

## MASS SPECTROMETRY AND PROTEOMICS APPLICATIONS

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**M**ass spectrometry (MS) is widely recognized as a powerful analytical tool for molecular research. MS is used by researchers around the globe to identify, quantify, and characterize biomolecules like proteins from any number of biological conditions or sample types. As instrumentation has advanced, and with the coupling of liquid chromatography (LC) for high throughput LC MS/MS, a proteomics experiment measuring hundreds to thousands of proteins/protein groups is now commonplace. While expert practitioners who best understand the operation of LC MS systems tend to have strong backgrounds in physics and engineering, consumers of proteomics data and technology are not exposed to the physio chemical principles underlying the information they seek. Since articles and reviews tend not to focus on bridging this divide, our goal here is to span this gap and translate MS ion physics into language intuitive to the general reader active in basic or applied biomedical research. Here, we visually describe what happens to ions as they enter and move around inside a mass spectrometer. We describe basic MS principles, including electric current, ion optics, ion traps, quadrupole mass filters, and Orbitrap FT analyzers.

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