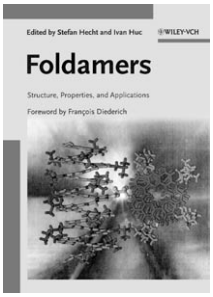
Structurally Sound Information

Foldamers: Structure, Properties, and Applications

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

Wiley-VCH, Weinheim 2007. xxii + 434 pp., hardcover € 159.00.—ISBN 978-3-527-31563-5



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.

Aurora Clark
Washington State University (USA)
DOI: 10.1002/cmdc.200700242

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-

