



COLLOQUIUM

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Mass Spectrometry Based Proteomics

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Abstract

Mass spectrometry (MS) has become an indispensable technique for proteomics studies whose goal is to identify and quantify proteins from complex mixtures. Protein level study of cellular functions is fundamental to the emerging field of Systems Biology and discovering biomarkers. MS based proteomics relies on the availability of the genome sequence databases, and many technological advances (ionization and chromatography techniques) have greatly contributed to its rapid popularity.

In this presentation, some of the major issues related to quantitative proteomics based on Liquid Chromatography – Mass Spectrometry (LC-MS) will be outlined and a suit of tools to address them will be discussed.