Microcharacterization of Proteins (2nd edn)

edited by R. Kellner, F. Lottspeich, H.E. Meyer, Wiley-VCH, Weinheim, XXI + 325 pp. ISBN: 3-527-30084-8, DM 158.00.

This book is the second edition of the well-known first one based on a meeting on methods in protein chemistry organized in 1994 at the Max Planck Institute for Biochemistry in Martinsried. This is a most welcome update considering the dramatically increasing number of sequenced genes from which the number of identified gene products is comparatively small. Biochemists and molecular biologists are about to cut down this discrepancy. The revolutionary developments which have been achieved in protein analysis during the last years as well as "a change in our attitude to the proteins...considered as members of pathways and networks" (R. Kellner, F. Lottspeich & E. Meyer) initiated the new field of proteome research ("proteomics") in understanding the quantitative protein expression pattern of a cell or a whole organism. Researchers in the field became aware that a proteome is a highly dynamic object, influenced by numerous environmental and biological parameters. "Analysis of proteins, which are the real players and tools in a cell, is a supplementary and inevitable approach to understand the biological events in a cell" (F. Lottspeich & R. Kellner).

The book, written by 33 experts in the various fields of protein research, is divided into 18 chapters, grouped into four sections. Section one gives an overview on microcharacterization of proteins. The following ones are on microseparation techniques, sample preparation and bioanalytical characterization. Fully automated, high-throughput methods for protein analysis in research on proteomes are described. The methods introduced comprise analytical and preparative gel-electrophoretic techniques, electroblotting, capillary electrophoresis, high performance liquid chromatography (HPLC), techniques of chemical and enzymatic protein fragmentation, amino acid and protein sequence analyses, matrix-assisted laser desorption/ionization (MALDI) and electrospray (ESI) mass spectrometry as well as Fourier-transform ion cyclotron resonance (FT-ICR) mass spectrometry. The last two chapters of the book are on computer sequence analyses, one on internet resources for protein identification and characterization and the other one on protein sequences and genome databases.

The book combines basic concepts and practical applications. It is well illustrated and the many mispellings and typographical errors found in the first edition are corrected. The specialized chapters give deep background information on the various methods and most of the practical parts are highly recommended for those stepping into the experimental approach to proteomics, graduate students as well as experienced researchers. The book should be available in any library of natural sciences.

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