

Mass Spectrometry of Protein Interactions

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Mass Spectrometry of Protein Interactions is the newest addition to Wiley's highly successful series in mass spectrometry (series editors Dominic Desiderio and Nico Nibbering). This relatively small-volume book (less than 140 pages) is a collection of six short chapters, each focusing on a distinct MS-based approach to study protein interactions. As stated in the preface, the editor's goal was to present the latest achievements and challenges in this vast and rapidly growing field. Three chapters in the book (1, 3, and 5) clearly reached this goal.

Chapter 1 (contributed by J. A. Loo and C. S. Kaddis) focuses on direct characterization of protein complexes by ESI MS and mobility analyzers. The chapter includes a discussion of fundamental aspects of the behavior of non-covalent complexes in the absence of solvent. The authors also provide necessary background information on the hardware needed for such measurements, as well as useful hints for sample preparation.

Chapter 3 (contributed by J. R. Engen and colleagues) discusses use of hydrogen exchange for characterization of protein interactions. It contains very useful background information on the fundamental aspects of the hydrogen-exchange methodology and presents some of the examples of how it was used in the authors' laboratory to address specific questions related to protein interactions with small molecules, peptides, and other proteins.

Chapter 5 (contributed by A. Sinz) discusses various techniques based on chemical cross-linking. This chapter contains very useful reference material on cross-linking chemistry and specifics of experimental procedures suitable for various applications. Discussion of issues related to data interpretation contains examples of experimental works carried out in the author's laboratory. Authors of these three chapters do an admirable job in presenting state-of-the-art techniques to readers who may not be familiar with the latest achievements in

this field. However, even seasoned MS practitioners will find these chapters a useful resource.

Several other MS-based techniques are presented throughout the rest of the book. Chapter 2 (contributed by K. M. Downard) focuses on using MALDI MS to detect protein complexes. Most of the discussion is focused on the experimental work carried out in the 1990s and the discussion of the more recent work is very brief in comparison. This chapter will also disappoint readers with the graphics quality because most figures appear to be low-resolution scanned images with missing and/or difficult to read parts.

Chapter 4 (contributed by M. Monti and P. Pucci) discusses the use of an established technique of limited proteolysis for characterization of protein complexes. Although the examples of the authors' own work presented in this chapter are very interesting, I was somewhat disappointed to see very minimal discussion of MS aspects of such experiments. The quality of illustrations is also disappointing, as the low-resolution grayscale protein images provide hardly any help in reading this chapter.

Chapter 6 (contributed by K. M. Downard and S. D. Maleknia) presents a method that uses radical probes and mass spectrometry to study protein interactions. Although this chapter provides useful background information on this powerful technique, I felt that the selection of applications used by the authors to illustrate its use is heavily biased toward very early work. In addition to the synchrotron-generated radicals, this chapter also discusses other means of producing radicals in solution to probe protein structure (however, it is puzzling that most of it is devoted to oxidation in the ESI source, a technique that was never used for structural work except for a couple of small model polypeptides).

Two themes are notably absent from the book. No chapter deals with selective chemical labeling, an experimental technique whose capabilities are magnified when it is used in combination with mass spectrometry. Selective chemical labeling was applied successfully in the past several years to study structural aspects of a wide range of protein interactions, and it continues to gain popularity at a steady pace. Undoubtedly, inclusion of a chapter focusing on this subject would have been a very welcome addition to the book. Another rather surprising omission in the book is interactomics, a subject highly relevant to the theme of the book. Mass spectrometry is one of the major experimental tools in this rapidly growing field, and I believe the value of the book would have risen considerably by including a chapter on this subject.