

STATE-OF-THE-ART LECTURE S4

Driving biological discovery using mass spectrometry

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A component to understanding biological processes involves identifying the proteins expressed in cells as well as their modifications and the dynamics of processes. Several major technologies, but especially mass spectrometry, have benefited from large scale genome sequencing of organisms. The sequence data produced by these efforts can be used to interpret mass spectrometry data of proteins and thus enables rapid and large-scale analysis of protein data from experiments. Advances in multi-dimensional separations as well as mass spectrometry have improved the scale of experiments for protein identification. This has improved the analysis of protein complexes, and more complicated protein mixtures. Subtractive data analysis approaches have also improved the ability to identify the components of large structures such as the centrosome and proteins associated with chromatin. Experiments to identify centrosome proteins and chromatin associated proteins using subtractive approaches will be described.