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(54) Title: METHODS FOR THE DEVELOPMENT OF A BIOMOLECULE ASSAY

(57) Abstract: The present teachings provide methods for the development of a mass spectrometric based assay for a protein in a sample using parent-daughter ion transition monitoring (PDITM). In various aspects, the present teachings provide methods for developing a mass spectrometric based assay for a protein in a sample without the use of a standard for the protein. In various embodiments, the sample comprises proteolytic fragments of a protein which is present in low abundance in the physiological fluid from which it is derived.

METHODS FOR THE DEVELOPMENT OF A BIOMOLECULE ASSAY

RELATED APPLICATIONS

This application claims priority to Provisional Patent Application number 60/727,187, filed October 13, 2005, the contents of which are hereby incorporated by reference.

INTRODUCTION

In many applications of the analysis of a biological sample there is a desire to obtain absolute or relative quantitative information for a set of proteins present at low concentrations in the sample. This can be especially true in biomarker discovery and validation, and is non-trivial for several reasons, for example, extremely high sensitivity may be required to achieve appropriate detection limits and the complexity of the sample (e.g., large numbers of proteins present at concentrations spanning several orders of magnitude) may cause interferences that compromise the detection limit. In addition, although the protein of interest or its corresponding DNA sequence may be known, standard samples of the protein of interest may not be available; hence, the development of an assay or method that can quantitate the amount of protein in the sample can be extremely difficult.

Traditionally, most clinically relevant markers are detected by immunoassays that provide precise measures of serum protein levels in relation to disease progression or therapy. However, a growing number of candidate protein markers are being discovered through proteomic and transcriptional profiling methods and often there are no antibody reagents available for their precise quantification in human clinical samples. In addition, most clinically relevant biomarkers are present at low concentrations in biological samples. The development of practical approaches for the quantitative analysis of biomarkers across multiple samples derived from body fluids, tissues, or other biological matrices is necessary in order to confirm that these proteins are reliable predictors of disease and may eventually be used as a clinical diagnostic.

SUMMARY

The present teachings provide methods for the development of a mass spectrometric based assay for a protein in a sample using parent-daughter ion transition

monitoring (PDITM). In various aspects, the present teachings provide methods for developing a mass spectrometric based assay for a protein in a sample without the use of a standard for the protein. In various embodiments, the sample comprises proteolytic fragments of a protein which is present in low abundance in the physiological fluid from which it is derived.

The methods of the present teachings can be applied to develop a mass spectrometric based assay for a protein present in any of a number of biological samples, including, but not limited to, physiological fluids, and cell or tissue lysates. The biological samples can be from different sources, conditions, or both; for example, control vs. experimental, samples from different points in time (e.g. to form a sequence), disease vs. normal, experimental vs. disease, contaminated vs. non-contaminated, etc. Examples of physiological fluids, include, but are not limited to, blood, serum, plasma, sweat, tears, urine, cerebrospinal fluid, peritoneal fluid, lymph, vaginal secretion, semen, spinal fluid, ascetic fluid, saliva, sputum, breast exudates, and combinations thereof.

In various embodiments, methods of the present teachings can be applied to develop a mass spectrometric based assay for a protein in blood at a concentration of less than about 100,000 attomoles/microliter, less than about 10,000 attomoles/microliter, less than about 1,000 attomoles/microliter, less than about 100 attomoles/microliter, less than about 10 attomoles/microliter, and/or less than about 1 attomoles/microliter. Such methods, for example, can be used in various embodiments to develop a protein biomarker assay.

To develop a mass spectrometric based protein assay, the present teachings use a mass spectrometric technique of parent-daughter transition monitoring. The term "parent-daughter ion transition monitoring" or "PDITM" refers to, for example, a measurement using mass spectrometry whereby the transmitted mass-to-charge (m/z) range of a first mass separator (often referred to as the first dimension of mass spectrometry) is selected to transmit a molecular ion (often referred to as "the parent ion" or "the precursor ion") to an ion fragmentor (e.g., a collision cell, photodissociation region, etc.) to produce fragment ions (often referred to as "daughter ions") and the transmitted m/z range of a second mass separator (often referred to as the second dimension of mass spectrometry) is selected to transmit one or more daughter ions to a detector which measures the daughter ion signal. The combination of parent ion and daughter ion masses monitored can be referred to as the "parent-daughter ion transition"

monitored. The daughter ion signal at the detector for a given parent ion-daughter ion combination monitored can be referred to as the "parent-daughter ion transition signal". In the present teachings, where the parent ion is generated for a proteolytic fragment of a protein and the ion signal of a daughter ion is measured, the daughter ion signal at the detector for a given proteolytic fragment ion-daughter ion combination monitored can be referred to as the "parent-daughter ion signal".

The parent-daughter ion signal, and other ion signals described herein, can be based, for example, on the intensity (average, mean, maximum, etc.) of the daughter ion peak, the area of the daughter ion peak, or a combination thereof.

In various embodiments, parent-daughter ion transition monitoring comprises multiple reaction monitoring (MRM) (also referred to as selective reaction monitoring). In various embodiments of MRM, the monitoring of a given parent-daughter ion transition comprises using as the first mass separator a first quadrupole parked on the parent ion m/z of interest to transmit the parent ion of interest and using as a second mass separator a second quadrupole parked on the daughter ion m/z of interest to transmit daughter ions of interest. In various embodiments, a PDITM can be performed, for example, by parking the first mass separator on parent ion m/z of interest to transmit parent ions and scanning the second mass separator over a m/z range including the m/z value of the daughter ion of interest and, e.g., extracting an ion intensity profile from the spectra. A tandem mass spectrometer (MS/MS) instrument or, more generally, a multidimensional mass spectrometer (MS^n) instrument, can be used to perform PDITM, e.g., MRM. In various embodiments, the mass spectrometer is a triple quadrupole linear ion trap mass spectrometer.

In various aspects, the present teachings provide methods for developing a mass spectrometric based assay for a protein in a sample without the use of a standard for the protein, comprising the steps of: (a) predicting one or more of the proteolytic fragments of a protein based on one or more of an amino acid sequence for the protein and a translation of a gene sequence for the protein; (b) predicting one or more of the fragments produced from one or more of the proteolytic fragments of the protein when the proteolytic fragment is subjected to collision induced dissociation; (c) providing a sample containing proteolytic fragments of a protein; (d) loading at least a portion of the sample on a chromatographic column; (e) subjecting at least a portion of the eluent from the chromatographic column to multiple reaction monitoring, where the transmitted parent

ion m/z range of each multiple reaction monitoring scan includes a m/z value of one or more of the predicted proteolytic fragments of the protein and the transmitted daughter ion m/z range of each multiple reaction monitoring scan includes a m/z value one or more of the predicted collision induced dissociation fragments of the of the predicted proteolytic fragments; (f) measuring the ion signal of the m/z value range encompassing one or more of the predicted collision induced dissociation fragments m/z value using said multiple reaction monitoring; (g) performing a substantially full product ion scan on a m/z value range encompassing a predicted proteolytic fragment m/z value when the measured ion signal corresponding to one or more collision induced dissociation fragments of the predicted proteolytic fragment is above a specified signal threshold; (h) measuring the ion signals associated with the parent-daughter ion transitions of said substantially full product ion scan; and (i) selecting as the parent-daughter ion transition for an assay of the presence of the protein in a biological sample a parent-daughter ion transition of said substantially full product ion scan, wherein the selected parent-daughter ion transition for the assay corresponds to a transition where the transmitted parent ion is a proteolytic fragment of said protein, and wherein the selected parent-daughter ion transition has, relative to the measured ion signals associated with the other parent-daughter ion transitions for said protein, one or more of the approximately highest parent-daughter ion signal and the approximately highest signal-to-noise ratio. In various embodiments, the step of measuring the ion signal of the m/z value range encompassing one or more of the predicted collision induced dissociation fragments m/z value comprises: (1) sequencing the transmitted parent ion when the measured ion signal corresponding to one or more collision induced dissociation fragments of the predicted proteolytic fragment is above the specified signal threshold; and (2) performing said substantially full product ion scan on a m/z value range encompassing said sequenced transmitted parent ion when the sequence of the sequenced transmitted parent ion corresponds to a proteolytic fragment of the protein. In various embodiments, this step of measuring the ion signal further comprises a step of measuring the charge state of the transmitted parent ion when the measured ion signal corresponding to one or more collision induced dissociation fragments of the predicted proteolytic fragment is above a specified signal threshold.

In various aspects, the present teachings provide methods for developing a mass spectrometric based assay for detecting a low abundance protein in a blood sample

without the use of a standard for the protein comprising the steps of: (a) predicting one or more of the proteolytic fragments of a protein based on one or more of an amino acid sequence for the protein and a translation of a gene sequence for the protein; (b) predicting one or more of the fragments produced from one or more of the proteolytic fragments of the protein when the proteolytic fragment is subjected to collision induced dissociation; (c) providing a sample containing proteolytic fragments of a protein, wherein said sample is derived from a blood sample containing the protein in a concentration of less than about 100,000 attomoles/microliter; (d) loading at least a portion of the sample on a chromatographic column; (e) subjecting at least a portion of the eluent from the chromatographic column to multiple reaction monitoring, the transmitted parent ion m/z range of each multiple reaction monitoring scan including a m/z value of one or more of the predicted proteolytic fragments of the protein and the transmitted daughter ion m/z range of each multiple reaction monitoring scan including a m/z value one or more of the predicted collision induced dissociation fragments of the of the predicted proteolytic fragments; (f) measuring the ion signal of the m/z value range encompassing one or more of the predicted collision induced dissociation fragments m/z value using said multiple reaction monitoring; (g) performing a substantially full product ion scan on a m/z value range encompassing a predicted proteolytic fragment m/z value when the measured ion signal corresponding to one or more collision induced dissociation fragments of the predicted proteolytic fragment is above a specified signal threshold; (h) measuring the ion signals associated with the parent-daughter ion transitions of said substantially full product ion scan; and (i) selecting as the parent-daughter ion transition for an assay of the presence of the protein in a biological sample a parent-daughter ion transition of said substantially full product ion scan, wherein the selected parent-daughter ion transition for the assay corresponds to a transition where the transmitted parent ion is a proteolytic fragment of said protein, and wherein the selected parent-daughter ion transition has, relative to the measured ion signals associated with the other parent-daughter ion transitions for said protein, one or more of the approximately highest parent-daughter ion signal and the approximately highest signal-to-noise ratio. In various embodiments, the step of measuring the ion signal of the m/z value range encompassing one or more of the predicted collision induced dissociation fragments m/z value comprises: (1) sequencing the transmitted parent ion when the measured ion signal corresponding to one or more collision induced dissociation fragments of the predicted

proteolytic fragment is above the specified intensity threshold; and (2) performing said substantially full product ion scan on a m/z value range encompassing said sequenced transmitted parent ion when the sequence of the sequenced transmitted parent ion corresponds to a proteolytic fragment of the protein. In various embodiments, this step of measuring the ion signal further comprises a step of measuring the charge state of the transmitted parent ion when the measured ion signal corresponding to one or more collision induced dissociation fragments of the predicted proteolytic fragment is above a specified signal threshold.

In various aspects, the present teachings provide methods for developing a mass spectrometric assay for a protein in a sample without the use of a standard for the protein comprising the steps of: (a) predicting one or more of the proteolytic fragments of a protein based on one or more of an amino acid sequence for the protein and a translation of a gene sequence for the protein; (b) predicting one or more of the fragments produced from one or more of the proteolytic fragments of the protein when the proteolytic fragment is subjected to collision induced dissociation; (c) providing a sample containing proteolytic fragments of a protein; (d) loading at least a portion of the sample on a chromatographic column; (e) subjecting at least a portion of the eluent from the chromatographic column to multiple reaction monitoring, the transmitted parent ion m/z range of each multiple reaction monitoring scan including a m/z value of one or more of the predicted proteolytic fragments of the protein and the transmitted daughter ion m/z range of each multiple reaction monitoring scan including a m/z value one or more of the predicted collision induced dissociation fragments of the of the predicted proteolytic fragments; (f) measuring the ion signal of the m/z value range encompassing one or more of the predicted collision induced dissociation fragments m/z value using said multiple reaction monitoring; (g) measuring the charge state of the transmitted parent ion when the measured ion signal corresponding to one or more collision induced dissociation fragments of the predicted proteolytic fragment is above a specified signal threshold; (h) sequencing the transmitted parent ion when the measured ion signal corresponding to one or more collision induced dissociation fragments of the predicted proteolytic fragment is above the specified signal threshold; (i) performing a substantially full product ion scan on a m/z value range encompassing said sequenced transmitted parent ion when the sequence of the sequenced transmitted parent ion corresponds to a proteolytic fragment of the protein; (j) measuring the ion signals associated with the parent-daughter ion

transitions of said substantially full product ion scan; and (k) selecting as the parent-daughter ion transition for an assay of the presence of the protein in a biological sample the parent-daughter ion transition which has, relative to the measured ion signals associated with the other parent-daughter ion transitions for said protein, one or more of the approximately highest parent-daughter ion signal and the approximately highest signal-to-noise ratio.

As understood by one of ordinary skill in the art, the term "full product ion scan" refers to a mass spectrometric scan over m/z values corresponding to product ions of a parent ion that has been subjected to fragmentation. As used herein, the term "full product ion scan" does not require that scans encompass all m/z values from zero up to the highest m/z value possible for a product ion. As understood by those of ordinary skill in the art, mass spectrometers can be limited in the lower m/z value limit they can effectively reach and product ions below a certain mass may not be of interest, e.g., free hydrogen ion fragments (H^+). For example, a mass spectrometric scan for product ions from about 30 amu to a m/z value corresponding to the highest possible product ion mass can be considered a "full product ion scan" even though ions with a mass of less than about 30 amu will not be scanned or detected.

In various embodiments of the various aspects of the present teachings, an assay for the presence of one or more specific proteins (e.g., biomarker proteins) in a biological sample is developed where the protein is present in low abundance in the sample such as, for example, a blood sample. In various embodiments, the sample contains the protein in a concentration of less than about 100,000 attomoles/microliter, less than about 10,000 attomoles/microliter, less than about 1,000 attomoles/microliter, less than about 100 attomoles/microliter, less than about 10 attomoles/microliter, and/or less than about 1 attomoles/microliter. In various embodiments, mass spectrometric based assay for a protein in a sample of the present teachings can be extended to lower protein concentrations, e.g., by reducing the dynamic range of the protein concentration in the sample. For example, detection of lower concentrations of a protein of interest in a complex mixture can be achieved by removal of more abundant proteins, enrichment of the protein of interest in the sample, or combinations thereof, to increase, for example, the relative amount of the protein of interest in the sample loaded on the chromatographic column.

In various embodiments, the sample is prepared from extracts of cells, tissues and physiological fluids. Examples of physiological fluids, include, but are not limited to, blood, serum, plasma, sweat, tears, cerebrospinal fluid, urine, peritoneal fluid, lymph, vaginal secretion, semen, spinal fluid, ascetic fluid, saliva, sputum, breast exudates, and combinations thereof. The samples can be derived from different sources, conditions, or both; for example, control vs. experimental, samples from different points in time (e.g. to form a sequence), disease vs. normal, experimental vs. disease, contaminated vs. non-contaminated, etc.

A wide variety of approaches can be used to generate proteolytic fragments of the protein of interest. Suitable techniques for generating proteolytic fragments from proteins include any sequence specific cleavage process. Examples of suitable enzymatic sequence specific cleavage techniques include cleavage with proteases, such as, for example, serine proteases, and thiol proteases. For example, proteolytic fragments (e.g., peptides) can be generated from a protein by the enzymatic hydrolysis of peptide bonds with trypsin to produce a plurality of peptide proteolytic fragments.

In various embodiments, the sample containing proteolytic fragments of a protein further comprises a concentration standard for one or more of the predicted proteolytic fragments of the protein that is created after, and based on, the present teachings select the proteolytic fragment for use as an assay for said protein. The concentration standard can be, for example, a stable isotope labeled peptide corresponding to one of the proteolytic peptides generated from the protein of interest.

In various aspects, provided are assays designed to determine the presence of a protein of interest in one or more samples. The assay can be, for example, a biomarker validation assay, used to aid in the discovery of various biochemical pathways, for drug discovery or a diagnostic assay. The assay can, for example, be diagnostic of a disease or condition, prognostic of a disease or condition, or both.

In various aspects, the present teachings provide articles of manufacture where the functionality of a method of the present invention is embedded as computer-readable instructions on a computer-readable medium, such as, but not limited to, a floppy disk, a hard disk, an optical disk, a magnetic tape, a PROM, an EPROM, CD-ROM, or DVD-ROM.

BRIEF DESCRIPTION OF THE DRAWINGS

The foregoing and other aspects, embodiments, objects, features and advantages of the present teachings can be more fully understood from the following description in conjunction with the accompanying drawings. In the drawings, like reference characters generally refer to like features and structural elements throughout the various figures. The drawings are not necessarily to scale, emphasis instead being placed upon illustrating the principles of the present teachings.

Figure 1 is a simplified schematic diagram of the mass spectrometer system used in the Examples.

Figure 2 schematically depicts various embodiments of a method for the development of an MRM-based assay for the validation of biomarkers.

Figures 3A and 3B depict MRM and MS/MS experimental on a fibronectin peptide as discussed in Example 1.

Figure 4A depicts data for the peptides of the 53 proteins of Example 2 and Figure 4B depicts the range of abundance of these proteins in the samples analyzed in Example 2.

Figures 5B and 5C show correlation plots of peak areas of MRM transitions between a parallel depleted/digestion experiment and a parallel digestion experiment, respectively of Example 2 on the same plasma sample.

Figures 6A and 6B compare MRM data of Example 3 for a peptide fragment of L-selectin from the sample, Figure 6A, to that for an isotope labeled synthetic peptide Figure 6B.

Figure 7 schematically depicts refinement of predicted MRM transitions based on measured parent-daughter ion signals.

Figure 8 is a plot of peak CV versus peak area for two experiments (digested plasma and depleted plasma) of Example 2.

Figures 9A and 9B illustrate the effects of the depletion of the six most abundant proteins from plasma in Example 2.

Figures 10A and 10B depict the distribution of CV values for five experimental sets of Example 2.

DETAILED DESCRIPTION OF VARIOUS EMBODIMENTS

To develop a mass spectrometric based protein assay, the present teachings use a mass spectrometric technique of parent-daughter ion transition monitoring. In various embodiments, parent-daughter ion transition monitoring comprises multiple reaction monitoring (MRM). Referring to Figure 1, a MRM scan can be conducted, for example, by setting a first mass separator **101** to transmit the mass of a proteolytic fragment of interest (i.e., the parent ion **102)** to the ion fragmentor **103**. The first mass separator **101** can be set, e.g., by setting the first mass separator to transmit ions in a mass window about 3 mass units wide substantially centered on the mass of a proteolytic fragment. In various embodiments, the collision energy of the ion fragmentor **103** can be selected to facilitate producing the selected charged fragment of this peptide (the daughter ion) in the ion fragmentor (here, the ion fragmentor comprises a collision gas for conducting CID and a quadrupole, to facilitate, e.g., collecting ion fragments **104** and fragment ion transmittal). The second mass separator **105** is set to transmit the daughter ion (or ions) **106** of interest (e.g., by setting the second mass separator to transmit ions in a mass window about 1 mass unit wide substantially centered on the mass of a daughter ion) to a detector **107** to generate an ion signal for the daughter ion (or ions) transmitted.

In various embodiments, MRM parameters, for each parent ion-daughter ion combination, can be chosen to facilitate optimizing the signal for the selected daughter ion (or ions) associated with that parent ion (proteolytic fragment of the protein of interest). In various embodiments, dwell times typically between, but not limited to, about 10ms to about 200ms can be used on the mass separators in this experiment and the ability to rapidly change between MRM transitions can allow multiple components in a mixture to be monitored in a single LC-MS run. For example, 50-100 different components can be monitored in a single time period in a single LC-MS run. The use of specific time periods can allow more MRM transitions to be monitored in a single LC-MS run.

A wide variety of mass analyzer systems can be used in the present teachings to perform PDITM. Suitable mass analyzer systems include two mass separators with an ion fragmentor disposed in the ion flight path between the two mass separators. Examples of suitable mass separators include, but are not limited to, quadrupoles, RF multipoles, ion traps, time-of-flight (TOF), and TOF in conjunction with a timed ion selector. Suitable ion fragmentors include, but are not limited to, those operating on the

principles of: collision induced dissociation (CID, also referred to as collisionally assisted dissociation (CAD)), photoinduced dissociation (PID), surface induced dissociation (SID), post source decay, or combinations thereof.

Examples of suitable mass spectrometry systems for the mass analyzer include, but are not limited to, those which comprise a triple quadrupole, a quadrupole-linear ion trap, a quadrupole TOF systems, and TOF-TOF systems.

Suitable ion sources for the mass spectrometry systems include, but are not limited to, electrospray ionization (ESI), matrix-assisted laser desorption ionization (MALDI), atmospheric pressure chemical ionization (APCI), and atmospheric pressure photoionization (APPI) sources. For example, ESI ion sources can serve as a means for introducing an ionized sample that originates from a LC column into a mass separator apparatus. One of several desirable features of ESI is that fractions from the chromatography column can proceed directly from the column to the ESI ion source.

In various embodiments, the mass spectrometer system comprises a triple quadrupole mass spectrometer for selecting a parent ion and detecting fragment daughter ions thereof. In various embodiments, the first quadrupole selects the parent ion, herein referred to as Q1. The second quadrupole, herein referred to as Q2, is maintained at a sufficiently high pressure and voltage so that multiple low energy collisions occur causing some of the parent ions to fragment. The third quadrupole, Q3, is selected to transmit the selected daughter ion to a detector.

In various embodiments, one or more of the quadrupoles in a triple quadrupole mass spectrometer can be configurable as a linear ion trap (e.g., by the addition of end electrodes to provide a substantially elongate cylindrical trapping volume within the quadrupole). In various embodiments, the first quadrupole Q1 selects the parent ion. The second quadrupole Q2 is maintained at a sufficiently high collision gas pressure and voltage so that multiple low energy collisions occur causing some of the parent ions to fragment. The third quadrupole Q3 is selected to trap fragment ions and, after a fill time, transmit the selected daughter ion to a detector by, e.g., pulsing an end electrode to permit the selected daughter ion to exit the ion trap. Desired fill times can be determined, e.g., based on the number of fragment ions, charge density within the ion trap, the time between elution of different peptides, duty cycle, decay rates of excited state species or multiply charged ions, or combinations thereof.

Referring to Figure 2, depicted is a schematic diagram illustrating various embodiments of the present teachings for developing a mass spectrometric based assay for the detection of the presence of a protein in a sample. In various embodiments, the present teachings determine initial putative MRM transitions for the protein of interest based on a known or predicted sequence of the protein of interest. Protein sequence information can obtained from a number of sources, including, but not limited to, amino acid sequence databases (e.g., Celera, SwissProt, etc.), DNA databases, translations of a gene sequence, direct experimental determination, and combinations thereof. The methods of the present invention predict from the protein sequence **210** the proteolytic fragments of the protein (e.g., peptide fragments) and predict the fragments (daughter ions) of these proteolytic fragments that result from fragmentation of the proteolytic fragment by the fragmentation method of the ion fragmentor. In various embodiments, the ion fragmentation method comprises collision-induced-dissociation (CID), and the predicted daughter ions are those that result from CID of the corresponding proteolytic fragment. Accordingly, the proteolytice fragments (e.g., peptides) generated from a theoretical proteolysis of the protein can be used to determine one or more daughter ions for the corresponding proteolytic fragment and thereby determine initial parent -daughter ion transitions **220** for monitoring by MRM. These transitions are often listed using the notation MS1/MS2, where MS1 refers to the nominal mass-to-charge ratio transmitted by the first mass separator (and hence the nominal proteolytic fragment m/z) and MS2 refers to the nominal m/z transmitted by the second mass separator (and hence the nominal proteolytic fragment daughter ion m/z).

A sample, which contains proteolytic fragments of the protein of interest, is then subjected to an MRM experiment. Prior to the MRM experiment, the sample can be subjected to processing steps to, for example, concentrate the sample, fractionate out interfering sample, remove at least a portion of the more abundant proteins, etc. At least a portion of the sample is loaded onto a chromatographic column and at least a portion of the eluent is directed to a mass spectrometry system. The mass spectrometry system is used to perform MRM using one or more of the initial parent-daughter ion transitions, and the parent-daughter ion transition signals are measured **230.** To confirm the identity of the peptides being detected by MRM, an information-dependent acquisition experiment can be used to obtain dependent MS and MS/MS spectra of the peptides **240.** In various embodiments, for example, when the ion signal is above a specified signal

threshold, a substantially full product ion scan is performed on the corresponding proteolytic fragment. In various embodiments, when the ion signal is above a specified signal threshold, several linear ion trap scans are triggered, to provide, e.g., an enhanced resolution scan (a high-resolution scan using the linear ion trap) to confirm the charge state and monoisotopic mass of the peptide, and/or an enhanced product ion scan (an MS/MS scan using the linear ion trap) to confirm the sequence of the peptide.

For example, a full product ion scan can be performed on the transmitted parent ion and the parent ion sequenced in order to confirm the identity of the detected parent ion as a predicted proteolytic fragment from the desired protein. Preferably, the parent ions are fragmented in a collision cell to a series of fragment ions, among which are a ladder of ions with sequentially decreasing numbers of amino acids. Since the fragmentation can occur anywhere along the peptide, a spectrum of the observed mass to charge ratios is generated. Typically, two prominent sets of ions are observed in the fragmentation spectrum. One set is a sequence ladder with amino acid deletions from the C-terminal end of the peptide (often referred to as the y series), while the other set is a sequence ladder with amino acid deletions from the N-terminal end (often referred to as the b series). Complete or partial amino acid sequence information for the parent ions is then obtained by interpretation of the fragmentation spectra. As the different amino acids within a peptide each have different masses, the fragmentation spectrum of a peptide is usually characteristic of the peptide sequence.

In various embodiments, the experimentally measured full scan MS/MS spectra are used to refine the initial predicted parent-daughter ion transitions to generate a refined set of PDITs and the step of performing MRM and measuring the resultant parent-daughter ion transition signals are measured **230** is repeated using one or more of the refined parent-daughter ion transitions. This process of refining and measuring can be repeated.

The methods of the present teachings then select a parent-daughter ion transition as an assay of the presence of the protein in the biological sample **250.** The parent-daughter ion transition is selected based on (i) the parent ion of the parent-daughter ion transition is a proteolytic fragment of said protein; and at least one of the following, (ii) the selected parent-daughter ion transition has, relative to the measured ion signals associated with the other parent-daughter ion transitions for the protein, the approximately highest ion signal (as determined by peak area in this Example); (iii) the

selected parent-daughter ion transition has, relative to the measured ion signals associated with the other parent-daughter ion transitions for the protein, the approximately highest signal-to-noise ratio; (iv) the selected parent-daughter ion transition has, relative to the measured ion signals associated with the other parent-daughter ion transitions for the protein, the ion signal with the approximately smallest amount of error in the ion signal; and/or (v) the selected parent-daughter ion transition has one or more of a lower limit of quantitation (LOQ), signal-to-noise ratio, and/or parent-daughter ion signal, greater than a specified threshold value.

In various embodiments, the daughter ions for the selected parent-daughter ion transition can be selected based on one or more of their: level of detection (LOD), limit of quantitation (LOQ), signal-to-noise (S/N) ratio, mass similarity with other daughter ions of other peptides, etc. In various embodiments, the LOQ ranges from about attomole levels (10^{-18} moles) to about femtomole levels (10^{-15} moles) of sample on the LC column used, with a dynamic range of about three to about four orders of magnitude above the LOQ.

In various embodiments, the methods of the present teachings include a step of sample preparation to increase the sensitivity of the assay (e.g, to facilitate detecting lower protein concentrations). Several approaches can be used to increase the sensitivity of the assay, including, but not limited to, reducing the dynamic range of the protein concentration in the sample, increasing the relative concentration of the protein of interest in the sample, and combinations thereof. For example, lower concentrations of a protein of interest can be achieved by removal of more abundant proteins, enrichment of the protein of interest in the sample, or combinations thereof, to increase, for example, the relative amount of the protein of interest in the sample loaded on the chromatographic column. Although, mass spectrometers can theoretically detect a single molecule, typical chromatographic columns have practical limits to the amount of protein that can loaded on them.

In various embodiments, the sample containing proteolytic fragments of a protein further comprises a concentration standard for one or more of the predicted proteolytic fragments of the protein that is created after, and based on, the present teachings select the proteolytic fragment for use as an assay for said protein. The concentration standard can be, for example, a stable isotope labeled peptide corresponding to one of the proteolytic peptides generated from the protein of interest. It is to be understood that in

various embodiments the present teachings provide methods for the development of a mass spectrometric based assay for a protein in a sample without the use of a standard for the protein. In various embodiments, the present teaching thus provide methods for determining the concentration standard, if any, to be used in a mass spectrometric assay for a protein in a sample.

In another aspect of the present teachings, the functionality of the methods described above may be implemented as computer-readable instructions on a general purpose computer. The computer may be separate from, detachable from, or integrated into a mass spectrometry system. The computer-readable instructions may be written in any one of a number of high-level languages, such as, for example, FORTRAN, PASCAL, C, C++, or BASIC. Further, the computer-readable instructions may be written in a script, macro, or functionality embedded in commercially available software, such as EXCEL or VISUAL BASIC. Additionally, the computer-readable instructions could be implemented in an assembly language directed to a microprocessor resident on a computer. For example, the computer-readable instructions could be implemented in Intel 80x86 assembly language if it were configured to run on an IBM PC or PC clone. In one embodiment, the computer-readable instructions be embedded on an article of manufacture including, but not limited to, a computer-readable program medium such as, for example, a floppy disk, a hard disk, an optical disk, a magnetic tape, a PROM, an EPROM, CD-ROM, DVD-ROM.

The following examples illustrate experiments which use various principles of the present teachings. The teachings of these examples are not exhaustive and are not intended to limit the scope of the present teachings.

EXAMPLE 1: Detection and Confirmation of Fibronectin in Depleted Human Plasma

In this example, the detection and confirmation of fibronectin in human plasma (which was depleted of the 6 typically highest abundance plasma proteins: albumin, IgG, IgA, transferrin, haptoglobin, and antitrypsin) is shown. This can be a valuable step in the confirmation of the assay; e.g., to have sequence confirmation information (full scan MS/MS) for every MRM transition at the specific retention time to be used for

quantitation, for increased confidence in assay results. Fibronectin is typically present in human plasma at a concentration of about 5397 amol/ μL.

Preparation of Sample

In this Example, the sample comprised human plasma. The plasma sample was depleted of the 6 typically highest abundant proteins (albumin, IgG, IgA, transferrin, haptoglobin, and antitrypsin) using the Multiple Affinity Removal System ("MARS" spincolumn: Agilent Technologies), and the samples desalted by filtration prior to loading on the chromatographic column. The plasma samples were also denatured, reduced, alkylated and then digested with trypsin prior to column loading.

Chromatography

Human plasma (0.01 μL) was loaded on a C18 column (75μm x15cm, LC Packings) and components separated by reversed-phase HPLC using a 40 minute gradient (2-35% acetonitrile in 0.1% formic acid). In some cases, a precolumn desalting step was used (C18 trap, 300 μm x 5mm, LC Packings).

Mass Analyzer System

MRM analysis was performed using the NanoSpray® source on an Applied Biosystems/MDS Sciex 4000 Q TRAP® system (Q1 – unit resolution, Q3 – unit resolution). MRM transitions for each peptide were either predicted based on MS/MS spectra or designed based on the peptide sequence. MRM-Initiated Detection and Sequencing using a MIDAS™ brand workflow as illustrated was used to confirm every MRM transition and retention time in the final assay.

Discussion

Figure 3A shows a MRM transition (647.3 / 789.4) for DLQFVEVTDVK peptide of fibronectin **302** for about 0.01 μL of plasma loaded onto a chromatography column (i.e., a loaded sample with about 54 amol of the protein). Figure 3A also shows an MRM transition signal **304** for this Example. In this Example, the detection of the peptide by MRM drives the acquisition of MS/MS to confirm the peptide sequence and identify the detected peptide by a MS/MS experiment to provide sequence information on the daughter ion of the proteolytic fragment (peptide) of fibronectin. Figure 3B provides an

example of such MS/MS data **306**. Although the digested sample is a highly complex mixture of peptides (proteolytic fragments), only a single peak is observed in the MRM survey scan data **304**. The full product ion scan MS/MS data **306** shown in Figure 3B (stars shows Q3 mass used in MRM of Figure 3A) was used to confirm that the single peak observed in the MRM scan **304** is DLQFVEVTDVK, the targeted proteolytic fragment (peptide) from fibronectin. This example illustrates that peptides from the targeted protein of interest which, although present in low abundance, can be detected by MRM and confirmed by MS/MS in a complex biological mixture.

EXAMPLE 2: Assessments on Whole and Depleted Human Plasma Samples

This Example provides data and assessment of various embodiments of the present teachings as applied to peptides (protein proteolytic fragments) representing 53 proteins in human plasma using a multiplexed approach. Of these, 47 produced quantitative data with within-run coefficients of variation (CV) (n=10) of 2-22% (78% of assays had CV < 10%). A number of peptides gave CV's in the range 2-7% in 5 experiments (10 replicate runs each) continuously measuring 137 MRM's, demonstrating the precision achievable in complex digests using the present teachings. Depletion of 6 the typically high abundant proteins by immunosubtraction (as described below) improved CV's compared to whole plasma, but analytes could be detected in both sample types (depleted and undepleted). Replicate digest and depletion/digest runs yielded correlation coefficients (R^2) of >99.5% and >98.9% respectively. Absolute analyte specificity for each peptide was demonstrated using MRM-triggered MS/MS scans. Reliable detection of L-selectin (measured at 0.67 μg/ml) and fibronectin indicate that proteins down to the υg/ml level can be quantitated in plasma with minimal sample preparation, yielding a dynamic range of about 4 to 5 orders of magnitude in a single experiment. In various embodiments, additional upfront sample preparation can be performed to facilitate detection of lower abundance proteins using the present teachings. Thus, in various embodiments, the present teachings can provide a robust platform for biomarker validation.

Figure 4A depicts LC chromatogram data for the peptides of the 53 proteins (only 10 proteins are labeled due to space considerations in the figure) and Figure 4B depicts the range of abundance of these proteins in the samples analyzed in this Example. The

diamond-shaped symbols in Figure 4B represent theoretically predicted values and the square-shaped symbols representing experimental results of this example.

Reagents

Chemicals were obtained as follows: trypsin (Promega), sodium dodecyl sulfate (Bio-Rad Laboratories), iodoacetamide (Sigma), formic acid (Sigma), tris-(2-carboxyethyl)phosphine (Sigma) and acetonitrile (Burdick and Jackson).

Sample Protein Depletion and Digestion

All experiments were performed on aliquots of a single human plasma sample from a normal volunteer. For the depleted sample preparation, the six typically highest abundant proteins were depleted from the plasma using the Multiple Affinity Removal System ("MARS" spincolumn: Agilent Technologies) substantially according to the manufacturer's recommended protocol. Depleted sample was then exchanged into 50 mM ammonium biocarbonate using a VivaSpin concentrator (5000 MWCO, VivaScience). Undepleted plasma was also desalted before digestion.

Both depleted or undepleted plasma samples were denatured and reduced by incubating proteins in 0.05% SDS and 5mM tris-(2-carboxyethyl)phosphine at 60 °C for 15 minutes. The sample was then made 10mM in iodoacetamide and incubated for 15 minutes at 25 °C in the dark. Trypsin was added in one aliquot (protease:protein ratio of 1:20) and incubated for 5 hours at 37 °C.

Prediction of Proteolytic Fragments of the Proteins

In the present Example, three basic approaches were taken to prediction of the protein proteolytic fragments and MRM transitions: (1) *in silico* digestion from sequence databases and prediction of CID peptide fragment ions, (2) prediction from available LC-MS/MS proteomics survey data, and (3) the present teachings, a comprehensive MRM testing of all of a protein's candidate peptides using the MIDAS™ workflow. To further assess the methods of the present teachings, random MRM transitions were also generated.

In Silico

The *in silico* methods assembled a set of 177 proteins and protein forms that are demonstrated or potential plasma markers of some aspect of cardiovascular disease (see, e.g., Anderson, N. L. (2005) Candidate-based proteomics in the search for biomarkers of cardiovascular disease. *J Physiology* **563.1,** 23-60, the entire contents of which is incorporated herein by reference) and a subset of 62 proteins selected for which an estimate of normal plasma abundance was available. Predicted tryptic peptides for each of these were generated, along with relevant Swissprot annotations and a series of computed physico-chemical parameters: e.g., amino acid composition, peptide mass, Hoop-Woods hydrophilicity (see, e.g., Hopp, T. P. and Woods, K. R. (1981) Prediction of protein antigenic determinants from amino acid sequences. *Proc Natl Acad Sci U S A* **78,** 3824-8, the entire contents of which is incorporated herein by reference) and predicted retention time in reversed-phase (C18) chromatography (see, e.g., Krokhin, O. V., Craig, R., Spicer, V., Ens, W., Standing, K. G., Beavis, R. C. and Wilkins, J. A. (2004) An improved model for prediction of retention times of tryptic peptides in ion pair reversed-phase hplc: Its application to protein peptide mapping by off-line hplc-maldi ms. *Mol Cell Proteomics* **3,** 908-19, the entire contents of which is incorporated herein by reference). An index of the likelihood of experimental detection was derived from a data set reported by Adkins (Adkins, J. N., Varnum, S. M., Auberry, K. J., Moore, R. J., Angell, N. H., Smith, R. D., Springer, D. L. and Pounds, J. G. (2002) Toward a human blood serum proteome: Analysis by multidimensional separation coupled with mass spectrometry. *Mol Cell Proteomics* **1,** 947-55.) the entire contents of which is incorporated herein by reference, by counting the number of separate "hits" for the peptide in the data set divided by the number of hits for the most frequently detected peptide from the same protein. An overall index of peptide quality was generated according to a formula that gave positive weights to P, KP, RP and DP content, and negative weights to C, W, M, chymotrypsin sites, certain SwissProt features (carbohydrate attachment, modified residues, sequence conflicts, or genetic variants), and mass less than 800 or greater than 2000. The 3619 tryptic peptides predicted for the 62 protein marker candidates (6 to 497 peptides per target) ranged in length from 1 to 285 amino acids. Within the range of 8-24 aminoacids, 721 peptides had a c-terminal Lys and 690 a c-terminal Arg. In this Example, peptides from 30 of these target proteins ending in C-terminal Lyswere were selected for further study. Finally, based on simple CID fragmentation rules, the fragment ions were

predicted and used to create the MRM transitions (e.g., the first and second y ion above the parent m/z value).

LC-MS/MS proteomics survey data

Peptides were also selected based on a direct proteomics survey experiment. In this case a classical LC-MS/MS analysis of plasma digests in which the major ions observed by full scan MS were subjected to MS/MS using the ion trap capabilities of the 4000 Q TRAP instrument was carried out. The identified peptides showing the relatively best signal intensity and chromatographic peak shape for a given parent protein were selected. In addition, the GPM database of Beavis (see, e.g., Craig, R., Cortens, J. P. and Beavis, R. C. (2004) Open source system for analyzing, validating, and storing protein identification data. *J Proteome Res* **3,** 1234-42, the entire contents of which is incorporated herein by reference) was used to select peptides from target proteins that were frequently detected (multiple experiments). From the full scan MS/MS data, the most intense y-ion observed was used as the fragment ion for the MRM transition.

MRM testing

An adaptation of the MIDAS™ brand workflow was also used (see, e.g., Unwin, R. D., Griffiths, J. R., Leverentz, M. K., Grallert, A., Hagan, I. M. and Whetton, A. D. (2005) Multiple reaction monitoring to identify sites of protein phosphorylation with high sensitivity. *Mol Cell Proteomics* **4,** 1134-1144, the entire content of which is incorporated herein by reference) to look for measurable tryptic peptides from a variety of plasma proteins. In this approach, the protein sequence is digested *in silico*, likely y-ion fragments are predicted, and theoretical MRM's generated for all the peptides in an acceptable size window. These MRM's are then used as a survey scan in a data dependent experiment to detect specific peptide peaks, and each resulting MRM peak is examined by full scan MS/MS to obtain sequence verification of the hypothesized peptide. From the full scan MS/MS data obtained, the most intense y-ion observed was used as the fragment ion for the MRM transition, this provides a further refinement over that predicted here *in silico*.

Random MRMs

Two approaches were used to generate pseudo-random MRM's for the present Example. In the first case, 100 MS1 values distributed randomly (by the Excel RAND function) between 408.5 and 1290.2 (the max and min of an early set of real MRM's were tested) were used and paired with MS2 values chosen randomly between this MS1 and the max of the real MRM's (1495.6), thus mimicking the properties of the real MRM's (which are generally +2 charge state peptides and +1 charge fragments). In a second set 131 MS1 values chosen randomly from among MS1 values in a large table of real MRM's were paired with MS2 values chosen randomly from the real MS2 values of the same list, imposing only the constraint that each MS2 had to be between 1 and 2 times the paired MS1 mass (to approximate our selection criteria for real MRM's).

Labeled Peptide Internal Standards: polySIS

A series of stable isotope labeled internal standard (SIS) peptides was added to samples in selected experiments by spiking with the tryptic digest of a polyprotein ("polySIS") to assess the performance of various embodiments of the methods of the present teachings and to provide a proof-of-concept for the assessment of the commercial potential of the methods. However, stable isotope peptides could come from any of a number of sources including, but not limited to, chemical synthesis of a peptide using an isotope labeled amino acid, and/ or chemical labeling of synthetic peptides with labeling reagents (e.g., ICAT™, iTRAQ™). It is to be understood, however, that the use of a standard peptide in this example was for the purpose of assessing the methods of the present teachings and that a standard peptide is not required for use of the methods of the present teachings.

Briefly, this polySIS protein was produced by cell-free transcription and translation of a synthetic gene coding for 30 concatenated tryptic peptide sequences (derived from 30 plasma proteins) in the presence of U-$^{13}C_6$ U-$^{15}N_2$ labeled lysine (a total mass increment of 8 amu compared to the natural peptide). Of these peptides, 13 were used in the present studies (the remainder were not reproducibly detected with peak area > 1e4). The positioning of the label atoms at the extreme c-terminus of each peptide has the effect that all fragments that contain the c-terminus (i.e., the y-ions) show the

mass shift due to the label, whereas all the fragments that contain the n-terminus (and hence have lost one of more c-term residues: the b-series ions) have the same masses as the corresponding fragments from the natural (sample-derived) target protein. These features (shifted y-ions, normal b-ions) provide a simplification in interpreting the fragmentation patterns of the SIS peptides. To determine the absolute concentration of polySIS protein, an aliquot was diluted with 1M Urea, 0.05% SDS and 50 mM Tris, pH8 and subjected to N-terminal Edman sequencing, yielding an initial concentration of 5±1 picomole/μL. A tryptic digest of the polySIS protein was spiked into whole and depleted human plasma digests at the final concentrations as shown in Table 1.

Data Acquisition and Processing

Plasma digests with and without added polySIS standards were analyzed by electrospray LC-MS/MS using LC Packings (a division of Dionex, Sunnyvale CA) or Eksigent nanoflow LC systems (Table 1) with 75 micron diameter C18 PepMap reversed phase columns (LC Packings), and eluted with gradients of 3-30% acetonitrile with 0.1% formic acid. A column oven (Keystone Scientific, Inc.) was used to maintain the column temperature at 35 °C. Electrospray MS data were collected using the NanoSpray® source on a 4000 Q TRAP hybrid triple-quadrupole/linear ion trap instrument (Applied Biosystems/MDS Sciex) and the peaks integrated using quantitation procedures in the Analyst software 1.4.1 (IntelliQuan algorithm). MRM transitions were acquired at unit resolution in both the Q1 and Q3 quadrupoles to maximize specificity.

MRM Transitions

In this Example, in an initial approach to the selection of representative peptides for MRM assays, a single peptide of 8 to 18 amino acids was chosen from each of 30 proteins spanning a broad range of plasma concentrations ($6.6x10^8$ down to 1 fmol/ml normal concentration) based on computed characteristics alone (see, e.g., Anderson, N. L., Anderson, N. G., Haines, L. R., Hardie, D. B., Olafson, R. W. and Pearson, T. W. (2004) Mass spectrometric quantitation of peptides and proteins using stable isotope standards and capture by anti-peptide antibodies (siscapa). *J Proteome Res* **3,** 235-44, the entire contents of which is incorporated herein by reference). MRM's were designed assuming doubly charged peptide ions, and using fragments selected as likely y-ions above the m/z of the 2+ parent ion, with collision energies assigned by a generic formula

(CE = 0.05*m/z +5) and the peptides expressed as a concatamer polySIS protein containing single copies of each peptide labeled with U-$^{13}C_6$ U-$^{15}N_2$ lysine. When a tryptic digest of the polySIS was analyzed, all 30 peptides were detected by MRM's. When a digest of whole human plasma was added to the polySIS peptides, 19 of the labeled polySIS peptides were detected by the same MRM's, but only 11 of the plasma digest-derived unlabeled cognate peptides were detected (by the same MRM's adjusted for isotope label masses).

Since different peptides from a single protein can vary widely in detectability by ESI-MS, an alternative approach to MRM design was also pursued based primarily on experimental data from a conventional peptide survey scan approach and applying the selection criteria to peptides with demonstrated detectability. Using a 3 hour LC gradient, MS/MS scans were collected for the major doubly or triply charged ions across the separation using information-dependent data acquisition (IDA), and a second run performed using time-filtered exclusions of the peptide ions detected in the first run. The combined results identified 54 plasma proteins, ranging in abundance from albumin down to fibronectin (normal plasma concentration of about 1μg/ml). This experimental MS/MS data provided explicit information for peptide selection, charge state and most abundant y-ion m/z value under the specific conditions used (i.e., electrospray ionization with collisional peptide fragmentation), allowing improved design of MRMs. When these MRMs were then used to analyze the same sample in a subsequent run, triggering MS/MS scans at any MRM signal, most of the peptides were detected as peaks in the chromatogram and identified by database search. In most of these MRM chromatograms, only a single peak was detected.

Because peptide detection sensitivity using MRM is expected to be greater than that achieved in a full scan MS survey approach, a comprehensive *de novo* MRM design method was explored for those proteins not detected in the above survey experiment. Using an adaptation of a novel software tool, the MIDAS™ brand workflow (see above), a large set of MRM's was generated for each of a series of target proteins by selecting all predicted tryptic peptides in a useful size range, together with multiple high-mass y-ion fragments of each. These MRMs were then tested in LC-MS/MS runs of the unfractionated plasma digest, grouped in panels that included all the predicted tryptic peptides of one or two proteins at a time (50 to 100 MRMs per run), with MS/MS scans triggered on any peaks observed. Of 12 proteins examined, 9 produced at least one MRM

with a signal-to-noise ratio (S/N) of greater than about 20. The obtained full scan MS/MS data was used to refine the MRM transition for improved detection in the final assay.

MRM results from the above approaches were pooled, and a set of optimized MRMs assembled that covered a total of 60 peptides representing 53 proteins in human plasma (see Table 2: seven proteins were represented by two peptides). This set includes 18 peptides selected by the *in silico* approach (8 of the initial 30 *in silico* peptides were eliminated as likely to be of too low abundance for detection, and better alternative peptides were selected from experimental data for 4 others). For all but one of the peptides, two fragments of the peptide (i.e., using two MRM's per peptide) were measured, yielding 119 MRM's. Finally MRM's for 18 stable isotope labeled internal standard ("SIS") versions of target peptides (i.e., the tryptic digest of the polySIS protein) spiked into the digest plasma samples were included. The resulting set of 137 MRM's was measured in all the replicate runs described in this Example, using a 18 msec dwell time per MRM, and a resulting cycle time of about 3 sec between measurements.

After the final MRM method was constructed, each MRM transition and respective retention time was validated again as indicative of each specific peptide. Full scan MS/MS was acquired upon the appearance of the MRM signal, and each resultant spectrum was manually inspected to determine matching to the specific peptide.

Discussion

An important component to the early and late stage validation of biomarkers in any body fluid is the ability to prepare and analyze many samples in parallel in a highly reproducible manner. In the present example, mass spectrometric MRM assays were designed from tryptic peptides representing 53 proteins in human plasma (see, Table 2, for a list of the proteins). In this Example, proteins down to about 1 μg/mL concentration in plasma, with minimal sample preparation, were reliably detected in both digested and depleted/digested human plasma, producing a dynamic range of about 5 orders of magnitude in this single method, as illustrated, for example, in Figure 4B. Thus, in various embodiments, the present teachings can provide a robust platform for biomarker validation.

Six experimental sets (A-F) were performed. In each experiment, the same set of 137 MRM's was measured during sequential replicate LC-MS/MS runs of a single

sample (same injection volume), and the appropriate peaks integrated using Analyst™ brand software to yield a value (peak area) for each MRM in each run. The reproducibility of the LC MRM method was assessed by measuring 10 LC-MRM replicates on the same sample. Experiments A-E (10 replicate runs each) are summarized in Table 1. These experiments included tryptic digests of both whole (unfractionated) human plasma (B,C) and plasma depleted of abundant proteins (A,D,E); high (B,E) and low (A,C,D) total peptide loadings; and different chromatographic setups. One objective of the experiments of this Example was to assess the performance of the MRM's in various typical plasma digest experiments. The reference peptide load (experiment A) was derived from tryptic digestion of the protein contained in 10 nL of plasma after subtraction of the most abundant proteins (about80% of protein mass). This loading, comprising an estimated 60-70 ng of total peptides, proved to be a loading compatible with nanoflow chromatography of the MRM peptides. Experiments B and E used higher loadings to explore the tradeoff between peak stability (chromatographic quality, adversely affected by increased load) and signal-to-noise (S/N) ratio (improved by increased analyte quantity). In this Example, the loading of 60-70 ng, of the conditions investigated, was shown to be optimal. Chromatographic elution times were reproducible, showing, average CV's of 2% (experiment D) and 2.5% (experiment E).

Reproducibility Discussion

The reproducibility of both the depletion and digestion step of the plasma preparation was explored by both performing the sample preparation on aliquots of the same plasma samples on different days and by taking one sample, splitting it in two and performing parallel depletions, followed by a further split of each to perform parallel digestions on the same day. All samples were then assayed and correlated. The results suggest that these types of sample preparation techniques can be performed in a highly reproducible manner.

Reproducibility of Sample Preparation Across Disparate Preparations

Referring to Figures 10A and 10B, Figure 10A shows a histogram of CV's of MRM values (peak areas) for five experiments (A-E) across all 137 MRM's, such data was used to assess replicate reproducibility. The CV's were determined by performing 10 replicate injections on each sample, measuring the peak areas of each MRM transition,

then calculating the average, standard deviation and coefficient of variation on each MRM across the 10 replicates. Figure 10A shows histograms of the coefficients of variation (CV: standard deviation divided by mean peak area) for the 5 experiments (individual values for each MRM are presented in Table 2 which provides mean values and CV's for 10 replicate analysis across the 5 experiments). In the analyses of the depleted plasma, more than 60% of the MRM 's shown within-run CV's of less than 10%, and almost half have CV's below 5%. A number of these MRM's (e.g., alpha-1-antichymotrypsin, apolipoprotein E, hemopexin, heparin cofactor II, plasminogen, prothrombin, fibrinogen gamma chain, complement C4 and factor B) showed an average within-run CV of 3-4% across three experiments, precision equivalent to that of typical good clinical immunoassays. Analyses of whole (undepleted) plasma digests showed generally higher CV's (20-50% of MRM's with CV < 10%). These reproducibility measures were computed on raw peak areas, without correction using internal standards. Four of the measured proteins were expected to be removed by the protein immunodepletion process used. In comparing average peak areas obtained in analyses of digests of whole and depleted samples, substantial reductions in albumin (1.3e8 reduced to about1e4), transferrin (1.5e5 reduced to about5e3) and haptoglobin (4.6e6 reduced to about1e5) were found. In this Example, alpha-1-antitrypsin was not detected with sufficient reliability to confirm its removal at this time in the analysis of the data.

Multiple measurements of an MRM would be expected to improve CV's, and thus the experiments also examined whether the sum of the two fragments measured separately for 59 of the peptides exhibited a smaller CV across 10 replicate runs than the individual MRM's. As shown in Table 3, the average CV for the summed MRM's across 59 peptides is 1-3% lower than the averages of either individual MRM. If the summed CV is compared to the lower of the two fragment CV's for each MRM, the average reduction in CV in experiments A-E ranges from +0.7% to -0.1%. These small improvements in CV come at the cost of doubling the measurement time (or halving the number of peptides monitored).

The relationship between CV and peak area for experiments D and E, indicates at least for the data and conditions of this Example, that peak areas below 1e4 are unlikely to yield CV's below 10% (Figure 8). A cutoff of 1e4 corresponds to a signal-to-noise ratio of about 10, which is consistent with the quantitative goal of a S/N of 10 for a reported lower limit of quantitation. The highest peak areas measured (albumin peptides

in whole plasma digest samples) are above 1e8, demonstrating a maximal working dynamic range of greater than about 4 orders of magnitude above this cutoff.

Immunosubtraction Improves Reproducibility

In general in this Example, immunosubtraction of the most abundant proteins using the Agilent MARS column improved the performance of MRM's for non-subtracted proteins. This effect, it is believed, is not simply due to improved detection sensitivity, since there were few if any peptides in the current set that were detected in depleted but not whole plasma digests. Rather the effect of depletion it is believed appears to be manifested in improved chromatographic peak shape achieved by decreasing the total peptide loaded by about 4-5-fold and in MRM peak signal-to-noise, both of which contribute to improved CV's. Figures 9A and 9B illustrate the benefit of depletion in removing the albumin peptide (major peak in Figure 9A) and thus boosting the minor peaks in the depleted sample (Figure 9B). At very high loading of undepleted plasma digest, large shifts in peak retention times were noticed, but at loadings in the region of the nominal load the effect of high abundance peptides on MRM retention times was minor.

Assessment of Reproducibility of Immunodepletion and Digest

In a sixth experiment set (F series), MARS depletion on two aliquots of the same plasma sample was performed and then two aliquots of each depleted sample were separately digested (total of four samples,; e.g., F1_2 refers to the second digest of the first depletion). Four replicate runs of the 137 MRM's were carried out for each sample in randomized order to avoid any sequence effect. Figures 5B and 5C compare the mean peak areas of two digests of a single depleted sample (Figure 5C, F1_1 vs F1_2), two parallel depletion/digestions (Figure 5B, F1_1 vs F2_1). Duplicate digests show excellent comparability (R^2 = 0.995 and 0.998 for F1_1 vs F1_2 and F2_1 vs F2_2 respectively). Duplicate depletions (which necessarily include the effects of different digests as well) are only slightly worse (e.g., R^2 = 0.989 and 0.991 for F2_1 vs F1_1 or F2_2 vs F1_2 respectively). (!!We need to rename 5B and C to 5A and B)

Assessment of Sensitivity

Two proteins with relatively low normal concentrations in plasma were unequivocally detected among the MRM's tested: L-selectin and fibronectin. The soluble

form of L-selectin is a 33 kDa protein present in plasma at a normal concentration of about 0.67 μg/ml (26), or 20.3 pmol/ml. Fibronectin is a 260 kDa protein present in plasma at a normal concentration of about 1.4μg/ml (27, (28), or 5.4 pmol/ml. Given that an amount of digest corresponding to 0.01 μl plasma was loaded on column in experiment D, these peptides would be expected to be present on column at about 200 and about 50 amol, respectively. In the case of L-selectin a spiked SIS standard at 2.0 fmol was used to determine that the natural (sample-derived) peptide was present at 0.1 times the amount of SIS (single point quantitation), yielding a measured 200 amol and implied plasma concentration of 0.6-0.67 μg/ml, in good agreement with expectation. CV's for fibronectin in runs D and E were 4% and 4% respectively, and for L-selectin 22% and 11% respectively, indicating that L-selectin was near the lower limit (~1e4) for high-quality detection in these experiments.

At the present time and stage of the analysis of the data, six of the 53 selected target proteins were not reliably observed. A reproducible signal for the selected peptides from coagulation factor V, vitamin K-dependent protein C, or C4b-binding protein were not obtained. There were also instances in which peptides from more abundant proteins were not reliably detected at the present time and stage of the analysis of the data. The inter-alpha trypsin inhibitor light chain (despite the fact that a peptide from the heavy chain of this protein gave a good quality MRM), apolipoprotein C-II, and alpha-1-antitrypsin was not reliably detected at this time. It is believed that an alternative choice of peptides for these more abundant proteins can lead to more reliable detection: numerous alternative peptides exist for both the inter-alpha trypsin inhibitor light chain and alpha-1-antitrypsin, but for small proteins, such as apolipoprotein C-II, there may be no better alternative and additional enrichment of these peptides in the sample loaded on the column would be indicated.

Behavior of Random MRMs and Density of MRM Signals

Most of the non-randomly designed MRM's appeared to detect only a single peak during the LC run of a complex digest such as depleted plasma: while 73% had a peak area greater than about 32,000 (approximating a signal-to-noise value of 10 in this data) corresponding to the target peptide analyte, only about 8% had a second peak meeting the same peak area criterion. Experiments, therefore, were attempted to confirm that the density of peptide peaks in "MRM-space" was indeed low (equivalent to high MS/MS

detector specificity relative to sample complexity) by examining two types of randomized MRM's in the same depleted plasma digest sample. In a first set, 100 MRM's were generated with "parent" masses randomly distributed over the mass range of real peptides used in the 137 designed MRM's, and "fragment" masses randomly distributed between the "parent" mass and the maximum fragment mass among the designed MRM's ("random MRM's"). Of the 100 random MRM's, only 6 showed a peak with area greater than 32,000, and none of these peaks produced MS/MS spectra that led to a protein identification when searched with Mascot against SwissProt. A second set of 131 random MRM's was generated by randomly pairing parent ion and CID fragment ion masses from the set of designed MRM's detectable in plasma, excluding those cases where the fragment mass was lower than the parent ("random combination MRM's"). By using real peptide and fragment masses, these MRM's avoided potential bias arising from the tendency of real peptide masses to cluster around integral masses (the mass defect). In this second set, about 12% of the MRM's exhibited a peak with peak area greater than about 32,000, and none of these peaks gave MS/MS spectra yielding a protein identification. All the peaks observed in the random MRM sets occurred late in the LC gradient (after 100min), after the elution of a large majority of the designed plasma protein MRM's. These results suggest that the density of quantifiable features in MRM-space at the current sensitivity of these experiments, even for a very complex peptide sample and using unit resolution in both mass analyzers, is only 6-12%, of which a minority may be canonical tryptic peptides. The distribution of peak areas observed for random MRM's closely matches the distribution for second (non-target peptide) peaks in the non-randomly designed MRM's, indicating that these additional peaks represent a random background.

Despite the complexity of plasma digests (particularly those of depleted plasma, where a small number of superabundant peptides have been removed), most MRM's exhibited only a single peak across the peptide LC chromatogram. This observation is consistent with the low density of peaks in two sets of randomly distributed MRM's measured in depleted plasma digests, and demonstrates the specificity of the two-stage QqQ-MS selection process used as the detector. The existence of secondary peaks (whether or not they are actually tryptic peptides) in a subset (about 10%) of MRM's indicates that chromatographic elution time may be a factor in providing the absolute analyte specificity desired in these assays.

Refinement of Predicted MRM Transitions

Approximately half of the peptides chosen by purely *in silico* means and used to create the PolySIS peptides (13 of 30) were detected in plasma and produced MS signals greater than about 1e4. Although the prediction of ionization properties of tryptic peptides can be expected to improve substantially in the future, in the present Example experimental MS/MS data was used to refine the predictions to select more better parent-daughter ion transitions. Two experimental methods proved particularly useful in the present Example. High abundance peptides were detected in conventional LC/MS/MS data dependent full-scan MS experiments, in which a subset of high-signal peptides seen in MS1 are subjected to MS/MS. Lower abundance peptides were detected by using the present teachings, by constructing lists of candidate MRM's to all appropriately-sized predicted tryptic peptides from a target protein, and then characterizing any detected MRM peaks by MS/MS (the MIDAS workflow, in which MRM methods are designed using a specifically-designed script within the Analyst™ brand software). Since MRM's are typically more sensitive than full scan survey MS for detection of very low abundance components , the MIDAS approach allowed us to improve MRM's (parent-daughter ion transitions) for more lower abundance peptides and, in various embodiments of the present teachings, this approach is used in the methods of developing a mass spectrometric based assay for a protein in a sample. This process was facilitated by the combination of high-sensitivity triple quadrupole MRM and ion trap MS/MS scan capabilities on the hybrid triple quadrupole linear ion trap 4000 Q TRAP mass spectrometer.

An example of this refinement approach is schematically illustrated in Figure 7 for the protein coagulation factor XIIa light chain. Using the protein sequence from the SwissProt database for this protein, a list of 48 theoretical MRMs to 24 proteolytic peptides was generated and used as a survey scan. As an example, one of these MRMs is shown **702** and subsequent enhanced resolution scan **704** were conducted using *in silico* predicted parent-daughter ion transitions. Signal due to the predicted peptide was observed **706**. A full product ion scan **708** revealed that the predicted daughter ion **710** had substantially less signal intensity than another fragment **712**. The information from this scan **708** was used to refine the predicted MRM (parent-daughter ion) transition, and a new MRM was obtained **714** with higher signal-to-noise than the original MRM **702.**

This refinement process was done for two proteolytic peptides from this protein, but just one peptide was chosen for the final assay, based on its superior signal intensity and S/N.

Selection of a Parent-Daughter Ion Transition (MRM) for an Assay of a Protein

The parent-daughter ion transition (MRM) were identified from the 119 tested MRM's as possessing desirable properties for an assay for the respective protein is indicated by an "X" in the column "Best MRM" in Table 2. For 59 cases the fragment (daughter) ions were selected from two tested fragment ions; and for 7 cases the peptides (proteolytic fragment) were selected from cases where two peptides were tested per protein. Each of the 47 peptide sequences (of the 47 MRM assays) was verified as unique in the human proteome (represented by the Ensemble peptides), and occurred only once in the target protein. Three of the peptides (representing antithrombin III, apolipoprotein E and vitamin K-dependent protein C) occur in the mouse as well, and seven (apolipoprotein E and vitamin K-dependent protein C, complement C4 beta and gamma, fibronectin, haptoglobin beta, and inter-alpha trypsin inhibitor heavy chain) occur in the rat (all the other human sequences did not occur in the other species' Ensemble peptides).

Of the final 47 MRM assays, 12 were contributed by the *in silico* approach leading to the 30 polySIS peptides and one (hemopexin) by an earlier *in silico* effort (see, g.e., Anderson, N. L., Anderson, N. G., Haines, L. R., Hardie, D. B., Olafson, R. W. and Pearson, T. W. (2004) Mass spectrometric quantitation of peptides and proteins using stable isotope standards and capture by anti-peptide antibodies (siscapa). *J Proteome Res* **3,** 235-44, the entire contents of which are hereby incorporated by reference). A total of 8 *in silico* selections were replaced by peptides from the same target protein as a result of experimental testing (4 before and 4 after selection of the 137 MRM's), 2 subsequently failed and have not yet been replaced, and 8 were dropped before testing because of expected insufficient abundance. Thus 13 *in silico* selections survived, while 10 were replaced in testing. The distribution of CV's for the 47 best MRM's across the five experiments (A-E) is shown in Figure10B, e.g., in experiment D, 40 of these had CV's below 10% and 19 below 5%, illustrating the potential of this method for reproducibile quantitation.

One or more MRM transitions can then be selected as the parent-daughter ion transition for an assay of the presence of the protein in the biological sample (human plasma) were selected based on (i) the peptide (parent) of the parent-daughter ion

transition was a verified as a proteolytic fragment of said protein based on a full product ion scan of the peptide, and at least one of the following properties, (ii) the selected parent-daughter ion transition had, relative to the measured ion signals associated with the other parent-daughter ion transitions for the protein, the approximately highest ion signal (as determined by peak are in this Example); (iii) the selected parent-daughter ion transition had, relative to the measured ion signals associated with the other parent-daughter ion transitions for the protein, the approximately highest signal-to-noise ratio; and/or (iv) the selected parent-daughter ion transition had, relative to the measured ion signals associated with the other parent-daughter ion transitions for the protein, the ion signal with the approximately smallest amount of error in the ion signal (e.g., MRM chromatogram peaks isolated from other peaks and/or appearing in areas of low background typically have lower errors in the ion signal value when determined by peak area relative to peaks which are in regions of high background and/or overlap with other peaks).

Mutiplexing and Throughput Discussion

The multiplexing capability of LC-QqQ-MS platforms for measuring peptides in complex digests can be substantial, providing an opportunity to measure large panels of proteins accurately in each run. Based on the performance of the present set of 137 MRM's, which were all monitored continuously across the entire LC gradient as 18 msec sequential measurements, 100-200 MRM's might be used routinely to measure peptides in long LC gradients. Given reproducible chromatographic elution times, it is possible with existing systems to measure each MRM during a time window (e.g., static, dynamic, or combinations thereof) when the peak is expected to occur (e.g., a window of 10% of total run length, given an average 2-2.5% CV in peak elution time measured in our experiments D and E). Based on knowledge of elution time and column reproducibility, and selection of MRM's do not cluster too much in elution time, 10-fold more MRM's (1,000-2,000) could potentially be employed in a single LC MRM experiment.

An additional consideration for throughput of MRM measurements is the duration of the chromatography run. In replicate experiments D and E, a 30min gradient was used, which led to a total cycle time (including inter-sample wash) of 75 min. The analyte specificity indicated by the low density of peaks in MRM-space indicates that, in various embodiments, suitable MRM's for protein assays can be developed with less benefit from

chromatographic separation. The ability to focus MRM measurements in discrete time windows can allow more MRM's to be brought closer together in elution time used without sacrificing the required multiple measurements across each peak. In various embodiments, improvements in run time can be obtained in conjunction with a shift to higher flowrate (e.g,. capillary flow) systems to facilitate providing, e.g., increased robustness in routine operation.

EXAMPLE 3: Assessment of Quantitation Using an Internal Standard Peptide

Stable isotope labeled peptides can be included, although not required, in the methods of the present teachings to provide an internal standard for absolute protein quantitation in the final assay. In the initial assay, the peptides were added at a known amount and used as a reference against which to measure the amount of the corresponding protein in plasma. A single point concentration curve was generated: more accurate quantitation can be provided a multiple point concentration curve. As an example, Figures 6A and 6B shows the comparative MRM data for the proteolytic peptide fragment AEIEYLEK from L-selectin, Figure 6A, and that for an isotopically labeled fragment AEIEYLEK* of the standard. Using the ratios of the areas of the labeled (Figure 6B) and unlabeled peaks (Figure 6A) and the known labeled L-selectin peptide concentration (2 fmol on column), the plasma concentration of L-selectin was determined to be about0.7 μg/mL, in good agreement with the literature value for this protein of 0.67 μg/mL.

All literature and similar material cited in this application, including, patents, patent applications, articles, books, treatises, dissertations and web pages, regardless of the format of such literature and similar materials, are expressly incorporated by reference in their entirety. In the event that one or more of the incorporated literature and similar materials differs from or contradicts this application, including defined terms, term usage, described techniques, or the like, this application controls.

The section headings used herein are for organizational purposes only and are not to be construed as limiting the subject matter described in any way.

While the present inventions have been described in conjunction with various embodiments and examples, it is not intended that the present teachings be limited to such

embodiments or examples. On the contrary, the present inventions encompass various alternatives, modifications, and equivalents, as will be appreciated by those of skill in the art.

While the teachings have been particularly shown and described with reference to specific illustrative embodiments, it should be understood that various changes in form and detail may be made without departing from the spirit and scope of the teachings. Therefore, all embodiments that come within the scope and spirit of the teachings, and equivalents thereto are claimed. The descriptions and diagrams of the assays of the present teachings should not be read as limited to the described order of elements unless stated to that effect.

The claims should not be read as limited to the described order or elements unless stated to that effect. It should be understood that various changes in form and detail may be made without departing from the scope of the appended claims. Therefore, all embodiments that come within the scope and spirit of the following claims and equivalents thereto are claimed.

TABLE 1
Summary of Data Sets for Experiments A-F

Experiment	eps	Sample	LC system	Equivalent Plasma Volume Loaded (µL)	Load factor – total protein	Load factor – non-depleted proteins	PolySIS spike (fmol)
A	10	Depleted plasma digest	LC Packings	0.01	1	1	1.3
B	10	Whole plasma digest	LC Packings	0.01	10	1	1.3
C	10	Whole plasma digest	Eksigent	0.001	1	0.1	2.0
D	10	Depleted plasma digest	Eksigent	0.01	1	1	2.0
E	10	Depleted plasma digest	Eksigent	0.033	3.3	3.3	6.0
F1_1	4	Depletion 1, digest 1	Eksigent	0.01	1	1	-
F1_2	4	Depletion 1, digest 2	Eksigent	0.01	1	1	-
F2_1	4	Depletion 2, digest 1	Eksigent	0.01	1	1	-
F2_2	4	Depletion 2, digest 2	Eksigent	0.01	1	1	-

Replicate runs were performed with 30 minute washes between. Load is expressed as the equivalent volume of plasma from which the sample was derived.

TABLE 2

MRM Count	Protein	Peptide Sequence	RT in D	Best MRM	SIS	MS1/MS2	Mean Peak Areas					CV (%)				
							A	B	C	D	E					
	Afamin	DADPDTFFAK	1.5	X		563.8 / 825.4	1.7E+05	2.0E+05	3.2E+04	1.6E+05	3.7E+05			0		
						563.8 / 940.4	3.8E+04	5.9E+03	3.5E+04	3.1E+04	7.0E+04		5	7	0	0
	Alpha-1-acid glycoprotein 1	NWGLSVYADKPETTK	9.7			570.3 / 1052.5	2.3E+05	5.9E+04	1.9E+05	1.6E+05	3.1E+05		2			7
				X		570.3 / 575.3	3.9E+05	9.7E+04	3.3E+05	3.0E+05	5.9E+05		3			6
					X	575.6 / 1068.5	1.4E+04	2.3E+04	6.4E+03	9.0E+03	2.5E+04	1	1	1	5	6
	Alpha-1-antichymotrypsin	EIGELYLPK	2.4			531.3 / 633.4	5.0E+05	1.2E+05	7.5E+05	4.3E+05	9.9E+05					
				X		531.3 / 819.5	7.5E+05	1.6E+05	1.1E+06	5.7E+05	1.3E+06					
					X	535.3 / 827.5	4.7E+04	1.6E+05	5.7E+04	8.3E+04	2.0E+05		2			
	Alpha-1B-glycoprotein	LETPDFQLFK	7.7			619.4 / 995.5	2.1E+05	2.7E+04	1.9E+05	1.2E+05	3.0E+05			1		4
				X		619.4 / 894.5	5.2E+05	7.3E+04	5.0E+05	3.0E+05	8.1E+05					1
	Alpha-2-antiplasmin	LGNQEPGGQTALK	2.6	X		656.8 / 771.4	3.5E+05	7.8E+04	1.5E+05	2.2E+05	5.7E+05		0	0		
						656.8 / 900.5	3.7E+04	7.1E+03	1.4E+04	1.9E+04	4.9E+04		8	9	5	0
					X	660.8 / 779.4	1.8E+05	5.1E+05	4.4E+04	3.1E+05	9.5E+05		0			
	Alpha-1-antitrypsin	DTEEEDFHVDQVTTVK	7.4			631.3 / 790.4	8.5E+03	2.9E+03	3.5E+03	3.0E+03	1.8E+04	0	3	6	4	3
						631.3 / 889.5	1.3E+04	3.5E+03	4.5E+03	6.6E+03	4.1E+04	1	3	3	9	3
	Alpha-2-macroglobulin	LLIYAVLPTGDVIGDSAK	6.5	X		923.0 / 1059.5	4.1E+05	5.3E+04	1.6E+04	4.2E+05	4.3E+05	7	0	9		
						923.0 / 1172.6	1.5E+05	1.9E+04	6.2E+03	1.4E+05	1.4E+05	6	1	0	0	
	Angiotensinogen	ALQDQLVLVAAK	3.5			634.9 / 956.6	3.3E+04	1.6E+04	2.2E+03	1.6E+04	1.8E+04	0	6			3
						634.9 / 713.5	3.8E+04	2.0E+04	3.0E+03	2.4E+04	2.3E+04		1	6	0	6
					X	638.9 / 964.6	2.7E+04	7.3E+04	1.3E+05	4.5E+04	5.4E+04		7		0	

TABLE 2 (cont.)

MRM Count	Protein	Peptide Sequence	RT in D	Best MRM	SIS	MS1/MS2	Mean Peak Areas					CV (%)				
		PKDPTFIPAPIQAK	9.1			508.3 / 724.4	2.8E+04	3.3E+04	5.0E+04	1.6E+04	2.9E+04	4	7		5	1
				X		508.3 / 556.4	3.0E+04	1.2E+05	5.7E+04	1.8E+04	3.6E+04	0	9		4	5
	Antithrombin-III	DDLYVSDAFHK	9.2			437.2 / 803.4	9.1E+04	2.1E+04	1.4E+05	2.6E+04	4.2E+04			0	3	
				X		437.2 / 704.3	3.3E+05	7.5E+04	5.1E+05	9.3E+04	1.5E+05					
					X	439.9 / 811.4	4.5E+03	1.3E+04	4.2E+03	7.7E+03	1.2E+04	1	1	5	2	7
	Apolipoprotein A-I	ATEHLSTLSEK	2.1	X		405.9 / 664.4	2.1E+06	4.8E+05	4.3E+06	6.8E+05	1.6E+06					2
						405.9 / 777.5	1.9E+06	4.0E+05	3.8E+06	5.5E+05	1.3E+06					2
			2.1		X	408.5 / 672.4	2.2E+04	5.4E+04	2.9E+04	2.6E+04	6.6E+04	1		4		
	Apolipoprotein A-II precursor	SPELQAEAK	2.1			486.8 / 546.4	5.3E+05	2.9E+05	7.7E+05	1.1E+06	2.4E+06	9	1			0
				X		486.8 / 659.4	8.3E+05	5.4E+05	1.6E+06	2.1E+06	4.9E+06	9	4			1
	Apolipoprotein A-IV	SLAPYAQDTQEK	3.8	X		675.8 / 982.4	7.4E+04	1.8E+04	1.7E+04	6.1E+04	1.6E+05		0	5		
						675.8 / 1079.5	1.8E+05	3.6E+04	4.3E+04	1.3E+05	3.4E+05		6	1		
	Apolipoprotein B-100	FPEVDVLTK	2.8			524.3 / 803.5	5.1E+04	6.8E+04	4.2E+05	1.4E+05	3.0E+05					
				X		524.3 / 674.4	4.7E+04	5.8E+04	3.8E+05	1.2E+05	2.7E+05					
					X	528.3 / 811.5	7.1E+04	2.7E+05	8.4E+04	1.3E+05	2.8E+05					
		TEVIPPLIENR	2.9			640.8 / 838.4	6.4E+05	1.5E+05	1.0E+06	3.3E+05	8.1E+05		1			
						640.8 / 741.4	1.6E+05	3.6E+04	2.7E+05	7.7E+04	2.0E+05			1		0
	Apolipoprotein C-I lipoprotein	TPDVSSALDK	4.9	X		516.8 / 620.3	1.8E+04	7.2E+03	2.9E+04	2.1E+04	5.3E+04	2	8	7	0	
						516.8 / 719.4	1.3E+04	4.8E+03	2.2E+04	1.4E+04	3.7E+04	7	3	7	2	
	Apolipoprotein C-II lipoprotein	STAAMSTYTGIFTDQVLS VLK	6.2			745.1 / 1149.7	2.0E+04	4.4E+03	6.8E+03	8.1E+03	1.7E+04	5	1	6	2	7
			5.4			745.1 / 1002.6	1.9E+03	2.5E+03	9.2E+03	5.0E+02	5.3E+03	0	5	0	01	9

TABLE 2 (cont.)

MRM Count	Protein	Peptide Sequence	RT in D	Best MRM	SIS	MS1/MS2	Mean Peak Areas					CV (%)				
	Apolipoprotein C-III	DALSSVQESQVAQQAR	7.8			858.9 / 1144.6	1.0E+05	9.5E+04	1.5E+03	1.2E+05	3.6E+05		0		1	
				X		858.9 / 1417.7	1.7E+04	1.7E+04	2.6E+04	2.2E+04	6.4E+04	6	2	4	1	
	Apolipoprotein E	LGPLVEQGR	5.5			484.8 / 701.4	5.6E+04	2.5E+04	8.7E+03	5.7E+04	1.5E+05	0	7	6		
				X		484.8 / 588.3	1.6E+05	5.5E+04	2.0E+04	1.3E+05	3.5E+05		7			
	Beta-2-glycoprotein I	ATVVYQGER	2.4			511.8 / 652.3	7.4E+05	1.6E+05	1.6E+05	7.0E+05	1.8E+06		8			
				X		511.8 / 751.4	6.7E+05	1.5E+05	1.7E+05	7.0E+05	1.7E+06		5			
		EHSSLAFWK	9.3			552.8 / 838.5	3.0E+04	3.2E+03	2.4E+03	1.9E+04	6.0E+04	0	6	7	6	9
						552.8 / 664.4	6.1E+03	1.2E+03	3.1E+03	4.1E+03	1.8E+04	7	6	6	9	7
					X	556.8 / 846.5	4.6E+03	8.0E+03	5.1E+03	4.1E+03	2.2E+04	6	8	1	3	4
	C4b-binding protein alpha chain	LSLEIEQLELQR	7.0			735.9 / 915.5	1.2E+04	2.2E+03	2.3E+03	7.4E+03	5.1E+04	2	7	0	2	2
						735.9 / 1028.6	9.7E+03	2.0E+03	1.1E+03	6.5E+03	4.4E+04	6	1	5	6	1
	Ceruloplasmin	EYTDASFTNR	4.9			602.3 / 624.3	3.5E+05	7.8E+04	6.4E+04	4.1E+05	1.1E+06		9			
				X		602.3 / 695.3	3.0E+05	6.7E+04	5.4E+04	3.5E+05	9.2E+05		8			
	Clusterin	LFDSDPITVTVPVEVSR	8.5			937.5 / 1296.7	1.5E+05	3.2E+04	4.3E+05	2.4E+05	7.5E+05	9	3	9		
				X		937.5 / 686.4	3.1E+05	6.8E+04	9.1E+05	5.2E+05	1.7E+06	9	1	3		
	Coagulation factor V	DPPSDLLLLK	6.7			555.8 / 898.6	8.1E+03	1.8E+03	1.5E+04	7.3E+03	1.5E+04	8	6	0	9	7
					X	559.8 / 906.6	2.0E+04	6.8E+04	2.9E+04	3.4E+04	7.7E+04	4	2			
	Coagulation factor XIIa light chain	VVGGLVALR	9.7			442.3 / 784.5	2.6E+04	6.3E+03	1.1E+04	3.4E+04	5.6E+04	1	0	7		
				X		442.3 / 685.4	3.2E+05	8.0E+04	1.3E+05	4.1E+05	6.9E+05					
	Complement C3	TGLQEVEVK	5.0			501.8 / 731.4	1.7E+06	3.8E+05	5.7E+03	1.6E+06	4.0E+06		5			

TABLE 2 (cont.)

MRM Count	Protein	Peptide Sequence	RT in D	Best MRM	SIS	MS1/MS2	Mean Peak Areas					CV (%)				
				X		501.8 / 603.3	1.3E+06	2.9E+05	9.0E+03	1.2E+06	3.2E+06		5			
					X	505.8 / 739.4	1.7E+04	5.6E+04	3.5E+04	3.5E+04	1.0E+05	1	3	0	4	
	Complement C4 gamma chain	ITQVLHFTK	6.2			362.9 / 645.4	1.1E+05	2.6E+04	3.1E+04	9.4E+04	8.6E+04		0			2
				X		362.9 / 744.4	1.2E+05	3.2E+04	3.7E+04	1.2E+05	1.0E+05		8	2		
					X	365.6 / 653.4	1.3E+04	4.8E+04	5.8E+03	2.1E+04	2.5E+04	5	9		0	3
	Complement C4 beta chain	VGDTLNLNLR	0.9	X		557.8 / 629.4	8.9E+05	1.9E+05	1.0E+06	7.9E+05	1.4E+06					
						557.8 / 843.5	3.0E+05	6.5E+04	3.6E+05	2.8E+05	4.9E+05					
	Complement C9	AIEDYINEFSVR	8.3	X		728.5 / 1271.6	5.2E+04	9.6E+03	2.8E+04	2.3E+04	1.5E+05		1	4	0	
						728.5 / 1027.5	3.0E+04	6.1E+03	1.7E+04	1.3E+04	8.5E+04		0	4	0	
	Complement factor B	EELLPAQDIK	9.0	X		578.4 / 671.4	1.9E+06	3.3E+05	2.2E+06	1.8E+06	4.6E+06					
						578.4 / 784.5	2.7E+05	4.5E+04	3.0E+05	2.4E+05	6.1E+05			1		
	Complement factor H	SPDVINGSPISQK	6.3	X		671.4 / 830.4	7.2E+04	1.2E+04	1.1E+04	4.0E+04	1.1E+05		2	4	0	
						671.4 / 572.3	4.4E+04	8.5E+03	8.4E+03	2.6E+04	7.4E+04		3	7		0
	Fibrinogen alpha chain	TVIGPDGHK	1.7			462.3 / 723.4	4.4E+03	2.2E+05	3.8E+05	1.0E+06	2.4E+06	2	2			
						462.3 / 610.3	1.0E+03	1.7E+05	2.9E+05	8.5E+05	2.1E+06	1				
					X	466.2 / 731.4	2.8E+03	1.0E+05	5.7E+04	1.0E+05	2.4E+05	9	6		0	
		GSESGIFTNTK	4.7	X		570.8 / 780.4	1.0E+06	2.3E+05	1.1E+05	7.9E+05	1.9E+06		7			
						570.8 / 867.5	1.1E+06	2.2E+05	1.1E+05	7.5E+05	1.8E+06		7			
	Fibrinogen beta chain	QGFGNVATNTDGK	3.5	X		654.8 / 706.3	2.1E+06	3.4E+05	4.8E+05	9.3E+04	2.5E+05		6			
						654.8 / 805.4	6.2E+05	9.8E+04	1.4E+05	2.6E+04	6.8E+04		1		2	0
					X	658.8 / 714.3	6.1E+04	1.4E+05	1.3E+04	9.4E+04	2.9E+05		6			

TABLE 2 (cont.)

MRM Count	Protein	Peptide Sequence	RT in D	Best MRM	SIS	MS1/MS2	Mean Peak Areas					CV (%)				
	Fibrinogen gamma chain	DTVQIHDITGK	5.4			409.5 / 670.4	2.7E+05	7.1E+04	1.8E+06	2.2E+04	5.4E+04				1	
				X		409.5 / 533.3	2.6E+05	7.6E+04	1.6E+06	4.5E+04	1.1E+05					
					X	412.2 / 678.4	2.3E+04	5.5E+04	2.5E+04	2.6E+04	6.6E+04	3	4		7	
	Fibronectin	DLQFVEVTDVK	4.7	X		647.3 / 789.4	7.4E+04	2.9E+04	2.4E+04	8.2E+04	2.3E+05		3			
						647.3 / 690.4	1.0E+05	3.6E+04	8.1E+04	1.1E+05	3.0E+05			0		
		VTWAPPPSIDLTNFLVR	8.2			642.7 / 977.5	1.4E+04	4.5E+03	2.1E+03	1.6E+04	2.0E+04	1	7	4	4	1
						642.7 / 862.5	9.6E+03	3.7E+03	2.5E+03	1.2E+04	1.6E+04	7	8	5	0	8
	Gelsolin, isoform 1	TGAQELLR	4.8	X		444.3 / 786.5	1.1E+05	2.7E+04	1.0E+04	1.2E+05	3.1E+05		4			
						444.3 / 729.4	1.5E+05	3.5E+04	1.5E+04	1.6E+05	4.2E+05		3	4		
	Haptoglobin beta chain	VGYVSGWGR	8.2	X		490.8 / 562.3	4.2E+05	1.6E+06	4.6E+06	7.7E+04	1.9E+05					
						490.8 / 661.3	2.0E+05	8.1E+05	2.1E+06	4.1E+04	9.4E+04		1			
	Hemopexin	NFPSPVDAAFR	3.6	X		610.8 / 959.6	4.9E+06	8.8E+05	6.0E+06	3.8E+06	7.0E+06					
						610.8 / 775.3	3.3E+06	7.1E+05	4.2E+06	3.1E+06	5.9E+06					
	Heparin cofactor II	TLEAQLTPR	6.4	X		514.8 / 814.4	3.3E+05	9.0E+04	2.0E+04	3.2E+05	8.7E+05		2			
						514.8 / 685.4	2.9E+05	7.0E+04	1.8E+04	2.5E+05	6.8E+05		5			
	Histidine-rich glycoprotein	DSPVLIDFFEDTER	7.7	X		841.9 / 1171.5	7.7E+04	2.9E+04	3.1E+04	1.1E+05	1.5E+05	4	3	2		1
						841.9 / 1058.4	7.3E+04	2.9E+04	3.2E+04	1.1E+05	1.6E+05	3	6	2	0	1
	Inter-alpha-trypsin inhibitor heavy chain	AAISGENAGLVR	4.9	X		579.4 / 902.5	6.3E+05	1.7E+05	9.3E+04	6.3E+05	1.6E+06		7			
						579.4 / 629.4	1.7E+05	4.4E+04	2.3E+04	1.8E+05	4.6E+05		4			
	Inter-alpha-trypsin inhibitor light	AFIQLWAFDAVK	8.0			704.9 / 836.4	3.0E+04	5.3E+03	2.8E+03	2.9E+03	2.6E+03	3	1	2	0	9

TABLE 2 (cont.)

MRM Count	Protein	Peptide Sequence	RT in D	Best MRM	SIS	MS1/MS2	Mean Peak Areas					CV (%)				
						704.9 / 949.5	1.5E+04	2.9E+03	7.3E+02	1.2E+03	1.1E+03	4	7	2	6	9
	Kininogen	TVGSDTFYSFK	1.5	X		626.3 / 1051.4	8.7E+05	1.5E+05	9.0E+05	6.4E+05	1.4E+06					
						626.3 / 994.5	8.7E+04	1.4E+04	8.2E+04	5.6E+04	1.1E+05		0	8		5
	L-selectin	AEIEYLEK	6.9			497.8 / 794.4	1.9E+04	6.0E+03	5.6E+03	1.7E+04	4.7E+04	6	5	9	4	
				X		497.8 / 681.3	1.2E+04	3.4E+03	2.5E+04	1.3E+04	3.3E+04	7	2	5	2	1
					X	501.8 / 802.4	8.4E+04	3.0E+05	1.6E+03	1.7E+05	5.0E+05		4			
	Plasma retinol-binding protein precursor	YWGVASFLQK	5.1	X		599.8 / 849.5	9.5E+04	1.1E+04	1.3E+04	4.8E+04	6.1E+04		7	5	7	8
						599.8 / 693.4	5.9E+04	7.1E+03	1.1E+04	2.8E+04	4.2E+04		0	3	6	6
	Plasminogen	LSSPAVITDK	5.3			515.8 / 743.4	1.8E+05	8.8E+04	4.7E+04	1.7E+05	4.3E+05		8	1		
						515.8 / 830.5	1.2E+05	5.4E+04	3.2E+04	1.1E+05	2.7E+05		3	1		
					X	519.8 / 751.4	8.6E+04	3.0E+05	1.0E+04	1.8E+05	5.1E+05		5			
		LFLEPTR	9.1			438.3 / 615.4	5.3E+05	2.2E+05	1.2E+06	5.0E+05	1.2E+06		8			
				X		438.3 / 502.3	2.7E+05	1.1E+05	6.4E+05	2.9E+05	6.1E+05					
	Prothrombin	ETAASLLQAGYK	0.2			626.3 / 879.5	2.8E+05	4.3E+04	1.8E+05	1.3E+05	3.1E+05		0	0		
				X		626.3 / 679.4	3.9E+05	6.5E+04	2.3E+05	2.0E+05	5.2E+05					
					X	630.3 / 887.5	4.4E+04	1.5E+05	4.4E+04	7.7E+04	2.1E+05	3				
	Serum albumin	LVNEVTEFAK	9.3			575.4 / 937.4	1.6E+04	2.8E+07	1.7E+08	7.7E+03	1.7E+04	4	9		8	3
				X		575.4 / 694.4	1.1E+04	2.2E+07	1.3E+08	5.8E+03	1.2E+04	4				8
	Serum amyloid P-component	VGEYSLYIGR	1.3			578.8 / 1057.5	2.1E+04	1.6E+04	2.7E+04	1.0E+05	5.5E+04			7		1
				X		578.8 / 871.5	2.2E+04	2.0E+04	2.8E+04	1.2E+05	6.2E+04	1		2		0

TABLE 2 (cont.)

MRM Count	Protein	Peptide Sequence	RT in D	Best MRM	SIS	MS1/MS2	Mean Peak Areas					CV (%)				
	Transferrin	EDPQTFYYAVAVVK	0.3	X		815.4 / 1160.6	2.5E+03	2.3E+05	1.5E+05	4.8E+03	5.2E+03	0	1		1	4
						815.4 / 1288.7	8.9E+02	3.0E+04	2.0E+04	4.4E+02	6.5E+02	6	0	0	9	8
	Transthyretin	AADDTWEPFASGK	2.3			697.8 / 921.4	1.3E+05	8.4E+03	2.1E+05	7.7E+04	2.0E+05			6		
				X		697.8 / 606.4	5.7E+05	3.7E+04	9.3E+05	3.7E+05	9.7E+05			4		
	Vitamin D-binding protein	THLPEVFLSK	9.7	X		585.8 / 819.5	1.6E+05	2.4E+04	1.5E+05	9.6E+04	2.8E+05			7	2	7
						585.8 / 932.5	5.5E+04	3.9E+03	4.9E+04	3.2E+04	8.7E+04	3	4	4	2	4
	Vitamin K-dependent protein C	WELDLDIK	0.1			516.3 / 716.4	4.4E+02	2.3E+04	4.8E+03	5.9E+03	3.7E+04	1	1	5	0	7
						516.3 / 603.3	3.8E+02	1.7E+04	7.3E+03	1.2E+04	6.9E+04	8	1	0	7	3
					X	520.3 / 724.4	3.7E+04	8.4E+03	3.9E+04	5.7E+02	4.8E+02		2	2	4	2
	Vitronectin	DVWGIEGPIDAAFTR	6.4			823.9 / 947.5	6.7E+04	8.1E+04	4.7E+04	1.4E+05	2.7E+05	6	7	6		
						823.9 / 890.5	3.5E+04	4.1E+04	2.6E+04	7.7E+04	1.4E+05	5	9	2		
		FEDGVLDPDYPR	2.2	X		711.9 / 875.4	2.6E+05	8.5E+04	4.5E+05	1.7E+05	3.8E+05					
						711.9 / 1031.5	9.1E+04	2.7E+04	1.5E+05	5.5E+04	1.2E+05			4		
	Zinc-alpha-2-glycoprotein	EIPAWVPFDPAAQITK	6.2	X		891.9 / 1087.7	7.6E+03	3.4E+04	2.0E+05	1.4E+04	2.4E+04	0	9	2	3	5
						891.9 / 728.4	3.8E+03	1.7E+04	9.8E+04	7.3E+03	1.4E+04	3	8	7	2	9
						Average values:	**3.1E+05**	**4.7E+05**	**2.5E+06**	**2.6E+05**	**6.0E+05**	3	0	3	1	1

TABLE 3
CV using 2 fragments instead of 1

Experiment	Avg CV sum of frags	Avg CV frag 1	Avg CV frag 2
A	10.5%	11.8%	14.8%
B	16.2%	20.0%	19.4%
C	11.0%	13.0%	14.4%
D	8.0%	9.4%	12.3%
E	8.5%	9.4%	11.9%

CLAIMS

What is claimed is:

1. A method for developing a mass spectrometric based assay for a protein in a sample without the use of a standard for the protein, comprising the steps of:

predicting one or more of the proteolytic fragments of a protein based on or more of an amino acid sequence for the protein and a translation of a gene sequence for the protein;

predicting one or more of the fragments produced from one or more of the proteolytic fragments of the protein when the proteolytic fragment is subjected to collision induced dissociation;

providing a sample containing proteolytic fragments of a protein;

loading at least a portion of the sample on a chromatographic column;

subjecting at least a portion of the eluent from the chromatographic column to multiple reaction monitoring, the transmitted parent ion m/z range of each multiple reaction monitoring scan including a m/z value of one or more of the predicted proteolytic fragments of the protein and the transmitted daughter ion m/z range of each multiple reaction monitoring scan including a m/z value one or more of the predicted collision induced dissociation fragments of the predicted proteolytic fragments;

measuring the ion signal of the m/z value range encompassing one or more of the predicted collision induced dissociation fragments m/z value using said multiple reaction monitoring;

performing a substantially full product ion scan on a m/z value range encompassing a predicted proteolytic fragment m/z value when the measured ion signal corresponding to one or more collision induced dissociation fragments of the predicted proteolytic fragment is above a specified signal threshold;

measuring the ion signals associated with the parent-daughter ion transitions of said substantially full product ion scan; and

selecting as the parent-daughter ion transition for an assay of the presence of the protein in a sample a parent-daughter ion transition of said substantially full product ion scan, wherein the selected parent-daughter ion transition for the assay corresponds to a transition where the transmitted parent ion is a proteolytic

fragment of said protein, and wherein the selected parent-daughter ion transition has, relative to the measured ion signals associated with the other parent-daughter ion transitions for said protein, one or more of the approximately highest ion signal and the approximately highest signal-to-noise ratio.

2. The method of claim 1, wherein the sample containing proteolytic fragments of a protein is derived from at least one of a physiological fluid, a cell lysate, a tissue lysate, and combinations thereof.

3. The method of claim 2, wherein the physiological fluid comprises one or more of blood, serum, plasma, sweat, tears, urine, cerebrospinal fluid, peritoneal fluid, lymph, vaginal secretion, semen, spinal fluid, ascetic fluid, saliva, sputum, breast exudates, and combinations thereof.

4. The method of claim 2, wherein the physiological fluid comprises blood.

5. The method of claim 4, wherein the blood sample is depleted of at least six most abundant proteins before proteolytic fragmentation of the protein.

6. The method of claim 4, wherein the blood sample is plasma or serum.

7. The method of claim 4, wherein the blood sample contains the protein in a concentration of less than about 100,000 attomoles/microliter.

8. The method of claim 4, wherein the blood sample contains the protein in a concentration of less than about 10,000 attomoles/microliter.

9. The method of claim 4, wherein the blood sample contains the protein in a concentration of less than about 1,000 attomoles/microliter.

10. The method of claim 4, wherein the blood sample contains the protein in a concentration of less than about 100 attomoles/microliter.

11. The method of claim 4, wherein the blood sample contains the protein in a concentration of less than about 10 attomoles/microliter.

12. The method of claim 4, wherein the blood sample contains the protein in a concentration of less than about 1 attomoles/microliter.

13. The method of claim 1, wherein the proteolytic fragments of the protein comprise tryptic peptides.

14. The method of claim 1, wherein the sample containing proteolytic fragments of a protein further comprises a concentration standard for one or more of the predicted proteolytic fragments of the protein, said concentration standard selected based on the parent-daughter ion transition selected as an assay of the presence of the protein in the biological sample.

15. The method of claim 1, wherein the step of subjecting at least a portion of the eluent from the chromatographic column to multiple reaction monitoring comprises using a triple quadrupole ion trap mass spectrometer.

16. The method of claim 15, wherein the ion trap comprises a linear trap.

17. The method of claim 1, wherein the step of measuring the ion signal of the m/z value range encompassing one or more of the predicted collision induced dissociation fragments m/z value using said multiple reaction monitoring comprises:

sequencing the transmitted parent ion when the measured ion signal corresponding to one or more collision induced dissociation fragments of the predicted proteolytic fragment is above the specified signal threshold; and

performing said substantially full product ion scan on a m/z value range encompassing said sequenced transmitted parent ion when the sequence of the sequenced transmitted parent ion corresponds to a proteolytic fragment of the protein.

18. The method of claim 17, further comprising the step of:

measuring the charge state of the transmitted parent ion when the measured ion signal corresponding to one or more collision induced dissociation fragments of the predicted proteolytic fragment is above a specified signal threshold.

19. The method of claim 1, further comprising the steps of:

refining the mass values of the predicted proteolytic fragments of the protein and the mass values of the predicted collision induced dissociation fragments of the refined predicted proteolytic fragments based on at least one or more of the measured full product ion scans;

subjecting at least a portion of the eluent from the chromatographic column to multiple reaction monitoring, the transmitted parent ion m/z range of each multiple reaction monitoring scan including a m/z value of one or more of the refined predicted proteolytic fragments of the protein and the transmitted daughter ion m/z range of each multiple reaction monitoring scan including a m/z value one or more of the refined predicted collision induced dissociation fragments of the predicted proteolytic fragments; and

measuring the ion signal of the m/z value range encompassing one or more of the refined predicted collision induced dissociation fragments m/z value using said multiple reaction monitoring.

20. A method for developing a mass spectrometric based assay for a low abundance protein in a blood sample without the use of a standard for the protein, comprising the steps of:

predicting one or more of the proteolytic fragments of a protein based on an amino acid sequence for the protein;

predicting one or more of the fragments produced from one or more of the proteolytic fragments of the protein when the proteolytic fragment is subjected to collision induced dissociation;

providing a sample containing proteolytic fragments of a protein, wherein said sample is derived from a blood sample containing the protein in a concentration of less than about 100,000 attomoles/microliter;

loading at least a portion of the sample on a chromatographic column;

subjecting at least a portion of the eluent from the chromatographic column to multiple reaction monitoring, the transmitted parent ion m/z range of each multiple reaction monitoring scan including a m/z value of one or more of the predicted proteolytic fragments of the protein and the transmitted daughter ion m/z range of each multiple reaction monitoring scan including a m/z value one or more of the predicted collision induced dissociation fragments of the predicted proteolytic fragments;

measuring the ion signal of the m/z value range encompassing one or more of the predicted collision induced dissociation fragments m/z value using said multiple reaction monitoring;

performing a substantially full product ion scan on a m/z value range encompassing a predicted proteolytic fragment m/z value when the measured ion signal corresponding to one or more collision induced dissociation fragments of the predicted proteolytic fragment is above a specified signal threshold;

measuring the ion signals associated with the parent-daughter ion transitions of said substantially full product ion scan; and

selecting as the parent-daughter ion transition for an assay of the presence of the protein in a biological sample a parent-daughter ion transition of said substantially full product ion scan, wherein the selected parent-daughter ion transition for the assay corresponds to a transition where the transmitted parent ion is a proteolytic fragment of said protein, and wherein the selected parent-daughter ion transition has, relative to the measured ion signals associated with the other parent-daughter ion transitions for said protein, one or more of the approximately highest ion signal and the approximately highest signal-to-noise ratio.

21. The method of claim 20, wherein the blood sample is depleted of the six most abundant proteins before proteolytic fragmentation of the protein.

22. The method of claim 21, wherein the blood sample is plasma or serum.

23. The method of claim 20, wherein the blood sample contains the protein in a concentration of less than about 10,000 attomoles/microliter.

24. The method of claim 20, wherein the blood sample contains the protein in a concentration of less than about 1,000 attomoles/microliter.

25. The method of claim 20, wherein the blood sample contains the protein in a concentration of less than about 100 attomoles/microliter.

26. The method of claim 20, wherein the blood sample contains the protein in a concentration of less than about 10 attomoles/microliter.

27. The method of claim 20, wherein the blood sample contains the protein in a concentration of less than about 1 attomoles/microliter.

28. The method of claim 20, wherein the proteolytic fragments of the protein comprise tryptic peptides.

29. The method of claim 20, wherein the sample containing proteolytic fragments of a protein further comprises a concentration standard for one or more of the predicted proteolytic fragments of the protein, said concentration standard selected based on the parent-daughter ion transition selected as an assay of the presence of the protein in the biological sample.

30. The method of claim 28, wherein the step of subjecting at least a portion of the eluent from the chromatographic column to multiple reaction monitoring comprises using a triple quadrupole ion trap mass spectrometer.

31. The method of claim 30, wherein the ion trap comprises a linear trap.

32. The method of claim 20, wherein the step of measuring the ion signal of the m/z value range encompassing one or more of the predicted collision induced

dissociation fragments m/z value using said multiple reaction monitoring comprises:

sequencing the transmitted parent ion when the measured ion signal corresponding to one or more collision induced dissociation fragments of the predicted proteolytic fragment is above the specified signal threshold; and

performing said substantially full product ion scan on a m/z value range encompassing said sequenced transmitted parent ion when the sequence of the sequenced transmitted parent ion corresponds to a proteolytic fragment of the protein.

33. The method of claim 32, further comprising the step of:

measuring the charge state of the transmitted parent ion when the measured ion signal corresponding to one or more collision induced dissociation fragments of the predicted proteolytic fragment is above a specified signal threshold.

34. The method of claim 20, further comprising the steps of:

refining the mass values of the predicted proteolytic fragments of the protein and the mass values of the predicted collision induced dissociation fragments of the refined predicted proteolytic fragments based on at least one or more of the measured full product ion scans;

subjecting at least a portion of the eluent from the chromatographic column to multiple reaction monitoring, the transmitted parent ion m/z range of each multiple reaction monitoring scan including a m/z value of one or more of the refined predicted proteolytic fragments of the protein and the transmitted daughter ion m/z range of each multiple reaction monitoring scan including a m/z value one or more of the refined predicted collision induced dissociation fragments of the predicted proteolytic fragments; and

measuring the ion signal of the m/z value range encompassing one or more of the refined predicted collision induced dissociation fragments m/z value using said multiple reaction monitoring.

35. A method for developing a mass spectrometric based assay for a protein in a sample without the use of a standard for the protein, comprising the steps of:

predicting one or more of the proteolytic fragments of a protein based on an amino acid sequence for the protein;

predicting one or more of the fragments produced from one or more of the proteolytic fragments of the protein when the proteolytic fragment is subjected to collision induced dissociation;

providing a sample containing proteolytic fragments of a protein;

loading at least a portion of the sample on a chromatographic column;

subjecting at least a portion of the eluent from the chromatographic column to multiple reaction monitoring, the transmitted parent ion m/z range of each multiple reaction monitoring scan including a m/z value of one or more of the predicted proteolytic fragments of the protein and the transmitted daughter ion m/z range of each multiple reaction monitoring scan including a m/z value one or more of the predicted collision induced dissociation fragments of the of the predicted proteolytic fragments;

measuring the ion signal of the m/z value range encompassing one or more of the predicted collision induced dissociation fragments m/z value using said multiple reaction monitoring;

measuring the charge state of the transmitted parent ion when the measured ion signal corresponding to one or more collision induced dissociation fragments of the predicted proteolytic fragment is above a specified signal threshold;

sequencing the transmitted parent ion when the measured ion signal corresponding to one or more collision induced dissociation fragments of the predicted proteolytic fragment is above the specified signal threshold;

performing a substantially full product ion scan on a m/z value range encompassing said sequenced transmitted parent ion when the sequence of the sequenced transmitted parent ion corresponds to a proteolytic fragment of the protein;

measuring the ion signals associated with the parent-daughter ion transitions of said substantially full product ion scan; and

selecting as the parent-daughter ion transition for an assay of the presence of the protein in a biological sample the parent-daughter ion transition which has, relative to the measured ion signals associated with the other parent-daughter ion transitions for said protein, one or more of the approximately highest ion signal and the approximately highest signal-to-noise ratio.

36. The method of claim 35, wherein the sample containing proteolytic fragments of a protein is derived from at least one of a physiological fluid, a cell lysate, a tissue lysate, and combinations thereof.

37. The method of claim 36, wherein the physiological fluid comprises one or more of blood, serum, plasma, sweat, tears, urine, cerebrospinal fluid, peritoneal fluid, lymph, vaginal secretion, semen, spinal fluid, ascetic fluid, saliva, sputum, breast exudates, and combinations thereof.

38. The method of claim 35, wherein the physiological fluid comprises blood.

39. The method of claim 38, wherein the blood sample is depleted of at least the six most abundant proteins before proteolytic fragmentation of the protein.

40. The method of claim 38, wherein the blood sample is plasma or serum.

41. The method of claim 38, wherein the blood sample contains the protein in a concentration of less than about 100,000 attomoles/microliter.

42. The method of claim 38, wherein the blood sample contains the protein in a concentration of less than about 10,000 attomoles/microliter.

43. The method of claim 38, wherein the blood sample contains the protein in a concentration of less than about 1,000 attomoles/microliter.

44. The method of claim 38, wherein the blood sample contains the protein in a concentration of less than about 100 attomoles/microliter.

45. The method of claim 38, wherein the blood sample contains the protein in a concentration of less than about 10 attomoles/microliter.

46. The method of claim 38, wherein the blood sample contains the protein in a concentration of less than about 1 attomoles/microliter.

47. The method of claim 35, wherein the proteolytic fragments of the protein comprise tryptic peptides.

48. The method of claim 35, wherein the sample containing proteolytic fragments of a protein further comprises a concentration standard for one or more of the predicted proteolytic fragments of the protein, said concentration standard selected based on the parent-daughter ion transition selected as an assay of the presence of the protein in the biological sample.

49. The method of claim 35, wherein the step of subjecting at least a portion of the eluent from the chromatographic column to multiple reaction monitoring comprises using a triple quadrupole ion trap mass spectrometer.

50. The method of claim 35, wherein the ion trap comprises a linear trap.

51. The method of claim 35, further comprising the steps of:

refining the mass values of the predicted proteolytic fragments of the protein and the mass values of the predicted collision induced dissociation fragments of the refined predicted proteolytic fragments based on at least one or more of the measured full product ion scans;

subjecting at least a portion of the eluent from the chromatographic column to multiple reaction monitoring, the transmitted parent ion m/z range of each multiple reaction monitoring scan including a m/z value of one or more of the refined predicted proteolytic fragments of the protein and the transmitted daughter ion m/z range of each multiple reaction monitoring scan including a m/z

value one or more of the refined predicted collision induced dissociation fragments of the predicted proteolytic fragments; and

measuring the ion signal of the m/z value range encompassing one or more of the refined predicted collision induced dissociation fragments m/z value using said multiple reaction monitoring.

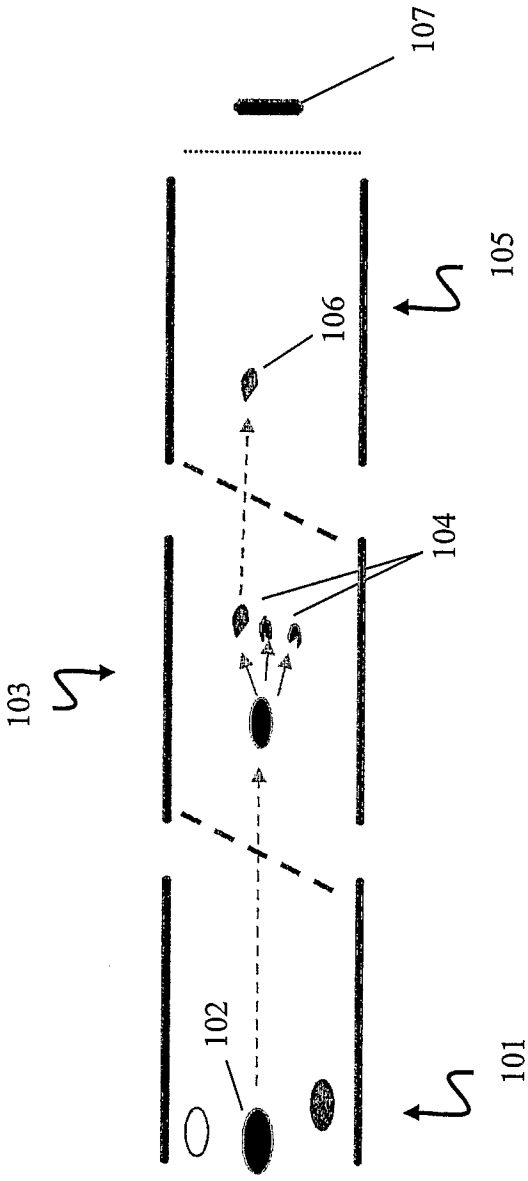


FIGURE 1

FIGURE 2

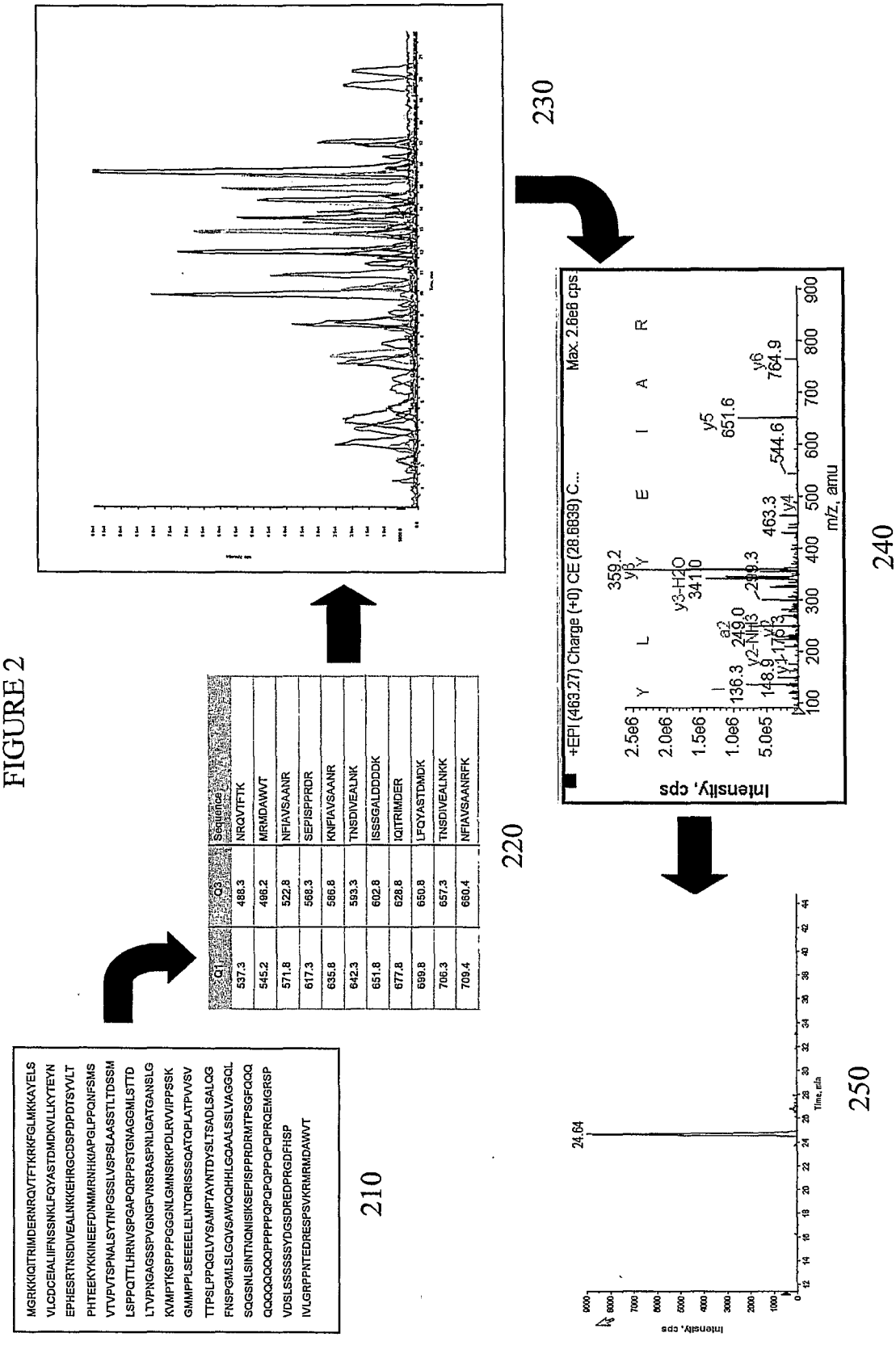
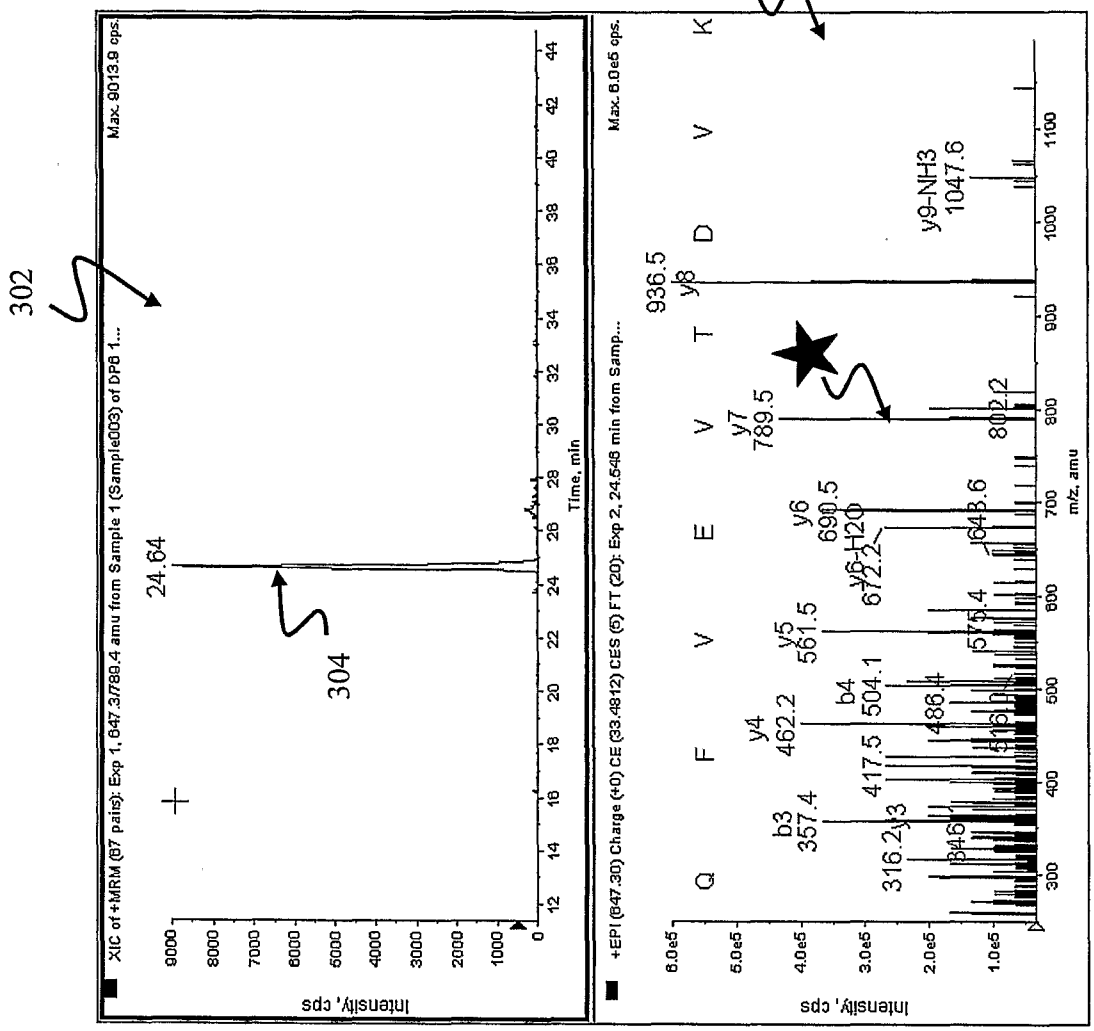

MGRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELS
VLCDCEIALIIFNSSNKLFQYASTDMDKVLLKYTEYN
EPHESRTNSDIVEALNKKEHRGCDSPDPDTSYVLT
PHTEEKYKKINEEFDNMMRNHKIAPGLPPQNFSMS
VTVPVTSPNALSYTNPGSSLVSPSLAASSTLTDSSM
LSPPQTTLHRNVSPGAPQRPPSTGNAGGMLSTTD
LTVPNGAGSSPVGNGFVNSRASPNLIGATGANSLG
KVMPTKSPPPPGGGNLGMNSRKPDLRVVIPPSSK
GMMPPLSEEEELELNTQRISSSQATQPLATPVVSV
TTPSLPPQGLVYSAMPTAYNTDYSLTSADLSALQG
FNSPGMLSLGQVSAWQQHHLGQAALSSLVAGGGL
SQGSNLSINTNQNISIKSEPISPPRDRMTPSGFQQQ
QQQQQQQQPPPPPQPQPQPPQPQPRQEMGRSP
VDSLSSSSSSSYDGSDREDPRGDFHSP
IVLGRPPATEDRESPSVKRMRMDAWVT
210
Q1 Q3 Sequence
537.3 498.3 NRQVTFTK
545.2 498.2 MRMDAWVT
571.8 522.8 NFIAVSAANR
617.3 568.3 SEPISPPRDR
635.8 586.8 KNFIAVSAANR
642.3 593.3 TNSDIVEALNK
651.8 602.8 ISSSGALDDDDK
677.8 628.8 IQITRIMDER
659.8 650.8 LFQYASTDMDK
706.3 657.3 TNSDIVEALNKK
709.4 680.4 NFIAVSAANRFK
220
230
+EPI (463.27) Charge (+0) CE (28.6839) C...
Max. 2.6e6 cps
Intensity, cps
m/z, amu
Y L E I A R
y5 651.6
y6 764.9
544.6
463.3
359.2
340.0
299.3
249.0
136.3
148.9
240
Intensity, cps
Time, min
24.64
250

FIGURE 3A

FIGURE 3B



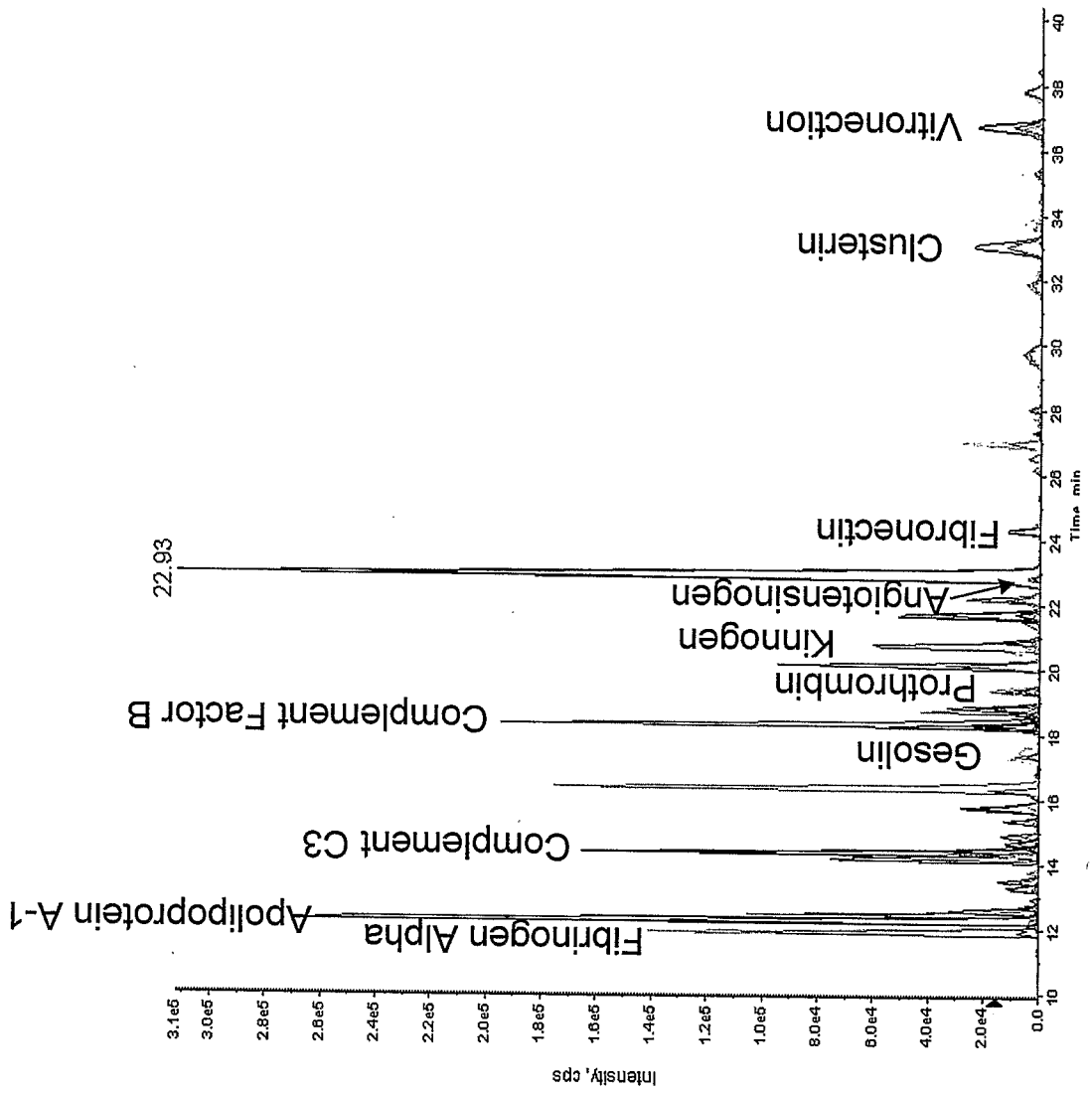

Intensity, cps
Time, min
22.93
Fibrinogen Alpha
Apolipoprotein A-1
Complement C3
Gesolin
Complement Factor B
Prothrombin
Kinnogen
Angiotensinogen
Fibronectin
Clusterin
Vitronection

FIGURE 4A

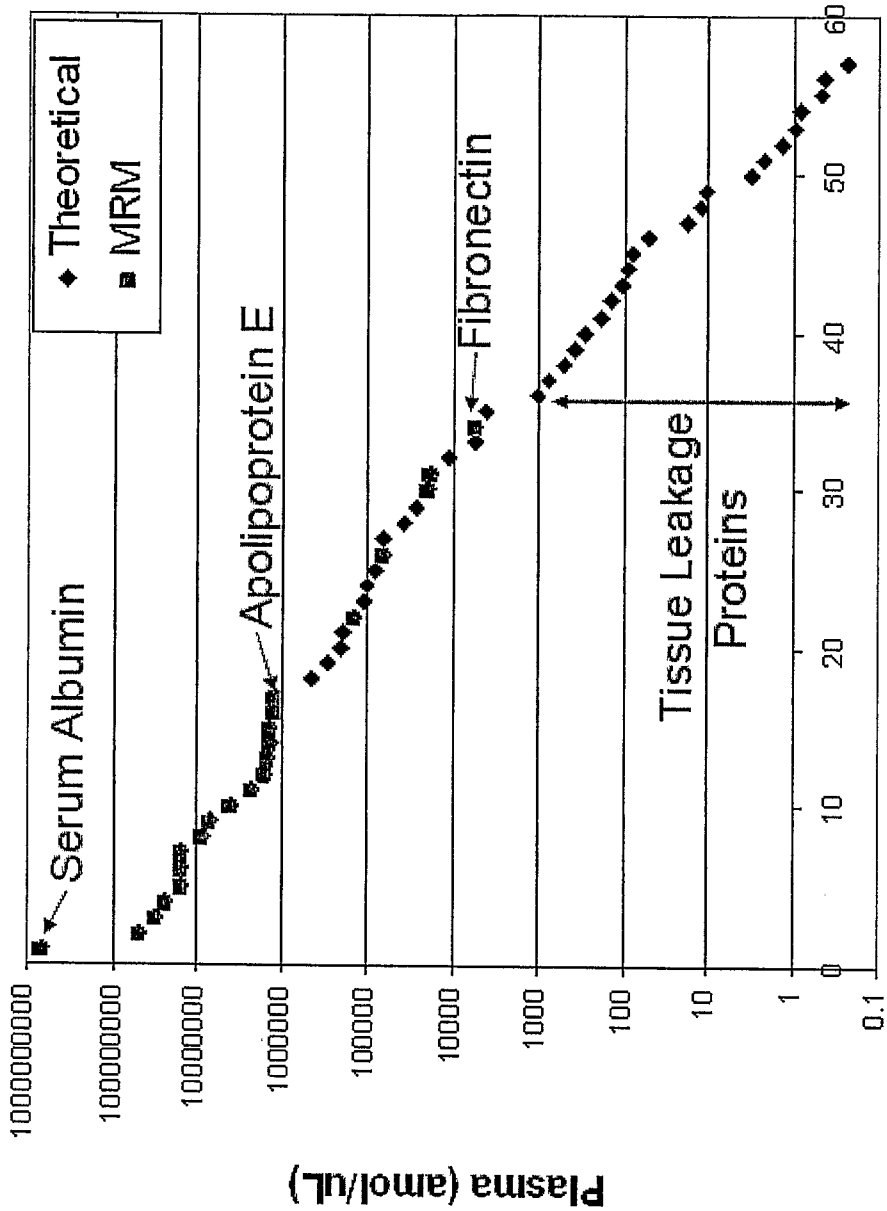

Theoretical
MRM
Serum Albumin
Apolipoprotein E
Fibronectin
Tissue Leakage
Proteins
Plasma (amol/uL)
1000000000
100000000
10000000
1000000
100000
10000
1000
100
10
1
0.1
0
10
20
30
40
50
60
Plasma Proteins

FIGURE 4B

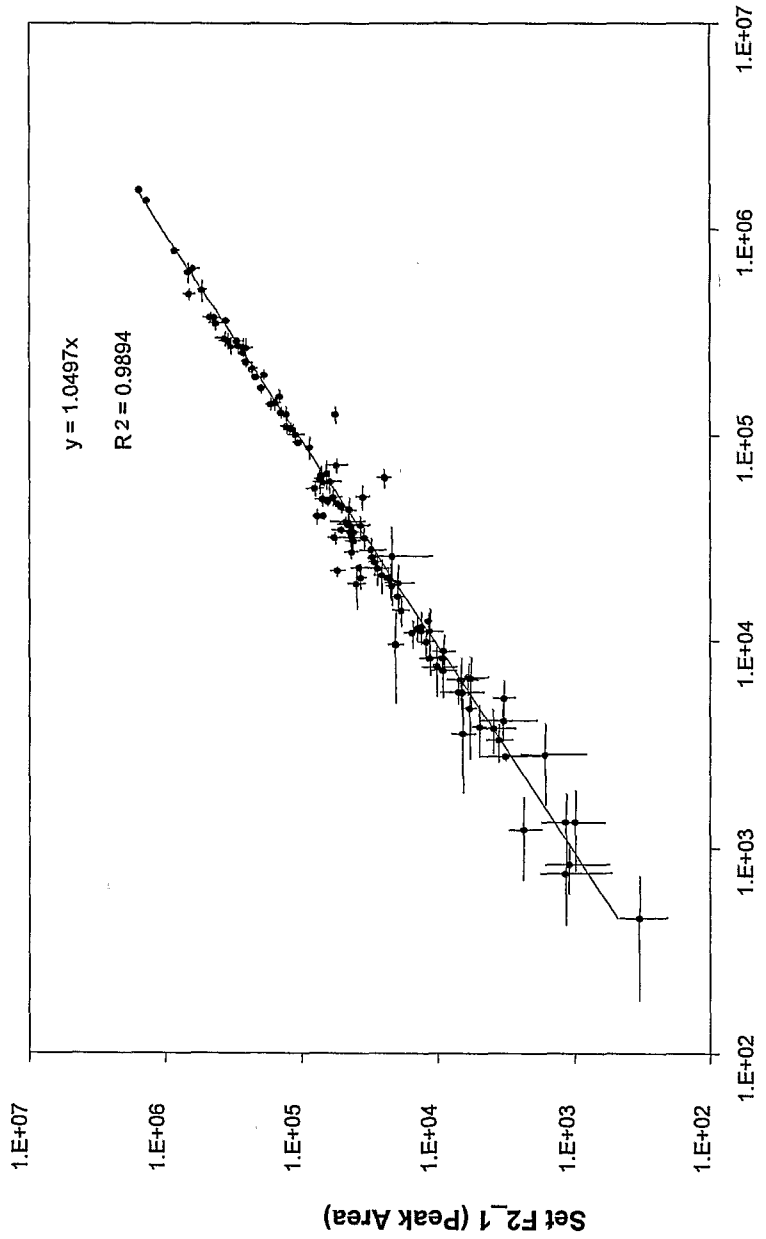

y = 1.0497x
R 2 = 0.9894
1.E+02
1.E+03
1.E+04
1.E+05
1.E+06
1.E+07
Set F1_1 (Peak Area)
Set F2_1 (Peak Area)

FIGURE 5A

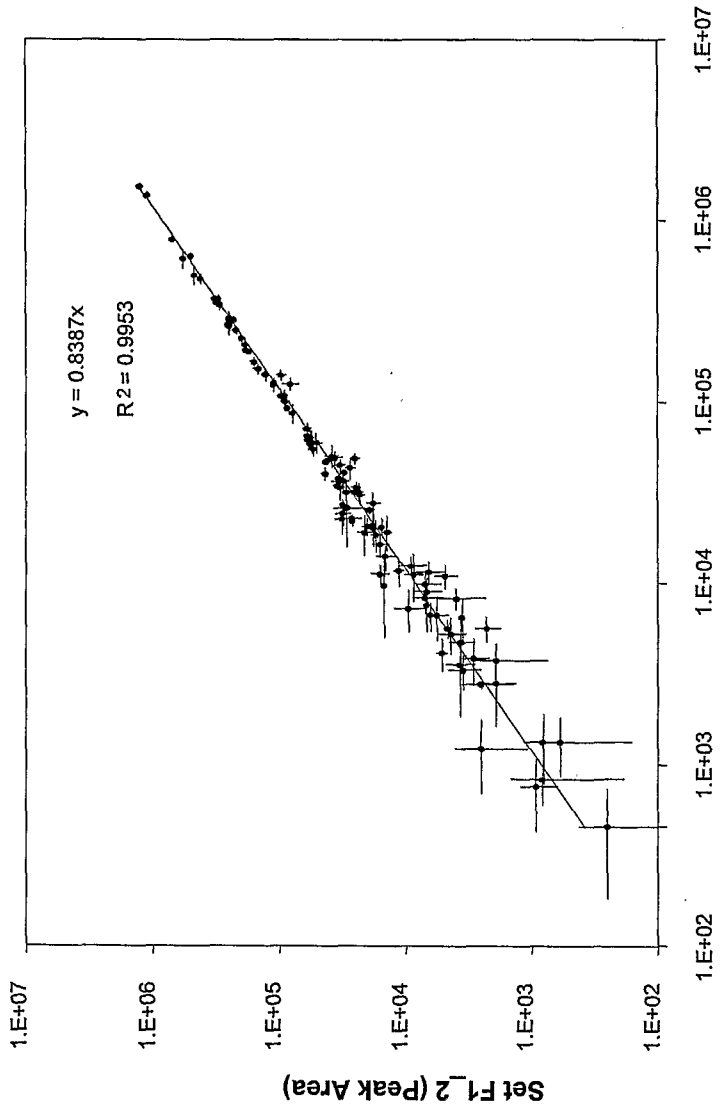

y = 0.8387x
R2 = 0.9953
Set F1_1 (Peak Area)
Set F1_2 (Peak Area)
1.E+02
1.E+03
1.E+04
1.E+05
1.E+06
1.E+07

FIGURE 5B

FIGURE 6A

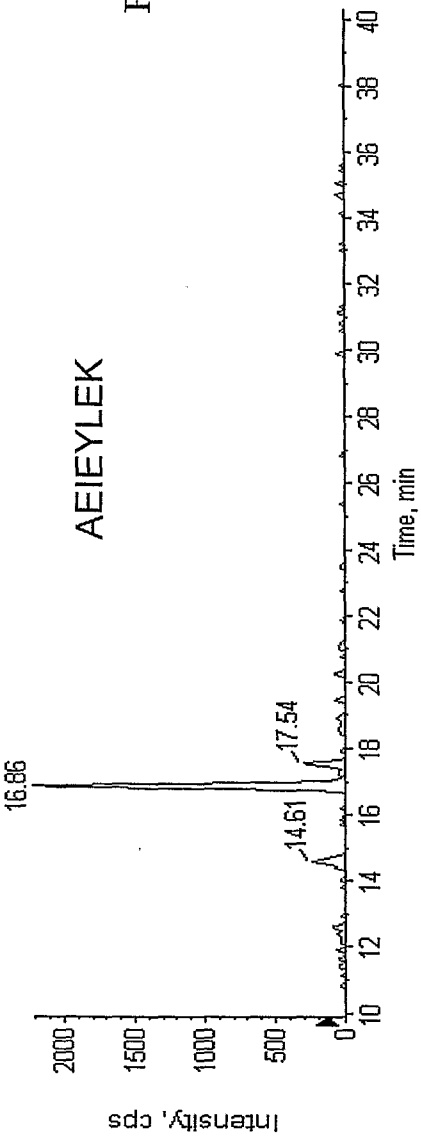
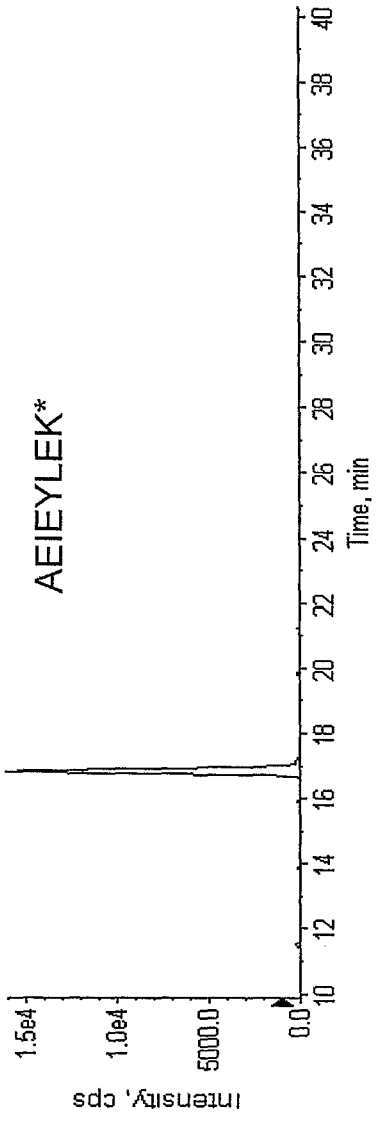


FIGURE 6B



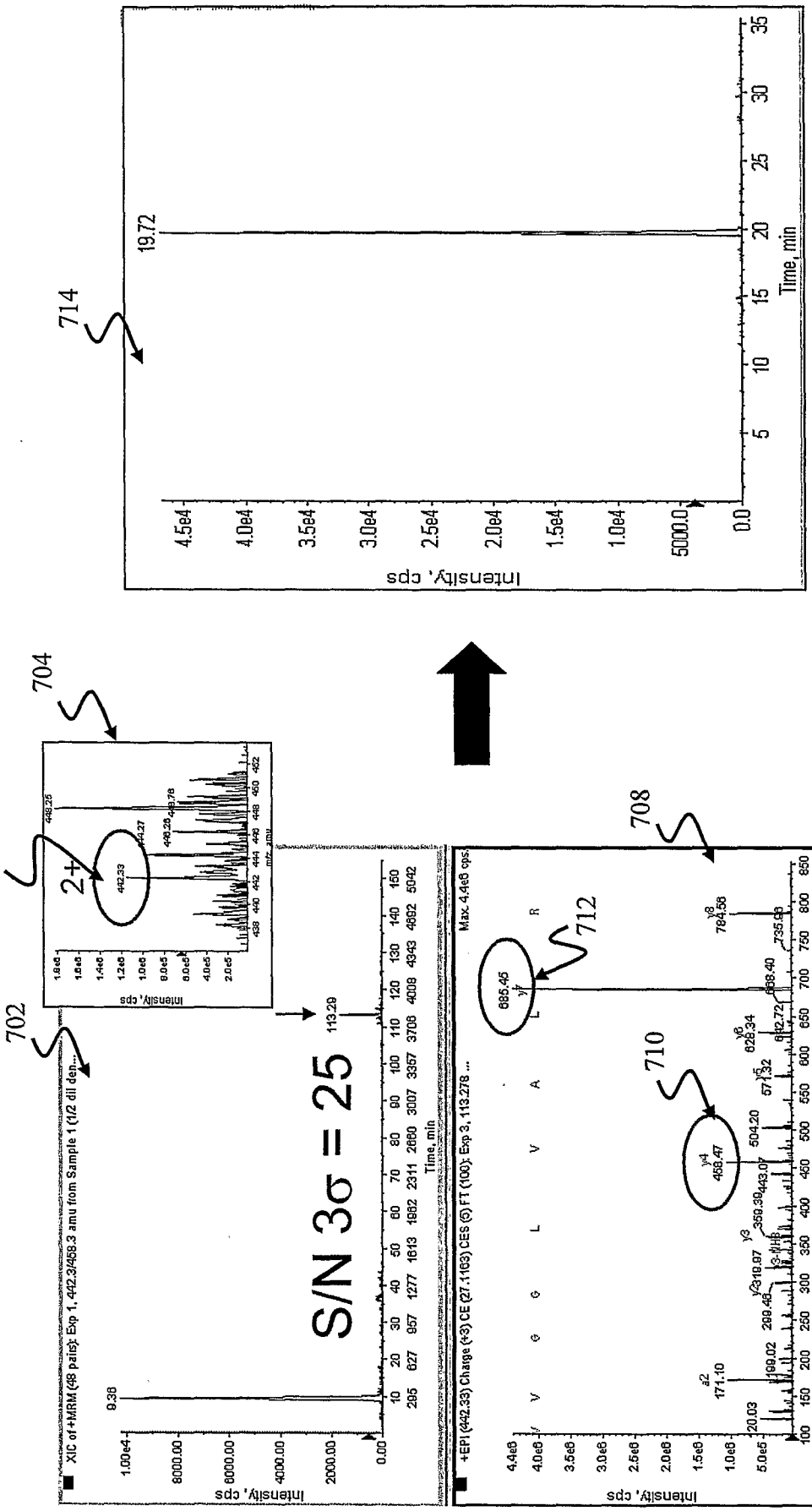

714
19.72
Intensity, cps
Time, min
704
706
2+
442.33
702
708
S/N 3σ = 25
XIC of +MRM (48 pairs): Exp 1, 442.3/458.3 amu from Sample 1 (1/2 dil den...
+EPI (442.33) Charge (+3) CE (27.1163) CES (5) FT (100); Exp 3, 113.278 ...
Time, min
m/z, amu
710
712
686.45
458.47

FIGURE 7

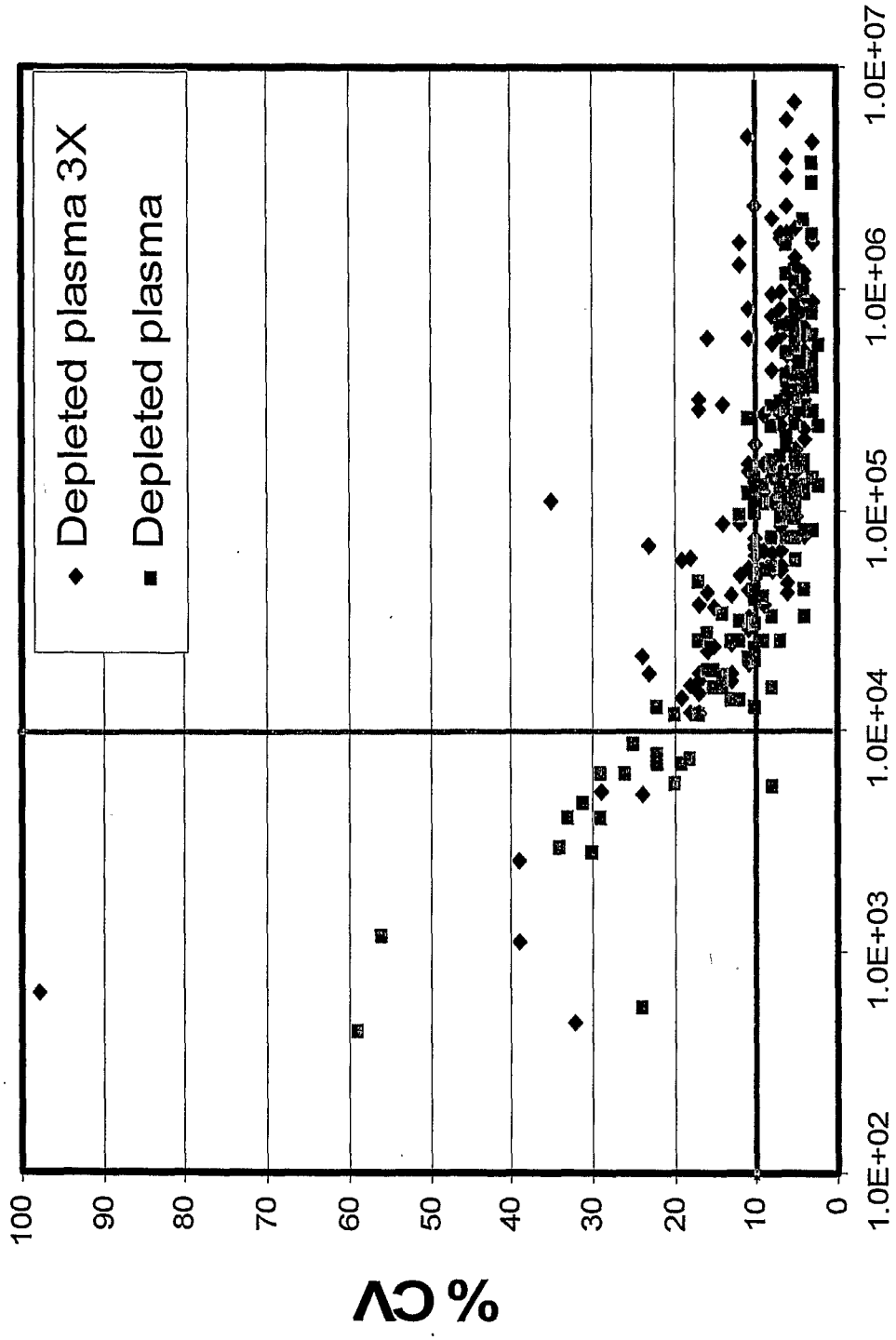
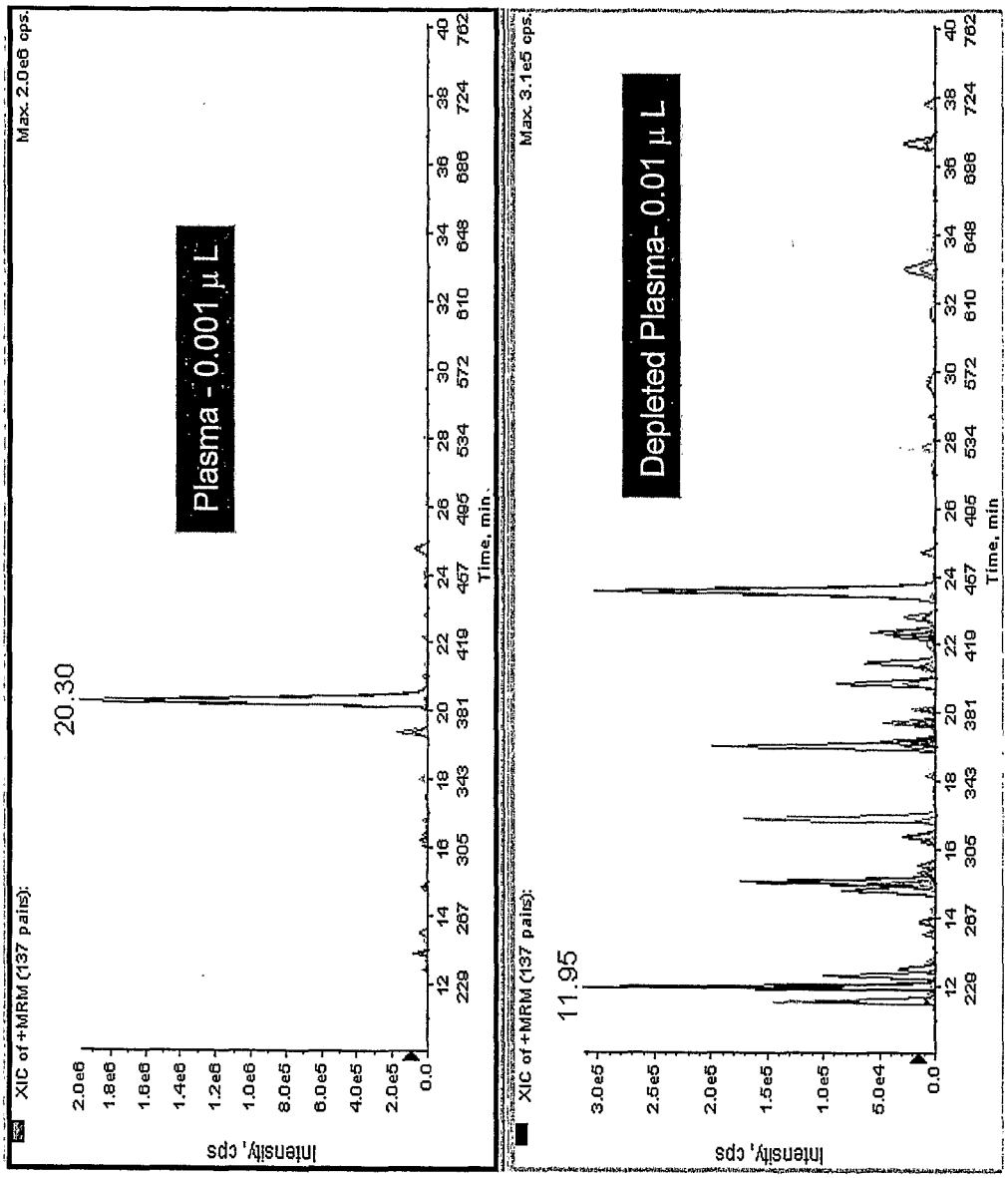

Depleted plasma 3X
Depleted plasma
CV %
Peak Area (log cps)
100
90
80
70
60
50
40
30
20
10
0
1.0E+02
1.0E+03
1.0E+04
1.0E+05
1.0E+06
1.0E+07

FIGURE 8

FIGURE 9A

FIGURE 9B



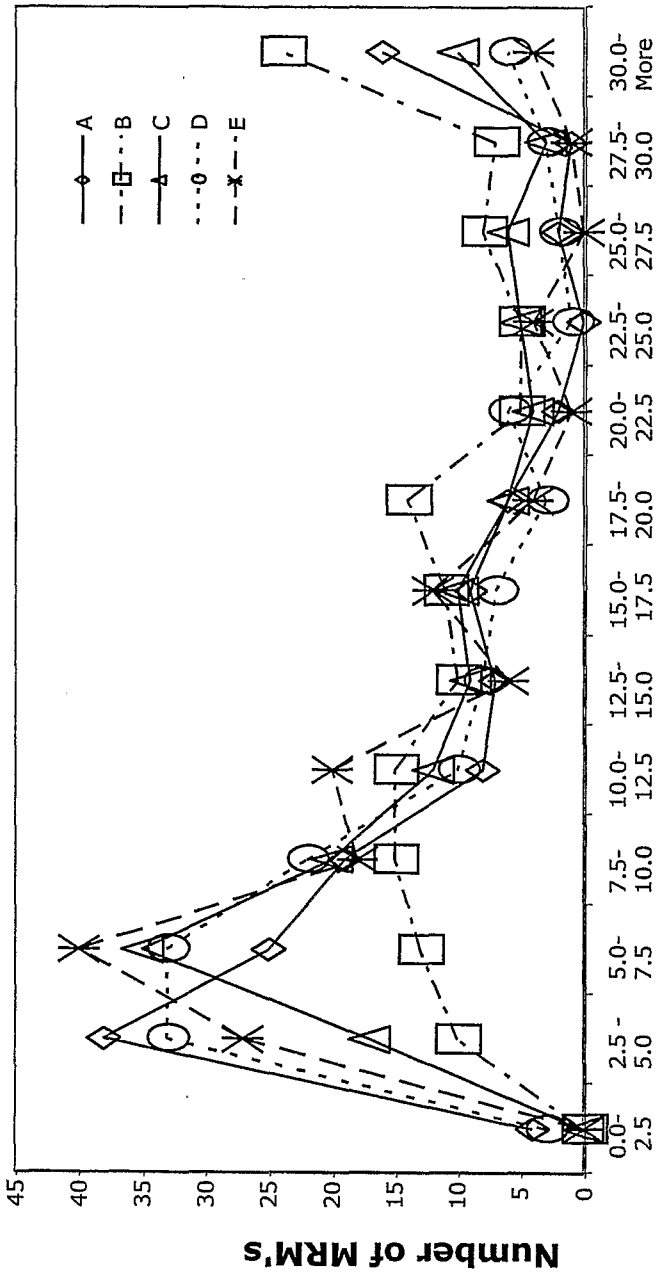

Number of MRM's
45
40
35
30
25
20
15
10
5
0
A
B
C
D
E
0.0-2.5
2.5-5.0
5.0-7.5
7.5-10.0
10.0-12.5
12.5-15.0
15.0-17.5
17.5-20.0
20.0-22.5
22.5-25.0
25.0-27.5
27.5-30.0
30.0-More
CV range (%)

FIGURE 10A

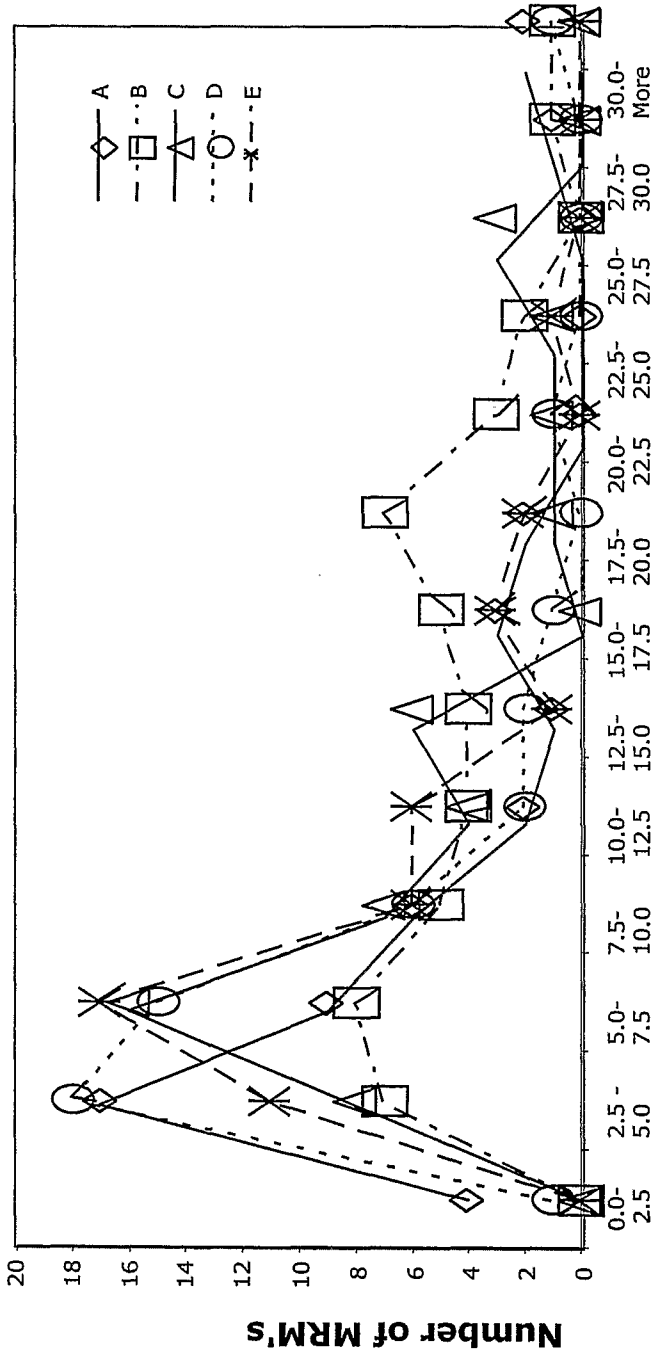

Number of MRM's
0
2
4
6
8
10
12
14
16
18
20
A
B
C
D
E
0.0-2.5
2.5-5.0
5.0-7.5
7.5-10.0
10.0-12.5
12.5-15.0
15.0-17.5
17.5-20.0
20.0-22.5
22.5-25.0
25.0-27.5
27.5-30.0
30.0-More
CV range (%)

FIGURE 10B