lian H, K and N proteins are the ones that most differ from the common structure in the book. For the H-Ras, no reference to either cDNA or gene sequence is given, nor is there any information on the chromosomal location of the genes in different organisms. For the newcomer to the field, such information is useful – even information that the information is not available. I have not attempted to check the information in the entries for correctness – there are bound to be mistakes (e.g. on p24 it is said that the *ras* effector domain was defined in yeast Ras. Not so, both groups defining the effector domain (one with analyses in *S. cerevisiae*) used mammalian H-Ras.) However, with the promise of the update site (discussed later) mistakes can be corrected.

It would have been useful if each entry also contained the precise name of the species of origin. One of the strengths of this collection of information is that it is derived from many systems, and the proteins from various species are presented next to each other. I realize that most accept the generic name yeast (as in 'isolated from a yeast library') as *S. cerevisiae*, however, *S. pombe* is also a yeast, and much Ras work has been done in this organism. Thus, it is only with the aid of careful screening of the references or prior knowledge of Ira that it is clear that the Msi2/Lte1 protein is a *S. cerevisiae* protein. Similarly, if outside the field, it would be impossible to know that the p62 entry refers to a human protein.

Throughout there is confusion between gene sequence and cDNA sequence. Of course, this is rampant in molecular biological scientific literature, however, since a very useful feature of this book is the Genbank accession numbers, it would have been reasonable to distinguish between chromosomal (gene) sequences and cDNA sequences.

In a field developing as fast as this, this type of book has a relatively brief utility life. According to the publishers(?), this will be circumvented by an exiting and potentially revolutionizing new companion to the book: a world wide web site (http://www.oup.co.uk/) containing update information from the individual authors to the editors and presented at the site.

Imagine what a gem such a site could be: Each protein has a moderator, a person monitoring the development, who would clear up confusion of duplicate names, sequencing mistakes, organism cross references, whatever! When I first tried the site there was no reference to the update information, only a description of the book. Now (August 96) there is a note to the effect that update information will be available when it exists – too bad that this is not taken advantage of, because, taken together, the book and the site would constitute a 'collector's item', a succinct up-to-date information on a large number of molecules of central interest to molecular cell biologists of today.

An excellent concept; a useful book.

Berthe Marie Willumsen

Protein Electron Transfer. Edited by D.S. Bendall. BIOS Scientific Publishers; Oxford, 1996. xvi+300 pp. $131.00 (hc). ISBN 1 85996 040 5

Electron transfer reactions are at the heart of essential cellular processes such as respiration and photosynthesis and are therefore central to biological energy conservation and utilization. Because in many cases only an electron is transferred from donor to acceptor without the making and breaking of chemical bonds, there is the possibility to understand these processes in a truly fundamental way. Indeed, electron transfer reactions are among the best understood of both chemical and biological processes. This area of science is one of the best examples of the coming together of Biology and Chemistry in a way that challenges and enriches both. This excellent book summarizes the current understanding of this exciting and fast-moving field.

The book consists of ten chapters and two appendices, all written by internationally recognized experts. The first chapter by Christopher Moser and Leslie Dutton is an overview of the problems addressed by the book and includes an introduction to the basic theory of electron transfer processes. It emphasizes the distance dependence of electron transfer and touches on how this relates to protein engineering. Chapter 2 by David Beratan and José Onuchic considers the detailed pathway that an electron follows in the electron transfer event and how this depends on the nature of the protein between the redox centers. The first two chapters are focused on intramolecular processes, where the electron transfer takes place within a single protein complex. These are the simplest cases and here the understanding is at a relatively advanced level. However, most electron transfers are intermolecular, with two reacting proteins colliding with each other in solution or on the surface of a membrane, finding the optimum orientation for the electron transfer to take place and then diffusing away to react with other oxidizing and reducing partners in the electron transfer chain. Chapter 3 by Derek Bendall discusses this important class of reactions, focusing on diffusional and electrostatic aspects. Chapter 4 by Scott Northrup is concerned with computer modeling of intermolecular electron transfer processes, emphasizing calculations on calculation of docking geometries and Brownian dynamics. Structures of electron transfer proteins and their complexes are the subject of Chapter 5 by Scott Matthews and Rosemary Durley. They focus on some of the systems where structures of noncovalently associated electron transfer proteins have been obtained. The next four chapters give detailed information about specific systems that have been extensively studied. These include the photosynthetic bacterial reaction center by William Parson, copper proteins by Ole Farver, heme proteins by G.R. Moore and ion translocating complexes by Peter Rich. The volume ends with the text of the Nobel lecture given by Rudolph Marcus, whose pioneering work on electron transfer theory earned him the Nobel prize in 1992.

Overall, I think this is an excellent book that should be useful to a wide range of researchers and advanced students. It provides authoritative and up-to-date coverage of a complex and interdisciplinary subject in a generally very accessible manner. The literature coverage is current through 1995. The selection of authors is a strength; in every case they are among the world experts in their particular areas. The inclusion of both intramolecular and intermolecular systems is also an attractive feature. The major shortcoming that I see in the book is the lack of any color figures. In many cases, in particular molecular structures and electrostatic potential maps, the presentation suffers significantly from not having the opportunity to color code the information. These systems are complex and it is now routine in the primary literature to include color figures. Presumably, this was done in order to save production costs. However, at $130, it is not an inexpensive book, considering its modest length. I think most readers would have been willing to pay a few dollars more for what would have been a significant improvement in presentation in many of the chapters.

Robert E. Blankenship

Receptors. Models for Binding, Trafficking, and Signalling. Edited by D.A. Lauffenburger and J.J. Linderman. IRL Press; Oxford, 1996. x+365 pp. £22.95 (pb)

'Receptors', first published in 1993, is now available as a paperback version. The book is a very comprehensive overview of the biology of cell surface receptors. The authors describe in detail the many important aspects of receptor studies, e.g. ligand-receptors interactions, trafficking and signal transduction. A major part of the book has been allocated the presentation of mathematically models describing receptor-related processes. For example, multivalency of either ligand or receptor is a common hurdle in ligand-receptor analyses and the book guides excellently the reader through the problems in this type of analyses. Most of the common methods in receptor biology are discussed. 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