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Book review

The Expanding Role of Mass Spectrometry in Biotechnology, Gary Siuzdak, MCC Press, San Diego, CA, USA, 2003, pp. 273, ISBN 0-9742451-0-0

This book has an excellent pedigree in the form of Siuzdak's first text published in 1996, "Mass Spectrometry for Biotechnology". Improvements in MS have continued at pace since that time and the technology has all but revolutionised the analysis of proteins. The advances now bring the same power to the analysis of other cellular macromolecules, including nucleic acids. The new book is aimed at more completely describing how the technology has changed and the exciting ways it has been applied – timely indeed.

The first two chapters describe the components of mass spectrometers and explain the principles involved. The main foci are (1) ionisation sources and their significance in the development of mass spectrometry in biomolecular analysis and (2) the principles of operation and current performance capabilities of mass analysers. Useful comparisons of performance characteristics are made for the different ionisation sources, mass analysers and ion detectors. There is good coverage here of the most commonly used mass alalysers, together with appropriate consideration of more specialised ones such as the quadrupole-time-of-flight mass analyser. A chapter on practical aspects of biomolecular analysis follows, with a predictable focus of electrospray ionisation (ESI) and matrix-assisted laser desorption/ionisation (MALDI). Amongst the many important considerations for making mass spectrometry experiments more useful are salt concentration, quantification, molecular weight calculation, isotope patterns, matrix selection and preparation, sample purity and speed analysis.

Three chapters are devoted to mass spectrometry of peptide and proteins. ESI, MALDI and desorption/ionisation on silicon (DIOS) are lauded as sensitive and gentle ionisation methods that, through a range of available mass analysers, are the basis of the fundamental tools for identifying proteins. A chapter on protein profiling explains the utility of MALDI and LC-MS/MS, and how mass spectrometry data can be used to interrogate protein databases. Recent advances and utilities of front-end techniques, such as isotope-coded affinity tagging, are also considered. There is a brief but useful chapter on protein structure characterisation, which explains how changes in protein conformation changes can be recognised with mass mapping.

The remaining four chapters in the book deal with high throughput analysis, non-protein applications of MS and some biochemical horizons for MS. Automated atmospheric pressure ionisation for high throughput analysis is considered at length and includes a case study entitled "1 Million Analyser/Year" – the task was to analyse one million discrete compounds in one year using an MS-based technique. Automating MALDI and DIOS-MS is also considered in the context of high throughput analysis. There is a chapter devoted to MS analysis of nucleic acids, carbohydrates and steroids, which presents an overview of the common techniques used for analysis of these compounds. Here, negative chemical-ionisation gas chromatography MS is discussed for the first time, while ESI, MALDI and DIOS are revisited. In a chapter on pharmacokinetics, the MS revolution of bioanalytical analysis in the drug discovery and development process is explained – from sample collection to multiple reaction monitoring using a triple quadrupole mass spectrometer. In the final chapter, the focus turns to how MS is

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being applied to significant biochemical problems, and includes the expanding role of MS in the field of metabonomics and in enzyme catalysis monitoring. The reader is left with the warm glow that often accompanies the end of a dramatic novel, when it becomes evident that the hero (MS) will prevail over the seemingly insurmountable odds.

There are a few editorial type errors – the odd subscript lacking in a chemical formula, a use of ml in place of μl – but lets not quibble, this book is an interesting and informative read. Each chapter opens with a perspective on the content and closes with a concise overview. Focus questions and lists of useful references are also provided. All these elements enhance the learning quality of the material, as does the ample scattering of colour illustrations. Whilst these figures are both informative and inventive, their effectiveness is often diminished by their inappropriate size.

The book has some recent and worth competitors, but none match Siuzdak's text for providing a readily digestible introduction to the current technology in its wide-scope application within biotechnology. It should appeal to bioscientist new to MS, as well as to scientists trained in more traditional MS techniques seeking to expand their horizons.

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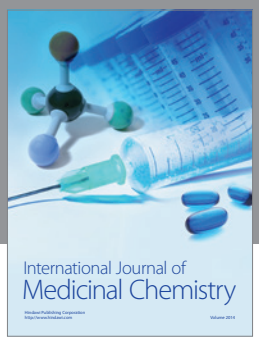

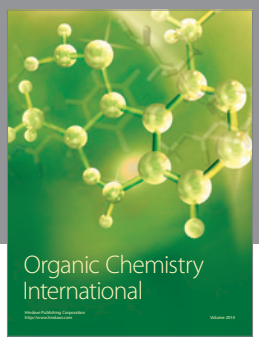

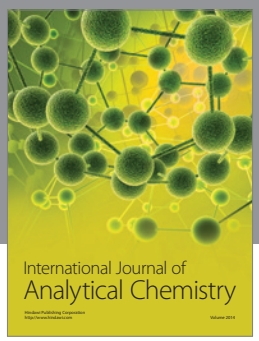

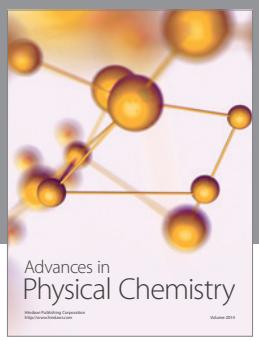

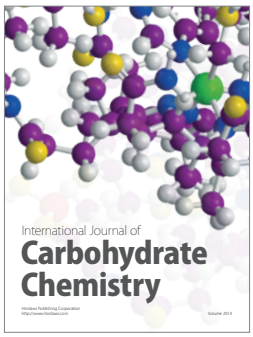

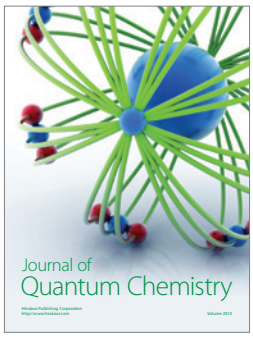

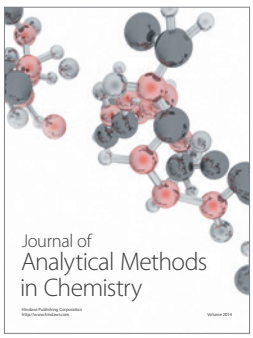

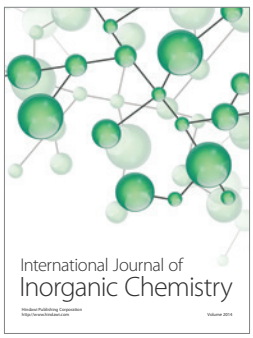

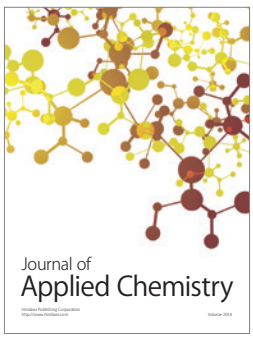

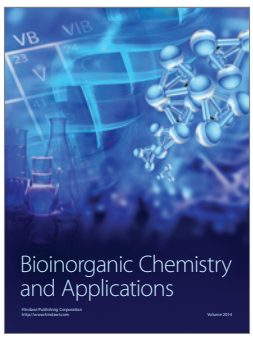

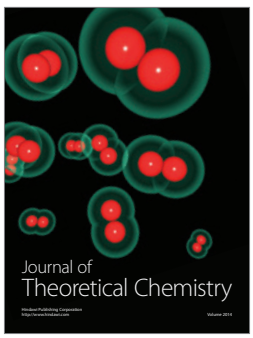

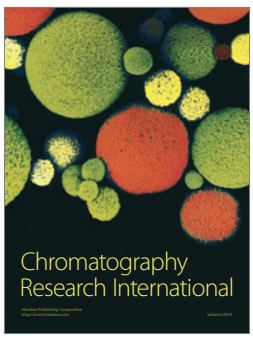

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