

Preface

The field of biological mass spectrometry is in the midst of a period of explosive growth. It is the major driver for proteomic data, which is central to modern efforts in cell and molecular biology, as well as systems biology and the identification of clinical biomarkers. It is very likely that the impact of mass spectrometry on biological understanding over the coming decades will be no less than the contribution that DNA and RNA sequencing technologies have had in modern biology.

The capability of mass spectrometry to determine large molecular masses was developing gradually, when, powered by certain technical developments it rapidly became possible to determine molecular masses of very large biological molecules like proteins and lipids, and from that derive their chemical identities. This transformed the investigation of biochemical processes in the laboratory, and enabled other applications such as identifying protein biomarkers in diseases. Initially the technology was employed for the assessment of macromolecular complexes but as it became possible to identify hundreds or even thousands of proteins in a sample, it rapidly emerged as a core driver of systems biology efforts. It is now being widely used to understand intra and intercellular signaling networks that regulate the function of cells and tissues.

Protein mass spectrometry is a powerful analytical technique albeit a complex one. Unlike many other methods, it does not yield a unique protein name as its output, because it generally involves a deduction of protein identity from determination of peptide fragmentation products. This requires sophisticated analytical approaches and chemical/biological knowledge to drive decision-making between alternate conclusions. Until the field evolves further and it becomes more definitive, it is important to understand and appreciate how determinations about protein identity from mass spectrometric data are made, because this could have a bearing on the application for which it is being used. It is for this reason it is incumbent on every user to have a good understanding of the method to be able to understand the limitations that may be present in the final conclusion.

This book is a general-purpose introduction to protein mass spectrometry for scientists and medical researchers and should satisfy at least three requirements. First, for someone just entering the field, it should provide a concise introduction to all branches of the biological mass spectrometric

method while citing the most recent and relevant work in the field. Second, it should provide biologists and medical researchers not only with information on the capabilities of the technique but also give an appraisal of the present limitations of the computer-analyzed mass spectrometric results. Third, in it specialists working in one branch of protein mass spectrometry should find brief, state-of-the-art information on other branches of the technique. This is what is attempted in the present book.

Over the years I have had the privilege of interactions with many of the scientists working in the field. I would like to thank them for clarifications of their work and to their publishers for the kind permission to use copyrighted material from their publications. To Profs Brian Chait, Alan Marshall, Akos Vertes, James Jorgenson, and David Fenyö I would like to express my special thanks. Kevin Blackburn and Dr John Tran were very helpful in answering my numerous queries.

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