What is claimed is:

1. A method for characterizing host-cell proteins in a sample matrix, comprising:

enriching host-cell proteins in the sample matrix by contacting the sample matrix with an affinity chromatography support;

performing fractionation on a flowthrough from the affinity chromatography; and

characterizing at least one of the host-cell proteins using a mass spectrometer.

2. The method of claim 1, wherein the affinity chromatography support is protein A chromatography support.

3. The method of claim 1 further comprising washing the affinity chromatography support with a wash buffer and collecting the flow-through.

4. The method of claim 1, wherein the affinity chromatography support comprises protein A or protein G.

5. The method of claim 4, wherein the protein A or the protein G is immobilized on agarose or sepharose resin.

6. The method of claim 1, wherein the mass spectrometer is a tandem mass spectrometer.

7. The method of claim 6, wherein the mass spectrometer is coupled with a liquid chromatography system.

8. The method of claim 7, wherein the liquid chromatography system is a nano-liquid chromatography system.

9. The method of claim 1 further comprising characterizing at least one of the host-cell proteins using High-Field Asymmetric Waveform Ion Mobility Spectrometry device.

10. The method of claim 1, wherein the sample matrix further comprises a protein of interest.

11. The method of claim 10, wherein the protein of interest is an antibody.

12. The method of claim 10, wherein the protein of interest is a fusion protein.

13. The method of claim 1, wherein the fractionation is a size-based fractionation.

14. The method of claim 1, wherein the fractionation is a hydrophobicity-based fractionation.

15. The method of claim 1, wherein fractionation is a charge-based fractionation.