

Mass Spectrometry Data Analysis in Proteomics

Edited by

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Mass Spectrometry Data Analysis in Proteomics is an in-depth guide to the theory and practice of analyzing raw mass spectrometry (MS) data in proteomics. As MS is a high throughput technique, proteomic researchers must attend carefully to the associated field of data analysis, and this volume outlines available bioinformatics programs, algorithms, and databases available for MS data analysis. General guidelines for data analysis using search engines such as Mascot, X tandem, and VEMS are provided, with specific attention to identifying poor quality data and optimizing search parameters. Several different types of MS data are discussed, followed by a description of optimal methods for conversion of raw data into peak lists for input to search engines. Choosing the most accurate and complete databases is emphasized, and a report of available sequence databases is included. Methods for assembling expressed sequence tags (ESTs) into assembled nonredundant databases are provided, along with protocols for further processing the sequences into a format suitable for MS data. *Mass Spectrometry Data Analysis in Proteomics* describes publicly available applications whenever possible.

FEATURES

- Essential reference for mass spectrometry (MS) in proteomics and glycomics
- Concise protocols for optimizing search parameters in MS search engines
- Practical guide to MS data analysis and bioinformatics
- Thorough review of available databases for proteomics researchers

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