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# 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

## CONTACT

University of California, San Diego Office of Innovation and Commercialization innovation@ucsd.edu tel: 858.534.5815.



#### OTHER INFORMATION

#### **KEYWORDS**

protein identification, peptides, mass spectrometry, proteomics, posttranslational modifications

# CATEGORIZED AS

▶ Computer

▶ Software

RELATED CASES

2006-817-0, 2006-817-1

University of California, San Diego
Office of Innovation and Commercialization
9500 Gilman Drive, MC 0910, ,
La Jolla, CA 92093-0910

Tel: 858.534.5815
innovation@ucsd.edu
https://innovation.ucsd.edu
Fax: 858.534.7345

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