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Book review

Igor A. Kaltashov, Stephen J. Eyles, Mass Spectrometry in Biophysics—Conformation and Dynamics of Biomolecules, Wiley, Hoboken, NJ, 2005, ISBN 0-471-45602-0, Price GBP 51.50, USD 89.95, or 75.00 €, 458 pages.

Mass spectrometry is an analytical tool which experiences an ever faster development perhaps comparable to that of NMR methods in the 1970s and 1980s. Due to the soft ionization techniques such as electrospray ionization and matrix assisted laser desorption/ionization, many of the limitations of early mass spectrometry have been waived. In particular, high to very high molecular masses can be accurately determined, even without inducing too much fragmentation in the ionization process. Since both ionization methods mentioned above are particularly suited for polar molecules, it is no surprise that biopolymers are first-choice targets for mass spectrometry.

However, the research areas of mass spectrometry and biochemistry/biophysics have long grown rather independently from each other. It is necessary to bridge language gaps. In order to marry both, an intense communication is required. Mass spectrometrists need to learn what the fundamental research problems are in biophysics in order to be able to judge how they can contribute. Biophysicists on the other end need to become aware of the enormous potential of mass spectrometry in order to find the right experiments for the questions they wish to address.

In view of this background, the present book comes perfectly in time. It not only intends to, but definitively succeeds in providing the bridge between the two communities. The first three chapters present concisely written overviews on basic concepts in molecular biophysics, on the “traditional” methods in this field and on biological mass spectrometry. The information is packed into dense, but still easy to read and well understandable chapters which are illustrated by clear graphics. Reading this book is rewarding, and I certainly enjoyed the introductory chapters on biophysics which familiarized me with the basics of biophysics of which I had only a vague idea beforehand.

The subsequent chapters are devoted to a number of intellectually highly interesting problems of fundamental relevance. Mass spectrometric experiments are described to extract information on the higher order structure of proteins, for examining the dynamics of biomolecules, and for investigating the kinetics of protein folding and enzyme catalysis. The authors also include mass spectrometric methods for the extraction of quantitative data on protein–ligand interactions. I had exceptional fun reading Chapters 8 and 11. Chapter 8 uses the folding and substrate binding of egg lysozyme as an example to compare different biophysical methods which shows how important the combination of them is. Some give overlapping data and thus confirm each other’s results, while others provide complementary information. Mass spectrometry reveals its power when it is used to unravel the existence of different parallel folding pathways for this enzyme—just to mention one example. Chapter 11 addresses the future and tries to define problems which still are left unsolved in order to define potential future research areas for biophysics-oriented mass spectrometrists.

The book contains a large number of graphics which are well chosen. It provides a large number of up-to-date references for further reading at the end of each chapter and is equipped with an easy to navigate table of contents and a useful index. So, to make it brief: it is a book which has been thoughtfully prepared with care and presents its contents in a clever way. I am sure that it will attract a large number of readers. I definitively have no hesitation to recommend it to researchers, including Ph.D. students, who are involved in one or both of the areas of mass spectrometry and biophysics.

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