Structurally Sound Information

Foldamers: Structure, Properties, and Applications

Edited by *Stefan Hecht* and *Ivan Huc*.

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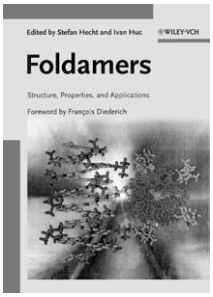

As aptly stated in the preface of *Foldamers*, "the aim of this book is to cover the breadth of the rapidly developing field of foldamer research and to unite the different aspects and schools by illustrating the generality of underlying concepts." Indeed, the collective authors of *Foldamers* accomplish a significant portion of this task over the course of 13 chapters that span synthetic oligomers, synthetic α-peptide sequences, artificial proteins, nucleic acids, and foldamers at interfaces. Each chapter is written by respected scientists within the field, and the editors have maintained an emphasis on the factors that dominate the folding processes of each system, including local rotational restrictions, interactions between sites both adjacent and remote, solvent effects, assembly hybridization, and steric and electrostatic effects (or combinations thereof).

Based on these interactions, the book could be divided into a discussion of predictable versus less-predictable folding structures (with an emphasis on the former). Much space is dedicated to foldamer synthesis, structure, and the kinetics of folding, whereas less effort is placed on optical, electrical, and other physical properties. Approximately half the book is associated with biological applications of foldamers, protein design, and the like. This is understandable, given the inspiration that foldamer chemists have had from the natural world. The coverage of biologically inspired systems is exceptional, however, from the standpoint of materials science, there is a deficiency of the subject content. The growing population of scientists who are exploring foldamers for molecular-, nano-, and even microscale materials science applications may not find sufficient information about the physical properties of folded versus unfolded structures to make this a useful addition to their libraries. Along this line, there is only a short discussion of the applications of theoretical models to: a) simulate the folding process, b) study the balance of interactions required to assemble a structure into a stable form, and c) examine the physical properties of foldamers as a function of organization. Though admittedly such research is at the state-of-the-art in computing capability (and the reviewer is biased in this regard), there is a growing body of recent publications within this theme, and the use of theory could have been more broadly integrated into multiple chapters.

The chapters cover the remaining state of research to the present time and integrate well with each other, often guiding the reader to complementary sections of the book that aid in effective reading. Given the burgeoning foldamer literature, the references are thorough and will be valuable to graduate students or experienced researchers entering this field. The index is sufficiently inclusive to be helpful. One of my favorite aspects of this book the "outlook", which not only summarizes each chapter but also highlights potential research areas in a way that captures the creativity and excitement of the authors. It is also clear that the authors put a great deal of time into the development of suitable figures that outline complex concepts, beautifully illustrate the intricate interaction mechanisms between subunits, and highlight kinetic and thermodynamic data associated with folding processes.

In summary, *Foldamers* is a delightful treatise on the subject area, provided that the reader is bent towards the biological realm (or are seeking to reproduce it). It is quite appropriate for the library of graduate students, junior scientists, or newcomers to the field. It would also be a suitable supplementary text to a graduate-level special topics class; it could also be integrated into a biochemistry or polymers course. Such versatility is hard to find, and the authors and editors should be commended for their hard work.

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Structural Genomics on Membrane Proteins

Edited by *Kenneth H. Lundstrom.*

CRC Press, Boca Raton 2006. 400 pp., hardcover £ 97.00.—ISBN 978-1-57444-526-8

Membrane proteins are one of the last frontiers in structural biology. Although roughly one third of all genes code for membrane proteins and around 60% of all drugs target membrane proteins, the discrepancy between importance and knowledge is best visualized by looking at the Protein Data Bank (PDB). The PDB currently holds 40000 three-dimensional protein structures, but fewer than 100 have been determined for integral membrane proteins. With few exceptions, such as bacterial and bovine rhodopsins or the nicotinic acetylcholine receptor, recombinant expression is required and is, in many cases, the first problem en-

countered. Many researchers are even convinced that the expression and purification of membrane proteins in a functional state and in sufficient quantity is the major bottleneck in the structural biology of membrane proteins.

In this book, approaches toward overcoming this barrier for membrane proteins are described from a structural genomics point of view. In general, structural genomics is an approach in which a large number of targets are produced in parallel by means of high-throughput technologies and subjected to structural studies. Dealing with structural genomics of membrane proteins in particular requires joint efforts in many areas of modern life sciences, which are covered by this book. Therefore, the reader is provided with detailed information about the overexpression of membrane proteins in bacterial, yeast, insect, and eukaryotic systems. Next, solubilization, purification, and crystallization strategies are described. However, the book is not restricted to X-ray crystallography. Rather, it provides a general overview of structural approaches suitable for membrane proteins, including electron microscopy of two-dimensional crystals, atomic force microscopy, and NMR.

It is quite frequently observed that overexpressed proteins do not adopt their native fold. Rather, these proteins are "deposited" within the cell in the form of inclusion bodies, which in principle can be refolded into their native three-dimensional structure. Much effort has been undertaken in the past to refold soluble proteins, but the refolding of membrane proteins is a rather new strategy toward the overproduction of a given protein of interest; *Structural Genomics on Membrane Proteins* also covers this promising strategy. Of course, structural genomics of membrane proteins requires parallelization and high-throughput technology. To satisfy this demand in the field of membrane proteins, chapters have also been included that cover production strategies, miniaturization, and an overview of structural genomic networks specialized in membrane proteins. These provide the reader with an opportunity to view the fascinating world of membrane proteins through the eyes of a structural genomics researcher. Notably, three chapters are devoted to current approaches in bioinformatics, molecular modeling of membrane proteins, and drug-discovery techniques for G-protein-coupled receptors. It is important to remember that it is not always necessary to remove membrane proteins from their natural environment, the biological membrane. Recent advances in fluorescence labeling of membrane proteins in living cells provide a new avenue to study the interactions of membrane proteins with other molecules within the cell and their spatial and temporal distribution and organization within the membrane.

Research on membrane proteins is an exciting field, and editor K. H. Lundstrom has organized material that covers the many aspects of this particular research area. This book provides insight into the various disciplines, approaches, problems, and solutions in membrane protein research. Clearly, it is a challenge to cover all aspects of this research area, but the editor and authors have achieved a balance between detail and importance without losing the main focus. Many leading experts have provided an excellent overview that is helpful for students and researchers who wish to familiarize themselves with this field. Also worth mentioning are the excellent table of contents and keyword index, which are very helpful in finding a given topic and its corresponding details. This book is also recommended for experts in membrane protein research or structural genomics because it not only provides an excellent overview, it also offers a detailed and balanced view on the daily challenges in working with these fascinating proteins, especially from a structural genomics perspective.

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Structural Genomics and High Throughput Structural Biology

Edited by *Michael Sundström*, *Martin Norin*, and *Aled Edwards*.

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Modern drug discovery suffers from low efficiency and high cost. One potential way to address these questions is through genomics research. Structural genomics has increasingly provided new means for enhancing structure-based drug design approaches. Also, the stricter demands on drug safety have presented a strong case for improved design of drugs with fewer side effects. Here, structure-based drug discovery might also play a significant role. In this sense, the new opportunities for drug development provided by structural genomics and high-throughput structural biology have recently received much attention. It is therefore with great pleasure that I welcome this new book by Sundström, Norin, and Edwards.

The editors have assembled an interesting mixture of authors representing important scientists in the field of structural biology from both academia and industry. The composition of the chapters is also successful and gives the reader a nice overview of structural genomics. Strong emphasis has been dedicated to the crystallization process and methods. The modeling aspects have also been described in detail with a special chapter dealing with the validation of structural information. I found most of the chapters very informative and highly adequate for getting a picture of the methodology, also for scientists not directly involved in crystallography and comparative modeling. The layout of the book is good. However, the size of the figures is generally too small and many of the structures suffer substantially from the black and white presentation.

The overview on structural genomics describes the field well and introduces the key players, such as the major structural genomics centers. The lessons learnt from the pilot phase of structural genomics are also interestingly presented. The following two chapters deal with protein purification and crystallization.

