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Book Review

Protein Structure: Determination, Analysis, and Applications for Drug Discovery
Daniel I. Chasman (Ed.); Marcel Dekker, Inc., New York, 2003, xiv + 606 pages, ISBN 0-8247-4032-7 ($195-00)

Although the identification of protein structures has been performed for many years and over 15,000 structures have been deposited in the Protein Data Bank, most are not unique and are variants of the same structures and sequences. Large assemblies of proteins performing a broad spectrum of biological roles outside the cell, within the membrane and inside the cell can only be understood adequately in the context of the descriptions provided by structural analysis. However, many classes of proteins, notably large protein complexes and membrane proteins, often still require years of intensive effort and imagination to identify their structures. Scientists have accepted that a "complete" set of structures can provide insights into the architecture of proteins and their relationship to function, as well as protein folding and evolution. However, such an undertaking seems impossible since it is neither feasible nor affordable to consider one-by-one structure determination of the entire universe of proteins. Therefore, their three-dimensional structures have already provided unique insight into their macromolecular function and mechanism, which has also become an important aid for targeted drug design. This book aims to provide current knowledge concerned with studying the structure of proteins and applications for drug discovery.

The main goal of *Protein Structure: Determination, Analysis, and Applications for Drug Discovery* is to be a comprehensive reference manual that can organise and help initiate in-depth studies. The volume is comprised of 20 different selected topics, divided into four parts, with the first part providing an introduction to structural genomics. The second part describes producing proteins, methods for solving structures by X-Ray crystallography and NMR, the computational strategies for determining structural information and comparative protein structure modeling. The third part describes analysis, mostly computational in nature, for gaining a deeper understanding of proteins from their structures including procedures for detecting errors in protein structures, finding functionally important links between protein sequence and structure, identifying biological properties from structure, data base repositories of protein structures (protein data banks) and the standards used to curate them and the importance of structure-based function annotation to drug discovery. The final part illustrates some potential uses of protein structure in the drug discovery process and discusses structure-based drug design, refining protein pharmaceuticals using structure, and the impact of genetic variation on protein function and pharmacology. The theme of structural genomics throughout the volume emphasises high-throughput methods, automation, and computation. Each group of authors surveys a field and supplies an extensive reference list for pursuing aspects of the topics that are not covered explicitly.

This volume can help to sustain and intensify interest in the renewed effort to learn about protein structure, its role in biology and some applications for drug discovery. It is an interesting and extremely informative reference volume, suitable for researchers and all individuals who would like to have a more detailed understanding about determination, analysis and use of structural information, especially in conjunction with a genomics perspective in any area of protein structure.

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