

What is claimed is:

1. A method of characterizing a sample, comprising:
providing the sample to a liquid chromatography system capable of sample separation to generate sample components;
analyzing sample components by multiplexed targeted selected ion monitoring (SIM) to generate an inclusion list; and
performing iterative mass spectral data-dependent acquisition (DDA) from the inclusion list, to identify individual sample components.
2. The method of claim 1, wherein the liquid chromatography system is a reversed phase liquid chromatography (RPLC) system.
3. The method of claim 1 or claim 2, wherein analyzing the fragmented sample by multiplexed targeted selected ion monitoring (SIM) to generate an inclusion list comprises utilizing an ion trap or orbitrap mass analyzer.
4. The method of any one of claims 1 to 3, wherein performing iterative mass spectral DDA comprises utilizing an ion trap or orbitrap mass analyzer fitted with a segmented quadrupole mass filter.
5. The method of any one of claims 1 to 4, wherein analyzing sample components by multiplexed targeted selected ion monitoring (SIM) to generate an inclusion list comprises segmenting mass to ratio window settings in which multiple segments are included and each segment has multiple windows.
6. The method of claim 5, wherein multiple segments is three segments.
7. The method of claim 5, wherein multiple segments is four segments.
8. The method of any one of claims 5 to 7, wherein multiple windows is 10 windows.
9. The method of any one of claims 5 to 8, wherein each window within a segment has the same window width.
10. The method of any one of claims 1 to 9, wherein the sample is cell culture medium.

11. The method of claim 9, wherein the method is for characterizing components and their metabolites within the cell culture medium.

12. The method of claim 10 or claim 11, wherein the cell culture medium is a soy-based cell culture medium.

13. The method of claim 10 or 11, wherein the cell culture medium is for a recombinant cell-based production system.

14. The method of any one of claims 1 to 10, wherein the method is for characterizing components and their metabolites within the cell culture medium following incubation with a recombinant cell-based production system.

15. The method of claim 14, wherein the recombinant cell-based production system is a mammalian system.

16. The method of claim 14, wherein the recombinant cell-based production system is for protein production.

17. The method of claim 16, wherein the protein is an antibody, a fusion protein, recombinant protein, or a combination thereof.

18. The method of claim 17, wherein the antibody is a monoclonal antibody.

19. The method of claim 18, wherein the monoclonal antibody is of isotype IgG1, IgG2, IgG3, IgG4, or mixed isotype.

20. A method of compound identification for cell culture medium analysis, comprising:

providing the sample of cell culture medium to a liquid chromatography system capable of sample separation to generate sample components;

analyzing sample components by multiplexed targeted selected ion monitoring (SIM) to generate an inclusion list; and

performing iterative mass spectral data-dependent acquisition (DDA) from the inclusion list, to identify individual compounds with the cell culture medium.

21. The method of claim 20, wherein the liquid chromatography system is a reversed phase liquid chromatography (RPLC) system.

22. The method of claim 20 or claim 21, wherein analyzing the fragmented sample by multiplexed targeted selected ion monitoring (SIM) to generate an inclusion list comprises utilizing an ion trap or orbitrap mass analyzer.

23. The method of any one of claims 20 to 22, wherein performing iterative mass spectral DDA comprises utilizing an ion trap or orbitrap mass analyzer fitted with a segmented quadrupole mass filter.

24. The method of any one of claims 20 to 23, wherein analyzing sample components by multiplexed targeted selected ion monitoring (SIM) to generate an inclusion list comprises segmenting mass to ratio window settings in which multiple segments are included and each segment has multiple windows.

25. The method of claim 24, wherein multiple segments is three segments.

26. The method of claim 24, wherein multiple segments is four segments.

27. The method of any one of claims 24 to 26, wherein multiple windows is 10 windows.

28. The method of any one of claims 24 to 27, wherein each window within a segment has the same window width.

29. The method of any one of claims 20 to 28, wherein the cell culture medium is a soy-based cell culture medium.

30. The method of any one of claims 20 to 29, wherein the cell culture medium is for a recombinant cell-based production system.

31. The method of any one of claims 20 to 30, wherein the cell culture medium sample is a cell culture medium sample obtained following incubation with a recombinant cell-based production system.

32. The method of claim 31 or claim 32, wherein the recombinant cell-based production system is a mammalian system.

33. The method of claim 31 or claim 32, wherein the recombinant cell-based production system is for protein production.

34. The method of claim 33, wherein the protein is an antibody, a fusion protein, recombinant protein, or a combination thereof.

35. The method of claim 34, wherein the antibody is a monoclonal antibody.

36. The method of claim 35, wherein the monoclonal antibody is of isotype IgG1, IgG2, IgG3, IgG4, or mixed isotype.