
Contents

Preface	v
Contributors	ix
1 Introduction to Proteomics Rune Matthiesen and Kudzai E. Mutenda	1
2 Extracting Monoisotopic Single-Charge Peaks From Liquid Chromatography-Electrospray Ionization–Mass Spectrometry Rune Matthiesen	37
3 Calibration of Matrix-Assisted Laser Desorption/Ionization Time-of-Flight Peptide Mass Fingerprinting Spectra Karin Hjernø and Peter Højrup	49
4 Protein Identification by Peptide Mass Fingerprinting Karin Hjernø	61
5 Generating Unigene Collections of Expressed Sequence Tag Sequences for Use in Mass Spectrometry Identification Jeppe Emmersen	77
6 Protein Identification by Tandem Mass Spectrometry and Sequence Database Searching Alexey I. Nesvizhskii	87
7 Virtual Expert Mass Spectrometrists v3.0: <i>An Integrated Tool for Proteome Analysis</i> Rune Matthiesen	121
8 Quantitation With Virtual Expert Mass Spectrometrists Albrecht Gruhler and Rune Matthiesen	139
9 Sequence Handling by Sequence Analysis Toolbox v1.0 Christian Ravnsborg Ingrell, Rune Matthiesen, and Ole Nørregaard Jensen	153
10 Interpretation of Collision-Induced Fragmentation Tandem Mass Spectra of Posttranslationally Modified Peptides Jakob Bunkenborg and Rune Matthiesen	169
11 Retention Time Prediction and Protein Identification Magnus Palmblad	195

12	Quantitative Proteomics by Stable Isotope Labeling and Mass Spectrometry Sheng Pan and Ruedi Aebersold	209
13	Quantitative Proteomics for Two-Dimensional Gels Using Difference Gel Electrophoresis David B. Friedman	219
14	Proteomic Data Exchange and Storage: <i>Using Proteios</i> Per Gärdén and Rikard Alm	241
15	Proteomic Data Exchange and Storage: <i>The Need for Common Standards and Public Repositories</i> Sandra Orchard, Philip Jones, Chris Taylor, Weimin Zhu, Randall K. Julian, Jr., Henning Hermjakob, and Rolf Apweiler	261
16	Organization of Proteomics Data With YassDB Allan L. Thomsen, Kris Laukens, Rune Matthiesen, and Ole Nørregaard Jensen	271
17	Analysis of Carbohydrates by Mass Spectrometry Kudzai E. Mutenda and Rune Matthiesen	289
18	Useful Mass Spectrometry Programs Freely Available on the Internet Rune Matthiesen	303
Appendix		307
Index		313



<http://www.springer.com/978-1-58829-563-7>

Mass Spectrometry Data Analysis in Proteomics

Matthiesen, R. (Ed.)

2007, X, 320 p. 87 illus., Hardcover

ISBN: 978-1-58829-563-7

A product of Humana Press