
Preface

When the last edition of this book was published in 2000, the field of proteomics was in its infancy. At that time, multidimensional liquid chromatographic separations were being introduced as an alternative to traditional gel-based techniques for separating complex protein and peptide mixtures prior to mass spectrometric detection. Today, this approach – referred to as shotgun proteomics – is considered routine for large-scale global analyses of protein mixtures.

Now in its adolescence, proteomics is fundamentally transforming biological and medical research. Much of this transformation can be attributed to technological advancements, particularly in mass spectrometry. Much wider accessibility of high-resolution and mass measurement accuracy instrumentation in recent years has initiated a new revolution in the field by providing more reliable data and shifting the focus from cataloging proteins to precisely quantifying changes in protein abundance over time and in response to stimuli. Advanced mass spectrometers and novel ion dissociation schemes such as electron transfer/capture dissociation make it possible to venture boldly into the maze of protein posttranslational modifications, which are an integral component of understanding functional proteomics in the spatial and temporal domains. Another area that has benefited from these advancements is top-down proteomics, an emerging method essential for characterizing various protein variants that has potentially high impact in biomedical research. Another breakthrough application that holds great potential in pharmaceutical as well as biomedical research is imaging mass spectrometry, which enables high-resolution spatial characterization of complex materials (such as tissues) with simultaneous information on chemical composition. By virtue of enhanced sensitivity, dynamic range, and throughput, these new tools are applied to generate robust quantitative measurements in support of clinical studies. However, before a proteomics platform can be used for routine clinical applications, certain challenges, such as the ability to provide the throughput needed to enable a statistically meaningful number of analyses for a clinical setting, must be overcome. Ion mobility separations have recently emerged as a means for significantly increasing throughput proteomics and as such are expected to have a transformational impact on the field of proteomics and its applications in broad areas of biological and medical research.

Spanning fields from microbial forensics and clinical applications to protein structure, dynamics, and function, the following chapters present new and updated methods for mass spectrometric characterization of proteins and peptides. As with the first two volumes, the intent of this latest edition of *Mass Spectrometry of Proteins and Peptides* is to provide the reader with step-by-step instructions, along with insight into the pitfalls and nuances of apparently straightforward techniques in the hope of facilitating new discoveries.

Mary S. Lipton
Ljiljana Paša-Tolic



<http://www.springer.com/978-1-934115-48-0>

Mass Spectrometry of Proteins and Peptides
Methods and Protocols, Second Edition

Lipton, M.S.; Pa#-Tolic, L. (Eds.)

2009, XIV, 470 p., Hardcover

ISBN: 978-1-934115-48-0

A product of Humana Press