What is claimed is:

1. A method for identifying at least one peptide or protein in a sample, comprising:

contacting the sample to a solid surface, wherein the solid surface comprises a hydrophobic group;

washing the solid surface using a mobile phase to produce at least one eluent, wherein the eluent comprises the at least one peptide or protein; and

characterizing the at least one peptide or protein in the at least one eluent using a mass spectrometer under native conditions, wherein a flow rate of the eluent to the mass spectrometer is between about 0.1 μL/min to about 3 μL/min.

2. The method of claim 1, further comprising generating at least one separation profile.

3. The method of claim 2, further comprising identifying or quantifying the at least one peptide or protein based on the at least one separation profile.

4. The method of claim 2, further comprising identifying or quantifying a level of post-translational modification or post-translational modification variation of the at least one peptide or protein based on the at least one separation profile or a comparison with another separation profile.

5. The method of claim 2, further comprising identifying or quantifying a level of glycosylation or glycosylation variation of the at least one peptide or protein based on the at least one separation profile or a comparison with another separation profile.

6. The method of claim 2, further comprising identifying or quantifying changes of masses or relative hydrophobicity of the at least one peptide or protein based on the at least one separation profile or a comparison with another separation profile.

7. The method of claim 2, further comprising separating or identifying an impurity in the sample based on the at least one separation profile or a comparison with another separation profile.

8. The method of claim 2, wherein the at least one peptide or protein is a drug, an antibody, a bispecific antibody, a monoclonal antibody, a fusion protein, an antibody-drug conjugate, an antibody fragment, or a protein pharmaceutical product.

9. The method of claim 8, further comprising quantifying a drug-to-antibody ratio of the antibody-drug conjugate based on the at least one separation profile or a comparison with another separation profile.

10. The method of claim 8, further comprising identifying or quantifying a drug location, a positional isomer or a degraded payload of the antibody-drug conjugate based on the at least one separation profile or a comparison with another separation profile.

11. The method of claim 8, further comprising identifying or quantifying a modification of a complementarity determining region of the antibody, the bispecific antibody, the monoclonal antibody, the antibody-drug conjugate or the antibody fragment based on the at least one separation profile or a comparison with another separation profile.

12. The method of claim 1, wherein the solid surface comprising the hydrophobic group is included in a chromatography column.

13. The method of claim 12, wherein the mass spectrometer is coupled online to the chromatography column.

14. The method of claim 1, wherein the hydrophobic group is phenyl, octyl, butyl, hexyl or propyl.

15. The method of claim 13, wherein a splitter is used to connect the mass spectrometer and the chromatography column.

16. The method of claim 15, wherein a makeup flow is introduced to the mobile phase between the mass spectrometer and the chromatography column.

17. The method of claim 15, wherein the splitter is used to divert a low flow to the mass spectrometer and a high flow to a detector.

18. The method of claim 1, wherein the mass spectrometer is an electrospray ionization mass spectrometer, nano-electrospray ionization mass spectrometer, a triple quadrupole mass spectrometer, a quadrupole mass spectrometer or a ultra-high mass range hybrid quadrupole mass spectrometer.

19. The method of claim 1, wherein the mass spectrometer comprises an orbitrap mass analyzer.

20. A system for identifying at least one peptide or protein, comprising:

a sample comprising the at least one peptide or protein;

a chromatography column comprising a hydrophobic group, wherein the chromatography column is capable of being washed by a mobile phase to generate an eluent; and

a mass spectrometer capable of characterizing or quantifying the at least one peptide or protein, wherein a flow rate of the eluent to the mass spectrometer is between about 0.1 μL/min to about 3 μL/min, the mass spectrometer is capable of being run under native conditions, and being coupled online to the chromatography column.

21. The system of claim 20, wherein a splitter is used to connect the mass spectrometer and the chromatography column.

22. The system of claim 21, wherein the splitter is used to divert a low flow to the mass spectrometer and a high flow to a detector.

23. The system of claim 20, wherein the eluent is characterized using the mass spectrometer under native conditions.

24. The system of claim 20, wherein a makeup flow is introduced to the mobile phase between the mass spectrometer and the chromatography column.

25. The system of claim 20, wherein the system comprises a diode-array detector or a photodiode array detector.

26. The system of claim 20, wherein the at least one peptide or protein is a drug, an antibody, a bispecific antibody, a monoclonal antibody, a fusion protein, an antibody-drug conjugate, an antibody fragment, or a protein pharmaceutical product.

27. The system of claim 20, wherein the mass spectrometer is an electrospray ionization mass spectrometer, nano-electrospray ionization mass spectrometer, a triple quadrupole mass spectrometer, or a ultra-high mass range hybrid quadrupole mass spectrometer.

28. The system of claim 20, wherein the mass spectrometer comprises an orbitrap mass analyzer.

29. The system of claim 20, wherein the hydrophobic group is phenyl, octyl, butyl, hexyl or propyl.