What is claimed is:

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

contacting the sample to a solid support, wherein at least one pharmaceutical product that is capable of interacting with the at least one peptide or protein has been attached to the solid support using a primary amine-epoxy reaction;

washing the solid support using at least one mobile phase solution to provide at least one eluent;

isolating the at least one peptide or protein from the eluent;

treating the isolated peptide or protein with a denaturation solution and/or an enzymatic digestion reaction to generate components of the isolated peptide or protein;

identifying the components of the isolated peptide or protein using a mass spectrometer.

2. The method of claim 1, wherein an isotype or subclass of the isolated peptide or protein is determined.

3. A method of claim 2, wherein the isolated peptide or protein is quantified using a mass spectrometer.

4. The method of claim 1, wherein the pharmaceutical product is a drug, a chemical compound, a nucleic acid, a toxin, a peptide, a protein, a fusion protein, an antibody, an antibody fragment, a Fab region of an antibody, an antibody-drug conjugate, or a protein pharmaceutical product.

5. The method of claim 1, wherein the at least one peptide or protein in the sample is an antibody that selectively binds to the pharmaceutical product attached to the solid support.

6. The method of claim 1, wherein the at least one peptide or protein in the sample is a human antibody, wherein an isotype of the human antibody is IgG1, IgG2, IgG3, IgG4, IgA1, IgA2, IgM, or IgE.

7. The method of claim 1, wherein the at least one peptide or protein in the sample is a mammalian antibody, wherein an isotype of the mammalian antibody is IgG1, IgG2, IgG3, IgG4, IgM, or IgA.

8. The method of claim 1, wherein the at least one peptide or protein in the sample is a human antibody, and wherein an amino acid sequence of the component of the isolated peptide or protein is GPSVFPLAPSSK, GLPAPIEK, WYVDGVEVHNAK, GLPSSIEK, DASGVTFTWTPSSGK, DASGATFTWTPSSGK, VSVFVPPR, or DFTPPTVK.

9. The method of claim 1, wherein the at least one peptide or protein in the sample is a mammalian antibody, wherein an amino acid sequence of the component of the isolated peptide or protein is GPSVFPLAPSSR, GPSVFPLASCSR, GPSVFPLVSCSR, GPSVFPLASSSR, QIEVSWLR, or DPSGATFTWTPSSGK.

10. The method of claim 1, wherein the sample is treated with a solution to reach a pH range of about 0.1-4.5 prior to contacting the solid support.

11. The method of claim 10, wherein the solution comprises acetic acid.

12. The method of claim 1, wherein the sample incubates with the solid support at room temperature for about 1 hour.

13. The method of claim 1, wherein the sample further comprises a salt and a surfactant.

14. The method of claim 1, wherein the sample further comprises BSA (bovine serum albumin), HEPES (4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid), sodium chloride, EDTA (ethylenediaminetetraacetic acid) and Tween-20 (polysorbate 20).

15. The method of claim 14, wherein the sample has a pH range of about 6-9.

16. The method of claim 1, wherein the solid support is washed using the at least one mobile phase solution that comprises a salt and a surfactant and at least another subsequent mobile phase solution that has a pH range of about 0.1 to 4.5.

17. The method of claim 16, wherein the at least one mobile phase solution comprises BSA (bovine serum albumin), HEPES (4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid), sodium chloride, EDTA (ethylenediaminetetraacetic acid) and Tween-20 (polysorbate 20) and has a pH range of about 6-9.

18. The method of claim 1, wherein the denaturation solution comprises about 5-10 M urea.

19. The method of claim 1, wherein an enzyme of the enzymatic digestion reaction is trypsin.

20. The method of claim 1, wherein the pharmaceutical product is attached to the solid support using a lysine residue of the pharmaceutical product.

21. The method of claim 1, wherein the mass spectrometer is an electrospray ionization mass spectrometer or nano-electrospray ionization mass spectrometer

22. The method of claim 1, wherein the mass spectrometer is coupled to a liquid chromatography system.

23. The method of claim 1, wherein the mass spectrometer is capable of performing LC-MS (liquid chromatography-mass spectrometry) or a LC-MRM-MS (liquid chromatography-multiple reaction monitoring-mass spectrometry) analyses.

24. The method of claim 1, wherein the mass spectrometer is a triple quadrupole mass spectrometer.

25. The method of claim 3, wherein the component of the isolated peptide or protein is at least about 0.01 ng, at least about 0.1 ng, at least about 0.2 ng, or at least about 0.3 ng.

26. The method of claim 3, wherein the method further comprises the steps of:

conducting peptide mapping of the isolated peptide or protein,

selecting unique peptides and fragment ions of the isolated peptide or protein to generate MRM (multiple reaction monitoring) transitions,

selecting top two or top three transitions of the unique peptides,

optimizing collision energy of the unique peptides,

subsequently generating a calibration curve, and

determining a LLOQ (lower limit of quantification) according to the calibration curve.

27. A system for identifying or quantifying at least one peptide or protein in a sample, comprising:

a solid support, wherein a pharmaceutical product that is capable of interacting with the at least one peptide or protein has been attached to the solid support using a primary amine-epoxy reaction;

at least one mobile phase solution for washing the solid support and capable of providing at least one eluent containing the at least one peptide or protein for isolating the at least one peptide or protein;

a denaturation solution and/or an enzymatic digestion solution capable of generating components from the isolated peptide or protein; and

a mass spectrometer capable of identifying or quantifying the components from the isolated peptide or protein.

28. The system of claim 27, wherein the mass spectrometer is capable of identifying or quantifying an isotype or subclass of the isolated peptide or protein.

29. The system of claim 27, wherein the pharmaceutical product is a drug, a chemical compound, a nucleic acid, a toxin, a peptide, a protein, a fusion protein, an antibody, an antibody fragment, a Fab region of an antibody, an antibody-drug conjugate, or a protein pharmaceutical product.

30. The system of claim 27, wherein the at least one peptide or protein in the sample is an antibody that selectively binds to the pharmaceutical product attached to the solid support.

31. The system of claim 27, wherein the at least one peptide or protein in the sample is a human antibody, wherein an isotype of the human antibody is IgG1, IgG2, IgG3, IgG4, IgA1, IgA2, IgM, or IgE.

32. The system of claim 27, wherein the at least one peptide or protein in the sample is a mammalian antibody, wherein an isotype of the mammalian antibody is IgG1, IgG2, IgG3, IgG4, IgM, or IgA.

33. The system of claim 27, wherein the at least one peptide or protein in the sample is a human antibody, and wherein an amino acid sequence of the component of the isolated peptide or protein is GPSVFPLAPSSK, GLPAPIEK, WYVDGVEVHNAK, GLPSSIEK, DASGVTFTWTPSSGK, DASGATFTWTPSSGK, VSVFVPPR, or DFTPPTVK.

34. The system of claim 27, wherein the at least one peptide or protein in the sample is a mammalian antibody, wherein an amino acid sequence of the component of the isolated peptide or protein is GPSVFPLAPSSR, GPSVFPLASCSR, GPSVFPLVSCSR, GPSVFPLASSSR, QIEVSWLR, or DPSGATFTWTPSSGK.

35. The system of claim 27, wherein the sample is treated with a solution to reach a pH range of about 0.1-4.5 prior to contacting the solid support.

36. The system of claim 35, wherein the solution comprises acetic acid.

37. The system of claim 27, wherein the sample incubates on the solid support at room temperature for about 1 hour.

38. The system of claim 27, wherein the sample further comprises a salt and a surfactant.

39. The system of claim 27, wherein the sample further comprises BSA (bovine serum albumin), HEPES (4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid), sodium chloride, EDTA (ethylenediaminetetraacetic acid) and Tween-20 (polysorbate 20).

40. The system of claim 39, wherein the sample has a pH range of about 6-9.

41. The system of claim 27, wherein the solid support is washed using the at least one mobile phase solution that comprises a salt and a surfactant and at least another subsequent mobile phase solution that has a pH range of about 0.1 to 4.5.

42. The system of claim 41, wherein the at least one mobile phase solution comprises BSA (bovine serum albumin), HEPES (4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid), sodium chloride, EDTA (ethylenediaminetetraacetic acid) and Tween-20 (polysorbate 20) and has a pH range of about 6-9.

44. The system of claim 27, wherein the denaturation solution comprises about 5-10 M urea.

44. The system of claim 27, wherein an enzyme of the enzymatic digestion solution is trypsin.

45. The system of claim 27, wherein the pharmaceutical product is attached to the solid support using a lysine residue of the pharmaceutical product.

46. The system of claim 27, wherein the mass spectrometer is an electrospray ionization mass spectrometer or nano-electrospray ionization mass spectrometer.

47. The system of claim 27, wherein the mass spectrometer is coupled to a liquid chromatography system.

48. The system of claim 27, wherein the mass spectrometer is capable of performing LC-MS (liquid chromatography-mass spectrometry) or a LC-MRM-MS (liquid chromatography-multiple reaction monitoring-mass spectrometry) analyses.

49. The system of claim 27, wherein the mass spectrometer is a triple quadrupole mass spectrometer.

50. The system of claim 27, wherein the system is capable of:

conducting peptide mapping of the isolated peptide or protein,

selecting unique peptides and fragment ions of the isolated peptide or protein to generate MRM (multiple reaction monitoring) transitions,

selecting top two or top three transitions of the unique peptides,

optimizing collision energy of the unique peptides,

subsequently generating a calibration curve, and

determining a LLOQ (lower limit of quantification) according to the calibration curve.