

Experimental Methods in Systems Biology

Part of the Coursera Certificate in Systems Biology

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Fall 2014, Week 3 Mass Spectrometry-Based
Proteomics



Outline

- What is Mass Spectrometry?
- General Components of a Mass Spectrometer
 - Separation
 - Ionization
 - Mass Analyzer
 - Fragmentation
- Quantification

 Mass spectrometer: an instrument in which ions are separated according to their mass—to charge ratio, and in which the number of ions is quantified electrically

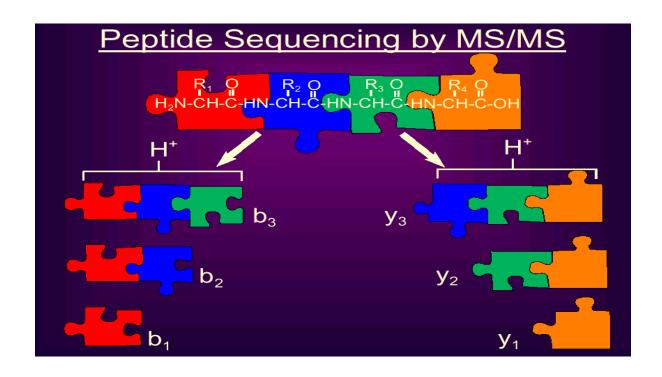
Two MS methods for protein ID

- Peptide mass fingerprinting (PMF): based on a collection of masses of peptides derived from proteolytic digestion of the proteins
 - Benefit: quick
 - Drawback: not able to handle mixtures
- Peptide sequencing by tandem MS (MS/MS): based obtaining partial peptide sequence information in MS/MS
 - Benefit: confident sequence/PTM site identification, easily coupled with HPLC for protein complex identification
 - Drawback: higher costs, more time consuming

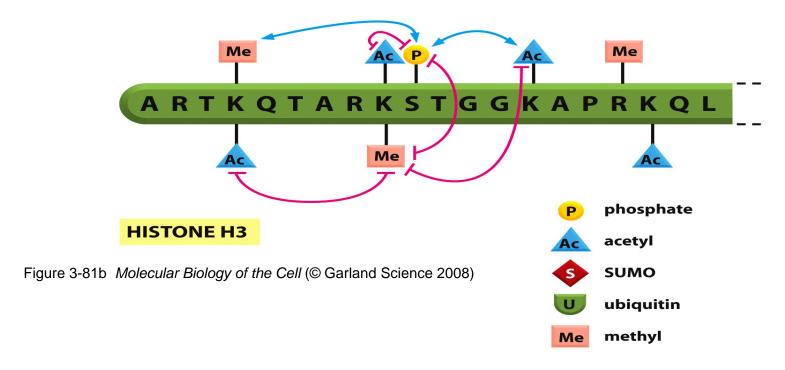
Peptide Sequencing by Tandem Mass Spectrometry

 Tandem mass spectrometry: ions separated according to their m/z value in the first stage analyzer are selected for fragmentation and the fragments are analyzed in a second analyzer. It is used for protein sequencing and PTM (post-translational modifications).

MS/MS Peptide Sequencing



PTMs and epigenetic regulation of histones



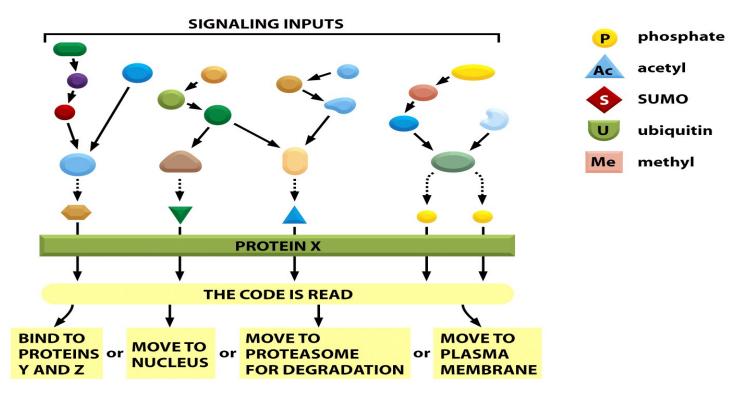
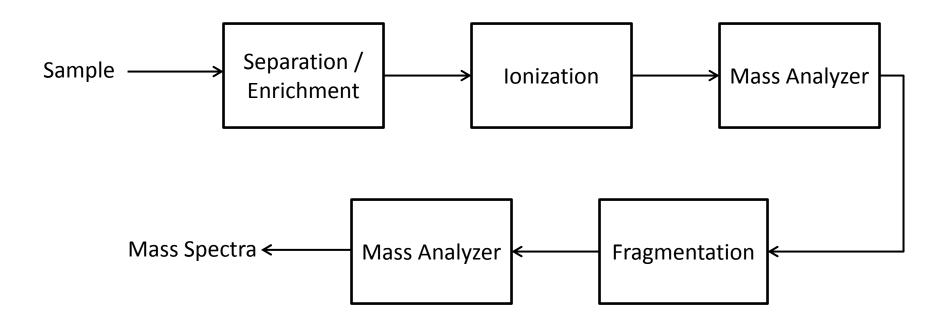


Figure 3-81c Molecular Biology of the Cell (© Garland Science 2008)

Applications

- Compare and/or quantify:
 - Total Protein Abundance
 - Post-translational modifications
 - Phosphorylation
 - Acetylation
 - Methylation
 - Hydroxylation
 - Glycosylation
 - Etc.
 - If it has mass and can be ionized, it can likely be analyzed by mass spectrometry

General MS/MS Setup for Proteomics



MS/MS Peptide sequencing and PTM identification

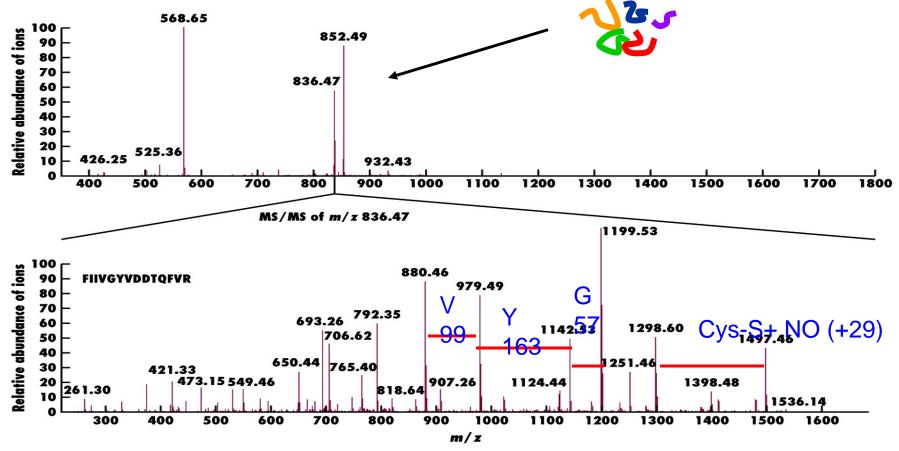


Figure 3-41b

Molecular Cell Biology, Sixth Edition
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