

Presentation title: An introduction to modern proteomic techniques

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Abstract:

In this lecture I will introduce and discuss many of the techniques currently used in proteomic research. Modern proteomics encompasses methods to separate complex protein mixtures, identify proteins and quantitate their levels in comparative studies. Mass spectrometry is now the prime method used in modern proteomic research with multiplexed labelling strategies proving popular for comparative quantitative analysis. However, there is still a place for classical techniques such as 2D gels and various protein chemistry methods. The analysis of protein post-translational modifications can also be studied using mass spectrometry and strategies to achieve this will be discussed.