## CLAIMS

WHAT IS CLAIMED IS:

1. An automated system for preparing a biological sample for mass spectrometry analysis comprising a network of units with differentiated functions in distinguishing states of the biological sample using a plurality of particles having surfaces with different physiochemical properties wherein:

(a) a first unit comprises a multichannel fluid transfer instrument for transferring fluids between units within the system;

(b) a second unit comprises a support for storing at least a portion of the biological sample;

(c) a third unit comprises a support for a sensor array plate comprising partitions that comprise the plurality of particles having surfaces with different physiochemical properties for binding a population of proteins within the biological sample;

(d) a fourth unit comprises supports for storing a plurality of reagents;

(e) a fifth unit comprises supports for storing a reagent to be disposed of; and

(f) a sixth unit comprises supports for storing consumables used by the multichannel fluid transfer instrument;

wherein the system is programmed to perform a series of steps comprising: i. contacting the biological sample with the partitions of the sensor array plate; ii. incubating the biological sample with the plurality of particles contained within the partitions of the sensor array plate, wherein the plurality of particles comprise a plurality of magnetic particles in a solution with different physiochemical properties for binding the population of proteins within the biological sample, and wherein each particle type of the plurality of particles is configured to bind to at least 300 different proteins to thereby form protein coronas; iii. transferring the sensor array plate to a magnetized support to remove all components from the partitions except the plurality of magnetic particles and the population of proteins interacting with the plurality of magnetic particles; and iv. preparing a sample for mass spectrometry by adding a solution to the plurality of magnetic particles such that a population of peptide analytes are desorbed from the plurality of magnetic particles, wherein the preparing comprises alkylation and protease digestion.

2. The automated system of claim 1, wherein the first unit comprises a degree of mobility that enables access to all other unit within the system.

3. The automated system of either of claims 1 or 2, wherein the first unit comprises a capacity to perform pipetting functions.

4. The automated system of any one of claims 1-3, wherein the support of the second or third unit comprises support for a single plate, a 6 well plate, a 12 well plate, a 96 well plate, or a rack of microtubes.

5. The automated system of any one of claims 1-4, wherein the automated system comprises a thermal unit capable of modulating the temperature of said support for storing at least a portion of the biological sample.

6. The automated system of any one of claims 1-5, wherein the second or third unit comprises a rotational unit capable of physically agitating or mixing the biological sample.

7. The automated system of any one of claims 1-6, wherein the plurality of particles having surfaces comprise a plurality magnetic nanoparticles in a solution with different physiochemical properties for binding the population of proteins within the biological sample.

8. The automated system of any one of claims 1-7, wherein the thermal unit is capable of modulating the temperature of said magnetized support and the biological sample and incubated for an additional amount of time.

9. The automated system of any one of claims 1-8, wherein the fourth unit comprises a set of reagents for:

(a) generating the sensor array plate;

(b) washing an unbound biological sample; or

(c) preparing the sample for mass spectrometry.

10. The automated system of any one of claims 1-9, wherein (i) contacting the biological sample with a specified partition of the sensor array plate comprises pipetting a specified volume of the biological sample into the specific partition of the sensor array plate.

11. The automated system of any one of claims 1-10, wherein (i) contacting the biological sample with a specified partition of the sensor array plate comprises pipetting a volume

corresponding to a 1:1, 1:2: 1:3, 1:4, 1:5, 1:6, 1:7, 1:8, 1:9, 1:10, 1:15, or 1:20 ratio of a plurality of particles in a solution to the biological sample.

12. The automated system of any one of claims 1-11, wherein (ii) incubating the biological sample with the plurality of magnetic particles contained within the partition of the sensor array plate comprises an incubation temperature between 4° C to 40° C.

13. The automated system of any one of claims 1-12, wherein the second unit can facilitate a transfer of the sample for mass spectrometry to a mass spectrometry unit.

14. The automated system of any one of claims 1-13, wherein the partitions comprise 3 to 8 types of magnetic particles having surfaces with different physicochemical properties.

15. The automated system of any one of claims 1-14, wherein the plurality of magnetic particles is configured to bind to at least 600 different proteins.

16. The automated system of any one of claims 1-15, wherein the plurality of magnetic particles is located in different partitions on the sensor array plate.

17. The automated system of any one of claims 1-16, wherein at least two distinct types of magnetic particles that differ from each other in at least one physicochemical property are located in the same partition on the sensor array plate.

18. The automated system of any one of claims 1-17, wherein the sample for mass spectrometry comprise the population of proteins.

19. A method for generating a subset of biomolecules from a biological sample for mass spectrometry, comprising:

providing the biological sample to the automated system of any one of claims 1-18, wherein the automated system contacts the biological sample with a plurality of magnetic particles to generate biomolecule coronas, wherein the automated system processes the biomolecule coronas to generate the subset of biomolecules, and wherein a dynamic range of the subset of biomolecules is compressed relative to a dynamic range of biomolecules present in the biological sample.