

Presentation title:

How does measuring the mass of peptides enable us to determine their amino acid sequence?

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Abstract

In this presentation we will discuss how measuring the mass of peptides can be used to determine their amino acid sequence. We will start by examining the features of a typical tandem mass spectrum of a peptide, and seeing how these can be matched against genomic sequence data to generate an identification. We will use several different freely available web-based searching tools to produce real-time identifications of individual peptides all the way through to files containing large sets of tandem mass spectra. Lastly, we will discuss how it is important for some interpretation of the results produced by such programs to ensure that the results are meaningful.