

Acceleration And Improvement Of Protein Identification By Mass Spectrometry

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Preface.- Acknowledgements.- List of Contributors.- 1: Introduction: Proteins analysis using mass spectrometry.- 2: Molecular scanner development: Toward clinical molecular scanner for proteome research: Parallel protein chemical processing before and during western-blot.- 3: Quantitation during electroblotting step: Enhanced protein recovery after electrotransfer using square wave alternating voltage.- 4: Signal treatment and virtual imaging (1/2): A molecular scanner to highly automated research and to display proteome images.- 5: Signal treatment and virtual imaging (2/2): Visualization and analysis of molecular scanner peptide mass spectra.- 6: Improvement in the peptide mass fingerprint protein identification (1/2): Hydrogen/deuterium exchange for higher specificity of protein identification by peptide mass fingerprinting.- 7: Improvement in the peptide mass fingerprint protein identification (2/2): MALDI-MS/MS with high resolution and sensitivity for identification and characterization of proteins.- 8: Proteomic and mass spectrometry: Some aspects and recent developments.- 9: Conclusions and perspectives.- Appendix.- Abbreviations used in this book.- Abbreviations for usual amino acids and chemical constants.- Index. EAN/ISBN : 9781402033193 Publisher(s): Springer Netherlands Discussed keywords: Massenspektrometrie Format: ePub/PDF Author(s): Bienvenut, Willy Vincent

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