Book Review

Crystallography Made Crystal Clear: A Guide for Users of Macromolecular Models by Gale Rhodes

Academic Press, New York, 1993. 202 pages. $34.95

Reviewed by Norma Allewell, Department of Biochemistry, University of Minnesota

In recent years, there has been an explosion of interest in determining crystal structures and analyzing solved structures, fuelled by the development of recombinant DNA methods, user-friendly data collection systems and computer packages for data analysis, and molecular graphics. Although the need for an introductory guide to crystallography has been recognized for some time, it has gone unmet. *Crystallography Made Clear: A Guide for Users of Macromolecular Models* bridges the gap between brief chapters in textbooks in biochemistry and proteins and complete treatments aimed at the professional crystallographer.

In this 200-page paperback, Gale Rhodes provides a road map through the crystallographer's maze. An overview chapter is followed by chapters on crystallizing proteins, collecting data, calculating Fourier transforms and phases, refining structures, obtaining and judging molecular models, reading crystallographic papers, and tools for studying proteins. The preface states that the book is intended for protein researchers who are not crystallographers, both those who never intend to be and those who are not yet.

Much of the book reads like a transcript of discussions between a wise and tolerant old crystallographer walking a novice through his/her first structure determination. All of the problems one encounters, from recognizing twinned crystals and visualizing the geometry of a precession camera, through identifying heavy atom binding sites from Patterson maps, to fitting electron density maps and refining the structure are dealt with patiently and creatively. Although all of the standard derivations are here, the text has a light touch which both novices and noncrystallographers will appreciate. Some sections clearly aimed at readers with a very modest background in the physical sciences may be a little frustrating to the budding crystallographer, while the mathematical sections will probably not win over very many molecular biologists, despite the quote from Jacob Bronowski in the preface that likens the verbal argument in mathematical writing to the melody in music, intrinsically satisfying, with the equations corresponding to the accompaniment that becomes more satisfying with repetition. The thirteen color plates are excellent.

Although the title does not indicate that only proteins will be discussed, this is in fact the case. Given this restriction and the brevity of the text, it is remarkably complete. Even Harker sections, the "hand problem," and the difference between constraints and restraints are dealt with, although the coverage of topics is not even. Indexing reflecting planes and reflections, the principle of contour maps and a specific graphics package are covered in detail, while refinement packages and issues of molecular motion and disorder receive relatively little attention. The most recent developments, for example, the use of robots in crystallization, tend to be slighted.

The most useful chapters for those who simply want to explore solved structures will be the last two, entitled "A User's Guide to Crystallographic Models" and "Tools for Studying Proteins." The former makes some important statements about the limitations of molecular models and walks the reader through two papers describing first the cloning and crystallizing ALBP (adipocyte lipid binding protein) and, second, the completed structure. The second chapter provides a tour through a typical molecular modeling program, the UCSD Molecular Modeling System.

This book will be useful in many contexts—in elementary courses in crystallography, in biochemistry courses as an auxiliary text, in crystallographic laboratories as a handbook for novices, and in molecular biology laboratories as an introduction to the Protein Data Base and molecular graphics. It can be perused in an afternoon which will be well spent.