

# 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. More advanced methods for data analysis have allowed the analysis of data from non-sequenced organisms as well. Advances in separation technologies as well as mass spectrometers have improved the scale of experiments for protein identification. This has improved the analysis of protein complexes, and more complicated protein mixtures. Quantitative mass spectrometry can be used to study biological processes such as protein-protein interactions, development or the effects of gene mutations on pathways. Recent studies on the interactions of the Cystic Fibrosis Transport Regulator as it progresses through the folding pathway will be presented. This lecture will illustrate how mass spectrometry based methods can be used to learn about biological processes.

**MCI**  
*Topics in  
Museum  
Conservation*

**June 15, 2009**  
**10:45 am**

*MCI Theater*  
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