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COMPREHENSIVE ANALYTICAL CHEMISTRY

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D. BARCELÓ

VOLUME 46

PROTEOMICS AND PEPTIDOMICS

NEW TECHNOLOGY PLATFORMS ELUCIDATING BIOLOGY

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G. MARKO-VARGA

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Preface

The proteomics and peptidomics research areas including global expression analysis as well as focused approaches are developing rapidly and play a major role in modern life sciences. Bioanalytical chemistry has a central role in these developments where the qualitative and quantitative alterations in protein expressions is the key aspect of consideration within this field.

Proteomics and peptidomics, the detailed understanding of the role that proteins and peptides play in health and disease, is a necessary complement to genetic analysis.

The functional expression analysis of both proteins and peptides plays a central role in modern drug discovery as well as drug development, and is also a key research area in systems biology.

The fast progress within the proteomics field has opened up possibilities for direct intervention to the medical and clinical area where diseases, disease progression, as well as cause of disease can be investigated at a molecular level. As slight protein modifications that modestly changes the biomacromolecule sequence or structure, in many instances has direct impact on cellular biological functions. This is the case for biological pathways, represent the relationships, reactions as well as interactions, between biological molecules in the context of normal cellular functions as well as disease mechanisms.

My intention of presenting the protein and peptide expression analysis in this book was to capture the width as well as depth within the area and exemplify the variety as well as the traditional basis of analytical chemistry that is needed in order to move forward in expression analysis studies. As the field is emerging quickly, my intention was also to give overview on parts within the field combined with highly specialized and dedicated parts, which are intended to complement each other. The invitation to scientists active in the proteomics and peptidomics areas has a spread, both in terms of geography where several countries and continents are represented as well as in sex and age.

The aim was also to have a mixture of both young and ambitious scientists along with older and experienced ones that has been within the field and been part of forming the basis and the tools that we are using today. These developments has been covered in the first part of the book that covers the area of modern analytical technologies combined with traditional analytical techniques. The book covers both gel-based- and liquid phases-separation techniques, where single dimension approaches are outlined along with multi-dimensional separation solutions.

It is also a fact that the protein and peptide expression research field is strongly moving forward by novel technology developments that relates to miniaturization. Down-scaling certainly has helped, and has driven the biology interpretation of proteomics studies forward significantly and been an important improvement where many of the successes of the field can be accounted for. Post-translational modifications presented by protein modifications such as phosphorylation alterations are presented in addition to clinical peptide biomarker discovery studies, biomarker discovery, being important and central to research activity.

It is true that in many aspects the analysis of protein expression is no longer a strictly wet lab experience, and as an exercise the technology and mathematical advancements in computational biology are hot development areas for providing lot of opportunities in deep mining and resolving proteomic data. Mass spectrometry is the dominating technique. The massive amount of data generated holds a lot more information than we are able to interpret. New algorithms, softwares as well as the database query tools developed and used with the help of bioinformatics will be the final data delivery point in the process line where the link to biology.

In many discussions and arguments it has been (and probably will be in the future) debated whether it's the technology milestone achievements that drives biology, or the biology questions that drives the technology.

As in most arguments the life science field needs the integration and cross boundary scientific collaborations to progress. My intention has also been to try to capture this momentum of scientific activity.

The final part of the book presents data from disease area studies as well as molecular biology approaches, using derived human disease cells in dedicated studies where the activated and resting states of cells in diseases are outlined with respect to protein and peptide presentations.

There is an understanding of the complexity and diversity of singular protein species. But we have also become more sophisticated in our understanding of the relationships and roles, which proteins have in biological systems. This is especially true for the studies of functions of proteins, which in some cases are exquisitely specific and unique while in other cases wide ranging and multi-fold. The unraveling of these relationships of expression, structure, and function is the heart of protein science today in the modern life sciences. These challenges can and will be determined by peptide and protein expression studies, where the technology developments in some aspect will be the biology driver.

I would finally like to acknowledge and express my sincere gratitude to my fellow colleagues who are the authors and contributors to this volume in the chapters that follow.

You responded to my invitation and I am very thankful.

György Marko-Varga
Lund, Sweden and Tordas, Hungary 2005

including cancer and cell biology proteomics applications. Finally, I would like to thank all the contributing authors of this book for their time and efforts in preparing this excellent and useful book on proteomics.

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