Patterson search correlation or molecular replacement methods have proved effective for solution of structures where a similar structure is already known. As the database of protein folds increases, these methods are finding increased application. The accounts of molecular replacement methods provide a sound background and give useful advice, for example for those problems where the starting model may not be an accurate representation of the structure sought. The book ends with 'horizon' methods. There is an entertaining description of crystal structures of racemic mixtures, although the methods are restricted to those molecules that can be synthesized and crystallized in both D and L forms. The sections on *ab initio* phasing using very high resolution data and the computation of very low resolution phases, that will allow us to bridge the gap between electron microscopy and X-ray crystallography images, point the way to the future.

This is an excellent volume. It is recommended to all graduate students and postdoctoral workers in macromolecular crystallography. I shall be purchasing both volumes for my laboratory and I shall expect to refer to my copy frequently.

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Macromolecular crystallography. Part B. Advances in Enzymology, Vol. 277. Edited by CHARLES. W. CARTER JR and ROBERT M. SWEET. New York: Academic Press, 1997. Pp. xxxiii + 664. Price $99.00. ISBN 0-12-182178-1

Volumes 276 and 277 in *Methods In Enzymology* describe the tools of the trade for macromolecular crystallography, using as a template the eponymous first pair published some 12 years ago. The problems to be solved remain the same: get crystals, collect data, determine phases, interpret the map, refine the structure (taking into account the normally low data-to-parameter ratio), evaluate the quality, make a picture, and publish, roughly in that order. The tools for solving these problems have advanced as far as new technologies (faster computers, new detectors, more intense X-ray sources) permit. The chapters in Volume 277, Part *B* of the work, describe horizon methods in phasing, the various approaches to map enhancement, interpretation, and refinement, evaluation of 'correctness', tools for conveying structural information to the consumer, suites of programs currently in use for the practicing macromolecular structuralist, and databases that contain the results of these experiments. The articles are written by leaders in their respective fields; not surprisingly and very pleasantly, a fair amount of individual personality shines through the writing.

The degree of technical understanding required for individual chapters makes it likely that these volumes will be used more by practitioners than by the 'educated layman' or even by consumers of structural information. Direct methods of phasing for macromolecules are not yet in the hands of the non-experts, despite substantial strides forward in this area, but the chapters describing these efforts are rewarding. In my view the field will have been put into the hands of consumers of structural information when user-friendly programs become available, but clearly this can only be done when the theory itself has matured. Thus, in my experience, first *PROLSQ/PROTIN* made refinement a commonly used tool, and now *TNT*, *X-PLOR* and *ARP* have become industry standards, but all after the pioneering efforts of Lyle Jensen to show that refinement was possible. Lyle's article on refinement and reliability of macromolecular models is characteristically clear and unassuming, full of nuggets of wisdom, as are the articles by the authors of these last three programs. Without the graphics programs *FRODO*, and now *O*, we as a commmunity would be nowhere, and the practical wisdom in the chapter describing map fitting is priceless. The chapter entitled 'Model phases: probability and bias' by Randy Read is also exceptionally understandable (check out the figure on page 113!). The *SHELX* chapter is also very readable, and perhaps inclusion of this program signals best the connections with the small molecule world as to how to get the most out of one's data. The *CCP*4 federation of programs continues to be invaluable. Its continued responsiveness (part of the original intent of the project) to changes in the field is particularly useful. I confess to focusing on programs with which I have personal familiarity: a reviewer more familiar with *PHASES* and *CHAIN* and a different lineage of programs would, I am sure, find equal words of praise for these chapters. Unfortunately, there is not a chapter from Duncan McRee on the *XTALVIEW* system, but perhaps his own book *Practical Protein Crystallography* (Academic Press, 1993) obviated that need.

I recognize that completely automatic map interpretation (once direct phasing is a *fait accompli*) is required for the field to realize its full potential, but for me and many others such a success will be at the expense of the personal thrill of recognition in interpreting electron density and of the realization of both just how much information really is in those data and of what has to be left unmodelled! I believe that the analytical approach to map interpretation will not be successful until enough noise is removed from the maps, at which point normal interpretation is easy, albeit tedious. However, automatic map interpretation may indeed put structure determination into the hands of the biologist or enzymologist. The chapter by Fortier on this subject, that describes the renewal of efforts initiated by Carroll Johnson over a two decades ago, will perhaps be the most novel to a macromolecular crystallographer, and it points to an area that should be watched closely. The still not-quite-automatic state of the horizon phase determination methods should suggest to the consumer that s/he should still rely on experimental phases and collaborators experienced in these traditional tools. The tools described in these volumes must be understood by the practitioners, although not all by everyone. Individuals will prefer, probably, the tools with which they have grown up in their scientific career, until a problem arises their tools can't handle properly, at which point they will turn to new ones.

I think future volumes will have to include chapters from consumers. The large numbers of structures we already have, and the even larger numbers to come, demand new methods for accessing, understanding and representing them. Two of the favorite tools for producing publication quality images, *RASTER3D* and *RIBBONS*, are well described in this volume,

but animation, as can be seen in several new web sites, will eventually be necessary to capture the molecular cinematography we desire. The chapter on detecting folding motifs, by Kleywegt and Jones, describes tools for detecting similar folds, even during the process of map fitting, and includes good references to the larger community of structural consumers interested in classifying protein folds and detecting similarities. The chapter on the Protein Data Bank might be that most appreciated by the consumer of molecular structures, although they probably will be already familiar with its contents from use of the PDB.

The chapters on diffuse scattering and on Laue diffraction are new to these volumes; both are lucid accounts of the state of forefront areas of research which are key to obtaining experimental information on the dynamics of molecules from X-ray data. Diffuse scattering measurement and Laue diffraction techniques clearly will not be appropriate for all problems, but it will be exciting to see what well chosen experimental systems can yield.

In the *Introduction* the editors speak of a move towards macromolecular service crystallography, the subject of an editorial by Ed Lattmann in an issue of *Proteins, Structure and Function*, some years back, to which I remember reacting quite negatively at the time. I am coming around! There are indeed many problems (mutants, structures with already known folds) that might fruitfully be regarded as treatable in such a way, but only if reliable structures are forthcoming. Recognizing that while structure determination usually provides correct structures because it is such an iterative and self-correcting method if an investigator heeds the warning signs, there still need to be independent measures of how good the resultant models are. Chapters describing these measures are new to these volumes. Unfortunately, there is not a chapter about the now commonly used *PROCHECK/WHATCHECK* programs that at least check self consistency. Brünger's chapter on the free *R* factor is excellent as is the chapter on *X-PLOR* itself; however an overall statistic still cannot replace honest evaluation of what remains in all electron-density maps from data with *R* factors in the high teens. Future volumes could fruitfully include a chapter on how to tell what is significantly different from one structure to the next: indeed it would have been useful to include some of Cruikshank's recent work on this problem in this volume. So, the practicing crystallographer should have Volume 277 on the bookshelf (to accompany volume 276, as recommended above by Professor Johnson). Should the collaborator of a practicing crystallographer also acquire them? Hard to say. A teacher of structure determination will want these articles for reference, and it is convenient to have them all together. It will be interesting to see who will write the successors to these chapters in ten years, or if the field will actually require successors. I think it probably will!

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