

NMR QUANTIFICATION OF BRANCHED CHAIN AMINO ACIDS**Related Applications**

[0001] This application claims the benefit of and priority to U.S. Provisional Application Serial No. 61/711,471, filed October 9, 2012, and U.S. Provisional Application Serial No. 61/831,353, filed June 5, 2013, the contents of which are hereby incorporated by reference as if recited in full herein. This application also claims priority to and is a continuation-in-part of U.S. Patent Application Serial No. 13/801,604, filed March 13, 2013, U.S. Patent Application Serial No. 13/830,199, filed March 14, 2013, U.S. Patent Application Serial No. 13/830,784, filed March 14, 2013, PCT Application Serial No. PCT/US2013/041274, filed May 16, 2013, PCT Application Serial No. PCT/US2013/043343, filed May 30, 2013, and PCT Application Serial No. PCT/US2013/044679, filed June 7, 2013, the contents of which are hereby incorporated by reference as if recited in full herein.

Field of the Invention

[0002] The present invention relates generally to the quantification of branched chain amino acids using NMR. The invention may be particularly suitable for NMR analysis of human blood plasma or serum.

Background

[0003] Branched chain amino acids (BCAAs), which include valine, isoleucine and leucine, may have associations with various diseases, such as metabolic diseases. They may also be used in therapeutic interventions and as dietary supplements.

Summary

[0004] Embodiments of the invention provide methods, systems, circuits, analyzers and computer program products for NMR quantification of at least one branched chain amino acid.

[0005] Embodiments of the invention are directed to methods of quantifying a branched chain amino acid (BCAA) in an *in vitro* unfiltered biosample from a patient. The method may include electronically obtaining a composite NMR spectrum which includes a target fitting region of the biosample; electronically deconvolving the composite NMR spectrum using a defined deconvolution model with at least one BCAA fitting region; and

electronically generating a measure of the at least one BCCA using computational fitting functions.

[0006] Embodiments of the invention provide methods of determining concentrations of BCAAs. The method can include placing at least one unfiltered *in vitro* serum or plasma sample in an NMR spectrometer having a static magnetic field B_0 ; electronically obtaining an NMR spectrum of the sample that includes peaks associated with a plurality of BCAAs; deconvolving the NMR spectrum using defined curve fitting functions; computing unitless intensity signals from the deconvolved spectrum associated with respective BCAAs; then electronically calculating concentrations of the plurality of BCAAs using respective correlations of values of the computed intensity signals with known concentrations of corresponding BCAAs.

[0007] The electronically calculating concentrations can be carried out for each of the plurality of BCAAs using a respective defined linear equation associated with concentrations over at least a normal biological range.

[0008] The linear equation can optionally also include outliers of high and/or low values.

[0009] The method can include for each NMR spectrum of each respective sample before the deconvolving, electronically evaluating at least one reference peak in the NMR spectrum to assess magnetic field inhomogeneity and/or to select an appropriate fitting function or linewidth thereof. The linewidth and/or lineshape of the at least one reference peak can be associated with magnetic field B_0 inhomogeneity and/or homogeneity.

[0010] The method can include applying scalar coupling information to BCAA peaks in the obtained NMR spectrum to thereby facilitate fitting during the deconvolving.

[0011] The scalar coupling information can identify multiple peaks which are separated by a consistent distance as measured in Hertz, irrespective of magnetic field strength, and the deconvolving can include fitting functions that can be constrained to a separation distance at or near the distance to thereby constrain the fitting.

[0012] The method can include for each sample, before the deconvolving, electronically determining a location, lineshape and/or linewidth of at least one endogenous or exogenous reference peak(s) present in respective samples that has shape characteristics dependent on homogeneity of B_0 .

[0013] The method can include computationally determining lineshape and/or linewidth characteristics of each NMR spectrum for respective samples before the deconvolving step using at least one reference peak to account for differences in magnetic

field homogeneity characteristics associated with a respective individual NMR spectrum, then selecting a defined deconvolution model with fitting functions having a linewidth and/or lineshape corresponding to the at least one reference peak such that different samples can be evaluated differently using (a) different fitting functions and/or (b) different linewidths.

[0014] In some embodiments, the electronically calculating the concentrations can include applying a scalar concentration value defined as a linear function of concentrations versus unitless intensity signal correlations for each BCAA.

[0015] In some embodiments, the plurality of BCAAs can include valine, isoleucine and leucine, and the deconvolving can be carried out using a baseline that is fit using protein and lipoprotein components.

[0016] The method can include, before the deconvolving, electronically evaluating at least one pH chemical-shift invariant reference peak in the obtained NMR spectrum associated with an endogenous or exogenous analyte or component of the sample, then determining a location of BCAA peaks in the NMR spectrum.

[0017] In some embodiments, the electronically obtaining can be carried out using between about 10 seconds to about 5 minutes of NMR acquisition time (AT) for a single NMR spectrum per sample.

[0018] In some embodiments, the electronically obtaining can be carried out using between about 16-96 scans for a respective sample NMR spectrum, and the electronically calculating the BCAA concentrations can be carried out using a single NMR spectrum per sample.

[0019] The method can include transmitting a pulse sequence that attenuates signal from lipoproteins and proteins in the sample to a greater degree than signal from small molecule BCAAs.

[0020] In some embodiments, the pulse sequence can include a Carr-Purcell-Meiboom-Gill (CPMG) pulse sequence with a defined delay that attenuates the lipoprotein and protein signals.

[0021] The CPMG pulse sequence can have a delay of between about 60 ms to about 400 ms. In some embodiments, the CPMG pulse sequence can have a delay of about 100 ms.

[0022] According to some embodiments, the CPMG pulse sequence can have a delay of about 200 ms, and the method can include electronically correcting the calculated concentrations for quantification errors associated with attenuation of signal intensity of the BCAAs associated with the CPMG pulse sequence.

[0023] In some embodiments, the CPMG pulse sequence can have a delay of about 300 ms, and the method can include electronically correcting the calculated concentrations for quantification errors associated with attenuation of signal intensity of the BCAAs associated with the CPMG pulse sequence.

[0024] In further embodiments, the CPMG pulse sequence can have a delay of about 400 ms, and the method can include electronically correcting the calculated concentrations for quantification errors associated with attenuation of signal intensity of the BCAAs associated with the CPMG pulse sequence.

[0025] In certain embodiments, the method can include transmitting a first lipoprotein pulse sequence and obtaining a first NMR spectrum associated with lipoproteins and proteins in the sample while the sample is in the NMR spectrometer and transmitting a second pulse sequence to obtain the NMR spectrum associated with the BCAAs that is configured to attenuate protein and lipoprotein signals before or after the first pulse sequence to obtain the NMR spectrum of the BCAAs. Both pulse sequences and subsequent NMR spectra can be obtained within about 2 minutes to about 6 minutes of NMR signal acquisition time per sample.

[0026] In some embodiments, the method can include flowing respective samples into the NMR spectrometer before the obtaining step. The obtaining can be carried out by serially obtaining respective NMR spectrums at a rate that is between about 50 and 250 unfiltered samples per 8 hours.

[0027] In some embodiments, the plurality of BCAAs includes valine, isoleucine and leucine, and valine and leucine can be quantified using less scans associated with the obtained NMR spectrum than isoleucine.

[0028] In some embodiments, the NMR spectrum used to calculate valine and leucine can be generated using between 16-96 scans. The NMR spectrum used to calculate isoleucine can be generated using 96 scans.

[0029] In some embodiments, the electronically calculating can be carried out using a respective defined linear concentration equation for each BCAA to provide a clinically relevant concentration measurement of at least normal biological concentration ranges.

[0030] In some embodiments, the first pulse sequence can include the pulse sequence shown in Figure 6.

[0031] The method can include, in some embodiments, electronically calculating a ratio or weighted index that is predictive of a clinical outcome or disease risk or identifies an efficacy of a drug or drug candidate. The ratio or weighted index can have at least one of the

following: (a) a numerator comprising at least one of the unitless signals or calculated concentrations of one or more of the BCAAs; (b) a denominator comprising at least one of the unitless signals or calculated concentrations of one or more of the BCAAs; or (c) a numerator and a denominator that includes at least one of the unitless signals or calculated concentrations of one or more of the BCAAs.

[0032] In some embodiments, the method can include electronically calculating a ratio and/or weighted index that is predictive of a clinical outcome or disease risk or identifies an efficacy of a drug or drug candidate. The ratio or weighted index includes in the denominator or numerator or in both the denominator and numerator at least one of the unitless signals or calculated concentrations of one or more of the BCAAs.

[0033] The method can include, in some embodiments, electronically calculating a ratio and/or weighted index that is predictive of a clinical outcome or disease risk or identifies an efficacy of a drug or drug candidate, wherein the ratio and/or weighted index includes in the denominator or numerator or in both the denominator and numerator at least one of the unitless signals or calculated concentrations of one or more of the BCAAs and a unitless signal or concentration measurement of an amino acid.

[0034] Certain embodiments of the present invention are directed to a circuit configured to provide measurements of BCAAs. The circuit includes at least one processor configured to carry out the steps of any of the methods of the present invention.

[0035] Further embodiments of the present invention are directed to a computer program product for evaluating *in vitro* patient biosamples. The computer program product includes: a non-transitory computer readable storage medium having computer readable program code embodied in the medium. The computer-readable program code includes computer readable program code configured to deconvolve a NMR spectrum with Branched Chain Amino Acid (BCAA) peaks of respective unfiltered patient samples using defined fitting functions; computer readable program code that computes unitless intensity signals from the deconvolved spectrum associated with respective BCAAs; and computer readable program code configured to provide concentrations of the BCAAs for the unitless intensity signals.

[0036] The computer program product can be configured to carry out one or more of the method of the present invention.

[0037] Still other embodiments are directed to a system. The system includes an NMR spectrometer for acquiring at least one NMR spectrum of respective *in vitro* biosamples, the NMR spectrometer having a static magnetic field B_0 ; and at least one

processor in communication with the NMR spectrometer. The at least one processor is configured to, for a respective biosample, using the acquired at least one NMR spectrum: deconvolve the NMR spectrum using defined fitting functions; compute unitless intensity signals from the deconvolved spectrum associated with respective BCAAs; then calculate concentrations of the plurality of BCAAs using respective correlations of values of the computed intensity signals with known concentrations of corresponding BCAAs.

[0038] In some embodiments, the at least one processor can be configured to computationally determine lineshape and/or linewidth characteristics of each NMR spectrum for respective samples before the deconvolving step using at least one reference peak to account for differences in magnetic field homogeneity characteristics associated with a respective individual NMR spectrum, then select a defined deconvolution model with fitting functions having a linewidth and/or lineshape corresponding to the at least one reference peak such that different samples can be evaluated differently using (a) different fitting functions and/or (b) different linewidths.

[0039] In some embodiments, the at least one processor can be configured to, before deconvolving respective NMR spectrum for quantifying BCAA signals, evaluate at least one pH chemical-shift invariant reference peak in respective obtained NMR spectrums associated with an endogenous or exogenous analyte or component of the sample, then determine a location of BCAA peaks in the NMR spectrum.

[0040] In some embodiments, the at least one processor can be configured to calculate a ratio and/or weighted index that is predictive of a clinical outcome or disease risk or identifies an efficacy of a drug or drug candidate. The ratio and/or weighted index can include in the denominator or numerator or in both the denominator and numerator at least one of the unitless signals or calculated concentrations of one or more of the BCAAs.

[0041] The at least one processor can, in some embodiments, calculate respective concentrations by applying a scalar concentration value defined as a linear function of concentrations versus unitless intensity signal correlations for each BCAA.

[0042] In some embodiments, the BCAAs can include valine, isoleucine and leucine, and the deconvolving can be carried out using a baseline that is fit using protein and lipoprotein components.

[0043] In some embodiments, the system can be configured to transmit a first lipoprotein pulse sequence to obtain a first NMR spectrum associated with lipoproteins and proteins in the sample while the sample is in the NMR spectrometer and transmit a second pulse sequence to obtain the NMR spectrum associated with the BCAAs that is configured to

attenuate protein and lipoprotein signals before or after the first pulse sequence to obtain the NMR spectrum of the BCAAs. Both pulse sequences and subsequent respective NMR spectrums can be obtained within about 2 minutes to about 6 minutes of NMR signal acquisition time per sample.

[0044] In some embodiments, the at least one processor can be configured to carry out any of the methods of the present invention.

[0045] Further features, advantages and details of the present invention will be appreciated by those of ordinary skill in the art from a reading of the figures and the detailed description of the preferred embodiments that follow, such description being merely illustrative of the present invention. Features described with respect with one embodiment can be incorporated with other embodiments although not specifically discussed therewith. That is, it is noted that aspects of the invention described with respect to one embodiment, may be incorporated in a different embodiment although not specifically described relative thereto. That is, all embodiments and/or features of any embodiment can be combined in any way and/or combination. Applicant reserves the right to change any originally filed claim or file any new claim accordingly, including the right to be able to amend any originally filed claim to depend from and/or incorporate any feature of any other claim although not originally claimed in that manner. The foregoing and other aspects of the present invention are explained in detail in the specification set forth below.

[0046] As will be appreciated by those of skill in the art in light of the present disclosure, embodiments of the present invention may include methods, systems, apparatus and/or computer program products or combinations thereof.

Brief Description of the Figures

[0047] **Figure 1** is a flow chart of exemplary operations that can be used to calculate NMR measures of at least one BCAA according to embodiments of the present invention.

[0048] **Figure 2** is an NMR spectrum showing an example of a quantitative fitting of valine, isoleucine, and leucine according to embodiments of the present invention.

[0049] **Figures 3A-I** are graphs of exemplary linear concentration conversion models for BCAAs according to embodiments of the present invention.

[0050] **Figure 4** is an expansion of an ^1H NMR spectrum about a target branched chain amino acid methyl region according to embodiments of the present invention.

[0051] **Figure 5** shows exemplary fitting for three BCAAs as an expansion of respective defined peak regions in the same NMR spectrum according to embodiments of the present invention.

[0052] **Figure 6** is an exemplary pulse sequence using a standard "one-pulse" protocol with WET solvent suppression according to embodiments of the present invention.

[0053] **Figure 7** illustrates the first pulse sequence in **Figure 6** modified to include a CPMG sequence to attenuate signals associated with macromolecules and large aggregates such as proteins and lipoproteins according to particular embodiments of the present invention.

[0054] **Figure 8** is an array of CPMG acquired ^1H NMR spectra with respective different duration delay times according to embodiments of the present invention.

[0055] **Figure 9** is an expansion of the array of spectra of **Figure 8** according to embodiments of the present invention.

[0056] **Figure 10** is a schematic illustration of a system with a BCAA evaluation module and/or circuit using according to embodiments of the present invention.

[0057] **Figure 11** is a schematic illustration of a NMR spectroscopy apparatus according to embodiments of the present invention.

[0058] **Figure 12** is a schematic diagram of a data processing system according to embodiments of the present invention.

[0059] **Figure 13** is a flow chart of exemplary operations that can be used to calculate NMR measures of BCAA according to embodiments of the present invention.

[0060] **Figure 14A** is a flow diagram of an NMR valine test protocol according to embodiments of the present invention.

[0061] **Figure 14B** is a flow chart of exemplary pre-analytical processing that can be used prior to obtaining NMR signal of biosamples according to embodiments of the present invention.

[0062] **Figure 14C** is a flow diagram of operations that can be used to evaluate valine using NMR according to embodiments of the present invention.

[0063] The foregoing and other objects and aspects of the present invention are explained in detail in the specification set forth below.

Detailed Description of Embodiments of the Invention

[0064] The present invention now is described more fully hereinafter with reference to the accompanying drawings, in which embodiments of the invention are shown. This

invention may, however, be embodied in many different forms and should not be construed as limited to the embodiments set forth herein; rather, these embodiments are provided so that this disclosure will be thorough and complete, and will fully convey the scope of the invention to those skilled in the art.

[0065] Like numbers refer to like elements throughout. In the figures, the thickness of certain lines, layers, components, elements or features may be exaggerated for clarity. Broken lines illustrate optional features or operations unless specified otherwise.

[0066] The terminology used herein is for the purpose of describing particular embodiments only and is not intended to be limiting of the invention. As used herein, the singular forms "a", "an" and "the" are intended to include the plural forms as well, unless the context clearly indicates otherwise. It will be further understood that the terms "comprises" and/or "comprising," when used in this specification, specify the presence of stated features, integers, steps, operations, elements, and/or components, but do not preclude the presence or addition of one or more other features, integers, steps, operations, elements, components, and/or groups thereof. As used herein, the term "and/or" includes any and all combinations of one or more of the associated listed items. As used herein, phrases such as "between X and Y" and "between about X and Y" should be interpreted to include X and Y. As used herein, phrases such as "between about X and Y" mean "between about X and about Y." As used herein, phrases such as "from about X to Y" mean "from about X to about Y."

[0067] Unless otherwise defined, all terms (including technical and scientific terms) used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. It will be further understood that terms, such as those defined in commonly used dictionaries, should be interpreted as having a meaning that is consistent with their meaning in the context of the specification and relevant art and should not be interpreted in an idealized or overly formal sense unless expressly so defined herein. Well-known functions or constructions may not be described in detail for brevity and/or clarity. In case of a conflict in terminology, the present specification is controlling.

[0068] It will be understood that, although the terms first, second, etc. may be used herein to describe various elements, components, regions, layers and/or sections, these elements, components, regions, layers and/or sections should not be limited by these terms. These terms are only used to distinguish one element, component, region, layer or section from another region, layer or section. Thus, a first element, component, region, layer or section discussed below could be termed a second element, component, region, layer or section without departing from the teachings of the present invention. The sequence of

operations (or steps) is not limited to the order presented in the claims or figures unless specifically indicated otherwise.

[0069] The term "programmatically" means carried out using computer program and/or software, processor or Application Specific Integrated Circuit (ASIC) directed operations. The term "electronic" and derivatives thereof refer to automated or semi-automated operations carried out using devices with electrical circuits and/or modules rather than via mental steps and typically refers to operations that are carried out programmatically. The terms "automated" and "automatic" means that the operations can be carried out with minimal or no manual labor or input. The term "semi-automated" refers to allowing operators some input or activation, but the calculations and signal acquisition as well as the calculation of the concentrations of the ionized constituent(s) is done electronically, typically programmatically, without requiring manual input.

[0070] The term "about" as used herein refers to +/- 10% (mean or average) of a specified value or number.

[0071] "Branched chain amino acid" and "BCAA" as used herein refers to at least one of the following amino acids: valine, leucine, and isoleucine. As is known to those of skill in the art, branched chain amino acids are amino acids having a branched alkyl group side-chain. Valine has the chemical formula: $\text{HO}_2\text{CCH}(\text{NH}_2)\text{CH}(\text{CH}_3)_2$. Leucine has the chemical formula: $\text{HO}_2\text{CCH}(\text{NH}_2)\text{CH}_2\text{CH}(\text{CH}_3)_2$. Isoleucine has the chemical formula: $\text{HO}_2\text{CCH}(\text{NH}_2)\text{CH}(\text{CH}_3)\text{CH}_2\text{CH}_3$.

[0072] When a BCAA is measured by NMR, the value can be in a unitless measure of intensity. The intensity scale is constant such that the intensity of signals from different samples obtained under identical conditions can be directly compared. The intensities can be correlated to concentration. The BCAA unitless measurement may be multiplied by a defined conversion factor using calibration data to convert or translate the unitless value into concentration units, such as $\mu\text{mol/L}$ concentration units.

[0073] The BCAA measurements may need to be adjusted based on an experimental condition before the fitting process. That is, the evaluation of the actual concentration of one or more BCAAs may be based on intensity, line width, and/or lineshape of respective samples which may be evaluated under different experimental conditions which may induce a variation or deviation in NMR spectrum from a standard or baseline experimental condition(s). One or more experimental conditions can be automatically or electronically determined *in situ* and/or proximate in time to acquisition of NMR data of respective samples

for assessing one or more actual experimental conditions to allow a customization of a deconvolution model used, sample to sample. .

[0074] The term "experimental condition" as used herein, can include, but is not limited to, the sample pH, the degree of water suppression, BCAA peak attenuation associated with a pulse *sequence* (such as a CPMG delay), the homogeneity of the magnetic field, sample preparation (*e.g.*, proper mixing of the sample and/or addition of the sample into the flow cell so that it completely fills the flow cell), the shim state of the instrument, and any combination thereof.

[0075] The terms "CAD" and "CHD" are used interchangeably to correspond to a patient or subject's risk of developing or having coronary artery and/or coronary heart disease, respectively. The term cardio vascular disease (CVD) refers to a combined outcome that is typically CHD plus stroke.

[0076] As used herein, the chemical shift locations (ppm) refer to NMR spectra referenced internally to CaEDTA signal at 2.519 ppm. Thus, the noted peak locations discussed and/or claimed herein may vary depending on how the chemical shift is generated or referenced as is well known to those of skill in the art. Thus, to be clear, certain of the described and/or claimed peak locations have equivalent different peak locations in other corresponding chemical shifts as is well known to those of skill in the art.

[0077] The term "biosample" refers to *in vitro* blood, plasma, serum, CSF, saliva, lavage, sputum, urine, or tissue samples of humans or animals. Embodiments of the invention may be particularly suitable for evaluating human blood plasma, blood serum, or urine biosamples. The blood plasma, blood serum, or urine samples may be fasting or non-fasting. In certain embodiments of the invention, the biosample may be unfiltered human blood plasma or human blood serum.

[0078] The biosample may be unprocessed. An "unprocessed biosample" as used herein refers to a biosample that, unlike sample preparation for mass spectrometry analysis, is not subjected to processing that removes components in the biosample after it is obtained. Thus, once the biosample is obtained from a human or animal, components from the biosample are not removed. For example, once a blood serum biosample is obtained, the serum is not subjected to processing that removes components from the serum. In some embodiments, an unprocessed biosample is not subjected to filtering and/or ultrafiltration processes. An example of an unprocessed biosample is an unfiltered biosample that contains lipoprotein and protein components and a full complement of small molecule metabolites.

[0079] As those skilled in the art will recognize, various additives, standards, and/or diluents known to those of skill in the art may be added to the biosample to aid in the identification and/or quantification of components, such as BCAAs, in the biosample and/or to provide an experimental control. However, the addition of additives, standards, and/or diluents to a biosample does not refer to or encompass processing that causes the components in the biosample to be removed after the biosample is obtained. In certain embodiments, the biosample is an unfiltered biosample and is diluted with a diluent.

[0080] A diluent may be added to the biosample to form a sample mixture. Suitable diluents include, but are not limited to, buffer solutions and/or reference or calibration analytes, such as those known to those of skill in the art. Exemplary buffer solutions include, but are not limited to, acidic buffers, such as, but not limited to, a citrate, a phosphate, and/or an acetate buffer. In some embodiments, the diluent may comprise a pH buffer. The term "pH buffer" refers to a chemical or set of chemicals added to the biosample to create a defined pH-induced NMR peak shift in the NMR spectrum. Exemplary pH buffers include, but are not limited to, citrate phosphate buffers (e.g., citric acid and sodium dibasic phosphate, e.g., $C_6H_8O_7 \cdot H_2O$ and $Na_2HPO_4 \cdot 7H_2O$). For example, the biosample can comprise a citrate buffer and/or citrate phosphate buffer having a pH from about 2.6 to about 5.5 and comprising citric acid, sodium citrate, and/or sodium phosphate. Other exemplary buffers include, but are not limited to, an acetate buffer and/or an acetate phosphate buffer having a pH from about 3.7 to about 5.5 and comprising acetic acid, sodium acetate, and/or sodium phosphate. In some embodiments, the biosample comprises a citrate phosphate buffer comprising citric acid and sodium dibasic phosphate. Typically, a pH buffer is mixed with deionized water and added to the biosample to dilute the sample by a defined amount. However, pH buffer(s), where used, may also be added directly into a liquid or tissue biosample. In some embodiments, the NMR assay is performed on a sample mixture (e.g., the biosample and the diluent or diluted biosample) that may have a pH of between 4-10, such as, but not limited to, a pH of between about 7-8 or a pH of between about 7.2-7.6.

[0081] A biosample, diluent, and/or buffer may contain one or more endogenous and/or exogenous reference analyte(s) including, but not limited to, one or more of albumin, glucose, citrate, acetate or other acidic compounds as well any of the well established chemical shift or quantitation reference analytes such as formate, trimethylsilylpropionate (and isotopically labeled isomers), 4,4-dimethyl-4-silapentane-1-sulfonic acid (DSS), CaEDTA, and EDTA, for example.

[0082] In some embodiments, a biosample contains at least one endogenous or exogenous reference analyte. For example, a reference analyte can generate a reference peak or peaks associated with an endogenous or exogenous analyte. An example of an endogenous reference analyte is by way of example, but not limited to, glucose, that is present in the biosample. In some embodiments, the reference analyte has a chemical shift or quantitation peak(s) that is/are pH stable, meaning that the peak region and/or linewidth of the reference peak(s) over a pH range of between 4-10 does not substantially vary with pH (e.g., the peak region varies by less than about ± 0.1 ppm) or varies in chemical shift location and/or in size in a known or predictable manner in response to changes in pH.

[0083] In some embodiments, the diluent may comprise or be a reference or calibration analyte, such as, but not limited to, CaEDTA and/or citrate.

[0084] The sample mixture may comprise a biosample to diluent ratio in a range of 10:90 to 90:10. In certain embodiments, the biosample to diluent ratio is 50:50. Buffers and/or other additives, e.g., reference or calibration analytes, may be added to the sample mixture. In certain embodiments, a buffer may maximize the amount of biosample in the mixture (e.g., provide a biosample to diluent buffer ratio of 55:45 or greater). It is contemplated that, in some embodiments, low volume biosamples may be analyzed, such as ≤ 50 μ L or between about 10 μ L to about 50 μ L.

[0085] The term "patient" is used broadly and refers to an individual, human or animal, that provides a biosample for testing or analysis.

[0086] The term "clinical disease state" means an at-risk medical condition that may indicate medical intervention, therapy, therapy adjustment or exclusion of a certain therapy (e.g., pharmaceutical drug) and/or monitoring is appropriate. Identification of a likelihood of a clinical disease state can allow a clinician to treat, delay or *inhibit* onset of the condition accordingly. Examples of clinical disease states include, but are not limited to, metabolic disorders such as diabetes, CHD, CVD, stroke, type 2 diabetes, prediabetes, liver disease, cancer, and cancer cachexia.

[0087] The term "CPMG" refers to a Carr-Purcell-Meiboom-Gill pulse sequence. This is a series of phase defined radiofrequency pulses that provide means to attenuate signals from large, rapidly relaxing molecules such as proteins and lipoprotein particles.

[0088] A single NMR spectrum is generated in response to a defined pulse sequence. For example, one NMR spectrum is obtained using a one-pulse sequence and/or one NMR spectrum is obtained using a CPMG pulse sequence. Typically, a plurality of scans per NMR spectrum, such as between about 16-96 scans, are used to acquire signal to generate the

associated NMR spectrum using a signal averaging process so that signal has improved signal to noise (SNR).

[0089] Embodiments of the invention may provide a simple, fast and convenient assay for the quantification of one or more branched chain amino acids (BCAAs) in a biosample using NMR. In the assay, separate quantification of all three BCAAs may be accomplished using NMR spectra of an unfiltered sample, optionally with the use of a reference analyte for generating a reference peak(s). The sample can have an exogenous and/or endogenous reference analyte that provides at least one reference peak that can be evaluated for linewidth and/or lineshape that is associated with inhomogeneity of the B_0 static magnetic field of the NMR spectrometer. The shim state or B_0 homogeneity/inhomogeneity can be evaluated automatically for each sample or proximate in time to NMR acquisition time of a respective sample or set of samples using the reference peak(s).

[0090] The deconvolution model can be configured to select a computational fitting function (CFF) (e.g., curve fitting function) with appropriate linewidth and/or lineshape based on the reference peak(s) linewidth and/or lineshape as determined for each respective sample NMR spectrum for BCAA quantification.

[0091] Two or three BCAAs may be separately quantified in a biosample.

[0092] In certain embodiments, a NMR assay according to embodiments of the present invention may provide a composite measure of three BCAAs present in a biosample to generate a composite unitless score or concentration measure of valine, isoleucine, and leucine versus separate discrete scores or concentrations.

[0093] The quantified concentration measurements for one or more of the BCAAs, e.g., at least valine and leucine, can be carried out to provide measurements with spiked dialyzed standards, as shown below in Table 1. It is contemplated that the calibration data can provide concentration measurements, with measured percent coefficient of variances (CV) (% CVs) of less than 15% at the mean concentrations in a healthy population.

[0094] Table 1: Spiked dialyzed BCAA measurements.

spike	NMR Leucine	NMR Leucine	spike	NMR Valine	NMR Valine	spike	NMR Isoleucine	NMR Isoleucine
0	98.92	9.62	0	117.44	12.36	0	32.36	13.23
60	173.74	3.48	80	212.07	4.41	10	56.45	13.74
120	251.42	2.96	160	290.18	7.72	20	96.34	8.18
180	323.92	5.41	240	372.03	6.01	30	140.75	10.41
240	393.37	1.71	320	466.03	7.81	40	181.96	8.01
98.7 +/- 11.5			212.3 +/- 62.3			60.7 +/- 18.6		

[0095] BCAAs may be central components of energy metabolism. In some embodiments, a NMR assay according to embodiments of the present invention may provide a ratio of at least one BCAA to at least one BCAA or to a group of BCAAs. The ratio can be generated based on a different combination of defined BCAAs, and thus the combination may include one or more BCAAs present in the sample. Alternatively or in addition, a NMR assay according to embodiments of the present invention may provide a ratio of one or more BCAAs to another metabolite. The ratios may have diagnostic value and may be used in evaluating a patient's clinical disease state and/or provide metabolic status or other therapeutic or diagnostic information. For example, a ratio of at least one BCAA to at least one aromatic amino acid (*e.g.*, phenylalanine, tyrosine, tryptophan, and histidine) may be obtained according to embodiments of the present invention, and may be used to predict and/or diagnose a liver disease and/or provide information for treating a patient diagnosed with a liver disease. In some embodiments, a Fischer's ratio (*i.e.*, the sum of all three BCAAs to the sum of phenylalanine and tyrosine in the biosample) may be calculated according to embodiments of the present invention. Ratios of at least one BCAA with other exemplary metabolites include, but are not limited to, metabolites such as those participating in glycolysis and/or β -oxidation pathways. In some embodiments, a ratio with a BCAA component may be electronically calculated or obtained.

[0096] Identification and quantification of a particular BCAA in a biosample may be accomplished according to embodiments of the invention. In some embodiments, at least three BCAAs (*i.e.*, valine, leucine, and isoleucine) are identified in respective biosamples and each of the three BCAAs in the biosample can be separately quantified using a single NMR spectrum.

[0097] Alternatively or in addition, a composite score or concentration of the BCAAs can be generated.

[0098] In some embodiments, a weighted index, ratio or ratio with a weighted index having at least one of the unitless signal or concentrations of BCAAs can be calculated. The ratio and/or weighted index can be generated based on a regression analysis of outcomes for respective diseases that is predictive of a clinical outcome or disease risk or identifies an efficacy of a drug or drug candidate. The weighted index can weight one or more BCAA unitless signals or measurements more than another BCAA component or may multiply certain other risk components together forming a patient health or risk indicator score or index. In the below examples, "V" refers to valine, "IL" refers to isoleucine, and "L" refers to

leucine. Ratios include, but are not limited to: $V/(L+IL)$; I/IL ; V/L ; IL/V ; $V/(IL)$; $(VL)/IL$ and the like. Weighted indexes include, but are not limited to: $V \cdot \text{GlycA}/V(IL)(L)$; $IL/L(10)+V; V(L)(IL)/L \times 10$ and $V/(IL \times 10)$, for example. _ :

[0099] According to some embodiments of the present invention, a method may comprise acquiring an NMR spectrum of an unfiltered sample using a pulse sequence (Figure 1, block 100). The pulse sequence may suppress or attenuate macromolecule signals (e.g., lipoprotein and protein signals) in the spectrum, optionally, the pulse sequence may be optimized. The term "optimized", as used herein, means that the pulse sequence is configured so that macromolecule signals are attenuated in the NMR spectrum to remove or reduce interference with small molecule BCAAs to a sufficient degree to allow for the quantification of one or more BCAAs.

[00100] The suppression of macromolecular signals may be carried out in a manner that suppresses small molecule (i.e., compounds or molecules with a molecular weight of up to about 500 Daltons or less) signals by up to 40% (e.g., typically between about 2% to about 30%). For at least the larger attenuations, the suppression can be generated to yield predictable attenuations that can optionally be adjusted for using one or more quantification adjustment factors and/or models.

[00101] In certain embodiments, the NMR spectrum with a pulse sequence can generate a lipoprotein and/or protein signals and these signals may be accounted for computationally in a manner that allows for quantification of BCAAs.

[00102] Optionally, one or more reference peaks (e.g., 2, 3, 4, or more) may be identified and/or evaluated to identify and/or quantify a target BCAA peak or peaks for a respective BCAA (block 110). The reference peak(s) may be associated with an endogenous and/or exogenous reference analyte, which may be a pH chemical-shift invariant reference peak. A pH chemical-shift "invariant" reference peak is a peak that is pH insensitive over a pH of between about 4 to about 10 and has a chemical shift location that is within ± 0.1 ppm.

[00103] The one or more reference peaks may be electronically evaluated to determine their location, lineshape, and/or linewidth. The one or more reference peaks may be used to determine an experimental condition, such as, but not limited to, sample pH and/or magnetic field inhomogeneity. The one or more reference peaks may be determined for each sample and used to evaluate each sample NMR spectrum. The one or more reference peaks may thus be used to select a defined computational (e.g., curve) fitting function, linewidth of a CFF,

and/or for determining the location of one or more BCAA peaks and/or the measurement/concentration of a respective BCAA.

[00104] A computational (e.g., curve) fitting model may be used to deconvolve the NMR spectrum (block 120). The model may include defined mathematical deconvolution functions. The model may include fitting functions with determined lineshapes and/or linewidths to a targeted BCAA peak position. The model may include computational fitting functions with baseline contributions, such as, for example, as shown in **Figure 5**. The fitting functions can be any suitable function such as Lorentzians or Gaussians.

[00105] In some embodiments, the fitting model may involve using scalar coupling of the BCAAs. Scalar coupling is the spectroscopic phenomenon wherein a chemical species gives rise to multiple peaks which are separated by a consistent distance as measured in Hertz, irrespective of magnetic field strength. The fitting functions can be constrained to a separation distance at or very near this distance in order to constrain the fitting process.

[00106] A BCAA concentration may then be determined based on a BCAA peak area (block 130). Concentration conversion data may be obtained from linear mathematical equations or associated calibration lines or graphs or look-up tables or the like, may be used to determine the respective BCAA concentration. The calibration spectra are acquired under spectroscopic conditions which are identical to those used in the final assay, such as that shown in **Figures 3A-I**. As shown in **Figures 3A-I**, typical biological ranges for leucine, valine, and isoleucine are about $98.7 \pm 11.5 \mu\text{M}$, $212.3 \pm 62.3 \mu\text{M}$ and $60.7 \pm 18.6 \mu\text{M}$, respectively. In some embodiments, the calibration data may account for small differences in nuclear relaxation properties, typically less than 10%.

[00107] A respective single BCAA measurement or concentration may be used alone or in combination with another BCAA measurement or concentration or other metabolite measurement or concentration to evaluate a subject's clinical disease state and/or provide metabolic status or other therapeutic or diagnostic information. In some embodiments, a regression model may be used to correlate BCAA components into a composite BCAA number or score, weighted index and/or a BCAA ratio of different BCAA components with a particular therapeutic or diagnostic outcome.

[00108] In some embodiments, a pulse sequence can be configured to attenuate lipoproteins and proteins in an unfiltered biosample. One example is a CPMG sequence. Identification and/or quantification of other components (e.g., metabolites) in the biosample, such as, but not limited to, other amino acids (e.g., aromatic amino acids), organic acids, 2-

hydroxybutyrate, GlycA, GlycB, and/or lipoproteins may also be accomplished according to embodiments of the present invention.

[00109] In some embodiments, identification and/or quantification of a BCAA and an aromatic amino acid may be carried out with a sample mixture at a pH of about 7 or about 7.4.

[00110] The BCAA peak region may fall between about 0.85 ppm and about 1.10 ppm (at about 47°C sample temperature). The peak locations for valine, leucine, and isoleucine, at about 47°C sample temperature, may be as listed in the table in **Figure 2**.

[00111] In modeling the BCAA region of the NMR spectrum, an experimental and/or synthetic model may be used for a BCAA. The baseline may be modeled by CPMG processed experimental spectra of the individual protein and lipoprotein components that are known to contribute to this region. The model may also use synthetic functions such as, but not limited to, linear, quadratic and polynomial functions to fit the baseline component. The fitting approach may utilize the Lawson-Hanson non-negative linear least fitting method to achieve the best agreement between the experimental and modeled spectra.

[00112] **Figures 3A-I** show exemplary analytical models for BCAAs. In this example, a 100 ms delay CPMG pulse sequence was used. As can be seen in **Figures 3A-C**, the analytical models for leucine and valine were based on 16 scans and isoleucine was based on 96 scans. **Figures 3D-F** show the raw area NMR values for valine, leucine, and isoleucine based on 96 scans and **Figures 3G-I** show the converted NMR concentrations (μM) for the respective valine, leucine, and isoleucine values in **Figures 3D-F**. The concentrations can be calculated for normal biological ranges appropriating norms for each BCAA. Typical biological ranges for leucine, valine, and isoleucine are $98.7 \pm 11.5 \mu\text{M}$, $212.3 \pm 62.3 \mu\text{M}$ and $60.7 \pm 18.6 \mu\text{M}$, respectively, as described in Psychogios et al. (2011) The Human Serum Metabolome. PLoS ONE 6(2): e16957, Table 3. Concentrations (mean +/- standard deviation) of serum metabolites as determined by NMR.

[00113] According to some embodiments of the present invention, separate quantification of at least three BCAAs present in an unfiltered biosample may be accomplished without the need for an internal or external reference analyte.

[00114] Accurate quantification of BCAAs in an unfiltered biosample may be affected by B_0 homogeneities/inhomogeneities associated with the shimming of the spectrometer. Thus, in some embodiments, quantification may be carried out by selecting a deconvolution model with a CFF or a linewidth thereof on a sample to sample basis. For example, for each sample a linewidth and/or line shape of a defined reference peak(s) in the spectrum can be

evaluated. The reference peak(s) can include, but is not limited to, an EDTA peak and/or citrate peak.

[00115] A signature of at least one branched chain amino acids may be obtained according to embodiments of the present invention. An exemplary signature of all three branched chain amino acids is shown in **Figure 2**, which shows the fitting of the BCAA region of the spectrum. The signature shown in **Figure 2** was obtained from a 75:25 mixture of serum to citrate buffer (*i.e.*, diluent). The data was collected using a 16 scan CPMG experiment with an acquisition time of approximately 90 seconds and a 100 ms CPMG pulse train. The model included computationally derived basis functions for each of the three BCAAs as well as experimental protein and lipoprotein functions. The identification and/or quantification of signals of metabolites, including amino acids and organic acids, may also be obtained from such an experiment. According to some embodiments of the present invention, an experiment for the quantification of BCAAs as described herein may be appended to a standard Lipoprofile® lipoprotein analysis for high-throughput analysis of respective biosamples.

[00116] **Figure 4** shows an expansion of a ^1H NMR spectrum about the branched chain amino acid methyl region. The top spectrum was acquired with 96 scans and the bottom spectrum was acquired with 16 scans. In some embodiments, concentrations of leucine and valine can be calculated using less scans than isoleucine. Each BCAA can be calculated using the same NMR spectrum. Each BCAA can be evaluated using the same number of scans or a different number of scans.

[00117] Quantified measures of a BCAA in a biosample according to embodiments of the present invention may be used to determine a likelihood of a patient having or developing one or more defined clinical disease states. BCAAs may be associated with metabolic diseases, such as diabetes (*e.g.*, type 2 diabetes), CHD, liver diseases, and cancer. Accordingly, an assay of the present invention may be used to determine a patient's clinical disease state. In some embodiments, an assay according to embodiments of the present invention may be used to determine a patient's risk of developing a disease, such as, but not limited to a metabolic disease (*e.g.*, the patient's risk of incident diabetes).

[00118] According to some embodiments, an assay according to embodiments of the present invention may be used for disease prediction and/or intervention outcomes. In certain embodiments, the assay may be used as a predictor of improved insulin sensitivity in a patient and/or to determine if there has been an improvement in glycemic control in a patient. In other embodiments, the assay may be used in determining if there has been an enhancement

in liver regeneration in a patient or attenuation in muscle wasting in a patient, such as a cancer patient. In some embodiments, the assay may be used to determine the potential benefit and/or need for BCAA supplementation in a patient diagnosed with a wasting syndrome and/or severe inflammatory diseases (*e.g.*, sepsis, trauma, burn injury, etc.). In further embodiments, the assay may be used to guide and/or monitor the use of BCAAs in nutritional supplementation and/or improvement of health, wellness and/or athletic performance.

[00119] A defined mathematical deconvolution model can be used to quantify a BCAA. The "composite" or measured signal envelope C_m can be deconvolved to quantify the signal contributions of a BCAA and other contributing components such as lipoprotein subclass components. The deconvolution calculates signal amplitudes of the components contributing to the measured signal shapes and calculates the sum of the components. A close match between the calculated signal C and the measured signal C_m indicates the deconvolution successfully modeled the components that make up the NMR signal.

[00120] A curve fitting function or technique can be used according to embodiments of the present invention. The curve fitting may use different sets of basis functions that can vary biosample to biosample, which can include none, or one or more neighboring BCAA peaks that reside adjacent to a target BCAA peak.

[00121] The lineshape deconvolution can be achieved with a non-negative least squares fitting program (Lawson, CL, Hanson RJ, Solving Least Squares Problems, Englewood Cliffs, NJ, Prentice-Hall, 1974). This avoids the use of negative concentrations which will lead to error due especially in low signal to noise spectra. Mathematically, the lineshape analysis is described in detail for lipoproteins in the paper by Otvos, JD, Jeyarajah, EJ and Bennett, DW, Clin Chem, 37, 377, 1991. A synthetic baseline correction function may also be used to account for baseline offsets from residual protein components. This can take the form of a quadratic or other polynomial function. Weighting factors are determined and the fit can be optimized by minimizing the root mean squared deviation between the experimental and calculated spectrum. See, *e.g.*, U.S. Patent Nos. U.S. Patent Nos. 4,933,844 and 6,617,167 for a description of deconvolving composite NMR spectra to measure subclasses of lipoproteins, the contents of which are hereby incorporated by reference as if recited in full herein. See also, U.S. Patent No. 7,243,030 for a description of a protocol to deconvolve chemical constituents with overlapping signal contribution, the contents of which are hereby incorporated by reference as if recited in full herein.

[00122] **Figure 5** shows exemplary computational fitting for the three BCAAs. The panels on the left show the respective BCAA region from the expansions of the ^1H NMR spectral region about the branched amino acid methyl signals from the NMR spectrum on the right. For each amino acid a target peak or peaks for quantification have been boxed. The panels on the left show the "actual" spectrum (black), the "fitted" spectrum (light grey) with the associated fitting components (below). The fitting components (*e.g.*, gaussians or lorentzians or both) may contain experimental and/or computationally derived peaks and/or functions that model the contributions of the target analyte as well as the contributions from sources such as proteins, lipoproteins and known spectrometer induced offsets. In some embodiments, the fitting components may contain experimental and computationally derived peaks and functions that model the contributions of the target analyte as well as the contributions from sources such as proteins and lipoproteins. The factors and models may also provide for spectrometer induced offsets known to those of skill in the art such as DC offsets.

[00123] The pulse sequence parameters can include any appropriate parameters including solvent suppression scheme, pulse angle and acquisition time. However, generally stated, in some particular embodiments, the NMR signal acquisition time per scan, for any one biosample, can be between about 2-7 seconds (on average) and typically between about 5-6 seconds (on average), such as about 5.6 seconds (on average). In some embodiments, the total acquisition time is about 90 seconds (on average) or up to about 5 or 10 minutes (on average). The NMR analyzer may be configured to obtain at least 10 scans per biosample, typically between 10-256 scans, such as 16 scans, and possibly ≥ 96 , such as 96 scans or 128 scans with at least about 16K data points collected over a 4400 Hz sweep width, per sample, to obtain the NMR data used to measure BCAA. The BCAA scan can be carried out before or after a lipoprotein scan sequence, which typically employs a different pulse sequence to allow for quantification of lipoproteins.

[00124] In some embodiments, one element in the pulse sequence can be a solvent suppression scheme. A WET solvent suppression scheme uses a series of shaped pulses and pulsed field gradients over the course of, for example, about 80 ms. The 1D NOESY-presat scheme uses the first increment of a 2D Nuclear Overhauser Effect Spectroscopy (NOESY) experiment (Beckonert, O.; Keun, H. C.; Ebbels, T. M. et. al. *Nat. Protoc.* 2007, 2, 2692-2703). In this scheme, a continuous low power, frequency selective pulse on water resonance is applied during D1 and 'mixing' time. The PURGE solvent suppression scheme (Simpson, A. J.; Brown, S. A. *J. Magn. Reson.* 2005, 175, 340-346) uses a continuous low power,

frequency selective pulse on water resonance, relaxation gradients and echoes to attenuate the water signal.

[00125] The performance of all three sequences (and potentially other sequences known to those of skill in the art) is sufficient to achieve consistent solvent suppression in the spectra. Stated differently, a BCAA NMR signal may be obtained using CPMG and a WET, PRESAT, and/or PURGE protocol may be included as part of a pulse sequence. One advantage of the WET sequence is that it does not involve any low power saturation period which could perturb the protein baseline via spin diffusion. It also does not have any significant delays which could lead to signal attenuation via relaxation.

[00126] As is well known, a standard presaturation ("Presat") pulse sequence can be used in a pulse sequence to obtain the NMR spectrum for analyzing the BCAA signal. This pulse sequence involves a selective low power pulse targeting the water resonance and lasting several seconds. This is well established in NMR practice and is a robust and reliable method to attenuate the water signal.

[00127] In some embodiments, the WET water suppression scheme can be used. The WET sequence involves a series of short selective pulses targeting the water resonance. The entire scheme is prefixed to the pulse sequence as is the Presat, but only requires, for example, about 80 ms. The other advantage of the WET sequence is the fact that this sequence imposes only a minimal perturbation on the protein signals. Due to the length of a typical Presat sequence, some of the solvent saturation can be transferred to the protein which can lead to inconsistent contributions of the protein to the baseline. Other solvent presaturation schemes can be used, e.g., a PURGE sequence.

[00128] The flowcharts and block diagrams of certain of the figures herein illustrate the architecture, functionality, and operation of possible implementations of analysis models and evaluation systems and/or programs according to the present invention. In this regard, each block in the flow charts or block diagrams represents a module, segment, operation, or portion of code, which comprises one or more executable instructions for implementing the specified logical function(s). It should also be noted that in some alternative implementations, the functions noted in the blocks might occur out of the order noted in the figures. For example, two blocks shown in succession may in fact be executed substantially concurrently or the blocks may sometimes be executed in the reverse order, depending upon the functionality involved.

[00129] **Figure 6** illustrates a standard "one-pulse" sequence with WET solvent suppression. This leads to a spectrum in which the signals from the high concentrations of

proteins and macromolecular aggregates, e.g. lipoprotein particles, dominate the spectra. The lower concentration, small molecule metabolites are greatly obscured in these spectra. As shown in **Figure 6**, the WET solvent suppression scheme (Smallcombe, S. H.; Patt, S. L.; Keifer, P. A. *J. Magn. Reson., Ser. A* 1995, 117, 295-303) includes a series of solvent-directed selective pulses and pulsed field gradients followed by a read pulse and an acquisition time during which the signal is digitized for a fixed amount of time.

[00130] The second sequence shown in **Figure 7** incorporates a CPMG pulse train or sequence. This pulse train includes a series of refocusing π pulses (180 degrees) during which the signals from large, rapidly relaxing molecules are attenuated. The duration of this pulse train can be optimized to minimize the background signals from macromolecules, e.g. proteins and lipoprotein particles, while maintaining most of the signal intensity from the small molecules such as BCAA. This value is set to 100 ms, but other delays can be used. For example, CPMG pulse sequence delays may be set to 60 ms, 100 ms, 200 ms, 300 ms, or 400 ms. Thus, the CPMG pulse train shown in **Figure 7** is designed to attenuate the signals from the macromolecules which facilitate the detection of many more small molecule metabolites. This pulse sequence relies on the fact that the signals from macromolecules relax much faster than small molecules. The spin-echo train occurring can occur after the read pulse and is designed to maintain the small molecule magnetization while the signals from the macromolecules relax back to equilibrium. The duration of this spin echo train relates to the degree of attenuation of the macromolecule signals. This delay is typically set to between about 60 ms to about 400 ms (**Figure 8**). It is expected that there will be little perceptible change in performance over the range from about 60 ms to about 150 ms. In some cases this delay could be set to as high as about 400 ms if the benefit of increased attenuation of the proteins and lipoproteins offsets the reduced signal to noise. In some embodiments, attenuation of the BCAA NMR signal caused by the pulse sequence may be corrected using an adjustment factor.

[00131] In order to obtain an increased (e.g., maximum) signal from a molecule, a 90 degree pulse can be used and the time between these pulses should be in excess of 10 times the longitudinal relaxation time (T_1) of the signal. The T_1 for a BCAA at 400 MHz may be in a range of about 1.5 to about 3 seconds. This may not be a time efficient means to maximize the signal intensity so a compromise between pulse length and inter-pulse delay can be made. The relationship between signal intensity, T_1 , and pulse length is given by the Ernst angle equation. The first step in using this equation is to define the length of the entire pulse sequence. The length is defined by the required solvent suppression period, the CPMG

delay and the length of the data acquisition period needed to provide the required digitization of the FID. The Ernst angle equation is as follows:

$$\cos(\theta) = \exp(-(\text{total delay})/T1) \quad \text{EQUATION (1)}$$

[00132] In equation (1), the total delay equals the d1 delay (including solvent suppression), the CPMG time, plus the acquisition time. T1 represents the longitudinal relaxation time of the analyte signal of interest. It is noted that in front of the parentheses containing "total delay" is a negative sign. Solving for theta will give an optimal flip angle.

[00133] Using a standard set of experimental conditions, for example, a 1 second period for solvent suppression, 100ms CPMG, and an acquisition time of about 3 seconds, the Ernst angle may prescribe the tip angle (also known as the pulse length when described in microseconds) that is reduce from 90 degrees down to between 60 and 80 degrees. The equation is relatively insensitive in this region so it is unlikely that small errors in calibration or small differences in the T1 due to specific sample composition will lead to significant inefficiency.

[00134] The acquisition time (AT) is the time that the FID is digitized. The duration of AT is determined by both the relaxation time of the signal(s) being quantified and the required digitization. If the relaxation time of the signal being examined is longer than the AT then the FID will become truncated resulting in a signal with poor shape. As mentioned above, the T1 relaxation time for a BCAA may be less than about 3 seconds in serum and thus the acquisition time for a scan should be at least that long. The digitization rate of the spectrometer, i.e. the number of points taken per second of acquisition time, is determined by the sweep width of the spectrum. In some embodiments, a desired digital resolution uses at least 16K data points that are collected over the 4400Hz sweep width.

[00135] The most direct way to increase the detection sensitivity is to increase the number of scans. In some embodiments, the BCAA assay can be carried out on samples at about 47°C so that this assay can be easily interleaved or used with the current LipoProfile® assay from LipoScience, Inc. (Raleigh, NC). However, as the number of scans increases, the residence time of the sample in the probe at 47°C increases and the samples may become denatured. The challenge is to achieve the requisite signal-to-noise ratio for a BCAA peak to allow accurate and precise quantification over a desired biological range (at least those with adverse clinical association).

[00136] In some embodiments, the NMR assay may include a separate quantification for each BCAA and/or a total quantification of at least three of the BCAAs (*i.e.*, the

quantified sum of the BCAAs) present in a biosample, and each of the quantified measurements may be provided in a patient report for clinical consideration. It is contemplated that the separate or total quantification of the BCAAs in a single *in vitro* biosample may provide important clinical information and/or further improve a prediction or evaluation of a patient's risk of having a clinical disease state or being at increased risk for a clinical disease state.

[00137] **Figure 8** shows an array of CPMG acquired ^1H NMR spectra according to embodiments of the present invention. The spectra may be acquired using the CPMG sequence which suppresses the contributions to the spectrum from macromolecules such as proteins and macromolecular aggregates such as lipoproteins. As shown in **Figure 7** the CPMG pulse sequence may involve a pulse train of variable delay during which the signals from the large molecules decay away thereby enabling the detection of more of the small molecule metabolites. The longer CPMG delay times may lead to greater the attenuation of these signals. This delay may also attenuate the small molecule signals, but to a significantly lesser extent. **Figure 9** shows expansion of the array of CPMG spectra acquired with different total delay times. The expansion focuses on the methyl region of the BCAAs as previously shown in **Figure 4**. Notice that the signals in the lipoprotein region are significantly attenuated while the total intensity of the BCAA peaks is less affected.

[00138] Referring now to **Figure 10**, it is contemplated that the quantification of a BCAA may be carried out using a system 10 with an NMR clinical analyzer 22 as described, for example, with respect to **Figure 11** below and/or in U.S. Patent No. 8,013,602, the contents of which are hereby incorporated by reference as if recited in full herein. The analyzer 22 includes a spectrometer 22s and sample handler system.

[00139] The system 10 can include a BCAA analysis module and/or circuit 20 that can be onboard the analyzer 22 or at least partially remote from the analyzer 22. If the latter, the analysis module or circuit 20 can reside totally or partially on a server 150. The server 150 can be provided using cloud computing which includes the provision of computational resources on demand via a computer network. The resources can be embodied as various infrastructure services (e.g. computer, storage, etc.) as well as applications, databases, file services, email, etc. In the traditional model of computing, both data and software are typically fully contained on the user's computer; in cloud computing, the user's computer may contain little software or data (perhaps an operating system and/or web browser), and may serve as little more than a display terminal for processes occurring on a network of external computers. A cloud computing service (or an aggregation of multiple cloud resources) may

be generally referred to as the "Cloud". Cloud storage may include a model of networked computer data storage where data is stored on multiple virtual servers, rather than being hosted on one or more dedicated servers. Data transfer can be encrypted and can be done via the Internet using any appropriate firewalls to comply with industry or regulatory standards such as HIPAA. The term "HIPAA" refers to the United States laws defined by the Health Insurance Portability and Accountability Act. The patient data can include an accession number or identifier, gender, age and test data.

[00140] The results of the analysis can be transmitted via a computer network, such as the Internet, via email or the like to a patient, clinician site 50, to a health insurance agency 52 or a pharmacy 51. The results can be sent directly from the analysis site or may be sent indirectly. The results may be printed out and sent via conventional mail. This information can also be transmitted to pharmacies and/or medical insurance companies, or even patients that monitor for prescriptions or drug use that may result in an increase risk of an adverse event or to place a medical alert to prevent prescription of a contradicted pharmaceutical agent. The results can be sent to a patient via email to a "home" computer or to a pervasive computing device such as a smart phone or notepad and the like. The results can be as an email attachment of the overall report or as a text message alert, for example.

[00141] Referring now to Figure 11, a system 207 for acquiring and calculating the lineshape of a selected sample is illustrated. The system 207 includes an NMR spectrometer 22s for taking NMR measurements of a sample. In one embodiment, the spectrometer 22s is configured so that the NMR measurements are conducted at 400 MHz for proton signals; in other embodiments the measurements may be carried out at between 200 MHz to about 900 MHz or other suitable frequency. Other frequencies corresponding to a desired operational magnetic field strength may also be employed. Typically, a proton flow probe is installed, as is a temperature controller to maintain the sample temperature at 47 +/- 0.5 degrees C. However, other sample temperatures may be used during acquisition time. The spectrometer 22 is controlled by a digital computer 214 or other signal processing unit. The computer 211 should be capable of performing rapid Fourier transformations. It may also include a data link 212 to another processor or computer 213, and a direct-memory-access channel 214 which can connects to a hard memory storage unit 215.

[00142] The digital computer 211 may also include a set of analog-to-digital converters, digital-to-analog converters and slow device I/O ports which connect through a pulse control and interface circuit 216 to the operating elements of the spectrometer 22s. These elements include an RF transmitter 217 which produces an RF excitation pulse of the

duration, frequency and magnitude directed by at least one digital signal processor that can be onboard or in communication with the digital computer 211, and an RF power amplifier 218 which amplifies the pulse and couples it to the RF transmit coil 219 that surrounds sample cell 220 and/or flow probe 220p. The NMR signal produced by the excited sample in the presence of a 9.4 Tesla polarizing magnetic field produced by superconducting magnet 221 is received by a coil 222 and applied to an RF receiver 223. The amplified and filtered NMR signal is demodulated at 224 and the resulting quadrature signals are applied to the interface circuit 216 where they are digitized and input through the digital computer 211. The lipoprotein measurement and/or BCAA analyzer circuit 20 and/or module 350 (Figures 11-12) can be located in one or more processors associated with the digital computer 211 and/or in a secondary computer 213 or other computers that may be on-site or remote, accessible via a worldwide network such as the Internet 227.

[00143] After the NMR data are acquired from the sample in the measurement cell 220, processing by the computer 211 produces another file that can, as desired, be stored in the storage 215. This second file is a digital representation of the chemical shift spectrum and it is subsequently read out to the computer 213 for storage in its storage 225 or a database associated with one or more servers. Under the direction of a program stored in its memory or accessible by the computer 213, the computer 213, which may be a laptop computer, desktop computer, workstation computer, electronic notepad, electronic tablet, smartphone or other device with at least one processor or other computer, processes the chemical shift spectrum in accordance with the teachings of the present invention to generate a report which may be output to a printer 226 or electronically stored and relayed to a desired email address or URL. Those skilled in this art will recognize that other output devices, such as a computer display screen, electronic notepad, smartphone and the like, may also be employed for the display of results.

[00144] It should be apparent to those skilled in the art that the functions performed by the computer 213 and its separate storage 225 may also be incorporated into the functions performed by the spectrometer's digital computer 211. In such case, the printer 226 may be connected directly to the digital computer 211. Other interfaces and output devices may also be employed, as are well-known to those skilled in this art.

[00145] Certain embodiments of the present invention are directed at providing methods, systems and/or computer program products that use BCAA evaluations that may be particularly useful in automated screening tests of clinical disease states and/or risk assessment evaluations for screening of *in vitro* biosamples.

[00146] Embodiments of the present invention may take the form of an entirely software embodiment or an embodiment combining software and hardware aspects, all generally referred to herein as a "circuit" or "module."

[00147] As will be appreciated by one of skill in the art, the present invention may be embodied as an apparatus, a method, data or signal processing system, or computer program product. Accordingly, the present invention may take the form of an entirely software embodiment, or an embodiment combining software and hardware aspects. Furthermore, certain embodiments of the present invention may take the form of a computer program product on a computer-usable storage medium having computer-usable program code means embodied in the medium. Any suitable computer readable medium may be utilized including hard disks, CD-ROMs, optical storage devices, or magnetic storage devices.

[00148] The computer-usable or computer-readable medium may be, but is not limited to, an electronic, magnetic, optical, electromagnetic, infrared, or semiconductor system, apparatus, device, or propagation medium. More specific examples (a non-exhaustive list) of the computer-readable medium would include the following: an electrical connection having one or more wires, a portable computer diskette, a random access memory (RAM), a read-only memory (ROM), an erasable programmable read-only memory (EPROM or Flash memory), an optical fiber, and a portable compact disc read-only memory (CD-ROM). Note that the computer-usable or computer-readable medium could even be paper or another suitable medium, upon which the program is printed, as the program can be electronically captured, via, for instance, optical scanning of the paper or other medium, then compiled, interpreted or otherwise processed in a suitable manner if necessary, and then stored in a computer memory.

[00149] Computer program code for carrying out operations of the present invention may be written in an object oriented programming language such as Java7, Smalltalk, Python, Labview, C++, or VisualBasic. However, the computer program code for carrying out operations of the present invention may also be written in conventional procedural programming languages, such as the "C" programming language or even assembly language. The program code may execute entirely on the user's computer, partly on the user's computer, as a stand-alone software package, partly on the user's computer and partly on a remote computer or entirely on the remote computer. In the latter scenario, the remote computer may be connected to the user's computer through a local area network (LAN) or a wide area network (WAN), or the connection may be made to an external computer (for example, through the Internet using an Internet Service Provider).

[00150] **Figure 12** is a block diagram of exemplary embodiments of data processing systems **305** that illustrates systems, methods, and computer program products in accordance with embodiments of the present invention. The processor **310** communicates with the memory **314** via an address/data bus **348**. The processor **310** can be any commercially available or custom microprocessor. The memory **314** is representative of the overall hierarchy of memory devices containing the software and data used to implement the functionality of the data processing system **305**. The memory **314** can include, but is not limited to, the following types of devices: cache, ROM, PROM, EPROM, EEPROM, flash memory, SRAM, and DRAM.

[00151] As shown in **Figure 12**, the memory **314** may include several categories of software and data used in the data processing system **305**: the operating system **352**; the application programs **354**; the input/output (I/O) device drivers **358**; a BCAA Evaluation Module **350**; and the data **356**. The BCAA Evaluation Module **350** can deconvolve NMR signal to reveal a defined NMR signal peak region in proton NMR spectra of a respective biosample to identify a level of BCAA. The system **305** may also include one or more of a Clinical Disease State Evaluation Module or a Risk Prediction Module that considers the level of the measured BCAA or generates a ratio, composite risk number, or multi-parameter risk model.

[00152] The data **356** may include signal (constituent and/or composite spectrum lineshape) data **362** which may be obtained from a data or signal acquisition system **320** (e.g., NMR spectrometer **22s** and/or analyzer **22**). As will be appreciated by those of skill in the art, the operating system **352** may be any operating system suitable for use with a data processing system, such as OS/2, AIX or OS/390 from International Business Machines Corporation, Armonk, NY, WindowsCE, WindowsNT, Windows95, Windows98, Windows2000 or WindowsXP from Microsoft Corporation, Redmond, WA, PalmOS from Palm, Inc., MacOS from Apple Computer, UNIX, FreeBSD, or Linux, proprietary operating systems or dedicated operating systems, for example, for embedded data processing systems.

[00153] The I/O device drivers **358** typically include software routines accessed through the operating system **352** by the application programs **354** to communicate with devices such as I/O data port(s), data storage **356** and certain memory **314** components and/or the image acquisition system **320**. The application programs **354** are illustrative of the programs that implement the various features of the data processing system **305** and can include at least one application, which supports operations according to embodiments of the present invention. Finally, the data **356** represents the static and dynamic data used by the

application programs 354, the operating system 352, the I/O device drivers 358, and other software programs that may reside in the memory 314.

[00154] While the present invention is illustrated, for example, with reference to the Module 350 being an application program in Figure 12, as will be appreciated by those of skill in the art, other configurations may also be utilized while still benefiting from the teachings of the present invention. For example, the BCAA Module 350 may also be incorporated into the operating system 352, the I/O device drivers 358 or other such logical division of the data processing system 305. Thus, the present invention should not be construed as limited to the configuration of Figure 12, which is intended to encompass any configuration capable of carrying out the operations described herein.

[00155] In certain embodiments, the Module 350 includes computer program code for providing a level of BCAA which may be used as a marker to assess a clinical disease state or risk and/or to indicate whether therapy intervention is desired and/or track efficacy of a therapy or even an unintended consequence of a therapy.

[00156] Figure 13 is a flow chart of exemplary operations that can carry out embodiments of the present invention. A (measured) composite envelope NMR spectrum of NMR spectra of a fitting region of a biosample (e.g., blood plasma or serum) can be obtained (block 400). The NMR composite signal envelope is electronically deconvolved using a defined model having at least one BCAA peak region centered at a defined chemical shift location (e.g., between about 0.85 ppm and about 1.10 ppm) (block 402).

[00157] A defined number of (e.g., Lorentzian and/or Gaussian) curve fit functions for the peak region associated with a respective BCAA can be summed (block 415). A conversion factor can be applied to the summed functions to generate a calculated measurement of BCAA (block 420).

[00158] A CFF or linewidth of a CFF can be selected based on a linewidth of at least one reference peak that is associated with a measure of shim status of a spectrometer used to obtain the composite NMR spectrum (block 414).

[00159] The BCAA measurement can be provided in a patient and/or clinical trial report (block 422). The report can identify or alert as to whether he or she is at risk of having or developing a clinical disease state and/or whether additional screening may be appropriate, based at least in part on the BCAA measurement (block 424).

[00160] Figures 14A-14C are exemplary flow diagrams of operations that can be used to obtain NMR signal associated with valine according to embodiments of the present invention.

[00161] **Figure 14A** illustrates that a pre-analytical evaluation (block 610) can occur before a BCAA region, such as, for example, a valine region, of the NMR signal is determined (block 625), then deconvolved (block 650). **Figure 14B** illustrates an exemplary pre-analytical evaluation 610 which includes delivery verification of the sample into the flow cell as either complete failure (block 612) or partial injection failure (block 613), shimming verification (block 615), temperature verification (block 617) and a citrate tube detection (failure) (block 619), all using defined characteristics of signal associated with a defined diluent added to the sample. The shimming verification can include applying a quantitative shimming adjustment factor. Any suitable reference analyte may be used to generate the reference peak for use in the pre-analytical evaluation. The variables used in the evaluation will be determined based on the reference peak selected.

[00162] Referring again to **Figure 14A**, once the defined parameters are confirmed within limits, the pre-analytical quality control analysis can end (block 620) and the determination of the valine region can be identified (block 625) and the spectrum deconvolved and valine level calculated (block 650). Optionally, a post-analytical quality control can be electronically performed (block 655) and the results output (block 660). The results can be included in a test report with comments, visual indicia of high or low and the like (block 665).

[00163] Referring to **Figure 14C**, an exemplary method/analysis 700 of operations that can be used to quantify valine are shown. NMR signal can be electronically obtained of an *in vitro* biosample with a defined added diluent (block 702). The QC evaluation can be carried out (block 710). The valine region is determined (block 725). The valine region is deconvolved (block 750d) and an NMR derived value of valine is calculated (750c).

[00164] The diluents can comprise a reference analyte, such as, for example, calcium ethylenediamine tetraacetic acid (Ca EDTa) (block 703) or other suitable diluent that creates a reliable peak and behaves in a predictable manner. Well established chemical shift or quantitation reference analytes include, for example, formate, trimethylsilylpropionate (and isotopically labeled isomers), and EDTA.

[00165] The pre-analytical quality control evaluation 710 can be based on inspection of characteristics of a reference peak, such as, for example, an CaEDTA reference peak, and the system or processor can be configured not to perform the Valine test unless the NMR spectra have been acquired under specified conditions such as those shown in **Figure 14B**. The sample temperature can be 47 ± 0.5 °C in the flow cell for NMR scans/signal acquisition. The sample can comprise diluents in a 1:1 ratio (block 705) or other defined ratio (e.g., more

sample, less diluents or more diluent; less sample, e.g., 2:1 or more sample, less diluents, e.g. 1:2).

[00166] The test sample can be rejected with a defined error code if CaEDTA height > 140 for any acquired spectrum (block 719). This high value is indicative of detection of the citrate peak in conjunction with the CaEDTA peak. The citrate peak is introduced by collection of the specimen in an improper citrate tube. By disrupting the ability to locate the exact position of the CaEDTA peak, the citrate peak can disrupt the process for determining the Valine region.

[00167] The Valine region is located upfield relative to the position of the CaEDTA peak. The broad peaks beneath Valine are various methyl ($-\text{CH}_3$ -) protons of lipoproteins. The CaEDTA location can be determined at approximately 22258 ± 398 data points (block 721). The Valine region can be determined independently for each acquired spectrum. The Valine signal can be modeled with suitable data points using, for example, 25 data points (center ± 12 data points) for each peak of the quartet or 300 data points for the valine region of both doublets, but other numbers of data points may be used. The measurement of Valine can be carried out using one, two, three or all four peaks of the valine peak quartet.

[00168] All basis set spectra can be linearly interpolated before utilized by the non-negative least squares algorithm. The spectra to be analyzed and the basis set spectra can have a zero baseline offset modification before utilized by the non-negative least squares algorithm.

[00169] The start of the Valine region can be at about 2196-4355 data points, typically the latter when including both doublets, (the "Valine region offset") upfield from the location of the CaEDTA peak (block 722). In some embodiments, the start of the valine region is at 4355 data points upfield from the location of the CaEDTA peak.

In some embodiments, the valine quantification is carried out by characterizing the valine resonances at between 0.0-1.01 ppm as two doublets. Three or more valine experimental spectra stepped by two data points can be used as basis sets to model valine signal. The center valine peaks can be located by sliding three valine components ± 15 data points and determined through a least squares sum minimization. The valine signal can be modeled with a total of about 300 data points. The fitting algorithm may use the defined scalar coupling patterns of the experimental or computationally derived functions to help constrain and optimize the fitting.

[00170] Each basis set, including those used for the baseline but excluding the DC offset, are offset such that the lowest value is subtracted from the function (making the lowest point equal to 0). This prevents inclusion of a DC offset in the shapes they represent. The

[00171] Valine region from each acquired spectrum is deconvolved with a series of analyte and baseline functions which have been treated to the same type of pre-processing as the acquired spectra. The deconvolution coefficient for each component can be multiplied by an associated conversion factor. The resulting values are summed. Result values produced independently for each acquired spectrum can be averaged to generate final values to use in the measurement.

[00172] Data can be acquired using presaturation water suppression from a 1:1 diluted sample and can include about 16 scans, typically about 16 scans stored as 8 blocks of 2 (8 FIDs consisting of 2 scans each) (block 726).

[00173] The pulse sequence used in conjunction with presaturation water suppression can optionally include a presaturation (water suppression) pulse and a suitable excitation pulse. For example, FIDs can be acquired with 9024 data points with a sweep width of 4496.4 Hz, but as known to those of skill in the art other data points and sweep widths may be used. Each FID can be multiplied with a shifted Gaussian function:

$$e^{-\left(\frac{(t-gfs)}{gf}\right)^2}, \text{ or in computer terms, } \exp(-((t-gfs)/gf)^2), \text{ where } gfs = 0.2 \text{ seconds and } gf = 0.2 \text{ seconds.}$$

[00174] This can be performed prior to Fourier transformation with zero-filling which yields the frequency-domain GM spectrum for each FID consisting of 16,384 data points (block 727). Each FID can be multiplied by a mathematical function to increase signal to noise (*e.g.*, a decaying exponential) and/or resolution (*e.g.*, a Gaussian type function and/or any shifted version thereof). The spectra can be phased using the calibration-specified phase value. The spectra can be scaled (multiplied) by a calibration-specified scaling factor. All basis set spectra can be linearly interpolated before utilized by the non-negative least squares algorithm. The spectra to be analyzed and the basis set spectra can have a zero baseline offset modification before utilized by the non-negative least squares algorithm (*e.g.*, all components used for the model and the spectrum that will be analyzed can be linearly interpolated) (block 728). To determine the center of the valine fitting region, the valine

resonances between 0.9 and 1.0 as two doublets can be characterized and the center peaks can be identified by sliding three valine components ± 15 data points (block 729).

[00175] The foregoing is illustrative of the present invention and is not to be construed as limiting thereof. Although a few exemplary embodiments of this invention have been described, those skilled in the art will readily appreciate that many modifications are possible in the exemplary embodiments without materially departing from the novel teachings and advantages of this invention. Accordingly, all such modifications are intended to be included within the scope of this invention as defined in the claims. In the claims, means-plus-function clauses, where used, are intended to cover the structures described herein as performing the recited function and not only structural equivalents but also equivalent structures. Therefore, it is to be understood that the foregoing is illustrative of the present invention and is not to be construed as limited to the specific embodiments disclosed, and that modifications to the disclosed embodiments, as well as other embodiments, are intended to be included within the scope of the appended claims. The invention is defined by the following claims, with equivalents of the claims to be included therein.

That Which Is Claimed Is:

1. A method of determining concentrations of BCAAs, comprising:
placing at least one unfiltered *in vitro* serum or plasma sample in an NMR spectrometer having a static magnetic field B_0 ;
electronically obtaining an NMR spectrum of the sample that includes peaks associated with a plurality of BCAAs;
deconvolving the NMR spectrum using defined curve fitting functions;
computing unitless intensity signals from the deconvolved spectrum associated with respective BCAAs; then
electronically calculating concentrations of the plurality of BCAAs using respective correlations of values of the computed intensity signals with known concentrations of corresponding BCAAs.
2. The method of Claim 1, wherein the electronically calculating concentrations is carried out for each of the plurality of BCAAs using a respective defined linear equation associated with concentrations over at least a normal biological range.
3. The method of Claim 1, further comprising, for each NMR spectrum of each respective sample before the deconvolving, electronically evaluating at least one reference peak in the NMR spectrum to assess magnetic field inhomogeneity and/or to select an appropriate fitting function or linewidth thereof, wherein linewidth and/or lineshape of the at least one reference peak is associated with magnetic field B_0 inhomogeneity and/or homogeneity.
4. The method of Claim 1, further comprising applying scalar coupling information to BCAA peaks in the obtained NMR spectrum to thereby facilitate fitting during the deconvolving.
5. The method of Claim 1, further comprising, for each sample, before the deconvolving, electronically determining a location, lineshape and/or linewidth of at least one endogenous or exogenous reference peak(s) present in respective samples that has shape characteristics dependent on homogeneity of B_0 .

6. The method of Claim 1, further comprising, computationally determining lineshape and/or linewidth characteristics of each NMR spectrum for respective samples before the deconvolving step using at least one reference peak to account for differences in magnetic field homogeneity characteristics associated with a respective individual NMR spectrum, then selecting a defined deconvolution model with fitting functions having a linewidth and/or lineshape corresponding to the at least one reference peak such that different samples can be evaluated differently using (a) different fitting functions and/or (b) different linewidths.

7. The method of Claim 4, wherein the scalar coupling information identifies multiple peaks which are separated by a consistent distance as measured in Hertz, irrespective of magnetic field strength, and wherein the deconvolving comprises fitting functions that can be constrained to a separation distance at or near the distance to thereby constrain the fitting.

8. The method of Claim 1, wherein the electronically calculating the concentrations includes applying a scalar concentration value defined as a linear function of concentrations versus unitless intensity signal correlations for each BCAA.

9. The method of Claim 1, wherein the BCAAs comprise valine, isoleucine and leucine, and wherein the deconvolving is carried out using a baseline that is fit using protein and lipoprotein components.

10. The method of Claim 1, further comprising, before the deconvolving, electronically evaluating at least one pH chemical-shift invariant reference peak in the obtained NMR spectrum associated with an endogenous or exogenous analyte or component of the sample, then determining a location of BCAA peaks in the NMR spectrum.

11. The method of Claim 1, wherein the electronically obtaining is carried out using between about 10 seconds to about 5 minutes of NMR acquisition time (AT) for a single NMR spectrum per sample.

12. The method of Claim 10, wherein the electronically obtaining is carried out using between about 16-96 scans for a respective sample NMR spectrum, and wherein the electronically calculating the BCAA concentrations is carried out using a single NMR spectrum per sample.

13. The method of Claim 1, further comprising transmitting a pulse sequence that attenuates signal from lipoproteins and proteins in the sample to a greater degree than signal from small molecule BCAAs.

14. The method of Claim 13, wherein the pulse sequence comprises a Carr-Purcell-Meiboom-Gill (CPMG) pulse sequence with a defined delay that attenuates the lipoprotein and protein signals.

15. The method of Claim 14, wherein the CPMG pulse sequence has a delay of between about 60 ms to about 400 ms.

16. The method of Claim 15, wherein the CPMG pulse sequence has a delay of about 100 ms.

17. The method of Claim 15, wherein the CPMG pulse sequence has a delay of about 200 ms, the method further comprising electronically correcting the calculated concentrations for quantification errors associated with attenuation of signal intensity of the BCAAs associated with the CPMG pulse sequence.

18. The method of Claim 15, wherein the CPMG pulse sequence has a delay of about 300 ms, the method further comprising electronically correcting the calculated concentrations for quantification errors associated with attenuation of signal intensity of the BCAAs associated with the CPMG pulse sequence.

19. The method of Claim 15, wherein the CPMG pulse sequence has a delay of about 400 ms, the method further comprising electronically correcting the calculated concentrations for quantification errors associated with attenuation of signal intensity of the BCAAs associated with the CPMG pulse sequence.

20. The method of Claim 1, wherein the method includes transmitting a first lipoprotein pulse sequence and obtaining a first NMR spectrum associated with lipoproteins and proteins in the sample while the sample is in the NMR spectrometer and transmitting a

second pulse sequence to obtain the NMR spectrum associated with the BCAAs that is configured to attenuate protein and lipoprotein signals before or after the first pulse sequence to obtain the NMR spectrum of the BCAAs, wherein both pulse sequences and subsequent NMR spectra are obtained within about 2 minutes to about 6 minutes of NMR signal acquisition time per sample.

21. The method of Claim 1, further comprising flowing respective samples into the NMR spectrometer before the obtaining step, and wherein the obtaining is carried out by serially obtaining respective NMR spectrums at a rate that is between about 50 and 250 unfiltered samples per 8 hours.

22. The method of Claim 1, wherein the plurality of BCAAs includes valine, isoleucine and leucine, and wherein valine and leucine are quantified using less scans associated with the obtained NMR spectrum than isoleucine.

23. The method of Claim 1, wherein the NMR spectrum used to calculate valine and leucine is generated using between 16-96 scans, and wherein the NMR spectrum used to calculate isoleucine is generated using 96 scans.

24. The method of Claim 1, wherein the electronically calculating is carried out using a respective defined linear concentration equation for each BCAA to provide a clinically relevant concentration measurement of at least normal biological concentration ranges.

25. The method of Claim 20, wherein the first pulse sequence is the pulse sequence shown in Figure 6.

26. The method of Claim 1, further comprising electronically calculating a ratio or weighted index that is predictive of a clinical outcome or disease risk or identifies an efficacy of a drug or drug candidate, wherein the ratio or weighted index has at least one of the following: (a) a numerator comprising at least one of the unitless signals or calculated concentrations of one or more of the BCAAs; (b) a denominator comprising at least one of the unitless signals or calculated concentrations of one or more of the BCAAs; or (c) a numerator and a denominator that comprises at least one of the unitless signals or calculated concentrations of one or more of the BCAAs.

27. The method of Claim 1, further comprising electronically calculating a ratio and/or weighted index that is predictive of a clinical outcome or disease risk or identifies an efficacy of a drug or drug candidate, wherein the ratio or weighted index comprises in the denominator or numerator or in both the denominator and numerator at least one of the unitless signals or calculated concentrations of one or more of the BCAAs.

28. The method of Claim 1, further comprising electronically calculating a ratio and/or weighted index that is predictive of a clinical outcome or disease risk or identifies an efficacy of a drug or drug candidate, wherein the ratio and/or weighted index comprises in the denominator or numerator or in both the denominator and numerator at least one of the unitless signals or calculated concentrations of one or more of the BCAAs and a unitless signal or concentration measurement of an amino acid.

29. A circuit configured to provide measurements of BCAAs, comprising:
at least one processor configured to carry out the steps of any of Claims 1-28.

30. A computer program product for evaluating *in vitro* patient biosamples, the computer program product comprising:
a non-transitory computer readable storage medium having computer readable program code embodied in the medium, the computer-readable program code comprising:
computer readable program code configured to deconvolve a NMR spectrum with Branched Chain Amino Acid (BCAA) peaks of respective unfiltered patient samples using defined fitting functions;
computer readable program code that computes unitless intensity signals from the deconvolved spectrum associated with respective BCAAs; and
computer readable program code configured to provide concentrations of the BCAAs for the unitless intensity signals.

31. The computer program product of Claim 30, configured to carry out one or more of method Claims 2-28.

32. A system, comprising:
an NMR spectrometer for acquiring at least one NMR spectrum of respective *in vitro* biosamples, the NMR spectrometer having a static magnetic field B_0 ; and

at least one processor in communication with the NMR spectrometer, the at least one processor configured, for a respective biosample, using the acquired at least one NMR spectrum:

deconvolve the NMR spectrum using defined fitting functions;
compute unitless intensity signals from the deconvolved spectrum associated with respective BCAAs; then
calculate concentrations of the plurality of BCAAs using respective correlations of values of the computed intensity signals with known concentrations of corresponding BCAAs.

33. The system of Claim 32, wherein the at least one processor is configured to computationally determine lineshape and/or linewidth characteristics of each NMR spectrum for respective samples before the deconvolving step using at least one reference peak to account for differences in magnetic field homogeneity characteristics associated with a respective individual NMR spectrum, then select a defined deconvolution model with fitting functions having a linewidth and/or lineshape corresponding to the at least one reference peak such that different samples can be evaluated differently using (a) different fitting functions and/or (b) different linewidths.

34. The system of Claim 32, wherein the at least one processor is configured to, before deconvolving respective NMR spectrum for quantifying BCAA signals, evaluate at least one pH chemical-shift invariant reference peak in respective obtained NMR spectrums associated with an endogenous or exogenous analyte or component of the sample, then determine a location of BCAA peaks in the NMR spectrum.

35. The system of Claim 34, wherein the at least one processor is configured to calculate a ratio and/or weighted index that is predictive of a clinical outcome or disease risk or identifies an efficacy of a drug or drug candidate, wherein the ratio and/or weighted index comprises in the denominator or numerator or in both the denominator and numerator at least one of the unitless signals or calculated concentrations of one or more of the BCAAs.

36. The system of Claim 34, wherein the at least one processor calculates respective concentrations by applying a scalar concentration value defined as a linear function of concentrations versus unitless intensity signal correlations for each BCAA.

37. The system of Claim 34, wherein the BCAAs comprise valine, isoleucine and leucine, and wherein the deconvolving is carried out using a baseline that is fit using protein and lipoprotein components.

38. The system of Claim 34, wherein the system is configured to transmit a first lipoprotein pulse sequence to obtain a first NMR spectrum associated with lipoproteins and proteins in the sample while the sample is in the NMR spectrometer and transmit a second pulse sequence to obtain the NMR spectrum associated with the BCAAs that is configured to attenuate protein and lipoprotein signals before or after the first pulse sequence to obtain the NMR spectrum of the BCAAs, wherein both pulse sequences and subsequent respective NMR spectrums are obtained within about 2 minutes to about 6 minutes of NMR signal acquisition time per sample.

39. The system of Claim 34, wherein the at least one processor is configured to carry out any of the methods of Claims 1-28.