That Which Is Claimed Is:

1. A method of evaluating a subject's risk of developing type 2 diabetes, comprising:

programmatically calculating a diabetes risk index of a subject using at least one defined mathematical model of risk of developing type 2 diabetes that includes a measurement of at least one lipoprotein component and at least one of a measurement of (i) GlycA or GlycB or (ii) at least one branched chain amino acid, obtained from at least one *in vitro* biosample of the subject.

2. The method of Claim 1, wherein one or more of the at least one lipoprotein component forms a numerator, denominator or multiplication factor of at least one interaction parameter.

3. The method of Claim 1, wherein the defined mathematical model of risk comprises GlycA, wherein the at least one lipoprotein component comprises an interaction parameter defined by the measurement of GlycA multiplied by a concentration of a defined subpopulation of high density lipoprotein (HDL) particles.

4. The method of Claim 1, wherein the at least one lipoprotein component of the defined mathematical model of risk comprises a first interaction parameter of the measurement of GlycA multiplied by a concentration of a defined subpopulation of high density lipoprotein (HDL) particles and a second interaction parameter of HDL size multiplied by the concentration of the defined HDL subpopulation, wherein the HDL subpopulation comprises only medium HDL particle subclasses with diameters between about 8.3 nm (average) to about 10.0 nm (average).

5. The method of Claim 1, further comprising programmatically defining at least two different mathematical models of risk of developing type 2 diabetes, the at least two different mathematical models including one for subjects on a statin therapy that includes at least one lipoprotein component that is statin insensitive and one for subjects not on a statin therapy.

6. The method of Claim 1, further comprising programmatically defining at least two different mathematical models of risk of developing type 2 diabetes, at least one of which is used for the programmatic calculation, the at least two different mathematical models with

different lipoprotein components including one for fasting biosamples and one for non-fasting biosamples.

7. The method of Claim 1, further comprising programmatically generating a report with a graph of risk of progression to type 2 diabetes in the future versus ranges of glucose levels with a visual indication of higher and lower risk values with respect to the calculated diabetes risk index for ease of identifying or understanding risk stratification for a particular glucose level.

8. The method of Claim 1, wherein the diabetes risk index is a numerical score within a defined score range, the method further comprising an electronic analysis circuit in communication with a display of an electronic device configured to allow a user to enter one or more of (i) a glucose value, (ii) a glucose value and a diabetes risk index score, or (iii) a diabetes risk index score, and wherein the diabetes risk index score stratifies risk of developing type 2 diabetes in the future for patients having the same glucose value when the glucose value is in an intermediate risk range associated with when fasting plasma glucose levels are between 90-110 mg/dL, A1C % levels are between 5.7-6.4 or oral glucose tolerance levels are between 140-199 mg/dL.

9. The method of Claim 1, wherein the at least one defined mathematical model of risk includes NMR derived measurements of GlycA and Valine and at least one interaction parameter comprising a high density lipoprotein (HDL) particle subpopulation.

10. The method of Claim 1, wherein the diabetes risk index is a numerical score within a defined score range, with scores associated with a 9th or 10th decile, fourth quartile (4Q) or fifth quintile (5Q) of a population norm reflecting an increased or high risk of developing type 2 diabetes relative to a first quartile or first quintile (1Q).

11. The method of Claim 1, wherein the diabetes risk index is a numerical score within a defined score range that is obtained independent of a glucose measurement of the subject, the method further comprising identifying respective subjects that are at highest increased risk of developing type 2 when the diabetes risk score is at a high end of the score range and/or when the score is associated with a 10th decile, a fourth quartile (4Q) or a fifth quintile (5Q) of a population norm.

12. The method of Claim 1, wherein the diabetes risk index is a numerical score within a defined score range or is provided in deciles, quartiles or quintiles of a population norm, the method further comprising evaluating a glucose level of a respective subject, wherein when fasting plasma glucose levels are between 90-110 mg/dL, A1C % levels are between 5.7-6.4 or oral glucose tolerance levels are between 140-199 mg/dL and when the diabetes risk index score is in a fourth quartile (4Q), a fifth quintile (5Q) or a 10th decile of a population norm associated with a high end of the score range, a subject is at increased risk of developing diabetes.

13. The method of Claim 1, wherein the diabetes risk index is a numerical score within a defined score range, with scores associated with a fourth quartile (4Q), fifth quintile (5Q) or 10th decile of a population norm reflecting an increased or high risk of developing type 2 diabetes, and wherein the diabetes risk index score stratifies risk of developing type 2 diabetes in the future for patients having the same glucose value when the glucose value is in an intermediate risk range associated with when fasting plasma glucose levels are between 90-110 mg/dL, A1C % levels are between 5.7-6.4 or oral glucose tolerance levels are between 140-199 mg/dL.

14. The method of Claim 1, wherein the defined mathematical risk model includes only NMR derived measurements of a respective subject's at least one *in vitro* blood plasma or serum biosample.

15. The method of Claim 1, further comprising, before the programmatic calculation,
placing the *in vitro* biosample of the subject in an NMR spectrometer ;
obtaining at least one NMR spectrum of the biosample;
deconvolving the obtained at least one NMR spectrum; and
calculating NMR derived measurements of GlycA and a plurality of selected lipoprotein subclassess based on the deconvolved at least one NMR spectrum.

16. The method of Claim 15, further comprising calculating a measurement of Valine as one of or as the only branched chain amino acid.

17. The method of Claim 1, wherein the at least one defined mathematical model includes selected lipoprotein components comprising at least two of the following: (i) concentration of a defined subpopulation of medium size high density lipoprotein (HDL) particles with HDL particle subclasses with diameters between 8.3 nm (average) to about 10.0 nm (average); (ii) an interaction parameter defined HDL size multiplied by the concentration of the medium defined HDL subpopulation; (iii) an interaction parameter defined by the concentration of the medium HDL subpopulation multiplied by GlycA; (iv) an lipoprotein insulin resistance index; (v) large VLDL subclass particle number; (vi) medium VLDL subclass particle number; (vii) total HDL subclass particle number; (viii) medium HDL subclass particle number; and (ix) VLDL particle size.

18. The method of Claim 17, wherein the selected lipoprotein components include (i)-(iv) of the listed lipoprotein components.

19. The method of Claim 1, wherein the at least one of the at least one lipoprotein components of the at least one defined mathematical model includes one or more of: VLDL subclass particle size (vsz3), a ratio of medium HDL-P to total HDL-P (HMP_HDLP) multiplied by GlycA and a ratio of VLDL size by a sum of large VLDL-P and medium VLDL-P.

20. The method of Claim 1, wherein the at least one lipoprotein component comprises at least one interaction parameter that includes a concentration of a subpopulation of high density lipoprotein (HDL) particles as a multiplication factor or a numerator or denominator of a ratio.

21. The method of Claim 1, further comprising, before the programmatic calculation:

electronically obtaining a composite NMR spectrum of a GlycA fitting region of the biosample of the subject, wherein the GlycA fitting region extends from 1.845 ppm to 2.080 ppm, and wherein the GlycA peak region is centered at 2.00 ppm;

electronically deconvolving the composite NMR spectrum using a defined deconvolution model with high density lipoprotein (HDL) components, low density lipoprotein (LDL) components, VLDL (very low density lipoprotein)/chylomicron components, and curve fit functions associated with at least a GlycA peak region; and

programmatically generating the measurement of GlycA using the curve fit functions.

22. The method of Claim 21, further comprising electronically applying a conversion factor to the measure of GlycA to provide the measure in μmol/L before the programmatic calculation of the diabetes risk index.

23. The method of Claim 21, wherein the curve fit functions are overlapping curve fit functions, and wherein the measure of GlycA is generated by summing a defined number of curve fit functions, and wherein the deconvolution model further comprises a protein signal component for protein having a density greater than 1.21 g/L.

24. The method of Claim 1, further comprising, before the programmatic calculation:

electronically obtaining an NMR spectrum of a branched chain amino acid fitting region of the biosample of the subject;

electronically identifying a Valine signal as located upstream or downstream of a reference peak of a defined diluent in the biosample;

electronically deconvolving the composite NMR spectrum using a defined deconvolution model;

evaluating a line width of the reference peak during the obtaining step;

electronically quantifying Valine using the deconvolved NMR spectrum; and

electronically correcting the quantification of Valine using an adjustment factor based on the line width of the reference peak associated with shim status of an NMR spectrometer used to obtain the NMR spectrum.

25. The method of Claim 1, wherein the at least one defined mathematical model of risk includes a plurality of different defined models, including one that includes lipoprotein components that are insensitive to statin therapy, one that includes lipoprotein components that are sensitive to statin therapy, one that is for fasting biosamples and one that is for non-fasting biosamples.

26. A circuit configured to determine whether a patient is at-risk for developing type 2 diabetes and/or whether a patient has prediabetes, comprising:

at least one processor configured to electronically calculate a diabetes risk index based on at least one mathematical model of risk to convergence to type 2 diabetes that considers a measurement of at least one lipoprotein component and a measurement of either

(i) at least one branched chain amino acid or GlycA or (ii) at least one branched chain amino acid and GlycA, from at least one in vitro biosample of the subject.

27. The circuit of Claim 26, wherein the diabetes risk index is a numerical score within a defined score range, and wherein the circuit is in communication with or is configured with an electronic analysis circuit in communication with a respective display of remote electronic devices configured to allow a user to enter (i) a glucose value, (ii) a glucose value and a diabetes risk index score, or (iii) a diabetes risk index score, and wherein the circuit is configured to use a corresponding glucose value and a diabetes risk index score of a patient to stratify a risk of developing type 2 diabetes in the future for patients having the same glucose value when the glucose value is in an intermediate risk range associated with when fasting plasma glucose levels are between 90-110 mg/dL, A1C % levels are between 5.7-6.4 or oral glucose tolerance levels are between 140-199 mg/dL.

28. The circuit of Claim 26, wherein the at least one mathematical model of risk includes an NMR derived measurement of GlycA along with an NMR measurement of Valine, with Valine as the at least one branched chain amino acid, and wherein the at least one lipoprotein component includes a least one interaction parameter comprising a concentration of a sub-population of high density lipoprotein (HDL) particles.

29. The circuit of Claim 26, wherein the defined mathematical model of risk comprises GlycA, and wherein the at least one lipoprotein component comprises an interaction parameter of a measurement of GlycA multiplied by concentration of a defined subpopulation of high density lipoprotein (HDL) particles.

30. The circuit of Claim 26, wherein the at least one lipoprotein component of the defined mathematical model of risk comprises a first interaction parameter of a measurement of GlycA multiplied by a concentration of a defined subpopulation of high density lipoprotein (HDL) particles and a second interaction parameter of HDL size multiplied by the concentration of the defined HDL subpopulation.

31. The circuit of Claims 29 or 30, wherein the defined HDL subpopulation includes only medium HDL particle subclasses with diameters between 8.3 nm (average) to about 10.0 nm (average).

32. The circuit of Claim 26, wherein the at least one processor is configured to define at least two different mathematical models of risk of developing type 2 diabetes, the at least two different mathematical models including a first model for subjects on a statin therapy that includes lipoprotein components that are statin insensitive and a second model for subjects not on a statin therapy, wherein the second model includes at least some lipoprotein components that are different from the first model, and wherein the circuit is configured to identify subject and/or biosample characteristics to select the appropriate first or second model of risk for the calculation of the diabetes risk index score.

33. The circuit of Claim 26, wherein the at least one processor is configured to define at least two different mathematical models of risk of developing type 2 diabetes with different lipoprotein components, the at least two different mathematical models including one for fasting biosamples, and one for non-fasting biosamples, and wherein the circuit identifies subject and/or biosample characteristics to select the appropriate mathematical model of risk for calculation of the diabetes risk index score.

34. The circuit of Claim 26, wherein the at least one processor is configured to generate a diabetes risk index as a numerical score with a defined range with a scores at a high end of the scale representing increased risk, and wherein the at least one processor is configured to generate a report with a graph of risk of progression to type 2 diabetes in the future versus ranges of glucose levels and a comparative scale of risk associated with the diabetes risk index score.

35. The circuit of Claim 34, wherein the graph includes visual references of at least comparative low risk DRI scores associated with a first quartile, first quintile or first decile of DRI scores and high risk DRI scores associated with a fourth quartile, fifth quintile or 10th deciles of DRI scores based on a defined population to thereby allow for ease of identifying or understanding risk stratification.

36. The circuit of Claim 26, wherein the at least one processor is configured to evaluate a blood glucose measurement of the subject, wherein the diabetes risk index score is a numerical score within a defined score range, with scores associated with a fourth quartile (4Q), fifth quintile (5Q) or 10th deciles of a population norm reflecting an increased and/or

high risk of developing type 2 diabetes, and wherein the at least one processor is configured to generate a report that can stratify risk in subjects having the same glucose measurement and a different diabetes risk score.

37. The circuit of Claim 26, wherein the at least one defined mathematical model includes selected lipoprotein components comprising at least two of the following: (i) concentration of a defined subpopulation of medium size high density lipoprotein (HDL) particles with HDL particle subclasses with diameters between 8.3 nm (average) to about 10.0 nm (average); (ii) an interaction parameter defined HDL size multiplied by the concentration of the medium defined HDL subpopulation; (iii) an interaction parameter defined by the concentration of the medium HDL subpopulation multiplied by GlycA; (iv) an lipoprotein insulin resistance index; (v) large VLDL subclass particle number; (vi) medium VLDL subclass particle number; (vii) total HDL subclass particle number; (viii) medium HDL subclass particle number; and (ix) VLDL particle size.

38. The circuit of Claim 37, wherein the mathematical model includes all components (i)-(iv) of the listed lipoprotein components.

39. The circuit of Claim 37, wherein one of the lipoprotein components of the mathematical model is a ratio of medium HDL-P to total HDL-P.

40 The circuit of Claim 26, wherein the at least one mathematical model includes a plurality of lipoprotein components including VLDL subclass particle size (vsz3), a ratio of medium HDL-P to total HDL-P (HMP_HDLP) multiplied by GlycA and a ratio of VLDL size by a sum of large VLDL-P and medium VLDL-P.

41. 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 that provides at least one mathematical model of risk to progression to type 2 diabetes in the future, wherein the at least one mathematical model of risk to progression to type 2 diabetes includes a plurality of components, including at least

one lipoprotein component, at least one inflammatory biomarker and at least one branched chain amino acid; and

computer readable program code that calculates a diabetes risk index associated with a patient's biosample based on the at least one mathematical model of a risk of developing type 2 diabetes.

42. The computer program product of Claim 41; wherein the computer readable program code that provides the at least one mathematical model includes model components of NMR derived measurements of GlycA as the inflammatory marker and Valine as the at least one branched chain amino acid.

43. The computer program product of Claim 41, wherein the at least one mathematical model of risk includes NMR derived measurements of GlycA as the at least one inflammatory maker, Valine as the at least one branched chain amino acid and at least one interaction parameter as one or more of the at least one lipoprotein component, wherein the at least one interaction parameter comprises a concentration of a sub-population of high density lipoprotein (HDL) particles.

44. The computer program product of Claim 41, wherein the defined mathematical model of risk comprises GlycA as the inflammatory biomarker, and wherein the at least one lipoprotein component includes an interaction parameter of a measurement of GlycA multiplied by a concentration of a defined subpopulation of high density lipoprotein (HDL) particles.

45. The computer program product of Claim 41, wherein the at least one lipoprotein component includes an interaction parameter of a measurement of GlycA multiplied by a concentration of a defined subpopulation of high density lipoprotein (HDL) particles and a second interaction parameter of HDL size multiplied by the concentration of the defined HDL subpopulation.

46. The computer program product of Claims 44 or 45, wherein the defined HDL subpopulation includes only medium HDL particle subclasses with diameters between 8.3 nm (average) to about 10.0 nm (average).

47. The computer program product of Claim 41, further comprising computer readable program code configured to evaluate a glucose measurement of the patient, wherein the computer readable program code that calculates a diabetes risk index as a numerical score within a defined score range, with scores associated with a fourth quartile (4Q), fifth quintile (5Q) or 10th decile of a population norm reflect an increased or high risk of developing type 2 diabetes.

48. The computer program product of Claim 47, wherein the computer program product further comprises computer readable program code configured to identify respective patients that are at increased risk of developing type 2 diabetes when: (i) fasting blood glucose levels are between 90-110 mg/dL or when A1C % levels are between 5.7-6.4 or when oral glucose tolerance levels are between 140-199 mg/dL
and (ii) the diabetes risk score is in the 4Q,o5Q and/or 10th decile range.

49. The computer program product of Claim 41, wherein the at least one defined mathematical model includes selected lipoprotein components comprising at least two of the following: (i) concentration of a defined subpopulation of medium size high density lipoprotein (HDL) particles with HDL particle subclasses with diameters between 8.3 nm (average) to about 10.0 nm (average); (ii) an interaction parameter defined HDL size multiplied by the concentration of the medium defined HDL subpopulation; (iii) an interaction parameter defined by the concentration of the medium HDL subpopulation multiplied by GlycA; (iv) an lipoprotein insulin resistance index; (v) large VLDL subclass particle number; (vi) medium VLDL subclass particle number; (vii) total HDL subclass particle number; (viii) medium HDL subclass particle number; and (ix) VLDL particle size.

50. The computer program product of Claim 49, wherein the mathematical model includes components (i)-(iv) of the listed lipoprotein components.

51. The computer program product of Claim 41, wherein the mathematical model includes a ratio of medium HDL-P to total HDL-P.

52. The computer program product of Claim 41, wherein the at least one mathematical model includes a plurality of lipoprotein components including VLDL subclass

particle size (vsz3), a ratio of medium HDL-P to total HDL-P (HMP_HDLP) multiplied by GlycA and a ratio of VLDL size by a sum of large VLDL-P and medium VLDL-P.

53. The computer program product of Claim 41, further comprising:

computer readable program code that identifies and deconvolves a Valine fitting region of a composite NMR spectrum blood serum or plasma sample of a subject and generates a calculated measurement of Valine; and

computer readable program code that deconvolves a GlycA fitting region of the composite NMR spectrum, wherein the computer readable program code that deconvolves the composite NMR spectrum uses a defined GlycA deconvolution model with (i) high density lipoprotein (HDL) components, (ii) low density lipoprotein (LDL) components, (iii) VLDL (very low density lipoprotein)/chylomicron components, (iv) another defined protein signal component and (v) curve fitting functions applied to at least a GlycA peak region and generates a calculated measurement of GlycA.

54. A system, comprising:

an NMR spectrometer for acquiring at least one NMR spectrum of an *in vitro* biosample; and

at least one processor in communication with the NMR spectrometer, the at least one processor configured to determine, for a respective biosample using the acquired at least one NMR spectrum, a diabetes risk index score based on at least one defined mathematical model of risk to convergence to type 2 diabetes that includes at least one lipoprotein component, at least one branched chain amino acid and at least one inflammatory biomarker obtained from at least one in vitro biosample of the subject.

55. The system of Claim 54, wherein the at least one processor is configured to deconvolve the acquired at least one NMR spectrum and generate: (i) an NMR measurement of GlycA as at least one inflammatory biomarker: (ii) an NMR measurement of Valine as the at least one branched chain amino acid; and (iii) NMR measurements of lipoprotein subclasses, and wherein the at least one processor calculates the diabetes risk index score as a numerical score in a defined range using the NMR measurements of GlycA, Valine and the at least one lipoprotein component as components of the at least one defined mathematical model.

56. The system of Claim 54, wherein the defined mathematical model of risk comprises GlycA as the inflammatory biomarker, and wherein the at least one lipoprotein component comprises an interaction parameter with a concentration of a defined subpopulation of high density lipoprotein (HDL) subclasses or HDL particle size as a component of a mathematical ratio or product.

57. The system of Claim 54, wherein the at least one lipoprotein component comprises an interaction parameter a multiplied factor of GlycA and concentration of a defined subpopulation of high density lipoprotein (HDL) particles.

58. The system of Claim 54, wherein the at least one lipoprotein component of the defined mathematical model of risk comprises a first interaction parameter of a measurement of GlycA multiplied by a concentration of a defined subpopulation of high density lipoprotein (HDL) particles and a second interaction parameter of HDL size multiplied by the concentration of the defined HDL subpopulation.

59. The system of Claim 57 or 58, wherein the system calculates the concentration of the defined HDL subpopulation, and wherein the HDL subpopulation comprises only medium HDL particle subclasses with diameters between 8.3 nm (average) to 10.0 nm (average).

60. The system of Claim 54, wherein the at least one processor is configured to define at least two different mathematical models of risk of developing type 2 diabetes, the at least two different mathematical models including one for subjects on a statin therapy that includes lipoprotein components that are statin insensitive and one for subjects not on a statin therapy with at least one different lipoprotein component.

61. The system of Claim 54, wherein the at least one processor is configured to define at least two different mathematical models of risk of developing type 2 diabetes with different lipoprotein components, the at least two different mathematical models including one for fasting biosamples and one for non-fasting biosamples.

62. The system of Claim 54, wherein the at least one processor is configured to generate a report with a graph of risk of progression to type 2 diabetes in the future versus

ranges of glucose levels and a quartile, quintile or decile of risk based on a population norm associated with the diabetes risk index score.

63. The system of Claim 62, wherein the graph includes visual references of at least first (low) and fourth quartile or fifth quintile or 10th decile (high) DRI scores based on a defined population to thereby allow for ease of identifying or understanding risk stratification.

64. The system of Claim 54, wherein the defined at least one mathematical model includes NMR measurements of GlycA and a plurality of selected lipoprotein components using lipoprotein subclasses, sizes and concentrations measured from an *in vitro* blood plasma or serum biosample.

65. The system of Claim 54, wherein the at least one defined mathematical model includes selected lipoprotein components comprising at least two of the following: (i) concentration of a defined subpopulation of medium size high density lipoprotein (HDL) particles with HDL particle subclasses with diameters between 8.3 nm (average) to about 10.0 nm (average); (ii) an interaction parameter defined HDL size multiplied by the concentration of the medium defined HDL subpopulation; (iii) an interaction parameter defined by the concentration of the medium HDL subpopulation multiplied by GlycA; (iv) an lipoprotein insulin resistance index; (v) large VLDL subclass particle number; (vi) medium VLDL subclass particle number; (vii) total HDL subclass particle number; (viii) medium HDL subclass particle number; and (ix) VLDL particle size.

66. The system of Claim 65, wherein the selected lipoprotein components include items (i)-(iv) of the listed lipoprotein components.

67. The system of Claim 54, wherein the at least one lipoprotein component includes at least one of the following: VLDL subclass particle size (vsz3), a ratio of medium HDL-P to total HDL-P (HMP_HDLP) multiplied by GlycA and a ratio of VLDL size by a sum of large VLDL-P and medium VLDL-P.

68. A patient report comprising:

a diabetes risk index (DRI) score calculated based on a defined mathematical model of risk of progression to type 2 diabetes, wherein the model includes a measure of GlycA and at least one lipoprotein component, with scores associated with a fourth quartile, fifth quintile or 10th decile of a population norm associated with higher risk relative to a first quartile, quintile or decile.

69. The report of Claim 68, further comprising a graph showing a range of risk of diabetes conversion versus glucose level with different DRI scores defining different levels of risk for a respective glucose level for visual risk stratification information.

70. The report of Claim 68, further comprising a bar chart or graph illustrating a comparative risk stratification illustrating different levels or risk for different DRI scores for the same glucose level and the bar chart or graph includes an intermediate risk range of glucose associated with when fasting plasma glucose levels are between 90-110 mg/dL, A1C % levels are between 5.7-6.4 or oral glucose tolerance levels are between 140-199 mg/dL.

71. An NMR system comprising:

a NMR spectrometer;

a flow probe in communication with the spectrometer; and

at least one processor in communication with the spectrometer configured to obtain (i) NMR signal of a defined GlycA fitting region of NMR spectra associated with GlycA of a blood plasma or serum specimen in the flow probe; (ii) NMR signal of a defined branched chain amino acid fitting region of NMR spectra associated with the specimen in the flow probe; and (iii) NMR signal of lipoprotein subclasses;

wherein the at least one processor is configured to calculate measurements of (i) GlycA, (ii) at least one branched chain amino acid and (iii) the lipoprotein subclasses using the NMR signals, and wherein the at least one processor is configured to calculate a diabetes risk index that uses the calculated measurements of GlycA, the at least one branched chain amino acid and some of the lipoprotein subclasses.

72. The system of Claim 71, wherein the at least one processor comprises at least one local or remote processor, wherein the at least one processor is configured to calculate at least one interaction parameter.

73. The system of Claim 71, wherein the at least one interaction parameter includes a first interaction parameter defined by a measurement of GlycA multiplied by a concentration of a defined subpopulation of high density lipoprotein (HDL) particles.

74. The system of Claim 71, wherein the at least one processor calculates a first interaction parameter of a measurement of GlycA multiplied by a concentration of a defined subpopulation of high density lipoprotein (HDL) particles and a second interaction parameter of HDL size multiplied by the concentration of the defined HDL subpopulation.

75. The system of Claim 71, wherein the at least one processor calculates a concentration of a defined HDL subpopulation using HDL subclasses for at least one interaction parameter, wherein the HDL subpopulation comprises only medium HDL particle subclasses with diameters between 8.3 nm (average) to about 10.0 nm (average).

76. The system of Claim 71, wherein the at least one branched chain amino acid comprises Valine.

77. A method of monitoring a patient to evaluate a therapy or to determine whether the patient is at-risk of developing type 2 diabetes, comprising:

programmatically evaluating a plurality of NMR derived measurements of selected lipoprotein subclasses and at least one of (i) at least one branched chain amino acid or GlycA or (ii) at least one branched chain amino acid and GlycA, of at least one patient in vitro biosample;

programmatically calculating a diabetes risk index of respective patients using the NMR derived measurements; and

evaluating at least one of (i) whether the diabetes risk index is above a defined level of a population norm associated with increased risk of developing type 2 diabetes; and/or (ii) whether the diabetes risk index is increasing or decreasing over time to thereby evaluate change in risk status that may be in response to a therapy.

CLAIMS:

1. A method of evaluating a subject's risk of developing type 2 diabetes and/or of having prediabetes, comprising:

performing Nuclear Magnetic Resonance to determine the levels of at least one lipoprotein component, at least one branched chain amino acid and GlycA from an in vitro blood plasma or serum biosample from the subject, wherein GlycA is a composite Nuclear Magnetic Resonance signal from carbohydrate portions of acute phase reactant glycoproteins containing N-acetylglucosamine and/or N-acetylgalactosamine moieties that is detectable at about 2.00 ppm when Nuclear Magnetic Resonance measurements are performed at about 47 degrees C.; and

programmatically calculating a diabetes risk index score for the subject using a defined mathematical model of risk of developing type 2 diabetes that includes the Nuclear Magnetic Resonance measurements of GlycA, the at least one lipoprotein component and the at least one branched chain amino acid.

2. The method of claim 1, further comprising programmatically defining at least two different mathematical models of risk of developing type 2 diabetes, the at least two different mathematical models including one for subjects on a statin therapy that includes lipoprotein component that are statin insensitive and one for subjects not on a statin therapy.

3. The method of claim 1, further comprising programmatically defining at least two different mathematical models of risk of developing type 2 diabetes, the at least two different mathematical models with different lipoprotein components including one for fasting biosamples, and one for non-fasting biosamples.

4. The method of claim 1, further comprising programmatically generating a report with a graph of risk of progression to type 2 diabetes in the future over a 1-7 year period versus ranges of fasting glucose levels and a quartile of risk associated with the diabetes risk index score.

5. The method of claim 1, further comprising electronically generating reports that present the diabetes risk index score for respective subjects.

6. The method of claim 1, wherein the at least one defined mathematical model of risk includes NMR derived measurements of a plurality of selected lipoprotein components of the at least one biosample of the subject and an NMR measurement of valine as the at least one branched chain amino acid.

7. The method of claim 6, wherein the at least one defined mathematical model includes selected lipoprotein components comprising at least two of the following: large Very Low Density Lipoprotein subclass particle number, medium Very Low Density Lipoprotein subclass particle number, total High Density Lipoprotein subclass particle number, medium High Density Lipoprotein subclass particle number and Very Low Density Lipoprotein particle size.

8. The method of claim 1, further comprising programmatically evaluating a fasting blood glucose measurement of the subject using at least one in vitro biosample, wherein the diabetes risk index score is a numerical score within a defined score range, with scores associated with a fourth quartile or fifth quintile of a population norm reflecting an increased or high risk of developing type 2 diabetes within 5-7 years, and programmatically identifying respective subjects that are at increased risk of developing type 2 diabetes prior to onset of type-2 diabetes when (i) fasting blood glucose levels are between 90-110 mg/dL and (ii) the diabetes risk score is in the fourth quartile or fifth quintile range.

9. The method of claim 1, further comprising programmatically evaluating a fasting blood glucose measurement of the subject, wherein the diabetes risk index score is a numerical score within a defined score range, with scores associated with a fourth quartile or fifth quintile of a population norm reflecting an increased or high risk of developing type 2 diabetes within 5-7 years, the method further comprising programmatically identifying respective subjects that are at increased risk of developing type 2 diabetes prior to onset of type-2 diabetes when fasting blood glucose levels are between 90-125 mg/dL, wherein the programmatically identifying is carried out to stratify risk in subjects having the same fasting blood glucose and a different diabetes risk score.

10. The method of claim 1, wherein the defined mathematical risk model includes only Nuclear Magnetic Resonance derived measurements of a subject's in vitro blood plasma or serum biosample.

11. The method of claim 1, further comprising, before the programmatic calculation, placing a blood plasma or serum sample of the subject in an Nuclear Magnetic Resonance spectrometer;

obtaining at least one Nuclear Magnetic Resonance spectrum of the sample;

deconvolving the obtained at least one Nuclear Magnetic Resonance spectrum; and

calculating the Nuclear Magnetic Resonance levels of GlycA and the at least one lipoprotein component based on the deconvolved spectrum.

12. The method of claim 11, further comprising calculating the level of valine as the at least one branched chain amino acid.

13. The method of claim 1, wherein the diabetes risk index score has a defined numerical range, and wherein the method further comprises programmatically generating a report that identifies a respective subject as at risk of developing prediabetes if a fasting blood plasma or serum glucose value is between about 90-99 mg/dl and the diabetes risk index is in a fourth quartile or fifth quintile of a population norm.

14. The method of claim 1, wherein the at least one branched chain amino acid is valine.

15. The method of claim 14, further comprising, before the programmatic calculation;

electronically obtaining a Nuclear Magnetic Resonance spectrum of a valine fitting region of the biosample of the subject;

electronically identifying a valine signal as located upstream or downstream a defined number of data points of a peak of a defined diluent in the biosample;

electronically deconvolving the composite Nuclear Magnetic Resonance spectrum using a defined deconvolution model; and

electronically quantifying valine using the deconvolved Nuclear Magnetic Resonance spectrum for the Nuclear Magnetic Resonance measurement of valine.

16. The method of claim 1, wherein the at least one defined mathematical model includes a ratio of medium High Density Lipoprotein Particle number to total High Density Lipoprotein Particle number.

17. The method of claim 1, wherein the at least one defined mathematical model includes Very Low Density Lipoprotein subclass particle size, a ratio of medium High Density Lipoprotein Particle number to total High Density Lipoprotein Particle number multiplied by GlycA and a ratio of Very Low Density Lipoprotein size by a sum of large Very Low Density Lipoprotein Particle number and medium Very Low Density Lipoprotein Particle number.

18. The method of claim 1, wherein the at least one defined mathematical model includes a plurality of different defined models, including one that includes lipoprotein components that are insensitive to statin therapy, one that includes lipoprotein components that are sensitive to statin therapy, one that is for fasting biosamples and one that is for non-fasting biosamples.

19. The method of claim 1, wherein the generated report comprises:

the diabetes risk index score calculated based on a defined mathematical model of risk of progression to type 2 diabetes within the next 5-7 years, with values above a population norm associated with increased risk; and

a graph showing a percentage in a range of risk of diabetes conversion over a 1, 2, 3, 4, 5, 6, or 7 year risk window versus glucose level and an associated quartile or quintile of the patient's DRI risk score relative to a defined population.

20. The method of claim 19, wherein the generated report further comprises a comparative risk of a population with a lower or higher quartile or quintile DRI score and the same glucose measurement.

21. A method of evaluating a subject's risk of developing type 2 diabetes and/or of having prediabetes, comprising:

performing Nuclear Magnetic Resonance measurements to electronically obtain a composite Nuclear Magnetic Resonance spectrum of at least one lipoprotein component, at least one branched chain amino acid and a GlycA fitting region of at least one biosample of the subject, wherein the GlycA fitting region extends from 1.845 ppm to 2.080 ppm, wherein GlycA is a composite Nuclear Magnetic Resonance signal from carbohydrate portions of acute phase reactant glycoproteins containing N-acetylglucosamine and/or N-acetylgalactosamine moieties that is detectable at about 2.00 ppm when the Nuclear Magnetic Resonance measurements are performed at about 47 degrees C.;

electronically deconvolving the composite Nuclear Magnetic Resonance spectrum using a deconvolution model with high density lipoprotein components, low density lipoprotein components, very low density lipoprotein components, and curve fit functions associated with at least a GlycA peak region;

programmatically generating a measure of GlycA using the curve fit functions; and

programmatically calculating a diabetes risk index score of a subject using at least one defined mathematical model of risk of developing type 2 diabetes that includes the at least one lipoprotein component, the at least one branched chain amino acid and the measure of GlycA obtained from at least one biosample of the subject, wherein the method is carried out using a circuit with at least one processor in communication with at least one Nuclear Magnetic Resonance spectrometer.

22. The method of claim 21, wherein the at least one branched chain amino acid is valine.

23. The method of claim 21, wherein the curve fit functions are overlapping curve fit functions, and wherein the measure of GlycA is generated by summing a defined number of curve fit functions, and wherein the deconvolution model further comprises a protein signal component for protein having a density greater than 1.21 g/L.

24. A circuit configured to determine whether a patient is at-risk for developing type 2 diabetes within the next 5-7 years and/or whether a patient has prediabetes, comprising:

at least one processor configured to electronically calculate a diabetes risk index based on at least one mathematical model of risk to convergence to type 2 diabetes within 5-7 years that considers at least one lipoprotein component, at least one branched chain amino acid and GlycA from at least one in vitro biosample of the subject, wherein GlycA is a composite Nuclear Magnetic Resonance signal from carbohydrate portions of acute phase reactant glycoproteins containing N-acetylglucosamine and/or N-acetylgalactosamine moieties that is detectable at about 2.00 ppm when Nuclear Magnetic Resonance measurements are performed at about 47 degrees C.

25. The circuit of claim 24, wherein the at least one processor is configured to define at least two different mathematical models of risk of developing type 2 diabetes, the at least two different mathematical models including a first model for subjects on a statin therapy that includes lipoprotein components that are statin insensitive and a second model for subjects

not on a statin therapy, wherein the second model includes at least some lipoprotein components that are different from the first model, and wherein the circuit is configured to identify subject characteristics to select the appropriate first or second model of risk for the calculation of the diabetes risk index score.

26. The circuit of claim 24, wherein the at least one processor is configured to define at least two different mathematical models of risk of developing type 2 diabetes with different lipoprotein components, the at least two different mathematical models including one for fasting biosamples, and one for non-fasting biosamples, and wherein the circuit identifies subject characteristics to select the appropriate mathematical model of risk for calculation of the diabetes risk index score.

27. The circuit of claim 24, wherein the at least one processor is configured to generate a report with a graph of risk of progression to type 2 diabetes in the future over a 1-7 year period versus ranges of fasting glucose levels and a quartile of risk associated with the diabetes risk index score.

28. The circuit of claim 27, wherein the graph includes visual references of at least first (low) and fourth (high) quartile DRI scores based on a defined population to thereby allow for ease of identifying or understanding risk stratification.

29. The circuit of claim 24, wherein the at least one processor is configured to evaluate a fasting blood glucose measurement of the subject, wherein the diabetes risk index score is a numerical score within a defined score range, with scores associated with a fourth quartile or fifth quintile of a population norm reflecting an increased or high risk of developing type 2 diabetes within 5-7 years, and wherein the at least one processor is configured to identify respective subjects that are at increased risk of developing type 2 diabetes prior to onset of type-2 diabetes when fasting blood glucose levels are between 90-110 mg/dL and the diabetes risk score is in the fourth quartile or fifth quintile range.

30. The circuit of claim 24, wherein the at least one processor is configured to evaluate a fasting blood glucose measurement of the subject, wherein the diabetes risk index score is a numerical score within a defined score range, with scores associated with a fourth quartile or fifth quintile of a population norm reflecting an increased or high risk of developing type 2

diabetes within 5-7 years, the at least one processor configured to identify respective subjects that are at increased risk of developing type 2 diabetes prior to onset of type-2 diabetes when fasting blood glucose levels are between 90-125 mg/dL, and wherein the at least one processor is configured to generate a report that can stratify risk in subjects having the same fasting blood glucose and a different diabetes risk score.

31. The circuit of claim 24, wherein the at least one mathematical model includes a plurality of lipoprotein components comprising at least two of the following: large very low density lipoprotein subclass particle number, medium very low density lipoprotein subclass particle number, total high density lipoprotein subclass particle number, medium high density lipoprotein subclass particle number and very low density lipoprotein particle size.

32. The circuit of claim 24, wherein the at least one branched chain amino acid is valine.

33. 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 stored on the medium, the computer-readable program code comprising:

computer readable program code that provides at least one mathematical model of risk to progression to type 2 diabetes over a defined time period of between 1-7 years, wherein the at least one mathematical model of risk to progression to type 2 diabetes includes a plurality of components, including NMR derived measurements of GlycA and valine, wherein GlycA is a composite Nuclear Magnetic Resonance signal from carbohydrate portions of acute phase reactant glycoproteins containing N-acetylglucosamine and/or N-acetylgalactosamine moieties that is detectable at about 2.00 ppm when Nuclear Magnetic Resonance measurements are performed at about 47 degrees C.; and

computer readable program code that calculates a diabetes risk index associated with a patient's biosample based on the at least one mathematical model of a risk of developing type 2 diabetes.

34. The computer program product of claim 33, further comprising computer readable program code configured to evaluate a glucose measurement of the patient, wherein the computer readable program code that calculates a diabetes risk index as a numerical score within a defined score range, with scores associated with a fourth quartile or fifth quintile of a

population norm reflecting an increased or high risk of developing type 2 diabetes within 5-7 years.

35. The computer program product of claim 34, wherein the computer program product further comprises computer readable program code configured to identify respective patients that are at increased risk of developing type 2 diabetes prior to onset of type-2 diabetes when fasting blood glucose levels are between 90-110 mg/dL and the diabetes risk score is in the fourth quartile or fifth quintile range.

36. The computer program product of claim 34, wherein the computer program product is configured to generate a report that identifies respective subjects that are at increased risk of developing type 2 diabetes prior to onset of type-2 diabetes when fasting blood glucose levels are between 90-125 mg/dL, wherein the mathematical model stratifies risk in subjects having the same fasting blood glucose and a different diabetes risk score.

37. The computer program product of claim 34, wherein the at least one mathematical model includes a plurality of lipoprotein components comprising at least two of the following: large very low density lipoprotein subclass particle number, medium very low density lipoprotein subclass particle number, total high density lipoprotein subclass particle number, medium high density lipoprotein subclass particle number and very low density lipoprotein particle size.

38. The computer program product of claim 37, wherein the at least one branched chain amino acid is valine.

39. The computer program product of claim 33, further comprising:

computer readable program code that identifies and deconvolves a valine fitting region of a composite Nuclear Magnetic Resonance spectrum blood serum or plasma sample of a subject and generates a calculated measurement of valine for the Nuclear Magnetic Resonance derived measurement of valine; and

computer readable program code that deconvolves a GlycA fitting region of the composite Nuclear Magnetic Resonance spectrum, wherein the computer readable program code deconvolves the composite Nuclear Magnetic Resonance spectrum using a defined GlycA deconvolution model with (i) high density lipoprotein components, (ii) low density

lipoprotein components, (iii) very low density lipoprotein components, (iv) another defined protein signal component and (v) curve fitting functions applied to at least a GlycA peak region and generates a calculated measurement of GlycA for the Nuclear Magnetic Resonance derived measurement of GlycA.

40. A system, comprising:

an NMR spectrometer for acquiring at least one NMR spectrum of an in vitro biosample; and

at least one processor in communication with the NMR spectrometer, the at least one processor configured to determine for a respective biosample using the at least one NMR spectrum a diabetes risk index score based on at least one defined mathematical model of risk to convergence to type 2 diabetes within 5-7 years that considers at least one lipoprotein component, at least one branched chain amino acid and GlycA obtained from at least one in vitro biosample of the subject, wherein GlycA is a composite Nuclear Magnetic Resonance signal from carbohydrate portions of acute phase reactant glycoproteins containing N-acetylglucosamine and/or N-acetylgalactosamine moieties that is detectable at about 2.00 ppm when Nuclear Magnetic Resonance measurements are performed at about 47 degrees C.

41. The system of claim 40, wherein the at least one processor is configured to define at least two different mathematical models of risk of developing type 2 diabetes, the at least two different mathematical models including one for subjects on a statin therapy that includes lipoprotein components that are statin insensitive and one for subjects not on a statin therapy with at least one different lipoprotein component.

42. The system of claim 40, wherein the at least one processor is configured to define at least two different mathematical models of risk of developing type 2 diabetes with different lipoprotein components, the at least two different mathematical models including one for fasting biosamples and one for non-fasting biosamples.

43. The system of claim 40, wherein the at least one processor is configured to generate a report with a graph of risk of progression to type 2 diabetes in the future over a 1-7 year period versus ranges of fasting glucose levels and a quartile of risk associated with the diabetes risk index score.

44. The system of claim 43, wherein the graph includes visual references of at least first (low) and fourth (high) quartile DRI scores based on a defined population to thereby allow for ease of identifying or understanding risk stratification.

45. The system of claim 40, wherein the at least one defined mathematical model includes selected lipoprotein components comprising at least two of the following: large very low density lipoprotein subclass particle number, medium very low density lipoprotein subclass particle number, total high density lipoprotein subclass particle number, medium high density lipoprotein subclass particle number and very low density lipoprotein particle size.

46. The system of claim 43, wherein the at least one branched chain amino acid is valine.

47. A Nuclear Magnetic Resonance system comprising:

a Nuclear Magnetic Resonance spectrometer;

a flow probe in communication with the spectrometer; and

at least one processor in communication with the spectrometer configured to:

(a) obtain

(i) a Nuclear Magnetic Resonance signal of a defined GlycA fitting region of NMR spectra associated with GlycA of a blood plasma or serum specimen in the flow probe, wherein GlycA is a composite Nuclear Magnetic Resonance signal from carbohydrate portions of acute phase reactant glycoproteins containing N-acetylglucosamine and/or N-acetylgalactosamine moieties that is detectable at about 2.00 ppm when Nuclear Magnetic Resonance measurements are performed at about 47 degrees C.;

(ii) Nuclear Magnetic Resonance signal of a defined valine fitting region of Nuclear Magnetic Resonance spectra associated with the specimen in the flow probe; and

(iii) Nuclear Magnetic Resonance signal of at least one lipoprotein component of the blood plasma or serum sample in the flow probe;

(b) calculate measurements of GlycA, valine and the at least one lipoprotein component; and

(c) calculate a diabetes risk index using a defined mathematical model of risk of developing type 2 diabetes and/or having prediabetes that uses the calculated measurements of GlycA, valine and the at least one lipoprotein component.

48. The system of claim 47, wherein the at least one processor comprises at least one local or remote processor and/or at least one processor onboard the Nuclear Magnetic Resonance analyzer, wherein the at least one processor is configured to deconvolve at least one composite Nuclear Magnetic Resonance spectrum of the specimen to generate the calculated measurements of GlycA, valine and the lipoprotein parameters.

49. A method of monitoring a patient to evaluate a therapy or determine whether the patient is at-risk of developing type 2 diabetes or has prediabetes, comprising:

performing Nuclear Magnetic Resonance measurements to measure selected lipoprotein subclasses, valine and GlycA, wherein GlycA is a composite Nuclear Magnetic Resonance signal from carbohydrate portions of acute phase reactant glycoproteins containing N-acetylglucosamine and/or N-acetylgalactosamine moieties that is detectable at about 2.00 ppm when the Nuclear Magnetic Resonance measurements are performed at about 47 degrees C.;

programmatically providing at least one defined mathematical model of risk of progression to type 2 diabetes that includes a plurality of components including Nuclear Magnetic Resonance derived measurements of selected lipoprotein subclasses, valine and GlycA;

programmatically deconvolving at least one Nuclear Magnetic Resonance spectrum of respective in vitro patient blood plasma or serum samples and determining measurements of lipoprotein subclasses, GlycA and valine;

programmatically calculating a diabetes risk index score of the respective patients using the at least one defined model and corresponding patient sample measurements;

electronically generating a patient report providing the diabetes index risk score; and evaluating at least one of (i) whether the diabetes risk index is above a defined level of a population norm associated with increased risk of developing type 2 diabetes, and/or (ii) whether the diabetes risk index is increasing or decreasing over time in response to a therapy.

50. A circuit configured to determine whether a patient is at-risk for developing type 2 diabetes within the next 5-7 years and/or whether a patient has prediabetes, comprising:

at least one processor configured to electronically calculate a diabetes risk index based on at least one mathematical model of risk to convergence to type 2 diabetes within 5-7 years using Nuclear Magnetic Resonance derived measurements of GlycA, valine and a plurality of lipoprotein components, wherein GlycA is a composite Nuclear Magnetic

Resonance signal from carbohydrate portions of acute phase reactant glycoproteins containing N-acetylglucosamine and/or N-acetylgalactosamine moieties that is detectable at about 2.00 ppm when Nuclear Magnetic Resonance measurements are performed at about 47 degrees C.

51. A system, comprising:

a Nuclear Magnetic Resonance spectrometer for acquiring at least one Nuclear Magnetic Resonance spectrum of an in vitro biosample; and

at least one processor in communication with the Nuclear Magnetic Resonance spectrometer, the at least one processor configured to determine for a respective biosample, using the at least one Nuclear Magnetic Resonance spectrum, a diabetes risk index score based on at least one defined mathematical model of risk to convergence to type 2 diabetes within 5-7 years that considers at least one lipoprotein component, at least one branched chain amino acid and GlycA as at least one inflammatory biomarker obtained from at least one in vitro biosample of the subject, wherein GlycA is a composite Nuclear Magnetic Resonance signal from carbohydrate portions of acute phase reactant glycoproteins containing N-acetylglucosamine and/or N-acetylgalactosamine moieties that is detectable at about 2.00 ppm when Nuclear Magnetic Resonance measurements are performed at about 47 degrees C.; and

wherein the at least one processor is configured to deconvolve the at least one Nuclear Magnetic Resonance spectrum and generate:

(i) a Nuclear Magnetic Resonance measurement of GlycA:

(ii) a Nuclear Magnetic Resonance measurement of valine;

(iii) Nuclear Magnetic Resonance measurements of lipoprotein parameters; and

(iv) the diabetes risk index

using the Nuclear Magnetic Resonance measurements of GlycA, valine and the lipoprotein parameters as components of the at least one defined mathematical model.

52. A system, comprising:

a Nuclear Magnetic Resonance spectrometer for acquiring at least one Nuclear Magnetic Resonance spectrum of an in vitro biosample; and

at least one processor in communication with the Nuclear Magnetic Resonance spectrometer, the at least one processor configured to determine for a respective biosample using the at least one Nuclear Magnetic Resonance spectrum a diabetes risk index score

based on at least one defined mathematical model of risk to convergence to type 2 diabetes within 5-7 years that considers at least one lipoprotein component, at least one branched chain amino acid and GlycA as an inflammatory biomarker obtained from at least one in vitro biosample of the subject,

wherein GlycA is a composite Nuclear Magnetic Resonance signal from carbohydrate portions of acute phase reactant glycoproteins containing N-acetylglucosamine and/or N-acetylgalactosamine moieties that is detectable at about 2.00 ppm when Nuclear Magnetic Resonance measurements are performed at about 47 degrees C.; and

wherein the defined at least one mathematical model includes Nuclear Magnetic Resonance measurements of GlycA and a plurality of selected lipoprotein components using lipoprotein subclasses, sizes and concentrations measured from an in vitro blood plasma or serum biosample.