Biomedical Applications of Proteomics

J.-Ch. Sanchez, G. L. Corthals, and D. F. Hochstrasser (eds.). Wiley-VCH, Weinheim (2004). ISBN 3-527-30807-5. 435 pages, price: € 149.–.

This book provides within its 21 chapters an overview over applications of proteomics in the discovery of new prognostic, diagnostic, and therapeutic targets. In detail examples of applications are given for a selection of important research fields in life sciences like cardiovascular disorders, cancer, infectious diseases and the central nervous system as well as toxicology. The editors are experts in the use of proteomics applied to understand molecular coherences in biology and medicine. Jean-Charles Sanchez has been working since 15 years in the field of proteomics. He contributed to the development of two-dimensional polyacrylamide gel electrophoresis and related procedures and their application in biomarker discovery research. He is a founder of the Swiss Proteomics Society and Swiss-2D service. Garry L. Corthals has contributed to the proteome research for over 10 years now and has focused on the integration of mass spectrometry technologies for protein analysis in biomedical research. He currently heads the MS Group at the BPRG with the aim to improve and automate protein identification and characterization methodologies using 2-DE, mass spectrometry and bioinformatics. Denis F. Hochstrasser is the director of the Clinical Pathology Department and Head of the Clinical Chemistry Laboratory of the Geneva University Hospital. He is one of the well known pioneers in the development of proteomics and contributed to software development for proteome data processing and 2D-PAGE databases by the installation of EXPASY as the first life sciences-devoted web server. His current work is focused on the development of the Molecular Scanner, a technique for molecular imaging to enhance clinical proteomic analysis, e.g. in the drug discovery process. He is co-founder of the Swiss Institute for Bioinformatics and scientific founder of GeneProt and GeneBio.

The interest in proteomics is due the fact that the proteomic approach used for disease investigations could overcome some of the limitations of other approaches. Promising areas of proteome research goal the development of novel biomarkers for diagnosis as well as for the identification of new targets for therapeutics and include the illustration of alterations on the protein level from the whole-cell lysates up to subcellular structures and protein complexes. Currently there is intense interest in applying proteomics to enhance a better and profound understanding of disease processes, to develop new biomarkers for diagnostic purposes and early detection of disease, and to accelerate drug development processes and to evaluate the effect and toxicity of therapeutics. Considering the rapid increase of new applications of proteomics appearing in the literature in the last years, this book is a compendium of biomedical publications covering a wide range of state-of-the-art proteomic techniques and aimed to give a detailed view what current proteomic technologies can serve for in biomedical research. The clear style of the book and its straightforward presentations provide profound insight to scientists. Furthermore, it serves as a good resource for literature and techniques for academic and other researchers interested in the implementation of proteomics in biomedicine. The introduction by the editors represents excellently the framework in which the topic will be considered and furthermore addresses the difficulties of hypothesis-driven research.

The first part of the book is dedicated to the maturation of proteomics, the challenges of using results for diagnostic purposes as well as the availability of tissue samples for proteome studies, and the ethics involved in using human tissue for proteome-based studies.

Each part of the book is divided into several chapters written by experts who review the literature and discuss current advantages and challenges of proteomic research and the implemented techniques in a variety of diseases. These articles give a very clear introduction to the respective diseases, biological systems, analysis strategies and conclusions of the experiments and their impact on clinical applications. In some of the described studies not only gel-based proteome comparisons were described. For example, in the cancer section clinical markers and targets were identified for renal cancer and the qualitative and quantitative validation strategy was outlined comprising several methods like Western blot, immunohistochemistry, and SELDI. In addition, the pathological changes of urine and plasma analysis were characterized by proteome analysis.

Other contributors focus on the problem of posttranslational modifications of proteins. Proteomic tools to identify and validate such modifications and how they are linked to different diseases are presented as well. In the chapter on neurosciences, the authors review comprehensively neurological diseases like Parkinson’s disease or multiple sclerosis and common conditions upon which proteome analyses promise significant clinical impact. The final section on mass spectrometry and bioinformatics summarizes in excellent form the increasing importance of retrievable databases for protein identification.

Overall the editors provide a comprehensive overview on biomedical proteomics applications for both, protein analysts familiar with state-of-the-art proteome technologies as well as physicians in molecular medicine.

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