
Contents

<i>Preface</i>	v
<i>Contributors</i>	ix
1. Generation and Analysis of Multidimensional Protein Identification Technology Datasets.....	1
<i>Selene K. Swanson, Laurence Florens, and Michael P. Washburn</i>	
2. Quantitative Peptide and Protein Profiling by Mass Spectrometry	21
<i>Alexander Schmidt, Birgit Bisle, and Thomas Kislinger</i>	
3. Label-Free Relative Quantitation of Prokaryotic Proteomes Using the Accurate Mass and Time Tag Approach	39
<i>Kim K. Hixson</i>	
4. Classical Proteomics: Two-Dimensional Electrophoresis/MALDI Mass Spectrometry.....	65
<i>Ursula Zimny-Arndt, Monika Schmid, Renate Ackermann, and Peter R. Jungblut</i>	
5. The Use of Difference In-Gel Electrophoresis for Quantitation of Protein Expression	93
<i>Rajat Sapra</i>	
6. Liquid-Chromatography-Mass Spectrometry of Thylakoid Membrane Proteins.....	113
<i>Christian G. Huber, Anna-Maria Timperio, Hansjörg Toll, and Lello Zolla</i>	
7. High Accuracy Mass Spectrometry in Large-Scale Analysis of Protein Phosphorylation.....	131
<i>Jesper V. Olsen and Boris Macek</i>	
8. Manual Validation of Peptide Sequence and Sites of Tyrosine Phosphorylation from MS/MS Spectra.....	143
<i>Amy M. Nichols and Forest M. White</i>	
9. Assigning Glycosylation Sites and Microheterogeneities in Glycoproteins by Liquid Chromatography/Tandem Mass Spectrometry	161
<i>Yehia Mechref, Milan Madera, and Milos V. Novotny</i>	
10. Structure Analysis of N -Glycoproteins	181
<i>Stefanie Henning, Jasna Peter-Katalinic', and Gottfried Pohlentz</i>	
11. Capillary Zone Electrophoresis-Mass Spectrometry for the Characterization of Isoforms of Intact Glycoproteins.....	201
<i>Christian Neusüß, and Matthias Pelzing</i>	

12.	Top-Down Proteomics on a High-field Fourier Transform Ion Cyclotron Resonance Mass Spectrometer	215
	<i>Séverine A. Ouvry-Patat, Matthew P. Torres, Craig Gelfand, Hung-Hiang Quek, Michael Easterling, J. Paul Speir, and Christoph H. Borchers</i>	
13.	Capillary Isoelectric Focusing/Reversed Phase Liquid Chromatography/Mass Spectrometry.....	233
	<i>Cheng S. Lee and Brian M. Balgley</i>	
14.	Integrating Accelerated Tryptic Digestion into Proteomics Workflows	241
	<i>Gordon W. Slys and David C. Schriemer</i>	
15.	Hydrogen/Deuterium Exchange Mass Spectrometry	255
	<i>Xuguang Yan and Claudia S. Maier</i>	
16.	Mass Spectrometry Detection and Characterization of Noncovalent Protein Complexes	273
	<i>Sheng Yin and Joseph A. Loos</i>	
17.	Chemical Cross-Linking for Protein–Protein Interaction Studies.....	283
	<i>Xiaoting Tang and James E. Bruce</i>	
18.	Tissue Analysis with High-Resolution Imaging Mass Spectrometry	295
	<i>A.F. Maarten Altelaar and Ron M.A. Heeren</i>	
19.	Proteomic Global Profiling for Cancer Biomarker Discovery.....	309
	<i>Vitor Faca, Hong Wang, and Samir Hanash</i>	
20.	Analysis of Protein Glycosylation and Phosphorylation Using Liquid Phase Separation, Protein Microarray Technology, and Mass Spectrometry.....	321
	<i>Jia Zhao, Tasneem H. Patwa, Manoj Pal, Weilian Qiu, and David M. Lubman</i>	
21.	Transthyretin Mass Determination for Detection of Transthyretin Familial Amyloid.....	353
	<i>John F. O'Brien and H. Robert Bergen III</i>	
22.	Characterization of Microorganisms by MALDI Mass Spectrometry	367
	<i>Catherine E. Petersen, Nancy B. Valentine, and Karen L. Wahl</i>	
23.	Mass Spectrometric Characterization of Neuropeptides.....	381
	<i>Stephanie S. DeKeyser, James A. Dowell, and Lingjun Li</i>	
24.	Peptide and Protein Ion/Ion Reactions in Electrodynamic Ion Traps: Tools and Methods.....	395
	<i>Scott A. McLuckey</i>	
25.	Electron Capture Dissociation LC/MS/MS for Bottom–Up Proteomics	413
	<i>Roman A. Zubarev</i>	
26.	Two-Dimensional Ion Mobility Analyses of Proteins and Peptides	417
	<i>Alexandre A. Shvartsburg, Keqi Tang, and Richard D. Smith</i>	
27.	Proteomics for Validation of Automated Gene Model Predictions.....	447
	<i>Kemin Zhou, Ellen A. Panisko, Jon K. Magnuson, Scott E. Baker, and Igor V. Grigoriev</i>	

28. Support Vector Machines for Improved Peptide Identification from Tandem Mass Spectrometry Database Search	453
<i>Bobbie-Jo M. Webb-Robertson</i>	
<i>Index</i>	461