Principles of Mass Spectrometry

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Mass spectrometry is the principle analytical component of current proteomics. This lecture will focus on the physical basics of the method, available instrumentation, the interpretation of mass spectra as well as the application of mass spectrometry to peptide sequencing, the determination of post-translational proteins, protein quantification and intact protein measurements.

A mass spectrometer essentially consists of three parts: a) an ion source, b) a mass analyzer and c) a detection system. Mass spectrometric analysis requires the generation of ions from analyte molecules. The primary methods for this purpose in proteomics are electrospray ionization (ESI) and matrix-assisted laser desorption/ionization (MALDI). In any of the many available mass analyzers, ions are separated according to their mass-to-charge ratio (m/z) which provide the basis for the detection of analytes of different mass. The more common types of mass analyzers for proteomics are quadrupoles, time-of-flight instruments and several variants of ion traps. The detection system converts the physical ions into a digital signal. This is accomplished either by physical impact of ions on detectors such as multi channel plates (MCPs) or channeltrons, or by measuring image currents as in ion cyclotron resonance (ICR) or Orbitrap instruments.

In preparation of this lecture, students should familarise themselves with the following important concepts and keywords:

- Ions and isotopes
- Mass definitions: average or chemical mass, nominal mass, monoisotopic mass
- Mass resolution
- Precision and accuracy of mass measurement

Suggested reading: http://en.wikipedia.org/wiki/Mass_spectrometry