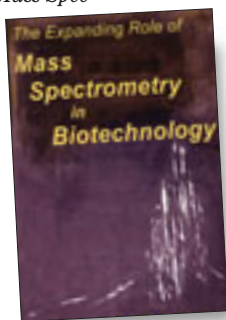


► **The Expanding Role of Mass Spectrometry in Biotechnology**

GARY SIUZDAK

MCC Press, San Diego, 2003, 274 pp,
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Targeted more at the biotechnology specialist than the physical chemist, Gary Siuzdak's *The Expanding Role of Mass Spectrometry in Biotechnology* provides a basic tutorial on the physics, chemistry, and applications of MS. Throughout, the explanations are accompanied by simple graphics that allow readers to better understand the science behind many of the papers they have skimmed over the years. Thus, the book would serve as a teaching aid in any laboratory or departmental library involved in biochemical and biomedical research.



The author is well situated to describe this subject, too. When he's not writing books on the application of MS technologies to the biological and biochemical sciences, Siuzdak is the director of the Scripps Center for Mass Spectrometry and associate professor of molecular biology at the Scripps Research Institute in La Jolla, CA. Likewise, his passion for the technique seems as boundless as his passion for life. This is exemplified by his department's website (<http://masspec.scripps.edu>), which has a section dedicated to all things MS, including several recent articles, both technical and historical, on MS methods and instrumentation, and a timeline of MS milestones, which he excerpts in the book.

The book can be divided roughly into two broad sections, the first of which describes MS in terms of its physics. In Chapter 1, Siuzdak offers a basic outline of the technology followed by brief descriptions of the various modes of ionization, including electrospray ionization (ESI), matrix-assisted laser desorption/ionization (MALDI), and fast atom/ion bombardment (FAB). To assist readers in determining which method best suits their needs, this chapter also

includes tables outlining the respective advantages and disadvantages of ESI and MALDI and a much larger table highlighting some features of each ionization method.

Chapter 2 moves the discussion from science to instrumentation, describing the premise behind mass analysis and the functions of the various mass analyzers, including time-of-flight (TOF), quadrupole, and Fourier transform-ion cyclotron resonance (FT-ICR). Likewise, Siuzdak offers a brief discussion of the various ion detectors and their respective advantages. Chapter 3 then rounds out the section, providing an analysis of many practical considerations of MS, including sensitivity, mass calculations, quantitation, and sample purity. At the end of this chapter,

Siuzdak provides a short table of frequently asked questions that the reader can use to troubleshoot experiments.

The next section of the book, encompassing Chapters 4 through 10, focuses on the actual application of MS to biotechnology. Given the technique's prevalence in proteomics, it is perhaps not surprising that the author begins his discussion with three chapters on protein characterization. Chapter 4 focuses on the application of ESI and MALDI MS to peptide and protein analysis, offering several step-by-step sample preparation procedures. Siuzdak pays particular attention to the ways in which sample type and concentration dictate the MS method used and describes methods of MS automation and hyphenation with LC.

Whereas Chapter 4 focuses on relatively pure protein samples, Chapter 5 describes the application of MS to protein profiling and peptide mass mapping. Among the topics discussed in this chapter are 1D and 2D gel electrophoresis, tandem MS, and isotope-coded affinity tags. The next chapter then continues this discussion by extending the technique into protein structure characterization. These efforts rely on combining MS with methods such as isotope labeling or partial proteolysis to identify con-

formational changes and chemical cross-linking or modification.

Chapter 7 takes what the reader has learned about MS and the relatively heterogeneous populations of proteins and peptides and applies it to the characterization of the more homogeneous nucleic acids, carbohydrates, and steroids. As with proteins, MS has been used to sequence DNA, and it can also analyze noncovalent interactions in complex sugar chains.

In Chapter 8, Siuzdak returns the reader to discussions about MS hardware and describes the many ways in which scientists have tried to expand the technology into the high-throughput realm. As he describes, this achievement has relied as much on software developments as instrumental modifications because the sheer volume of data produced in the high-throughput environment is unwieldy without supporting computational analysis and storage tools.

Siuzdak finishes his analysis of MS applications by looking, in the last two chapters, at how researchers have used MS to perform studies such as pharmacokinetics, metabolic profiling, natural product characterization, and enzyme catalysis monitoring. These methods have become critical to drug discovery and the development and analysis of biotherapeutics.

The Expanding Role of Mass Spectrometry in Biotechnology is well written and researched. It would be hard to find a book that better explains challenging concepts in such a reader-friendly manner.

—REVIEWED BY RANDALL C. WILLIS ■

► **moregoodreading**

Mass Spectrometry Basics

By Christopher G. Herbert and Robert A. W. Johnstone
CRC Press, 2003

Measuring Mass: From Positive Rays to Proteins

Michael A. Grayson, Ed.
Chemical Heritage Press, 2002