cussed. However, in the next version, newly developed methods as confocal scanning and plasmon surface resonance should be included.

In conclusion, the book is highly recommended for cell biologists working in the receptor field, in particular those approaching mathematical models for ligand/receptor interactions and trafficking.

Søren K. Moestrup

Crystallographic Methods and Protocols. Methods in Molecular Biology, vol. 56; Edited by C. Jones, B. Mulloy and M.R. Sanderson. Humana Press; Totowa, 1996. xii+394 pp. $69.50 (pb). ISBN 0-89603-259-0

As the field of Structural Biology expands, publishers everywhere recognize the need for text books concerning biomolecular crystallography (and NMR spectroscopy). Jan Drenth's book was probably the first useful text about protein crystallography to be published since Blundell and Johnson's seminal work of the mid-1970's, and it was rapidly followed by others. At the end of this year, the first of two long-awaited volumes of 'Methods in Enzymology' will hit the book stands, and the IUCr has commissioned a separate volume of the International Tables on the subject of macromolecular crystallography.

In the midst of this deluge of books comes 'Crystallographic Methods and Protocols'. In my opinion, the book fills an important (and probably profitable) niche in the market. The 'Methods in Enzymology' volumes are written by the experts in the various sub-disciplines, and they will no doubt be reference works for a decade to come. Drenth's book is very suitable for teaching and learning the principles of the trade, but does not provide much in terms of practical guidance. So: where does this leave the graduate student or cross-over molecular biologist who wants to learn how to collect and process data? It is precisely here that the present book comes into the picture, since it largely delivers what it promises: methods and protocols; very basic and down-to-earth, but all the more useful for inexperienced crystallographers. I suspect that the fact that the book succeeds in this is largely due to the fact that it has not been written by the 'prima donnas' in the field, but by the people who do the actual work (of course, I apologise to those contributing authors who do consider themselves to be prima donnas!). Another book that attempts to provide practical guidance is that of McRee, but the fact that his book is tied to one particular software package greatly diminishes its value. 'Crystallographic Methods and Protocols', on the other hand, will provide you with a list of programs (and contacts) for solving particular problems.

Judging from the reference lists, the manuscripts were written in 1993 (a few references to papers that appeared in 1994 have been added here and there). In a few cases this has led to chapters that feel slightly out-of-date, but on the other hand: a precession photo will be a precession photo. Actually, I was pleasantly surprised to find that both cryo-crystallography and MAD phasing are discussed in the book, the former in two different chapters, the latter in a chapter by itself.

The first chapter (Sanderson) is a very brief introduction to crystallography with a useful list of references to other books that go into more detail. In chapter 2, Skelly and Madden describe overexpression, isolation and crystallisation of proteins.

Chapters 3 and 4 were my personal favourites (probably because of my own clumsiness), and I suspect that these will also prove to be the most useful to novices in the field. In chapter 3, Abdel-Meguid, Jeruzalmi and Sanderson discuss the preliminary characterisation of crystals. They discuss symmetry, crystal mounting, precession photos, flash-freezing, spacegroup determination, and more. Elspeth Garman describes many types of data-collection equipment, and actually provides a step-by-step recipe for operating each and every one of them. In addition, she discusses practical aspects of data-processing and flash-freezing.

Chapters 5–7 describe the ins and outs of phasing, through MAD (Krishna Murty), Isomorphous Replacement (Abdel-Meguid) and Molecular Replacement (Tickle and Driessen) techniques. Due to the long production time of the book, the latter chapter has suffered somewhat, so that Navaza's excellent AMORE package is only mentioned briefly (in a note added in proof), but not discussed, and Tong's REPLACE suite (with 'locked' rotation and translation functions) is not mentioned at all. On the other hand, the discussion of various practical aspects of Molecular Replacement makes up for a lot. Similarly, the chapter on density modification (Podjarny, Rees and Urzhumtsev) refers only to programs that appeared before 1994, thereby missing GAP, DM, SOLOMON, RAVE and others (as well as multiple-domain and multiple-crystal form averaging, and solvent 'flipping'). In addition, some low-brow practical issues (such as the detection and importance of, and the distinction between proper, improper and purely translational NCS, and the importance of good mask and operator definitions) should have been discussed here.

Chapters 9 and 10 deal with refinement and model-building of structures. Westhof and Dumas have produced a chapter that they could have written 10 years ago almost without changing a word. When it comes to model-building, Westhof and Dumas promote FRODO – need I say more? Only in their very last note do they mention the fact that some of us are actually interested in tracing the chain in the correct direction. Apart from that, their ideas of good model-building and refinement practice (emphasising R factors and deviations from ideal geometry) largely date back to the 1980's, the dark ages of protein crystallography. The subject of tracking down errors and rebuilding the model to make it better would have deserved a chapter in its own right. Fortunately, Brünger makes up for this to some extent by discussing the use of cross-validation (the free R value) and the issue of the quality of crystal structures. Besides that, he presents a succinct description of energy-based refinement and simulation annealing, as well as models for bulk solvent and thermal motion.

The final four chapters discuss practical aspects of the crystallography of compounds other than 'simple proteins': oligonucleotides (Neidle), protein-DNA complexes (Brown and Freemont), viruses (Fry, Logan and Stuart), and membrane proteins (Newman). These chapters contain a wealth of information with respect to crystallisation conditions that have actually worked, and other aspects of the crystallographic structure-determination process that are different from those of proteins.

In summary: despite a few short-comings, I warmly recommend this book to newcomers to the field as a hands-on guide to many of the varied activities a macromolecular crystallographer faces. The book is a useful complement to more theoretical texts such as that of Drenth. Taken together, they can be put to good use for teaching both theory and practice of macromolecular crystallography. Naturally, neither book can or should replace actual supervision of students, in particular at those stages that require more intra-cranial than manual dexterity (i.e., every operation carried out with the aid of a computer program).

Gerard J. Kleywegt