book discuss aspects of glial cell-axonal interactions during development and repair. The discussion of the potential use of cultured glial cells to repair demyelinated lesions and to support the regeneration of traumatic CNS injuries is an interesting inclusion in the book, which, if possible, will revolutionise modern medicine. Invertebrates have for a long time represented a fruitful paradigm for the identification of regulatory genes that play roles in mammalian development and the final chapter in the book gives an interesting overview of glial cell development in the insect nervous system.

In conclusion, 'Glial Cell Development' gives an excellent overview of a broad range of topics in modern glial cell research and the book is valuable for researchers working in the field as well as for newcomers, students and others with interest in neurobiology.

Niels Aagaard

YAC Protocols. Methods in Molecular Biology, vol. 54. Edited by D. Markie. The Humana Press; Totowa, 1995. x+378 pp. $69.50 (pb). ISBN 0-896-03313-9

Laboratory or methods manuals are almost always useful publications: often they are the result of didactic efforts of their authors, enacted to finding a way to focus and verify their own protocols, otherwise frequently ill-defined. Of course they are (or are meant to be) of great help to colleagues in the field who desire to enrich their experimental tools with a novel technique. They could also represent, if and when the methodological details are accompanied by appropriate overviews, an advantageous observatory to newcomers to the field.

In order to meet all these plausible goals, a book of this sort requires inter alia a panel of authors and/or an editor who both share the awareness of the above scopes and possess the competence to present concisely the underlying theory and precisely the various protocols in question.

'YAC Protocols', volume 54 of the successful series 'Methods in Molecular Biology', gets close to responding fully to the aforementioned criteria. It is timely, since it appears almost 10 years after the publication in Science of the epochal YAC paper by Burke, Carle and Olson; 10 years in which the yeast artificial chromosomes (YAC) have contributed remarkably to the advancement of the various genome projects. Yet, it has been reliably stated that the YACs may have made their time at least as megacloning vectors, and are likely to yield the way to other cloning systems, possibly of prokaryotic origin, such as the PAC (phage P1-based artificial chromosomes) and the BAC (factor F-based artificial chromosomes), the main reason being the substantially unresolved problem of 'co-cloning' and this is an issue deserving some reflection.

Co-cloning is also known as 'chimerism'. It consists in the undesired apposition within the same YAC of fragments derived from unlinked regions of the genome under study: it is an inconvenience which could seriously mislead mapping and sequencing efforts. Admitted from the very beginning of the YAC technique, co-cloning has been unfortunately minimised by the original YAC apostles, who claimed it could be kept well below 10%; even if later acknowledged to be more conspicuous, it was deemed as marginally important, easy to be spotted and eventually eliminated in subsequent years (also through the use of recombinant deficient hosts). Yet, at the conclusion of the first 5 year phase (mapping) of the Human Genome Project, reliable commentators have issued a rather severe sentence of the future of the YACs, and this is so just because of the chimerism, now recognised to affect 50–60% of most of the generally available YAC libraries.

In front of all this, it is frankly a bit disappointing to see that a book on YAC protocols devotes only a few pages to the detection of chimerism (Chapter 11 deals with this problem and is one of the shortest), and neglects any discussion on the two distinguishable causes of co-cloning (co-ligation of different restriction fragments in vitro, and recombination between different constructs taken up in vivo by the same host cell), as well as on the possible remedies (dephosphorylation of the genomic fragments rather than of the chromosomal arms, or at least a ratio of dephosphorylated vector to phosphorylated insert higher than ten, as recommended in Chapter 1; and finally the use of a transformation ratio DNA/spheroplasted cells lower than here suggested, which turns out to be close to, if not higher than, ten, as well as the adoption of recombination defective strains as hosts, as already mentioned). This is an omission which seems to amount to considering co-cloning as unavoidable, a sort of 'original sin', which probably is not deserved.

On the positive side, it should be noticed that the various chapters are loaded with useful tips and information; if one wanders through the notes one has the chance of stumbling happily into real treasure chests of illuminating and curious details, of the nature one, in less competitive years and fields, used to learn by chatting with friendly colleagues in front of a beer during breaks at a meeting.

Thus, the chapters on the transfer of YAC into novel hosts, be they different yeast strains or mammalian cells, represent very instructive reading for those who intend to use the yeast artificial chromosomes as vector to dissect other more or less complex genomes, or for those who strive to exploit the YAC as intermediates of more ambitious constructs, such as the MAC (Mammalian Artificial Chromosome), probably likely to be used for manipulative rather than for analytical purposes. Not only for them, somehow broader surveys of the chromosome features, such as telomeres, and in particular centromeres and DNA replication origins (admittedly much simpler in yeast than in higher eukaryotes), would have contributed to a better and broader overview of the field of artificial chromosomes as the last addition to the synthetic approach to the study of life.

Vittorio Sgaramella

Guidebook to the Small GTPases. Edited by M. Zerial and L.A. Huber. A Sambrook and Tooze publication at Oxford University Press; Oxford, 1995. xix+476 pp. £29.50 (pb). ISBN 0-19-859944-7

This book puts together information on the small GTPases, a family of proteins where our knowledge has exploded in recent years. With the discovery of the regulatory role of the Ras protein, governed by its binding alternatively to GTP and GDP, and the discovery of a large number of homologous proteins with similar characteristics, a fruitful field of research has developed, leading to improved understanding of the regulatory proteins of several biological processes. The common biochemistry of these proteins, and the lack of homology of several proteins regulating or being regulated by similar structures are fascinating challenges for the interested molecular biologist, and much of the focus in the field today is on unraveling the mechanisms by which the small GTPases affect the activities of other proteins.

These characteristics makes it possible to use information from one biological system to the other – provided you get access to it. This is one aspect of the uses of this book.

In this guidebook, information on the GTPases themselves, the proteins that activate and inactivate them as well as their effectors (or presumed effectors) is given. They are organized in logical sections, where a common format has been attempted for each entry: After a brief summary, information on nucleotide sequence (gene), amino acid sequence (protein), posttranslational modifications, localization, interacting components (activators, inactivators, substrates) and functional studies (and references) is presented. Each protein is presented with one to two pages, with tabular material, drawings as well as the occasional picture presenting primary data. Needless to say, not all proteins have all information, and ironically, the mamma-

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 dis-