

# PROTEOMICS TODAY



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## Protein Assessment and Biomarkers Using Mass Spectrometry, 2D Electrophoresis, and Microarray Technology

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**MAHMOUD HAMDAN**

GlaxoSmithKline

**PIER GIORGIO RIGHETTI**

University of Verona, Italy

 **WILEY-  
INTERSCIENCE**

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Published by John Wiley & Sons, Inc., Hoboken, New Jersey.

Published simultaneously in Canada.

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***Library of Congress Cataloging-in-Publication Data***

Proteomics today: Protein assessment and biomarkers using mass spectrometry, 2D electrophoresis, and microarray technology / Mahmoud Hamdan, Pier Giorgio Righetti.

p. cm.

Includes bibliographical references and index.

ISBN 0-471-64817-5 (cloth)

1. Proteins—Spectra. 2. Mass spectrometry. 3. Proteomics. I. Hamdan, Mahmoud, 1947-II. Righetti, P. G.

QP551.M315 2005

572'.6—dc22

2004050921

Printed in the United States of America

10 9 8 7 6 5 4 3 2 1

To Fatima, Giovanna, Mohammed, Jamilah  
To my nephews Mohsin, Hamdan, Mahmoud and Suad  
M.H.



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## PREFACE

Prior to starting Part I of this book, and while searching existing literature on current proteomic activities, I came across a number of statements, that caught my attention and in a way have influenced my choice of the material in Part I. Therefore, it is reasonable to list them in here: First, mass spectrometry is a central component in modern proteomic research, second, the ability to determine statistically significant alterations in protein expression that might be provoked by disease, environmental, pharmacological, or genetic factors is a central component in current proteomic research, third, at the biochemical level, proteins rarely act alone; rather they interact with other proteins to perform a given cellular task. Although data obtained by various expression proteomics strategies have functional relevance by detecting changes in protein abundance, such measurements offer only an indirect readout of dynamics in protein activity. This means that numerous post-translational forms of protein regulation, including those governed by protein–protein interactions, remain undetected; and forth, biomarkers are not necessarily proteins. They can be DNA, RNA, or metabolites that can be associated with a measurable change with a given disease. Having stated that, protein-based analyses have two attractive features: First, proteins can be found regularly in blood, urine, and other biological fluids which make such approaches rather noninvasive, and second, proteins are the real executioners of various biological functions which make them key players in many diseases. To resolve the various issues contained within these statements, the last decade has witnessed an unprecedented use of a wide range of technologies and the fall of conventional barriers among the various disciplines. Within the wide host of technologies employed in the area of proteomic research, mass spectrometry emerges as a central component. The first three chapters of this book is an attempt to capture the recent contribution of this technology and its interaction with other technologies to tackle various proteomic challenges. The organization of Part I begins with a chapter dedicated to the major

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components of current mass spectrometers with a particular emphasis on the developments which have influenced sensitivity, resolution and the capability to perform various tandem mass spectrometry functions. Chapter 2 deals with the various approaches including mass spectrometry in the field of disease biomarkers. To provide a broader perspective of the role of mass spectrometry in this particular area, some material has been included that is not circumscribed by mass spectrometry, per se. I have dedicated Chapter 3 to the argument of protein quantification including the emerging strategies for the quantification of phosphorylated and glycosylated proteins.

Of course regardless of the size of any given book and the good intentions of the author, it would be a pure scientific arrogance to pretend that such book would provide a comprehensive coverage of the arguments raised within. On the other hand, I would like to think that this text will be looked upon by prospective readers as a contribution to a vast and continuously evolving debate, where single contributions are required to enrich and possibly stimulate such debate.

I can not end this Preface without acknowledging that the years I spent at the University of Wales, Swansea working with Professor J. H. Beynon (founding editor-in-chief of the journal, *Rapid Communications of Mass Spectrometry*) had an immense impact on my appreciation of mass spectrometry as a tool, that can be applied in a wide range of applications including present day proteomics.

Verona, Italy  
November 2004  
Mahmoud Hamdan

## ACKNOWLEDGMENTS

The author of Part I of this book would like to acknowledge the scientific inspiration and the lasting friendship of professors, Keith Birkinshaw, Pietro Traldi, and John H. Beynon. The author is also grateful for the support and patience of all members of the Mass Spectrometry & Separation Technologies group at GlaxoSmithKline Research Centre in Verona.

The striking developments in Part II of this book, reported as part of the research from my group in the field of immobilized pH gradients, would have been impossible without the heroic efforts of a group of close collaborators, among whom I would like to mention Drs. E. Gianazza, C. Gelfi, and M. Chiari. For our own developments in the field of capillary isoelectric focusing and the use of isoelectric buffers, I would like to express my appreciation of the work of Drs. C. Gelfi, A. Bossi, E. Olivieri, L. Castelletti, and B. Verzola. Our recent work in two-dimensional map analysis would have been impossible without the help and close collaboration of Drs. B. Herbert, A. Castagna, F. Antonucci, D. Cecconi, and N. Campostrini. The research from my own group reported here has been supported over the years by grants from MURST (Ministero Università e Ricerca Scientifica e Tecnologica), 1999 (Protein Folding) and 2000 (New Techniques in Proteome Analysis), by FIRB (2001), and by PRIN (2003). Finally, I would like to thank the colleagues who have supplied me with original photographs of their work.

M.H.

P.G.R.

