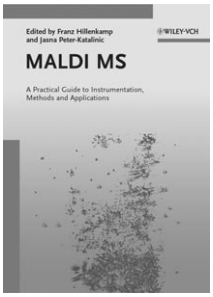
Critical Mass Spectrometry

MALDI MS: A Practical Guide to Instrumentation, Methods, and Applications

Edited by *Franz Hillenkamp* and *Jasna Peter-Katalinić*.

Wiley-VCH, Weinheim 2007. xvi + 345 pp., hardcover € 99.00.—ISBN 978-3-527-31440-9



Since the invention of matrix-assisted laser desorption/ionisation (MALDI) mass spectrometry 20 years ago this method has emerged, apart from electrospray, as one of the most important techniques for the identification and structure analysis of biological macromolecules such as proteins, peptides, and lipids. It has been developed for obtaining both accurate mass determination and primary sequence information. Desorption and subsequent mass measurement of macromolecules without significant fragmentation is a result of the soft ionization technique. Over the past decade this specific MS method has also been successfully applied to the characterization of synthetic polymers. MALDI MS provides absolute and accurate molecular masses for polymers with narrow polydispersity, information on repeat units, mass of end groups, molecular weight distribution, and structural information on the degree of polymerization and copolymerization. Latest results concern liquid chromatographic–MALDI MS coupling techniques.

A number of papers on MALDI MS have been published in recent years. This book gives a comprehensive overview of the methodological and instrumental enhancements of the technique along with different applications predominantly in the field of biosciences. The details of the MALDI process including analyte incorporation, the ablation/desorption process, and ionization are illustrated in a very clear and concise way. Various preparation techniques are presented. The second chapter describes the MALDI MS instrumentation. Many clear graphics illustrate the different operating modes and explain the equipment involved. The variety of lasers used for MALDI MS are also displayed. One section is dedicated to the fragmentation of molecular ions in the MALDI process and the tandem MS technique; another section deals with mass analyzers.

This book is the first monograph with a detailed description of mass spectrometers (FTMS, quadrupole ion trap, quadrupole time-of-flight (ToF), quadrupole FT, orbitrap), including future directions of the field. The first part is a very useful summary of the state of the art for beginners and advanced users. The chapters that follow contain many details of key applications concerning proteomics, biomarkers, nucleic acids, glycans, lipids, and polymers. The content is clearly structured, and specific aspects for each substance class are elaborated, for instance, sample preparation. Problems and limitations are critically discussed, such as the limitations of accuracy due to mass resolution.

The ninth and final chapter is dedicated to the special topic of small-molecule desorption/ionization mass analysis. MALDI was developed for large molecules, and small-molecule characterization has been "suppressed" until recently, not least because of competition by the ESI MS technique. The reasons for this, as discussed in the book, were low resolution of first-generation linear ToF instruments, matrix ion interference, and detector saturation in the low mass range. However, novel sample preparation approaches, new instrumentation, and optimization of the type of matrix are now available to overcome these shortcomings. Thus the potential of MALDI MS can be used for mixtures of both high- and low-molecular-weight compounds such as proteins and glucose, respectively. The book, including its extensive lists of references, is a practical and valuable guide for researchers at academic institutions and companies working in the field of bioanalytics.

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Functional Informatics in Drug Discovery

Edited by *Sergey Ilyin*.

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In recent years, "informatics" terms have become popular to describe research and development areas that integrate computational and experimental efforts in the greater life science arena. Of course, bioinformatics, medical informatics, and chemoinformatics have already become established fields. Other terms that are now in use include research informatics, molecular informatics, life science informatics, and drug discovery informatics. Many but not all of these terms have originated from drug discovery environments, and the boundaries between areas one attempts to cover are often rather fluid.

A new book, edited by Sergey Ilyin, adds yet another variant to the current spectrum of informatics terms: "functional informatics", also with a clear link to drug discovery. The editor positions this book as an "in-depth analysis of emerging trends and future opportunities in [technology] integration and interfacing

while maintaining a systematic or programmatic approach". It is meant to target a "heterogeneous audience, essentially anyone who seeks a greater understanding of the concepts and utilization of informatics".

The book consists of eight chapters, four of which are contributed by investigators from Johnson & Johnson, the pharmaceutical company to which the editor belongs. Therefore, it focuses to a significant extent on various drug discovery strategies that are being pursued at Johnson & Johnson. So far so good, but what exactly is "functional informatics" meant to be? At a closer look, only three of the eight chapters in this book have an immediate connection to applied informatics techniques. These contributions include a description of different automation strategies (Chapter 1), "neurally inspired algorithms" (Ch. 2), and the application and analysis of protein microarrays (Ch. 7). However, the remaining five chapters are fairly remote from the informatics arena, describing biomarkers in pharmacology (Ch. 3), strategies for CNS drug discovery (Ch. 4), antibody therapeutics in oncology (Ch. 5), genetic screening approaches and specialized screening libraries (Ch. 6), and finally, in a very short contribution, the use of laser microdissection in transciptomics (Ch. 8). The underlying approaches are often complex, and one can certainly see how the application of informatics techniques might help with experimental design or data analysis. Clearly, integrated experimental high-throughput approaches in biological screening, genomics, and proteomics require advanced computational infrastructures to be functional. However, as presented, these chapters primarily focus on the experimental study of biological functions and evaluation of opportunities for therapeutic intervention. Overall, the contributions in this book are indeed thematically heterogeneous (which is, per se, not a drawback) and only in part directly linked to informatics methods.

One can, of course, also view this compendium from a non-informatics-centric perspective. The majority of chapters nicely display advanced and integrated drug discovery strategies. While a number of contributions do not go much beyond the surface of the proposed informatics umbrella, they are generally written in an accessible style, explain scientifically complex aspects of modern drug discovery research in a concise manner, and are by and large well referenced, thereby providing the reader with a sound basis for further studies. The three more informatics-related chapters add a nice touch for those who are more interested in algorithms and computational approaches.

In summary, this book is not tailored to informatics experts and does not open up fundamentally new areas for applied informatics research. However, to a drug-discovery-oriented audience, it certainly has a number of interesting things to offer and is a meaningful addition to a series of drug discovery publications.

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