

PROTEINS AND PEPTIDES IDENTIFICATION FROM MS/MS DATA IN PROTEOMICS

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Abstract

Protein identification in biological samples is the most important task in proteomics. In the past decade, mass spectrometry (MS) became the method of choice for the identification of proteins. The purpose of this paper is to give an overview of MS-based protein identification methods, discuss their advantages and limitations and to highlight some recent advancements in this field.

Keywords: proteomics, tandem mass spectrometry MS/MS, database protein identification, de novo sequencing