CLAIMS

1. A method of identifying proteins in a sample, comprising:

(a) incubating a particle panel, the particle panel comprising a plurality of superparamagnetic iron oxide nanoparticles (SPIONs) comprising an iron oxide core and a polymer shell comprising an average particle size of about 200 nm to about 1 μm with distinct surface chemistries, with the sample to form a plurality of distinct biomolecule coronas corresponding to distinct SPION types of the particle panel, wherein at least one distinct SPION type of the particle panel comprises a positive surface charge, and at least one distinct SPION type of the particle panel comprises a negative surface charge from -60 mV to -30 mV in zeta potential, wherein the zeta potential is measurable with a concentration of 0.02 wt% in a solution in 5% pH 7.4 PBS at about 25°C with an about 1 minute equilibration time in the absence of biological sample, and, wherein the sample is plasma, serum, CSF, urine, tear, cell lysates, tissue lysates, cell homogenates, tissue homogenates, nipple aspirates, fecal samples, synovial fluid, whole blood, or saliva;

(b) magnetically isolating the particle panel from unbound protein in the sample to enrich proteins in the plurality of distinct biomolecule coronas; and

(c) assaying the plurality of distinct biomolecule coronas to identify at least 500 unique proteins from the enriched proteins**.**

2. The method of claim 1, wherein the assaying identifies from 500 to 20,000 unique proteins from the enriched proteins.

3. The method of claim 1 or 2, wherein the assaying identifies from 1,000 to 5,000 unique proteins from the enriched proteins.

4. The method of any one of claims 1-3, wherein the assaying identifies from 1,200 to 2,200 unique proteins from the enriched proteins.

5. The method of any one of claims 1-4, wherein an individual protein of the unique proteins comprises a peptide sequence having a minimum length of 7 amino acid residues.

6. The method of any one of claims 1-5, wherein the assaying comprises using mass spectrometry to identify the unique proteins in the sample.

7. The method of any one of claims 1-6, wherein the sample comprises a plurality of samples.

8. The method of claim 7, wherein the plurality of samples comprises at least two or more spatially isolated samples.

9. The method of claim 7 or 8, wherein the plurality of samples comprises at least 10 spatially isolated samples.

10. The method of claim 8 or 9, wherein the incubating comprises contacting the sample, which is provided in at least two or more spatially isolated samples with the particle panel at the same time, or wherein the magnetically isolating comprises magnetically isolating the particle panel from unbound protein in the at least two or more spatially isolated samples of the plurality of samples at the same time.

11. The method of any one of claims 1-10, further comprising repeating steps (a)-(c), wherein, when repeated, the incubating, isolating, and assaying yields a percent quantile normalized coefficient (QNCV) of variation of 20% or less, as determined by comparing a peptide mass spectrometry feature from at least three full-assay replicates for each particle type in the particle panel.

12. The method of any one of claims 1-11, wherein the assaying is capable of identifying proteins over a dynamic range of at least 7.

13. The method of any one of claims 1-12, further comprising washing the particle panel at least one time after the magnetically isolating the particle panel from the unbound protein.

14. The method of any one of claims 1-13, further comprising washing the particle panel at least two times after the magnetically isolating the particle panel from the unbound protein.

15. The method of any one of claims 1-14, further comprising, before the assaying of (c), (i) lysing the enriched proteins in the plurality of distinct biomolecule coronas, (ii) digesting the enriched proteins in the plurality of distinct biomolecule coronas to generate digested peptides, or (iii) purifying the digested peptides.

16. The method of claim 15, wherein the digesting the enriched proteins is performed in the presence of the plurality of SPIONs.

17. The method of claim 15 or 16, wherein the digesting is performed using a protease.

18. The method of any one of claims 1-17, wherein the assaying of (c) comprises using mass spectrometry to identify the unique proteins in the sample.

19. The method of any one of claims 1-18, wherein the assaying of (c) is performed in 2 to 4 hours.

20. The method of any one of claims 1-19, wherein the method is performed in 1 to 20 hours.

21. The method of any one of claims 1-20, wherein the isolating takes no more than 30 minutes.

22. The method of any one of claims 1-21, wherein the first distinct SPION type comprises a silica coating and the second distinct SPION type comprises a poly(N-(3-(dimethylamino)propyl) methacrylamide) (PDMAPMA) coating.

23. The method of any one of claims 1-21, wherein at least one distinct SPION type of the particle panel comprises a carboxylated polymer, an aminated polymer, a zwitterionic polymer, or any combination thereof.

24. The method of any one of claims 1-21, wherein at least one SPION type of the particle panel comprises an iron oxide core with a silica shell coating, an iron oxide core with a poly(N-

(3-(dimethylamino)propyl) methacrylamide) (PDMAPMA) coating, or an iron oxide core with a poly(oligo(ethylene glycol) methyl ether methacrylate) (POEGMA) coating.

25. The method of any one of claims 1-24, wherein the particle panel further comprises at least one distinct SPION type comprising a neutral surface charge.

26. The method of any one of claims 1-25, wherein the plurality of SPIONs comprise a heterogeneous size distribution.

27. The method of any one of claims 1-25, wherein the plurality of SPIONs comprise a homogeneous size distribution.

28. The method of any one of claims 1-25, wherein each distinct SPION type of the particle panel comprises a polydispersity index of less than 0.5.

29. The method of claim 28, wherein each distinct SPION type of the particle panel comprises a polydispersity index of less than 0.2.

30. The method of claim 29, wherein each distinct SPION type of the particle panel comprises a polydispersity index of less than 0.1.