



Acceleration and improvement of protein identification by mass spectrometry /

Bienvenut, Willy Vincent

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Monografía

"This volume presents a review of basic proteomic techniques as well as of "molecular scanner", a novel high throughput protein identification technique. The volume will serve as a valuable text to people new to the field of proteomic science introducing them to usual sample treatments, as well as post separation gel treatments. More importantly, protein identification techniques are described, especially peptide mass fingerprinting with MALDI-MS based methods."--Jacket

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Contenido: Introduction: Proteins analysis using mass spectrometry. -- Molecular scanner development: toward clinical molecular scanner for proteome research: parallel protein chemical processing before and during western-blot. -- Quantitation during electroblotting step: enhanced protein recovery after electrotransfer using square wave alternating voltage. -- Signal treatment and virtual imaging (1/2): a molecular scanner to highly automated research and to display proteome images. -- Signal treatment and virtual imaging (2/2): visualization and analysis of molecular scanner peptide mass spectra. -- Improvement in the peptide mass fingerprint protein identification (1/2): hydrogen/deuterium exchange for higher specificity of protein identification by peptide mass fingerprinting. -- Improvement in the peptide mass fingerprint protein identification (2/2): MALDI-MS/MS with high resolution and sensitivity for identification and characterization of proteins. -- Proteomic and mass spectrometry: some aspects and recent developments. -- Conclusions and perspectives

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