were measured by LC/MS as previously described in the preceding Example (Renal Assay LC/MS).

[0063] A time course of inosine, creatinine and NGAL levels following dichromate injection in a single dog is shown in Figure 2. Inosine concentrations dropped within 2 hours of dichromate treatment. Between about 60 and 70 hours post-treatment, inosine levels began to recover. *See,* Fatima, et al., Hum Exp Toxicol 2005, 24:631-8. Creatinine and NGAL were included as reference markers (Figure 2). In summary, these data illustrate that reduced inosine levels provide a marker for renal failure and tubular injury.

[0064] In an additional study, serum samples from dichromate-treated dogs were prepared and subjected to LC/MS as described above in Example 4. Figure 3 shows time course measurements of the relative concentrations of three peptides (SEQ ID NO:1 (Apolipoprotein C1); SEQ ID NO:23 (Kininogen); SEQ ID NO:25 (Inter-Alpha Inhibitor H4 (ITIH4))) in two dogs.

[0065] SEQ ID NO:1 (Apolipoprotein C1) levels increased between about 4 hours and about 48 hours of dichromate treatment (Figure 3A). Between about 84 and 108 hours post-treatment, peptide SEQ ID NO:1 (Apolipoprotein C1) levels began to recover (decrease). These data illustrate that increased SEQ ID NO:1 (Apolipoprotein C1) levels provide a marker for renal failure and tubular injury.

[0066] SEQ ID NO:23 (Kininogen) levels generally decreased within the first 1-2 days of dichromate treatment, and recovered (increased) during later time points (Figure 3B). These data illustrate that decreased SEQ ID NO:23 (Kininogen) levels provide a marker for renal failure and tubular injury.

[0067] SEQ ID NO:25 (Inter-Alpha Inhibitor H4 (ITIH4)) levels generally decreased by the day 2 of dichromate treatment, and recovered (increased) after day 2 (Figure 3C). These data illustrate that altered SEQ ID NO:25 (Inter-Alpha Inhibitor H4 (ITIH4)) levels provide a marker for renal failure and tubular injury.

SEQUENCE LISTING

[0068]

<110> IDEXX Laboratories, Inc.
Yerramilli, Murthy
Yerramilli, Mahalakshmi

<120> Markers for Renal Disease

<130> 10-712-WO

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Val

Claims

1. A method for diagnosing stage 1 to 5 of renal disease, the method comprising:

   (a) determining the amount of at least one polypeptide in a canine patient sample, wherein said polypeptide(s) comprise one or more of SEQ ID NO: 1, SEQ ID NO: 2, and SEQ ID NO: 3, and
   (b) comparing the amount of said at least one polypeptide in the canine patient sample to a control sample, wherein increased levels of said polypeptide in the canine patient sample versus the control sample is an indication of renal disease.

2. The method of claim 1, wherein the polypeptide comprises SEQ ID NO: 1.

3. The method of claim 1, wherein determining the amount of the polypeptide is performed by immunoassay.

4. The method of claim 1, wherein the renal disease is glomerular or tubular.

5. The method of claim 1, wherein the patient sample is blood, serum, plasma or urine.

Patentansprüche

1. Verfahren zur Diagnose von Stadium 1 bis 5 einer Nierenerkrankung, wobei das Verfahren umfasst:

   (a) Bestimmen der Menge mindestens eines Polypeptids in einer Patientenprobe eines Hundes, wobei diese(s) Polypeptid(e) eine oder mehrere von SEQ ID NO: 1, SEQ ID NO: 2 und SEQ ID NO: 3 umfassen, und
   (b) Vergleichen der Menge des mindestens einen Polypeptids in der Patientenprobe eines Hundes mit einer Kontrollprobe, wobei erhöhte Werte dieses Polypeptids in der Patientenprobe eines Hundes im Vergleich zu der Kontrollprobe ein Anzeichen für eine Nierenerkrankung ist.

2. Verfahren nach Anspruch 1, wobei das Polypeptid SEQ ID NO: 1 umfasst.

3. Verfahren nach Anspruch 1, wobei das Bestimmen der Menge des Polypeptids mit einem Immunoassay durchgeführt wird.

4. Verfahren nach Anspruch 1, wobei die Nierenerkrankung glomerulär oder tubulär ist.

5. Verfahren nach Anspruch 1, wobei die Patientenprobe Blut, Serum, Plasma oder Urin ist.

Revendications

1. Procédé de diagnostic d’une maladie rénale de stade 1 à 5, le procédé comprenant :

   (a) la détermination de la quantité d’au moins un polypeptide dans un échantillon de patient canin, dans lequel le(s)dit(s) polypeptide(s) comprend/comprennent une ou plusieurs de SEQ ID NO: 1, SEQ ID NO: 2, et SEQ ID NO: 3, et
   (b) la comparaison de la quantité d’au moins un polypeptide dans l’échantillon de patient canin avec un échantillon témoin, dans lequel des taux accrus dudit polypeptide dans l’échantillon de patient canin par rapport à l’échantillon témoin sont une indication d’une maladie rénale.

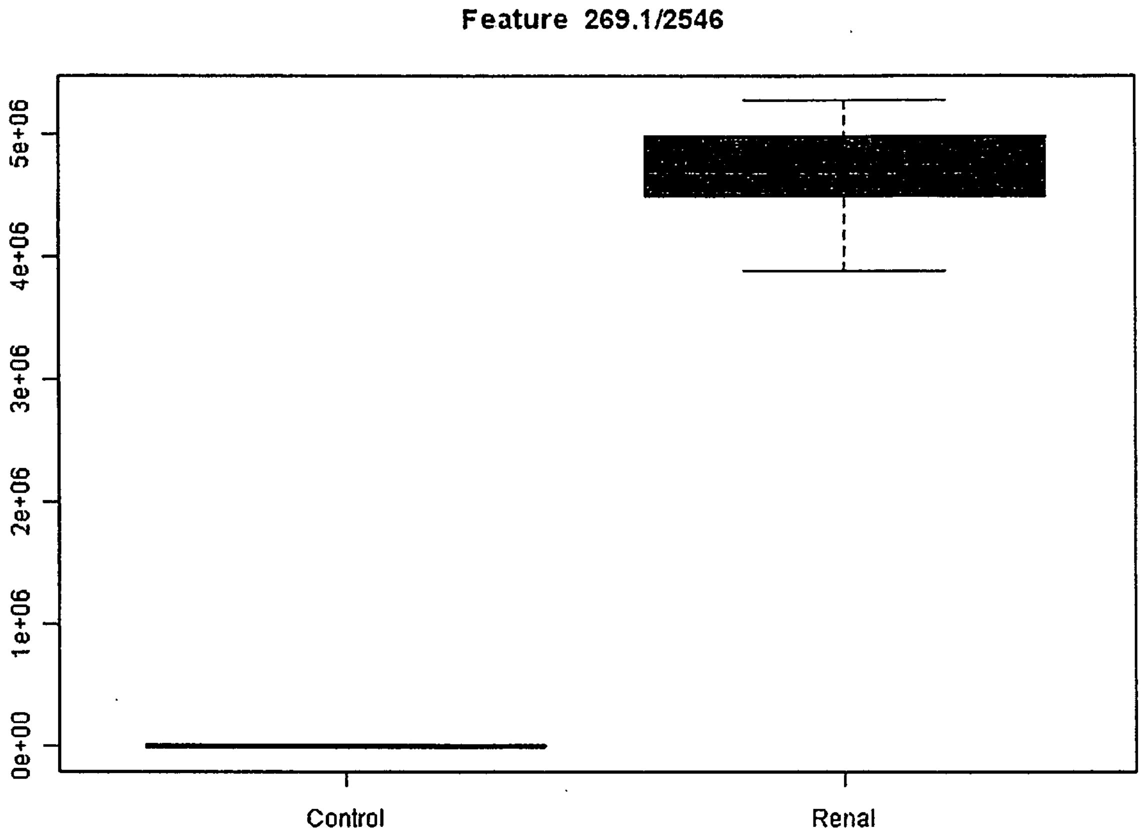
2. Procédé selon la revendication 1, dans lequel le polypeptide comprend SEQ ID NO: 1.

3. Procédé selon la revendication 1, dans lequel la détermination de la quantité du polypeptide est réalisée par dosage immunologique.

4. Procédé selon la revendication 1, dans lequel la maladie rénale est glomérulaire ou tubulaire.

5. Procédé selon la revendication 1, dans lequel l’échantillon de patient est du sang, du sérum, du plasma ou de l’urine.

Figure 1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5e+06
4e+06
3e+06
2e+06
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0e+00
Control
Renal

Figure 2

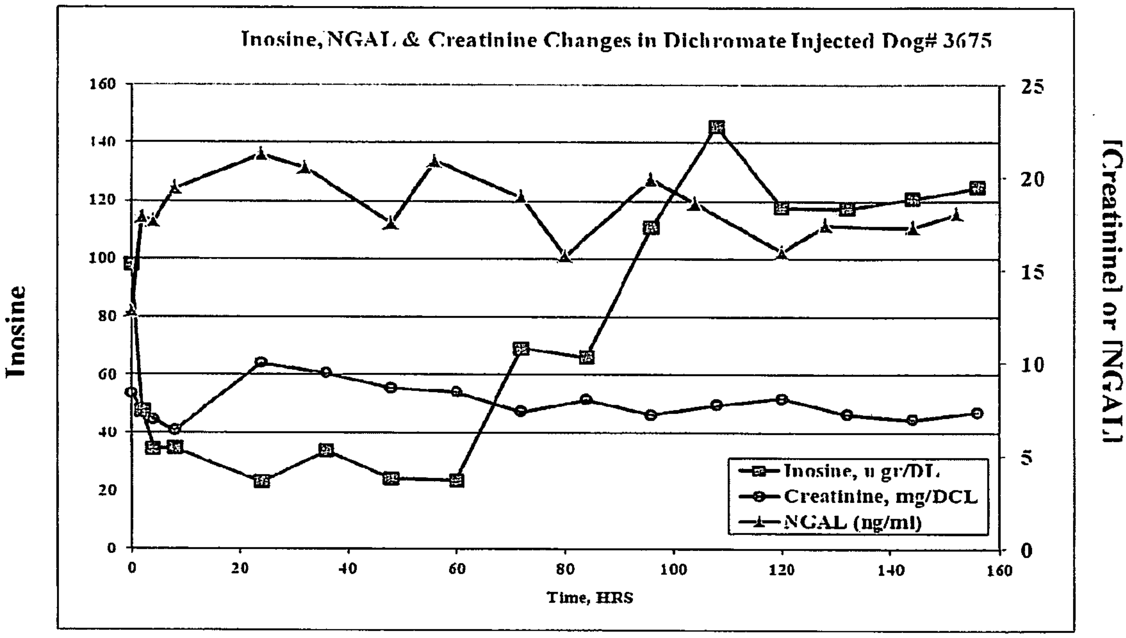

Inosine, NGAL & Creatinine Changes in Dichromate Injected Dog# 3675
Inosine
[Creatinine] or [NGAL]
Time, HRS
Inosine, u gr/DL
Creatinine, mg/DCL
NGAL (ng/ml)
0
20
40
60
80
100
120
140
160
0
5
10
15
20
25

Figure 3A

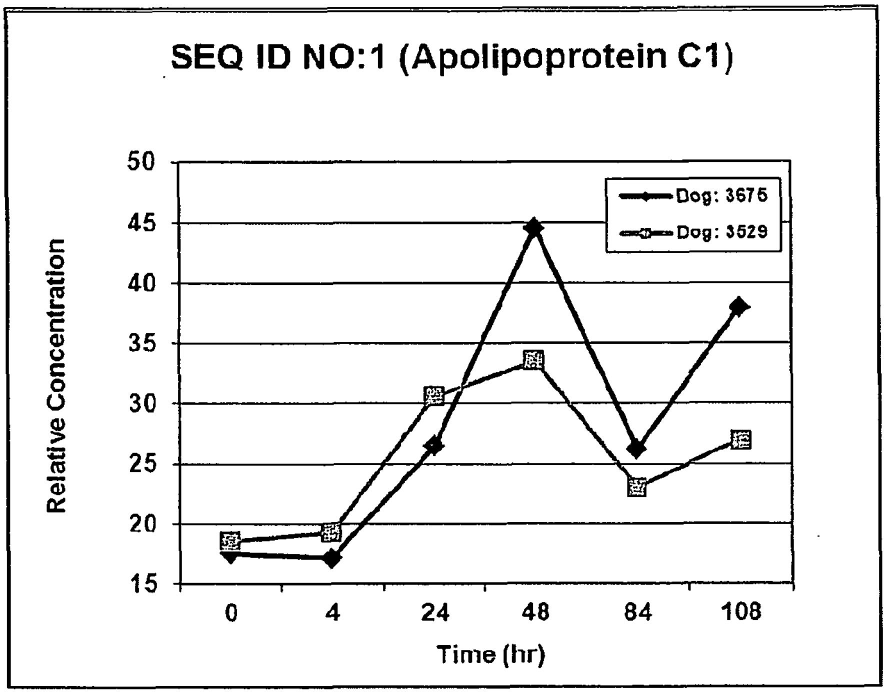


Figure 3B

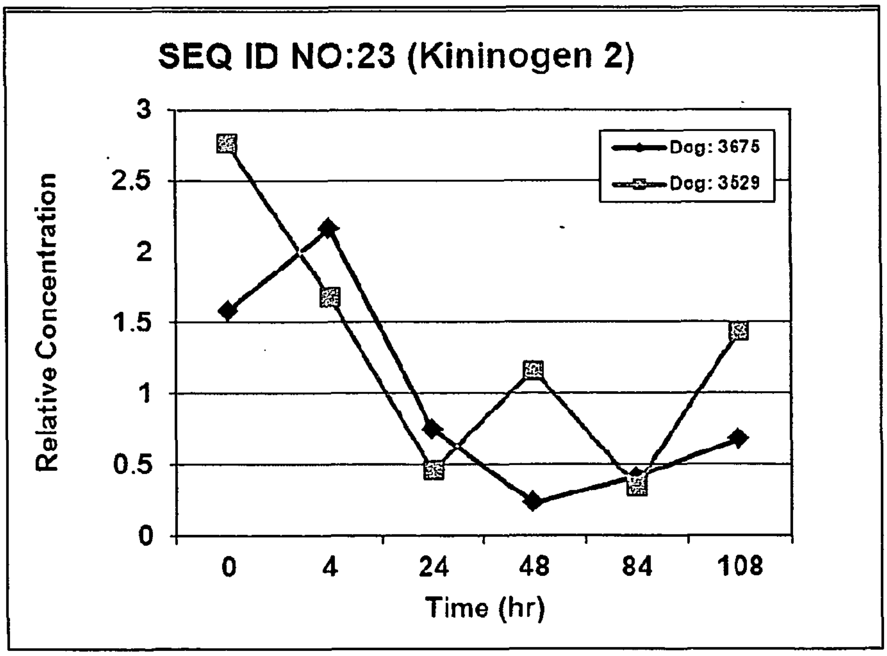
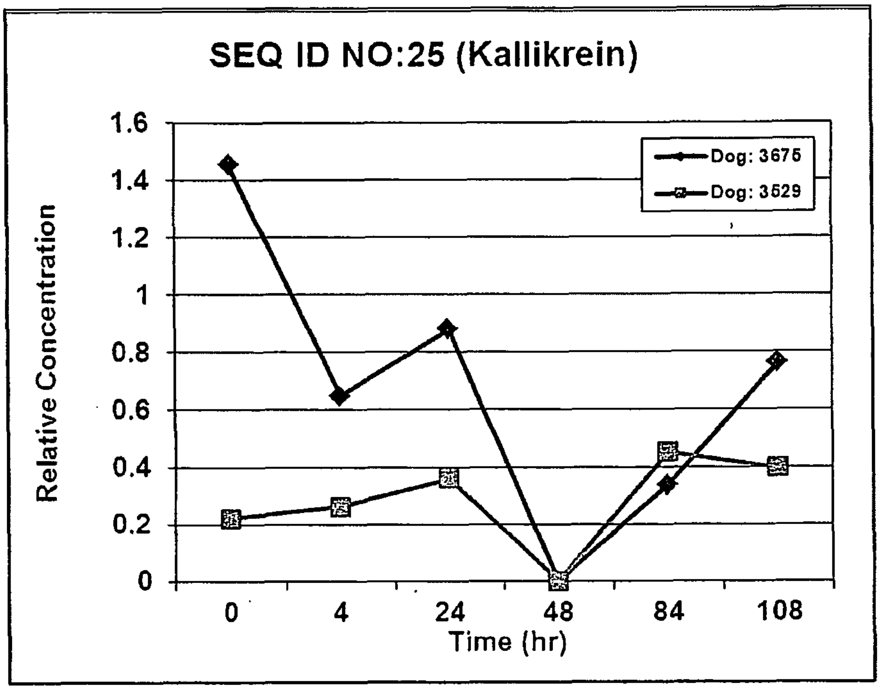


Figure 3C


SEQ ID NO:25 (Kallikrein)
Relative Concentration
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1.4
1.2
1
0.8
0.6
0.4
0.2
0
0
4
24
48
84
108
Time (hr)
Dog: 3675
Dog: 3529

REFERENCES CITED IN THE DESCRIPTION

This list of references cited by the applicant is for the reader's convenience only. It does not form part of the European patent document. Even though great care has been taken in compiling the references, errors or omissions cannot be excluded and the EPO disclaims all liability in this regard.

Patent documents cited in the description

- WO 2001079280 A **[0002]**
- US 20070087448 A1 **[0002]**
- US 4474893 A **[0013]**
- US 4816567 A **[0013]**
- US 4676980 A **[0013]**
- US 5482856 A **[0014]**
- US 5726010 A **[0019]**
- US 4554101 A **[0033]**

Non-patent literature cited in the description

- **PUPPIONE et al.** *Comparative Biochemistry and Physiology,* 2008, 290-296 **[0002]**
- **MAINO et al.** *Cytometry,* 1995, vol. 20, 127-133 **[0009]**
- **DEAN.** *Methods Mol. Biol.,* 1998, vol. 80, 23-37 **[0010]**
- **DEAN.** *Methods Mol. Biol.,* 1994, vol. 32, 361-79 **[0010]**
- **BAILEG.** *Methods Mol. Biol.,* 1994, vol. 32, 381-88 **[0010]**
- **GULLICK.** *Methods Mol. Biol.,* 1994, vol. 32, 389-99 **[0010]**
- **DRENCKHAHN et al.** *Methods Cell. Biol.,* 1993, vol. 37, 7-56 **[0010]**
- **MORRISON.** *Ann. Rev. Immunol.,* 1992, vol. 10, 239-65 **[0010]**
- **WRIGHT et al.** *Crit. Rev. Immunol.,* 1992, vol. 12, 125-68 **[0010]**
- **CHEN, Y. et al.** *J. Mol. Biol.,* 1999, vol. 293, 865-881 **[0013]**
- **KOHLER ; MILSTEIN.** *Nature,* 1975, vol. 256, 495 **[0013]**
- **STEPLEWSKI et al.** *P.N.A.S. U.S.A.,* vol. 82, 8653-1985 **[0013]**
- **SPRIA et al.** *J. Immunolog. Meth.,* 1984, vol. 74, 307 **[0013]**
- **JONES et al.** *Nature,* 1986, vol. 321, 522 **[0014]**
- **REICHMANN et al.** *Nature,* 1988, vol. 332, 323 **[0014]**
- **PRESTA.** *Curr. Op. Struct. Biol.,* 1992, vol. 2, 593 **[0014]**
- **REISENER et al.** *Trends Biotechnol.,* 1998, vol. 16, 242-246 **[0014]**
- Computational Molecular Biology. Oxford University Press, 1988 **[0027]**
- Biocomputing: Informatics And Genome Projects. Academic Press, 1993 **[0027]**
- Computer Analysis Of Sequence Data. Humana Press, 1994 **[0027]**
- **VON HEINJE.** Sequence Analysis In Molecular Biology. Academic Press, 1987 **[0027]**
- Sequence Analysis Primer. M Stockton Press, 1991 **[0027]**
- **DEVEREUX et al.** *Nuc. Acids Res.,* 1984, vol. 12, 387 **[0027]**
- **ATSCHUL et al.** *J. Molec. Biol.,* 1990, vol. 215, 403 **[0027]**
- Wisconsin Sequence Analysis Package. Science Drive. Genetics Computer Group, University Research Park, vol. 575 **[0027]**
- **SMITH ; WATERMAN.** *Adv. App. Math.,* 1981, vol. 2, 482-489 **[0027]**
- **TAM.** *J. Immunol. Methods,* 1996, vol. 196, 17-32 **[0032]**
- **JAMESON ; WOLF.** *CABIOS,* 1988, vol. 4, 181-186 **[0033]**
- **NABITY et al.** *J Vet Intern Med,* 2007, vol. 21, 425-430 **[0038]**
- **RUEGG et al.** *Toxicol Appl Pharmacol.,* 1987, vol. 90 (2), 261-7 **[0062]**
- **PEDRAZA-CHAVERRI et al.** *BMC Nephrology,* 2005, vol. 6, 4 **[0062]**
- **CHIUSOLO et al.** *Toxicol Pathol.,* 2010, vol. 38, 338-45 **[0062]**
- **FATIMA et al.** *Hum Exp Toxicol,* 2005, vol. 24, 631-8 **[0063]**

专利名称(译)	肾脏疾病的标志物		
公开(公告)号	EP2577315B1	公开(公告)日	2017-04-12
申请号	EP2011725846	申请日	2011-06-03
[标]申请(专利权)人(译)	艾德克斯实验室公司		
申请(专利权)人(译)	IDEXX实验室，INC.		
当前申请(专利权)人(译)	IDEXX实验室，INC.		
[标]发明人	YERRAMILLI MAHALAKSHMI ATKINSON MICHAEL RANDOLPH YERRAMILLI MURTHY V S N		
发明人	YERRAMILLI, MAHALAKSHMI ATKINSON, MICHAEL, RANDOLPH YERRAMILLI, MURTHY, V.S.N.		
IPC分类号	G01N33/68 G01N33/53 C07K14/775 C07K14/00		
CPC分类号	G01N33/5308 G01N33/6893 G01N2800/347 G01N2800/60 G01N33/92		
优先权	61/351183 2010-06-03 US 61/411280 2010-11-08 US		
其他公开文献	EP2577315A1		
外部链接	Espacenet		

摘要(译)

本发明提供了用于诊断肾病的试剂和方法。肌苷代谢物和蛋白质的差异水平：载脂蛋白CI，载脂蛋白C-II，纤维蛋白原α链或纤维蛋白原A-α链，激肽原，α间抑制剂H4（ITIH4），角蛋白I型细胞骨架蛋白10胱抑素A，胱抑素B和其他多肽及其片段提供肾病的生物标志物并在本文中描述。

Accession	No. Peptides	No. AAs	MW [kDa]	Description		Expression Levels
P56595	3	88	9.7	Apolipoprotein C-I OS=Canis familiaris GN=APOC1 PE=2 SV=1-[APOC1_CANFA]		Increased
	Sequence	m/z [Da]	MH+ [Da]	RT [min]		
	AGEISSTFERIPDKLKEFGNTLEDKA (SEQ. ID NO: 1)	965.83238	2895.48259	27.98		
	EISSTFERIPDKLKEFGNTLEDKA (SEQ. ID NO: 2)	923.14789	2767.42910	27.41		
	DKLKEFGNTLEDKA (SEQ. ID NO: 3)	536.61725	1607.83719	20.36		
Q28243	4	443	45.9	Fibrinogen A-alpha-chain (Fragment) OS=Canis familiaris PE=4 SV=1-[Q28243_CANFA]		Decreased
	Sequence	m/z [Da]	MH+ [Da]	RT [min]		
	IMGSDSDIFTNIGTPEFPSSGKTSSHSKQFVTSSTT (SEQ. ID NO: 4)	945.45618	3778.80288	26.50		
	THIMGSDSDIFTNIGTPEFPSSGKTSSH (SEQ. ID NO: 5)	738.34826	2950.37119	26.38		
	THIMGSDSDIFTNIGTPEFPSSGKTSSHS (SEQ. ID NO: 6)	1013.13733	3037.39743	26.25		
	IMGSDSDIFTNIGTPEFPSSGKTSSHS (SEQ. ID NO: 7)	933.76956	2799.29412	27.29		
P12278	6	101	11.2	Apolipoprotein C-II OS=Canis familiaris GN=APOC2 PE=2 SV=1 - [APOC2_CANFA]		Increased
	Sequence	m/z [Da]	MH+ [Da]	RT [min]		
	AHESQQDETTSSALLTQMQESLYSYWGTARSAAEDL (SEQ. ID NO: 8)	1335.61365	4004.82639	35.25		
	AHESQQDETTSSALLTQMQESL (SEQ. ID NO: 9)	1217.55859	2434.10991	28.22		