

METHODS IN MOLECULAR BIOLOGY

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Quantitative Proteomics by Mass Spectrometry

Second Edition

Edited by

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Cover image: This image is composed of 4 elements: A 3D image of a cell where the nucleus is visible, a double helix DNA that comes out of the nucleus and joins/morphs into a 3D ribbon structure of a protein. On top of these 3 elements there is a Mass Spectra.

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Preface

Tools for Next Generation Quantitative Proteomics by Mass Spectrometry

The proteome has been defined as the entire set of proteins expressed by a genome. The genome is relatively simple, and using today's technology the human genome of an individual can be routinely sequenced. The dynamic nature of the proteome, and its heterogeneous structure with many possible post-translational modifications, make the task of fully sequencing the complete human proteome out of reach. On one hand, "gene-centric" proteomic approaches that focus on identifying the genes that code for the expressed proteins (which is distinct from characterizing the complete molecular sequences of the proteins) are becoming routine, and many laboratories have undertaken large-scale protein identification projects. On the other hand, the characterization and quantification of post-translational modifications and the accurate and reproducible quantification of proteins from tissues, biofluids, and cell lines are more challenging, and fewer specialized laboratories have the tools and expertise to perform these experiments routinely.

This volume describes prominent methodologies developed by laboratories that have been leading the field of quantitative proteomics by Mass Spectrometry (MS). The procedures for performing the experiments are described in an easy-to-understand manner, with many technical details that usually are not reported in typical research articles.

This volume is not intended to be comprehensive with respect to all currently available methodologies for performing quantitative proteomics by MS, but it should provide a broad perspective of the methodologies used for quantifying proteins and post-translational modifications in different types of biomedical specimens.

The tools for performing quantitation of proteins by MS have gone through a major revolution in the last decade, and next-generation quantitative proteomics tools are already here. I hope that this volume will facilitate the dissemination of these tools.

Bethesda, MD, USA

Salvatore Sechi

Contents

<i>Preface</i>	<i>v</i>
<i>Contributors</i>	<i>ix</i>
1 Increased Depth and Breadth of Plasma Protein Quantitation via Two-Dimensional Liquid Chromatography/Multiple Reaction Monitoring-Mass Spectrometry with Labeled Peptide Standards	1
<i>Andrew J. Percy, Juncong Yang, Andrew G. Chambers, and Christoph H. Borchers</i>	
2 Quantitative Analysis of the Sirt5-Regulated Lysine Succinylation Proteome in Mammalian Cells	23
<i>Yue Chen</i>	
3 Determining the Composition and Stability of Protein Complexes Using an Integrated Label-Free and Stable Isotope Labeling Strategy	39
<i>Todd M. Greco, Amanda J. Guise, and Ileana M. Cristea</i>	
4 Label-Free Quantitation for Clinical Proteomics	65
<i>Robert Moulder, Young Ah Goo, and David R. Goodlett</i>	
5 Proteogenomic Methods to Improve Genome Annotation	77
<i>Keshava K. Datta, Anil K. Madugundu, and Harsha Gowda</i>	
6 Mass Spectrometry-Based Quantitative O-GlcNAcomic Analysis	91
<i>Junfeng Ma and Gerald W. Hart</i>	
7 Isolating and Quantifying Plasma HDL Proteins by Sequential Density Gradient Ultracentrifugation and Targeted Proteomics	105
<i>Clark M. Henderson, Tomas Vaisar, and Andrew N. Hoofnagle</i>	
8 A Method for Label-Free, Differential Top-Down Proteomics.	121
<i>Ioanna Ntai, Timothy K. Toby, Richard D. LeDuc, and Neil L. Kelleher</i>	
9 Multiplexed Immunoaffinity Enrichment of Peptides with Anti-peptide Antibodies and Quantification by Stable Isotope Dilution Multiple Reaction Monitoring Mass Spectrometry.	135
<i>Eric Kuhn and Steven A. Carr</i>	
10 High-Throughput Quantitative Proteomics Enabled by Mass Defect-Based 12-Plex DiLeu Isobaric Tags.	169
<i>Dustin C. Frost and Lingjun Li</i>	
11 Isotopic <i>N,N</i> -Dimethyl Leucine (iDiLeu) for Absolute Quantification of Peptides Using a Standard Curve Approach	195
<i>Tyler Greer and Lingjun Li</i>	

12	Selecting Optimal Peptides for Targeted Proteomic Experiments in Human Plasma Using In Vitro Synthesized Proteins as Analytical Standards	207
	<i>James G. Bollinger, Andrew B. Stergachis, Richard S. Johnson, Jarrett D. Egertson, and Michael J. MacCoss</i>	
13	Using the CPTAC Assay Portal to Identify and Implement Highly Characterized Targeted Proteomics Assays.	223
	<i>Jeffrey R. Whiteaker, Goran N. Halusa, Andrew N. Hoofnagle, Vagisha Sharma, Brendan MacLean, Ping Yan, John A. Wrobel, Jacob Kennedy, D.R. Mani, Lisa J. Zimmerman, Matthew R. Meyer, Mehdi Mesri, Emily Boja, Steven A. Carr, Daniel W. Chan, Xian Chen, Jing Chen, Sherri R. Davies, Matthew J.C. Ellis, David Fenyö, Tara Hiltke, Karen A. Ketchum, Chris Kinsinger, Eric Kuhn, Daniel C. Liebler, Tao Liu, Michael Loss, Michael J. MacCoss, Wei-Jun Qian, Robert Rivers, Karin D. Rodland, Kelly V. Ruggles, Mitchell G. Scott, Richard D. Smith, Stefani Thomas, R. Reid Townsend, Gordon Whiteley, Chaochao Wu, Hui Zhang, Zhen Zhang, Henry Rodriguez, and Amanda G. Paulovich</i>	
14	Large-Scale and Deep Quantitative Proteome Profiling Using Isobaric Labeling Coupled with Two-Dimensional LC–MS/MS	237
	<i>Marina A. Gritsenko, Zhe Xu, Tao Liu, and Richard D. Smith</i>	
15	Multiple and Selective Reaction Monitoring Using Triple Quadrupole Mass Spectrometer: Preclinical Large Cohort Analysis	249
	<i>Qin Fu, Zhaohui Chen, Shenyang Zhang, Sarah J. Parker, Zongming Fu, Adrienne Tin, Xiaoqian Liu, and Jennifer E. Van Eyk</i>	
16	Methods for SWATH™: Data Independent Acquisition on TripleTOF Mass Spectrometers	265
	<i>Ronald J. Holewinski, Sarah J. Parker, Andrea D. Matlock, Vidya Venkatraman, and Jennifer E. Van Eyk</i>	
17	Measurement of Phosphorylated Peptides with Absolute Quantification	281
	<i>Raven J. Reddy, Timothy G. Curran, Yi Zhang, and Forest M. White</i>	
18	Proteomic Analysis of Protein Turnover by Metabolic Whole Rodent Pulse-Chase Isotopic Labeling and Shotgun Mass Spectrometry Analysis.	293
	<i>Jeffrey N. Savas, Sung Kyu Park, and John R. Yates III</i>	
	<i>Index</i>	305

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