
BOOK REVIEW

The Proteomics Protocols Handbook

(Walker, J. (ed.) Humana Press, 2005, 988 p., \$175)

DOI: 10.1134/S0006297906060150

This book written by a representative group of authors consists of 73 chapters. It covers almost all major methods used for isolation, identification, and investigation of proteins in living systems.

Chapters 1-7 consider methods of protein extraction and solubilization, preparation of protein samples from plants, bacteria, yeasts, and animal tissues for two-dimensional gel electrophoresis.

Chapters 8-14 summarize the data on protein analysis using laser technique, fluorescence, isoelectrofocusing, and different variants of two-dimensional electrophoresis.

Chapters 15-23 consider various methods of protein staining with silver, zinc, and other sensitive reagents.

Chapters 24-29 deal with methods of protein separation by differential gel electrophoresis, approaches for statistical and computer analysis of proteins, and protein purification using various chromatographic methods.

Chapters 30-42 summarize the data on protein identification by various types of mass-spectrometry and combination of liquid chromatography and mass-spectrometry.

Chapters 43-45 highlight approaches used for analysis of proteins that have undergone various posttransla-

tional modifications: glycosylation, phosphorylation, and others.

Chapters 46-53 consider problems associated with elucidation of amino acid sequences in proteins, identification of protein domains, and characterization of protein sequence databases.

Chapters 54-59 analyze methods employed for studies of protein-protein (including antigen-antibody) interactions and also for antibody purification by affinity chromatography.

Chapters 60-66 consider problems of protein research using robotization, site-specific immobilization, and also modeling of protein structure.

Chapters 67-73 deal with: i) protein classification based on amino acid sequence and structure, classification of protein folds; ii) approaches used for protein crystallography; iii) methods applied for elucidation of protein structure on the basis of crystallographic data.

This is an excellent handbook that can be recommended for a large audience of molecular and cellular biologists, specialists in protein chemistry, biochemistry, and proteomics; it is also useful for biotechnologists, specialists in bioinformatics, and also for structural-functional studies of genomes.

*G. Ya. Wiederschain,
Doctor of Biological Sciences*