
BOOK REVIEW

Protein Misfolding and Disease. Principles and Protocol

(Bross, P., and Gregersen, N., eds., in the series *Methods in Molecular Biology*, Vol. 232, Walker, J. M., series ed., Humana Press, Totowa, New Jersey, 2003, 318 p., \$99.50)

This book consists of three sections containing 24 chapters. The first section entitled "General concepts and models" contains seven chapters where general problems of tertiary protein structure and its impairments under such pathological conditions as cystic fibrosis, α -1 antitrypsin insufficiency, Parkinson's disease, and cancer are highlighted. In the chapter 2 of this section the authors consider the role of molecular chaperones in protein folding. Chaperones bind to partially folded (unfolded) proteins and promote formation of native conformation (tertiary structure) by optimizing noncovalent interactions of side chains of amino acid residues. (However, they are not components of more complex conformational assemblies exhibiting biological activity.)

The second section of the book includes five chapters, where general methods of expression of recombinant proteins, expression of *E. coli* in yeast, site directed mutagenesis, and also method of analysis of protein maturation and degradation are considered.

The third section is the largest. It includes 11 chapters, which contain descriptions of methods for determi-

nation of protein aggregates and protein staining in various tissues, and also in cultured cells obtained from patients. This section also contains chapters that deal with studies of protein tertiary structure formation in cytoplasm, microsomes, and mitochondria.

The main advantage of this book is its introduction of basic knowledge on mechanisms responsible for formation of various conformational structures and detailed protocols of various methods used for studies of various important aspects in this field. Almost all chapters of this book contain numerous commentaries to methodological protocols and a basic bibliography on the discussed problems. An alphabetical index helps to find any information available in the book. This book is well illustrated with numerous photos, figures, schemes and tables, which help better understanding of the considered problems. I do believe that this book will be a very useful tool for specialists in protein chemistry and biochemistry, molecular biology and basic medicine, and also for teachers and their students studying principles of proteomics.

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