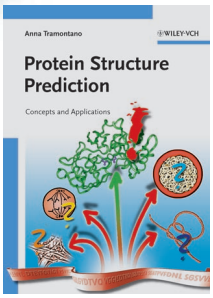
## Protein Structure Prediction




Concepts and Applications. By *Anna Tramontano*. Wiley-VCH, Weinheim 2006. 208 pp., softcover € 55.00.—ISBN 978-3-527-31167-5

With the advent of important initiatives in structural genomics, structure-based drug discovery, and in synthetic biology, the investigation of protein structure will remain a central research area of the life sciences in the foreseeable future. In addition to the elucidation of biological function, protein-based protocols have emerged as everyday laboratory tools in chemistry and nanotechnology, generating an interest in protein structure that extends beyond the life sciences research area.

As in many other areas of chemistry, computational methods are being used increasingly to complement experimental investigations of protein structure and function. Owing to the interdisciplinary nature of the protein structure prediction enterprise, many components of the presently most successful methods do not belong to the core curriculum of chemistry and physics. Consequently, the technological achievements in this field are difficult to assess for non-experts. Anna Tramontano's book *Protein Structure Prediction* fills a gap in the recent literature for researchers and graduate-level students alike, by describing the available methods and measures of their success, and providing a general insight into the state of the field. In this book, Anna Tramontano shares her insights into a research area to which she has contributed greatly, in part through her involvement as an assessor of the biannual protein structure prediction contests (CASP).

The book starts with a brief introduction to protein structure and its chemical and physical basis, which provides an easy point of departure from standard biochemical textbooks on the subject. It then moves on to an assessment of the quality of protein models. This is an important issue, because established measures of success in the field, such as GDT scores, alignment quality, and the like, are not easy to translate into absolute structure quality standards that are used to describe the resolution of experimental protein structures.

The author briefly reviews the available physics-based methodology for protein simulation, and concludes, correctly, that such methods have so far had little impact in leading to successful protocols for protein-structure prediction. The next three chapters, which constitute the core of the 200-page treatise, focus on present-day bioinformatics-based methods for protein-structure prediction, such as homology modeling, fold recognition methods, and fragment-based methods. Since all of these strategies originate from bioinformatics rather than from the physical sciences, these chapters are a welcome resource for researchers with a biochemical or biophysical background, who wish to understand the basis of these methods and learn about the most firmly established implementations. These chapters are augmented by a number of helpful worked examples, which illustrate key elements of the mathematical reasoning on which these techniques are based. They also contain a list of web links for many of the currently established protocols. The book is also useful for graduate-level students who are interested in the topic, but when it is used as a textbook the lecturer might provide more up-to-date references to the literature in this rapidly moving field.

A separate chapter is devoted to the important topic of membrane protein structure, which is particularly difficult to model because of the lack of available experimentally determined structures. The book concludes with a chapter that describes several examples of the successful application of protein structure prediction strategies for elucidating biological function. These examples illustrate nicely that protein-structure prediction has not yet matured to become a push-button machine, to which one could blindly submit sequences and obtain reliable structural models. From illustrative examples of situations where protein-structure prediction might be of use, the reader learns about strategies for tackling such complex problems. The examples are sufficiently embedded into a biological context that a non-expert reader can appreciate the issues and difficulties encountered in each of the prediction exercises. The book offers concise assessments of the effectiveness of computational models for drug discovery, for molecular replacement, and as a tool for structure determination by X-ray diffraction, all of which are very important areas for the application of protein structure prediction.

The book does not try to answer the notoriously difficult questions about the prospects for further progress on low-homology structures, but instead gives the reader information for evaluating the state of the art. It provides an up-to-date guide for the researcher who wishes to explore methods for applying protein-structure prediction to a particular problem, or wants to evaluate the quality of structural models obtained by such techniques. I hope that this clear and concise treatment will find many readers outside the bioinformatics community, and enable them to assess the state of the art and possibly benefit from recent developments.

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