Method for Identification of Peptides and Post-Translational Modifications

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TECHNOLOGY DESCRIPTION

The invention allows for the determination of amino acid sequence tags from tandem mass spectrometry spectral pairs and subsequent peptide and modification identification through a database search utilizing extremely fast pattern matching.

This invention would present an improved method over tools, such as SEQUEST and MASCOT, by never comparing a spectrum against a database and simultaneously allowing for higher sensitivity in the detection of post-translational modifications.

The invention is useful to anyone interested in identifying peptides, proteins and post-translational modifications on Tandem Mass Spectrometry data from biological samples

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OTHER INFORMATION

KEYWORDS

protein identification, peptides, mass spectrometry, proteomics, post-translational modifications

CATEGORIZED AS

- **Computer**
  - Software

RELATED CASES

2006-817-0, 2006-817-1