Mass Spectrometry of Peptides

Edited by Dominic M. Desiderio
CRC Press, Boca Raton, Florida
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This monograph contains 19 chapters authored by many of the leaders in the field. These contributions together provide one of the most thorough descriptions to date of the mass spectrometry of peptides. The book is clearly centered around peptides, *not* peptides and proteins. This distinction means there are relatively few pages given to the analysis of intact proteins, or of peptide mixtures derived from proteins. In most cases, the peptides are derived from nonproteinaceous sources or have been previously purified from a mixture. The categorization of the chapters into three sections (I—Ionization Methods, II—Instrumental Developments, and III—Analysis of Peptides) is somewhat confusing. Section I is mostly plasma desorption and its related applications, but no chapters cover fast-atom bombardment (FAB). In contrast, the chapters in Section III are exclusively applications of FAB. One or two of the chapters in Sections I and III could be exchanged for a more coherent presentation, especially for someone with little background in mass spectrometry.

About half of the chapters stand out as excellent presentations. "Fundamental Aspects of Protein Mass Spectrometry Using 252-Californium Plasma Desorption," by Macfarlane and co-workers, provides a clear overview of this technique. "Analysis of Peptides and Proteins by Plasma Desorption Mass Spectrometry," by Roepstorff, gives many practical suggestions and applications. "Four-Sector Tandem Mass Spectrometry of Peptides," by Ashcroft and Derrick, gives a good overview that is not found elsewhere. "Peptide Sequence Analysis by Triple Quadrupole and Quadrupole Fourier Transform Mass Spectrometry," by Hunt and colleagues, provides an excellent description of the data interpretation process and demonstrates the use of simple chemical reactions to enhance the information content of spectra. "Sample Preparation and Matrix Selection for Analysis of Peptides by FAB and Liquid SIMS," by Busch, is an extensive review of sample and matrix characteristics for FAB. "On-Line Methods for Peptide Analysis by Continuous-Flow FABMS," by Caprioli and co-workers, presents a well-illustrated overview of continuous-flow FAB. "The Mass Spectral Analysis of Hemoglobin Variants," by Lee and Rahbar, is a good illustration of the use of mass spectrometry to study amino acid substitutions in proteins. "Detection and Location of Disulfide Bonds in Proteins by Mass Spectrometry," by Smith and Sun, is excellent review of this topic. "Tandem Mass Spectrometry for Determining the Amino Acid Sequence of Cyclic Peptides and for Assessing Interactions of Peptides and Metal Ions," by Cerny and Gross, provides detailed approaches to data interpretation of the often complex spectra that arise from cyclic peptides. "Mass Spectrometry of Biologically Important Neuropeptides," by Desiderio, gives an excellent overview of this topic, including a significant discussion of sample preparation and important non-mass spectrometric adjunct techniques.

Of the other nine chapters, many are simply compilations of previously published examples. These serve to illustrate the utility of the technique further but give neither practical details nor any new understanding. The work is largely free from errors, either typographical or in content. Chapter 3 has several hand-labeled figures that reduce the overall appearance.

The book suffers most from the lack of discussion of electrospray ionization and matrix-assisted laser desorption/ionization, which were just beginning to see widespread use when the book was written in 1989. These two techniques have transformed the mass spectrometry of peptides and proteins to such an extent that without them the book loses much of its practical value, especially to the growing legions of biochemists who wish to acquire some understanding of mass spectrometry. Nonetheless, many of the approaches described are valuable and are independent of the ionization technique, and the book serves as an excellent, although, unfortunately, dated, reference.

Techniques in Protein Chemistry

Edited by Tony E. Hugli
612 pp., ISBN #0-12-682001-5 [paperback, $54.95], #0-12-682000-7 [hardcover, $99.00], 1989

Techniques in Protein Chemistry II

Edited by Joseph J. Villafranca
579 pp., ISBN #0-12-721957-9 [paperback, $49.95], #0-23-732958 [hardcover, $99.95], 1991

Techniques in Protein Chemistry III

Edited by Ruth Hogue Angeletti
544 pp., ISBN #0-12-058756-4 [paperback, $45.00], #0-12058755-6 [hardcover, $90.00], 1992

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The Protein Society held its first meeting in August 1987. After taking note of many excellent presentations, the Society's publications committee decided that publication of expanded abstracts would be worthwhile so that a larger audience could profit from the reports made at the conference.

Volumes I, II, III are reports of the 1989, 1990, and 1991 meetings, respectively. The first volume, *Techniques in Protein Chemistry*, was a collection of papers from the 1988 conference. Each volume has its own editor and is published by Academic Press in the "rapid manuscript reproduction" mode, which means that the expanded abstracts are camera-ready and are bound together with a soft cover and plastic comb.

The first volume contains 57 chapters that are divided into six sections: Protein Microsequence Analysis, Mass Spectrometry and NMR Spectroscopy, Amino Acid Analysis, Applications of HPLC, Protein Chemistry and Analysis, and Standard Test Peptide. Of course, the section on mass spectrometry, which contains eight chapters, will be of most interest to the readers of this journal. Subjects are tandem mass spectrometry for sequencing and methods for locating disulfide bonds.

The section on standard test peptide describes the synthesis of a test peptide containing a lysine (at position 18) in which both the α- and ϵ-amino acids are part of a peptide chain (the peptide has two N-termini). This unusual peptide was offered as an unknown, and the four reports on elucidating structure all made use of some form of mass spectrometry.

Although Volume I was not available to the reviewer, it undoubtedly is similar to Volumes II and III. Volume II contains 54 chapters divided again into six sections. Section VI is devoted to a mass spectrometry workshop. Fifteen expanded abstracts were gathered together. They cover strategies for sequencing another test peptide, this time a 26-residue one that had been purposely contaminated with a small peptide having a blocked amino terminus. Other chapters include discussions of electrospray, laser desorption, tandem mass spectrometry, and computer interpretation.

Volume III also offers testimony of the important role played by mass spectrometry in protein chemistry. The final section of the volume contains nine chapters on mass spectrometry subjects, including laser desorption, electrospray, tandem mass spectrometry, and plasma desorption, all applied to problems in peptide/protein structural studies. Discussion of the role of mass spectrometry in the structural determination of glycoproteins can also be found.

Although the chapters are not long (typically 6–10 pages, with abundant figures and tables), they do offer a useful and broad perspective on the role of mass spectrometry in the protein area. They serve a vital function in introducing newcomers, from both the protein and the mass spectrometry areas, to opportunities in the application of mass spectrometry to protein problems. In that way, the records of presentation at the meeting serve to bridge the two research areas. Furthermore, mass spectrometrists may readily examine the other methodologies used in protein chemistry. The Protein Society organizers and volume editors are to be congratulated for ensuring that these opportunities were not lost.