



## Proteome Research: Mass Spectrometry

Edited by Peter James,  
Springer-Verlag, 2001.  
Price \$50.00, £30.00.  
274 pages in softback

ISBN 3-540-67256-7

The sequencing of the human genome has provided such a wealth of information that it will still take years to appreciate the full impact this might have on our understanding of biology and medicine. Perhaps the biggest surprise, so far, has been the realization that the number of human genes encoded is much lower than anticipated and, in fact, not that much different from less developed species. The question has been raised as to how one can then explain that humans are so very different from yeast, worms or fruit flies. The answer, for many, lies in the biologically active products of our genes, the proteins, and this has focused the interest of scientists and investors alike to the new science of proteomics.

Proteomics – the study of many proteins in parallel – has evolved from traditional protein biochemistry into a fast-growing and rapidly evolving field. This has created an abundance of academic and industrial positions leading to a shortage of specialists. The resulting need for the training of newcomers to the field requires high quality training material.

The recently published book *Proteome Research: Mass Spectrometry* is well placed to become one of proteomics standard reference books. The book features 13 articles written by recognized experts in the field. It is superbly introduced by the editor, Peter James (Lund University, Sweden), who was one of the early pioneers of this area of research.

In the first part of the book, the initial two articles provide an introduction to the mass spectrometric techniques with a short, but concise, explanation of the fundamental principles, the various mass analysers and a thorough description of the many modes of operation. This is followed by two articles describing the coupling of liquid chromatography to the mass spectrometer (LC–MS), which highlights the importance of low flow–microscale chromatography for high sensitivity analysis. The first of these two LC–MS articles – written by D. Stahl and T. Lee – is worth reading and provides an excellent introduction to the issues surrounding a technically demanding method.

The second part of the book is devoted to the many ingenious ways in which the information content contained in the masses of peptides and peptide fragments can be used for protein identification, *de novo* sequencing and other aspects of protein characterization. There are four articles dealing with the subtleties of the various approaches used; for example, an article on peptide mass fingerprinting by P. Dainese and P. James, a very detailed description of the search engine SEQUEST by D. Tabb, J. Eng and J. Yates, an article introducing the theory and practical approaches for *de novo* sequencing by W. Staudenmann and P. James and a very stimulating article by Johnson on the automated interpretation of tandem mass spectra and homology searches. All four articles enable the reader to attain a high level of insight into the subject and are of value for both beginners and advanced practitioners.

In the third part of the book, two articles cover methods for the characterization of the most prominent post-translational modifications found in proteins; phosphorylation and glycosylation. This is followed in the last part by a listing of proteomics databases together with some useful information

on design and implementation of databases.

The book concludes with an outlook by Peter James in which he highlights a number of developments with the potential to change the *modus operandi* in proteomics. This book is certainly well orchestrated and features a number of high quality articles. However, there are some shortcomings that have to be addressed. There is no mention of orthogonal acceleration time-of-flight analysers that are in widespread use and no information on the promise of matrix-assisted laser desorption ionization (MALDI) on these instruments. A couple of the articles cover very specific approaches to the authors' laboratories, which could be difficult to implement without specialist knowledge. As the field is moving rapidly, some of the more recent approaches introduced since the articles were written, are consequently missing. However, this, cannot be avoided in a nascent field that is still being defined and is fuelled by a constant flow of new hardware, novel chemical approaches and ingenious software algorithms.

To conclude, the book *Proteome Research: Mass Spectrometry* provides the reader with a very good understanding of the key issues in the field and is worth reading.

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### What does the human genome sequence mean to you?

Commentaries relating to the publication of the draft sequences can be found both in print in several Trends titles, and online in the Commentary section of BioMedNet (updated daily at <http://news.bmn.com/commentary>).