

Preface

Mass spectrometry deals with the formation, manipulation, and measurement of charged substances in order to detect and identify them. Since its previous overview was published in this series (McCloskey, 1990), the Nobel Prize in Chemistry was awarded in 2002 to John B. Fenn and Koichi Tanaka for the discovery of two new methods for producing charged biomacromolecules from liquid and solid solution. These can be thought of as ways to isolate charged molecules in the gas phase that are formed simply from “normal acid-base protonation-deprotonation reactions” from volatile liquid buffers and solid matrices. Over the past two decades these techniques, electrospray (ESI) and matrix-assisted laser desorption (MALDI), have provided the remarkable window we needed to “see” into the machinery of cell biology and view its true molecular complexity for the first time.

These ways of producing ions work efficiently for virtually all biomacromolecules, so it is left to our scientific ingenuity to design ways to manipulate these charged molecules to elicit information that reveals their molecular structural nature. Hence, several generations of ion-optical and energy deposition strategies have emerged that make up the current tools of the trade—commercial mass spectrometers. It should be noted that the design and discovery of better strategies remains a vibrant, young pursuit.

Finally, advanced computational capabilities have evolved to record, process, and manage mass spectral information and provide interfaces with DNA and protein sequence repositories. The tools of bioinformatics are also being adapted and refined to provide visualization into our existing knowledge of biology.

But these developments represent just the beginning of positioning the kind of ingredients that will be employed to gain an understanding of human biology. This volume and its companion (Burlingame, 2005) are intended to describe the astounding strides that have brought us to our current methodological toolbox and also provide the foundation of knowledge indispensable to understanding the current practice of mass spectrometry, as well as to appreciate the rapidly expanding and accelerating horizons in this field.

Thus, this work is focused at the forefront of proteins and their complexities, including descriptions of the techniques and instrumentation being used, their sequence and structural identification based on interpretation of their tandem mass spectra, the strategies and issues in proteomics, studies of solution

structures and interactions using isotope exchange, studies of non-covalent complexes with metal ions and ligands, and use of sub-attomole isotopic bio-tracers using accelerator mass spectrometry. All of these contributions are written by authorities who have made seminal contributions to their respective topics.

These foundations provide insight into the forefront of the experimental and technological platforms necessary to pursue a variety of major research themes surrounding protein biology, including proteomics, protein-protein interactions, glycobiology, epi-genetics, and systems biology.

I am indebted to all of my colleagues who have participated in this work, to Candy Stoner for her assistance and talents during the preparation phase, and to Raisa Talroze for the completion of both volumes. I would like to acknowledge the NIH, National Center for Research Resources, for generous financial support (Grant RR 01614).

A. L. BURLINGAME

References

- Burlingame, A. L. (2005). "Mass Spectrometry: Modified Proteins and Glycoconjugates." *Meth. Enz.* **405**.
- McCloskey, J. A. (1990). Mass spectrometry. *Meth. Enz.* **193**, 960.