That Which Is Claimed Is:

1. A method of measuring GlycA, comprising:

electronically obtaining a composite NMR spectrum of a fitting region of a biosample of a subject;

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 a plurality of curve fit functions associated with at least a GlycA peak region; and

electronically generating a measure of GlycA using the curve fit functions.

2. The method of Claim 1, further comprising applying a conversion factor to the measure of GlycA to provide the measure in μmol/L.

3. The method of Claim 1, wherein the curve fit functions are overlapping Lorentzian functions, and wherein the measure of GlycA is generated by summing a defined number of Lorentzian functions.

4. The method of Claim 1, wherein the deconvolution model further comprises a protein signal component for protein having a density greater than 1.21 g/L.

5. The method of Claim 2, wherein the deconvolution model further comprises a protein signal component for protein having a density greater than 1.21 g/L, and wherein the method further comprises generating a risk predictor using a mathematical equation of:

HDL-P/LDL-P*GlycA,

wherein HDL-P is an NMR measure of HDL particle number and LDL-P is an NMR measure of LDL particle number and GlycA in the equation is the GlycA measurement, all in μmol/L.

6. The method of Claim 1, further comprising deconvolving another part of the NMR spectrum of the sample associated with a quartet of valine signals and generating an NMR measure of valine.

7. The method of Claim 5, further comprising providing the valine and GlycA measurement in a test report.

8. The method of Claim 1, wherein the plurality of curve fit functions are overlapping Lorentzian functions, and wherein the deconvolution model applies the Lorentzian functions to a subset of the fitting region that extends from a right side of the GlycA peak region of a chemical shift spectrum to a left side of a GlycB peak region.

9. The method of Claim 1, wherein the biosample comprises blood plasma or serum, wherein the electronically obtaining comprises obtaining NMR signal of the biosample while the biosample is at 47 degrees C +/- 0.2 degrees in an NMR flow probe of an NMR spectrometer, and wherein the fitting region extends from 1.845 ppm to 2.080 ppm, and wherein the GlycA peak region is centered at 2.00 ppm and wherein the method further comprises summing a defined number of a different set of curve fitting functions to generate a measure of GlycB.

10. The method of Claim 1, wherein the plurality of curve fit functions are applied to a fitting region that includes the GlycA peak region and extends to a GlycB peak region with between about 40-50 curve fit functions, and wherein the generating the measure of GlycA is carried out by summing values of a defined first subset of the curve fit functions, the method further comprising generating a measure of GlycB using a second smaller subset of the plurality of curve fit functions.

11. The method of Claim 1, wherein the defined deconvolution model includes metabolite A components.

12. A method of determining coronary heart disease (CHD) risk for a patient, comprising:

electronically evaluating NMR signal in a defined peak region of a proton NMR spectrum associated with GlycA of a biosample to determine a level of GlycA; and

determining a patient's risk of CHD based, at least in part, on the level of GlycA.

13. The method of Claim 12, further comprising electronically providing an electronic reference range of GlycA values with correlated CHD risk based on the reference range, with

higher values associated with increased risk, and wherein the determining the risk of CHD is carried out using the reference range.

14. The method of Claim 12, wherein an increased risk is associated with levels above a defined population norm.

15. The method of Claim 12, wherein the measuring and determining steps are carried out using at least one processor.

16. The method of Claim 12, wherein the measuring step comprises electronically obtaining NMR spectra of an *in vitro* blood plasma or serum patient biosample and deconvolving the composite NMR signal into a discrete GlycA NMR signal using a defined deconvolution model with at least (i) high density lipoprotein (HDL) components, (ii) low density lipoprotein (LDL) components, (iii) VLDL (very low density lipoprotein)/chylomicron components and (iv) a defined protein signal component.

17. The method of Claim 16, wherein the defined protein signal component is associated with protein density above 1.21 g/L.

18. The method of Claim 12, wherein the measuring step comprises electronically obtaining NMR spectra of an *in vitro* blood plasma or serum patient biosample and deconvolving the composite NMR signal into a discrete GlycA NMR signal having a peak centered at 2.00 ppm at 47 degrees C +/-0.2 using a defined deconvolution model with high density lipoprotein (HDL) components, low density lipoprotein (LDL) components, VLDL(very low density lipoprotein)/chylomicron components, a protein signal component associated with protein density above 1.21 g/L, and curve fitting functions applied to at least a GlycA peak region.

19. The method of Claim 18, wherein the curve fitting functions comprise overlapping Lorentzian functions.

20. The method of Claim 12, further comprising electronically generating a patient report and identifying the GlycA measurement and a risk summary, wherein increased levels of GlycA are associated with increased risk of CHD and a risk summary for the GlycA value.

21. The method of Claim 12, further comprising electronically calculating LDL-P and HDL-P from NMR spectra of the biosample, and wherein the determining step comprises identifying an increased risk of CHD when GlycA and LDL-P are above a respective population norm and HDL-P is below a population norm.

22. The method of Claim 12, further comprising deconvolving a composite NMR signal of the biosample to generate separate GlycA and GlycB peak regions, and wherein the electronically evaluating uses NMR signal of a peak region centered at 2.00 ppm for determining the level of GlycA and uses NMR signal of a peak region centered at 2.04 ppm for determining a level of GlycB.

23. 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 deconvolves a composite NMR spectrum of a fitting region of a plasma sample of a subject, wherein the computer readable program code deconvolves the composite NMR spectrum using a defined 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

computer readable program code that sums a defined number of the functions to generate a measurement of GlycA.

24. The computer program product of Claim 23, wherein the curve fitting functions comprise overlapping Lorentzian functions.

25. The computer program product of Claim 23, further comprising computer readable program code that applies a conversion factor to the summed Lorentzian functions to generate the measurement of GlycA in μmol/L.

26. The computer program product of Claim 23, further comprising computer readable program code that compares the GlycA measurement to a predefined range of

measurements having associated degrees of CHD risk, and computer readable program code that generates a patient report with the GlycA measurement and an associated with risk assessment.

27. The computer program product of Claim 23, wherein the computer program code that generates the measurement is configured to evaluate NMR spectra of an *in vitro* blood plasma or serum patient sample using NMR signal having a peak centered at about 2.00 ppm.

28. 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 obtain an NMR measurement of GlycA using the at least one NMR spectrum.

29. The system of Claim 28, wherein the at least one processor is configured to: (i) obtain a composite NMR spectrum of a fitting region of an in vitro plasma biosample; (ii) deconvolve the composite NMR spectrum using a defined deconvolution model with high density lipoprotein (HDL), low density lipoprotein (LDL), VLDL(very low density lipoprotein)/chylomicron components, a defined protein signal component, and curve fitting functions associated with at least a GlycA peak region; and (iii) electronically generate the NMR measurement of GlycA based on the curve fitting functions.

30. The system of Claim 29, wherein the curve fitting functions comprise overlapping Lorentzian functions, and wherein the at least one processor sums a defined number of the functions to generate the NMR measurement.

31. The system of Claim 29, wherein the at least one processor is configured to apply a conversion factor to the summed NMR measurement to generate a GlycA measurement in μmol/L.

32. The system of Claim 30, wherein the biosample is a blood plasma or serum sample, and wherein the at least one processor is configured to obtain a concentration measurement of high density lipoprotein particles (HDL-P) and a concentration measurement of low density lipoprotein particles (LDL-P).

33. The system of Claim 28, wherein the at least one processor is configured to deconvolve another part of the NMR spectrum of the sample associated with a quartet of valine signals and generate an NMR measure of valine.

34. The system of Claim 28, wherein the at least one processor is configured to generate patient reports summarizing a respective GlycA measurement and at least one lipoprotein subclass measurement and/or a Valine measurement.

35. The system of Claim 28, wherein the at least one processor is configured to use the GlycA measurement as a denominator in a defined all-cause death risk ratio and generate a risk number associated with a risk of all-cause death.

36. A patient report comprising:

a plurality of lipoprotein measurements including a quantitative measure of GlycA in μmol/L and/or arbitrary units.

37. The patient report of Claim 36, wherein the report also includes an NMR measurement of at least one of the following: (i) a low density lipoprotein particle number (LDL-P) in concentration units; (ii) a high density lipoprotein particle (HDL-P) number in concentration units; (iii) magnesium; or (iv) valine.

38. A patient report comprising a calculated ratio of measurements of valine, HDL-P and GlycA using a ratio of: (Valine*HDL-P)/GlycA.

39. An NMR analyzer 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 NMR signal of a defined single peak region of NMR spectra associated with GlycA of a fluid specimen in the flow probe and generate a patient report providing a GlycA level.

40. The NMR analyzer of Claim 39, wherein the at least one processor is configured to carry out the following or is in communication with at least one local or remote processor

that is configured to carryout out the following: (i) deconvolve a composite NMR spectrum using a defined deconvolution model with high density lipoprotein (HDL), low density lipoprotein (LDL), VLDL(very low density lipoprotein)/chylomicron components, a defined protein signal component, and curve fitting functions associated with at least a GlycA peak region; and (ii) electronically generate the GlycA level.

41. The analyzer of Claim 39, wherein the curve fitting functions comprise overlapping Lorentzian functions, and the at least one processor is configured to sum a defined number of the functions to generate the GlycA level.

42. The system of Claim 39, wherein the at least one processor is configured to apply a conversion factor to the to generate a GlycA measurement in μmol/L.

43. The system of Claim 39, wherein the at least one processor is configured to (a) deconvolve a 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 to provide the GlycA level and (b) deconvolve another part of the NMR spectrum of the sample associated with a quartet of valine signals and generate an NMR measure of valine.

44. The system of Claim 39, wherein the at least one processor is configured to (i) deconvolve an 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 metabolite A components, and (ii) sum a plurality of values of a defined subset of curve fit functions associated with a GlycA fitting region s to provide the GlycA level.

45. The system of Claim 39, wherein the at least one processor is configured to apply a plurality of curve fit functions to a fitting region that includes the GlycA peak region and extends to a GlycB peak region with between about 40-60 curve fit functions, and wherein the GlycA level is calculated by summing values of a defined first subset of the curve fit functions and applying a defined conversion value.

46. The system of Claim 39, wherein the at least one processor is configured to calculate a measure of GlycB by summing a second smaller subset of the plurality of curve fit functions and applying the defined conversion value.

47. The system of Claim 39, wherein the at least one processor is configured to calculate a ratio of measurements using at least one of the following: valine/GlycA, HDL-P/GlycA or (Valine*HDL-P)/GlycA.

48. A method to evaluate or predict all-cause death risk of a person, comprising:

electronically calculating a ratio of measurements of at least one of the following: Valine to GlycA, HDL-P to GlycA or (Valine*HDL-P)/GlycA; and

evaluating whether a person has an increased risk for all-cause death relative to a defined population, wherein a respective person has increased risk relative to the defined population when the calculated ratio is in a first tertile, first quartile or first quintile of the population.

49. The method of Claim 48, wherein the calculating is carried out using a ratio of (Valine*HDL-P)/GlycA.

50. A method of quantifying a level of metabolite A in a biosample, comprising:

deconvolving a defined metabolite A peak region of a proton NMR spectrum having signal associated with lipoproteins and a single peak associated with metabolite A;

applying a plurality of curve fitting functions to the metabolite A peak region; and

measuring a level of metabolite A using the applied curve fitting functions.

51. A method of quantifying valine in a biosample, comprising:

deconvolving an NMR spectrum using a deconvolution model of lipoproteins and protein components;

identifying a multiplet signal in a region between 0.90-1.01 ppm; and

calculating a level of valine in the biosample.

52. The method of 51, further comprising before the deconvolving step, applying a quality control pre-analytical analysis using acquired NMR spectra.

53. A method of measuring GlycB, comprising:

electronically obtaining a composite NMR spectrum of a fitting region of a biosample of a subject;

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 a plurality of curve fit functions associated with at least a GlycB peak region; and

electronically generating a measure of GlycB using the curve fit functions.

54. The method of any of Claims 10-15, further comprising generating a ratio of GlycA/GlycB or GlycB/GlycA.

CLAIMS:

1. A method of measuring GlycA, an NMR biomarker derived from a measure of composite NMR signal from carbohydrate portions of acute phase reactant glycoproteins containing N-acetylglucosamine and/or N-acetylgalactosamine moieties, comprising:

obtaining a composite NMR spectrum of a fitting region of a blood plasma or serum sample of a subject;

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

generating a measure of GlycA using the curve fit functions,

wherein the GlycA NMR biomarker is derived from NMR signal of the protons of N-acetylglucosamine and N-acetylgalactosamine methyl groups, and

wherein the GlycA peak region is centered at 2.00 ppm and the fitting region extends from 1.845 ppm to 2.080 ppm if the sample is at 47+/−0.2 degrees C. in an NMR spectrometer.

2. The method of claim 1, further comprising applying a conversion factor to the measure of GlycA to provide the measure in μmol/L.

3. The method of claim 1, wherein the curve fit functions are overlapping Lorentzian functions, and wherein the measure of GlycA is generated by summing a defined number of Lorentzian functions.

4. The method of claim 1, wherein the deconvolution model further comprises a protein signal component for protein having a density greater than 1.21 g/L.

5. The method of claim 2, wherein the deconvolution model further comprises a protein signal component for protein having a density greater than 1.21 g/L, and wherein the method further comprises generating a risk predictor comprising a mathematical equation of:

HDL-P/LDL-P*GlycA, HDL-P/GlycA, or Valine/GlycA,

wherein HDL-P is an NMR measure of HDL particle number and LDL-P is an NMR measure of LDL particle number and GlycA in the equation is the GlycA measurement, all in μmol/L.

6. The method of claim 1, wherein the plurality of curve fit functions includes between about 40-50 curve fit functions.

7. The method of claim 1, wherein the GlycA fitting region of the NMR spectrum is referenced internally to CaEDTA signal at 2.519 ppm.

8. The method of claim 1, further comprising obtaining a second measure of GlycA at a second point in time, wherein the GlycA values are compared to evaluate whether there is a change in inflammatory status over time due to age, medical intervention or a therapy.