

book reviews

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Protein Crystallography – A Concise Guide. By Eaton E. Lattman and Patrick J. Loll. Baltimore, Maryland, USA: John Hopkins University Press, 2008. Pp. 136. Price (hardback) US\$ 70. ISBN 9780801888069.

X-ray crystallography is one of the most important tools for the determination of structures of biological macromolecules. The structural model provides a wealth of information on the atomic scale. Knowledge of structures is one pre-requisite for a detailed understanding of the function of enzymes and the process of molecular recognition.

In recent years, structure determination has become easier and easier because of significant technical improvements related to protein production, purification, crystallization, data collection, phasing and refinement. Nevertheless, the steps from data collection *via* phasing to refinement especially require a profound knowledge of the underlying physical and mathematical principles in order to be performed correctly. There are numerous text books available which are specialized on one or more of these topics and which provide a profound and detailed insight. However, since these books make extensive use of mathematical derivations they are not well suited for those who are seeking a fast and comprehensive overview of structure determination by X-ray diffraction on single crystals. There is a huge community in the field of biochemistry which deals with protein structures and would like to know how they are determined and how their reliability can be evaluated. There are students who are uncertain whether structural biology is a field they would be able to cope with. There are scientists who want to know how the different terms which are frequently used in publications presenting new protein structures are defined. All these people don't want to read long text books dedicated to near experts.

This is the target audience for the 136-page paperback book written by Lattman and Loll. In the *Preface* the authors state that they have tried to provide an introductory guide to the most important topics of protein structure determination by crystallography for those who are seeking a basic grasp of crystallography. The authors have kept the visual pictures as simple as possible to be able to transmit the physical principles without putting too much emphasis on the derivation of the mathematical equations, which frequently is the reason why the novice reader puts aside a book on crystallography. The reader does not need to have prior knowledge of the basic physical and mathematical principles related to diffraction and structure determination. The authors provide a step-by-step introduction using well chosen and simple pictures. Nevertheless, by running through the pages of the book one will realize that complex equations are needed even for a simplified presentation of protein crystallography. The chapters

dealing with the Patterson function and functions associated with molecular replacement give a brief feeling to the 'newbie' of what one might be faced with if one wants to get more deeply involved in protein crystallography.

This book by Lattman and Loll bridges the gap between short descriptions and overviews of protein crystallography provided in reviews or dedicated chapters in textbooks for biochemistry and molecular biophysics, respectively, and the extensive monographs written for those who want to become experts in this field. The book starts with an introduction on what is diffraction, what are crystals and why to use diffraction of X-rays in order to solve protein structures with atomic resolution. These fundamental topics are explained in an easy-to-understand language supported by well chosen pictures. Therefore, this chapter serves as an elegant business card for the book and encourages the novice reader to continue on the tour through the theory behind protein crystallography. In the following six chapters the book serves as an explanatory guide for diffraction physics on protein crystals using an intuitive form for the introduction of the most important Fourier function, for phasing of diffraction data by isomorphous and molecular replacement, with a short introduction of the second most important Patterson function, and finishes with some crucial aspects of the refinement of protein structures. The book does not cover the different aspects of crystallization of proteins, symmetry within crystals, strategies of data collection, detailed model evaluation and internet-based tools dealing with structures. This might turn out to be a drawback compared with other introductory guides to crystallography. To overcome this shortcut, the authors provide after each chapter a short but very well selected and commented list of further readings, which will help the interested reader to find more specialized information dealing with these topics in more detail.

One special value of this book is the teaching of all the terms and statistics used and presented in scientific articles dealing with structures determined by X-ray crystallography. The non-expert will be able to judge the quality of the presented structures much better after having read this book. In this respect a special benefit of this book is its glossary. Many specialized treatises are lacking such a short collection of important terms and their definitions. Even terms not mentioned within the different chapters are included and short descriptions are given.

Scientists whose work is associated with structure determination by X-ray crystallography or who are interested in gaining a first insight into the complexity of structure determination by X-ray crystallography will find this book very useful. It plays on the same field as 'Crystallography made crystal clear: A guide of macromolecular models' by Gale

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Rhodes. Throughout the book the reader can tell that the authors are very experienced in teaching protein crystallography and that they know where the basic problems in understanding the first concepts of diffraction, phasing and structure refinement are. The book is written in a concise language and has the novice in mind throughout. Thus, it may become one of the best references for those who are not familiar with crystallography but want to know more about X-ray diffraction and the problems associated with it.

Professor Dr Axel J. Scheidig

Zoologisches Institut - Strukturbiologie
Zentrum fuer Biochemie und Molekularbiologie
Christian-Albrechts-Universität zu Kiel
Am Botanischen Garten 1-9
24118 Kiel
Germany