Preface

Unparalleled advances in macromolecular mass spectrometry continue at a rapid pace, and are providing ever more powerful tools to unravel and define the protein and glycolipid composition of cells on a global scale. Indeed, complex suites of proteins and glycolipids can be studied in concert and even in their functional biological context.

There is accelerating awareness in the biological research community that mass spectral strategies can provide crucial information to new areas, such as the challenging problems associated with the elucidation of protein signaling cascades and networks, temporal modulation of protein machine assembly and disassembly, and their posttranslational regulation. The broad utility and accessibility of this technology has begun to influence the design of experimental protocols in fields in which previously mass spectrometry had been only minimally involved. Since the continuing introduction of better technology platforms breed even higher quality experimentation, this trend will certainly continue but at an accelerated pace.

The more challenging biological problems drive tailoring and development of new methodologies, techniques, and instruments. Such development usually represents a mixture of multi-disciplinary, inter-dependent efforts involving sample handling, adaptation of techniques, which require gaining experience in their optimal use, and development of new software to enable the analysis of data and facilitate its comprehension.

This volume is a companion to Biological Mass Spectrometry in this series (Burlingame, 2005) and covers the additional topics and knowledge base essential for the understanding and practice of peptide and protein mass spectrometry, and glycolipidomics. These include protocols for sample preparation and clean up, proteolytic and chemical digests, factors essential for measurement of the molecular weight accurately, and then introduction into the mass spectrometer.

In addition, this volume describes the strategies employed for structural analyses of the two most pervasive classes of protein posttranslational modification, namely phosphorylation and the three major types of protein glycosylation. Many of these experiments utilize capillary HPLC coupled with electrospray ionization and tandem mass spectrometry. These treatments are followed by case studies of two protein machines, the proteasome and spliceosome, and the identification of MHC antigens. These examples reveal archetypal insights into how and why mass spectrometry revolutionized our

global understanding of the functional modulation of protein assemblages, complexes, and organelles so quickly. Finally, comprehensive treatments of both endogenous and bacterial glycolipid analyses are presented. All of these contributions are written by authorities who are world leaders in their fields. These authors have provided a detailed view into the classes of biopolymers that are readily tractable together with our state of knowledge about the biological context. In addition, projections of the technical developments and challenging problems ahead are indicated.

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