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Book reviews

Post-Translational Processing. A Practical Approach; Edited by S.J. Higgins and B.D. Hames, Oxford University Press; Oxford, 1999. xx+317 pp. £ 31.95 (pb). ISBN 0-19-963795-4

The 'Practical Approach' series of books has been a valuable laboratory resource to many people for many years. The aim of these books is to present a subject in sufficient detail to perform experimental procedures, but at a level appropriate for a relative novice in a given field. This is sometimes a difficult balancing act to achieve, and leaves the authors at risk of being hoist by their own petard. Too much detail can render the material dense and unreadable to all but a select few, while too little detail can leave the reader thirsting for more information. Whether or not such a balance is achieved, however, depends greatly on the scientific background of the reader. The subject of this review is the latest addition to this series, entitled 'Post-translational Processing: A Practical Approach'. I think that as a whole this delicate balance is achieved reasonably well, making this a very valuable and highly readable book.

The first chapter present a good overview of techniques used for sequence analysis of proteins. Although the title of the chapter includes the term 'expressed proteins' the information contained within is not restricted solely to expressed proteins. For example, methods of dealing with proteins containing a blocked N-terminus are presented and discussed, even though this rarely occurs in expressed proteins and is much more common in purified native proteins. The chapter focusses mostly on chemical and enzymatic sequencing of proteins, at both the N-terminus and C-terminus, but also includes a section on mass spectrometric analysis of proteins. It should be noted that great advances have been made in tandem mass spectrometric identification of proteins in recent years, and therefore this chapter does not contain the most up-to-date information in this area.

Chapter 2 is concerned with protein folding and import into organelles, focussing mainly on protein import into different organelles, with a brief discussion of analysis of protein folding. This chapter covers a wide subject area, so it cannot be considered a comprehensive review. Nonetheless, it is a very well presented description of protein translocation, particularly the section on mitochondria, which includes many detailed protocols and a good list of references for further reading. There are several hard-to-find protocols included for highly useful but relatively unusual techniques, such as blue native gel electrophoresis of protein complexes.

Chapter 3 is a necessarily brief overview of the analysis of protein phosphorylation, a subject broad enough that it has been the subject of entire books, rather than chapters. Various protein phosphorylation systems are covered, including tissue samples, isolated samples and cell-free protein preparations. Analytical methods for the characterization of the nature and extent of protein phosphorylation are discussed in detail, concentrating mostly on techniques using radioactivity. This section would benefit greatly from the inclusion of some information concerning some of the more recent work in this field using direct mass spectrometric determination of phosphate location and distribution in phosphoproteins. The latter part of the chapter deals with the analysis of protein kinases and phosphatases, and represents a good introduction to the complex nature of the experiments needed to characterise these enzymes.

Chapter 4 covers another very wide-ranging subject, protein glycosylation. Indeed, as mentioned very early in the chapter, numerous books have been devoted to this subject alone, including one previous title in the practical approach series. This chapter is devoted mainly to the analytical methods used to characterise carbohydrates, and thus does not aim to provide much information about the biological role of glycosylation. All stages of the glycosylation characterization process are covered, including initial detection of the presence of carbohydrate, information that can be deduced from whole glycoproteins, the mapping of glycosylation sites, and the analysis of the structure of individual glycans. A large number of techniques are explained in detail, including recent developments in hydrazinolysis and fluorescent labelling. However, the chapter does seem to be heavily weighted in favour of methodology applicable to mammalian *N*-linked glycan structures, and gives little consideration to the techniques used in determination of more unusual structures such as *O*-linked glycans from various biological sources. In addition, there is no mention in either chapter 3 or 4 of the phosphoglycosylation modification that is found in various parasitic organisms.

Chapter 5 provides a summary of the field of lipid modification in proteins. This is focussed mainly on glycosylphosphatidylinositol (GPI) anchors of proteins, but also includes discussion of amino-terminal acylation and cysteine prenylation. The section on GPI anchors includes all the detailed information necessary for the detection and identification of GPI anchor lipid groups attached to protein, including discussion of metabolic labelling, release of anchored proteins by bacterial phosphatidylinositol-specific phospholipase C, and detection of the cross-reacting determinant (CRD) antigenic epitope. The chapter does not include discussion of the detailed structural characterization of individual GPI anchor structures, which is usually performed principally by mass spectrometry and chromatography in conjunction with enzymatic digestion, but the reader is referred to other volumes in this series where this subject area is covered in detail.

Chapter 6 is fairly specific in subject matter, even though the title of the chapter, proteolytic processing, is very broad indeed. The chapter is mainly devoted to the prohormone convertase enzymes, PC1 and PC2. Detailed protocols and descriptions are included for both assaying intracellular enzyme levels, and overexpression of the same enzymes.

Chapters 7 and 8 cover the same subject, protein degradation, in mammalian and yeast cells, respectively. The discussion of mammalian cells is focussed mainly on protein degradation involving the ubiquitin system and lysosomes, while the discussion on yeast cells is centred mainly on degradation occurring in the proteasome and the vacuole. Both chapters present detailed protocols for many experiments in this area, including isolation of the relevant subcellular organelles, labelling of proteolytic substrates and quantification of rates of degradation of individual proteins. Chapter 8 also contains an informative introduction to the advantages of using yeast as a system for the study of cell biology in general, and protein degradation in particular.

Overall, this book is probably best for those who are relatively new to some of the highly specialised areas involved, as it presents a good general overview of the topics covered. Those who are already experts in particular areas will find many of the experimental protocols to be lacking in explanation of finer points, and also possibly somewhat outdated due to the rapid evolution of analytical techniques in certain areas. However, it would be impractical to cover the entire field of post-translational processing in great detail in a single reasonably sized volume, and thus it is highly useful that the chapters all include appropriate referencing for the reader who wants to find out more on any given subject. In summary, this is an informative and practically useful book, and represents a worthy addition to the 'Practical Approach' series.

Paul A. Haynes

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DNA Repair Protocols. Eukaryotic Systems; Edited by D.S. Henderson, Humana Press; Totowa, New Jersey, 1999. xix+641 pp. $ 79.50 (pb). ISBN 0-896-03590-5

After the first golden age of DNA repair, led by pioneers like Paul Howard-Flanders and Richard Setlow in the 1960s and 70s, the field of DNA repair passed through a period of less progress and reduced enthusiasm. However, during the last decade several remarkable breakthroughs have been made, which highlights the importance of this field and its overlap with many other research fields. In particular, the interrelationship between the '3 Rs', replication, repair and recombination of DNA, has been demonstrated repeatedly and now constitutes a more integral view of DNA metabolism. In its infancy, DNA repair experiments were restricted to simple, genetically tractable systems, whereas now the spectrum has been widened to a host of organisms which all yield important information. The revitalization of the DNA repair field stems partly from technical advances, partly from novel approaches to the cloning of repair genes in mammalian cells and partly from complex biochemical assays of the functions of repair enzymes.

This book is volume 113 in the series entitled 'Methods in Molecular Biology'. It contains a number of the protocols which promoted the upsurge in the DNA repair field. The book is organized into four major sections:

1. Mutant isolation and gene cloning,
2. Recognition and removal of inappropriate or damaged bases,
3. DNA strand breakage and repair,
4. DNA damage tolerance mechanisms and regulatory responses.

The list of authors contains many of the leading scientists within the field, although some are missing. Some contributions appear to have been written 2–3 years ago, but this is, in most cases, not a problem, since the procedures still represent the state of the art. The protocols are all published elsewhere, but they are collected here in a form where detailed instructions and explanations are given and emphasized. As such, the book represents an important contribution. In addition, since many procedures of general interest are described in an easily accessible way (e.g. different application of PCR, agarose electrophoresis, transfection of mammalian cells, labelling of DNA, nucleic acid hybridization, isolation of cell components and flow cytometry), any lab working with DNA will benefit from this book. Thus, although the format indicates a book where one would read one article and then never open the book again, its contents will stimulate use on a number of occasions. The plastic spiral binding suggests that the publisher has ambitions that this will be a heavily used reference book for lab use, but I doubt that it has the nature and quality for that.

Section 1 contains eight articles to describe methods to identify the genes encoding proteins involved in DNA repair. For aficionados, the book contains descriptions of different methods to detect a plethora of specific DNA lesions, including base damages (section 2) and strand breaks (section 3) of different sorts, along with equally sophisticated methods to detect the repair of these lesions. Section 4 contains 'miscellaneous' subjects that apparently could not be fitted into the first three sections. These articles are more remote from the DNA repair field, but most of them are valuable and clearly relevant for the scope of this book.

The introductions to the articles often contain overlapping and redundant information, which is difficult to avoid in a multi-authored book. However, as an example, the numerous explanations of nucleotide excision repair could have been avoided if the editor had assigned the job of giving a thorough description to one of the authors, at the same time informing the others that this description could be referred to. Some authors also include valuable information about the 'sociology' of their field, i.e. where can one get information about strains, enzymes, sequence banks, societies and material to start up experiments in this particular field. Protocols for most experimental eukaryotic organisms are described, from yeast through plants, worms, flies and frogs to mammals.

Another laudable quality of this book is the standardization of the descriptions in Materials and methods. Since (almost) all articles are organized similarly, it is relatively easy to find what you want. Also, technical details have been standardized. It is a blessing to see that centrifugations are described by their *g* value rather than a non-informative rpm number. At the end of each article, there is a 'Notes' section with detailed explanation of specific technical points. For a novice it is good to be reminded that ethidium bromide is a mutagen and that lids should be loosened before putting flasks in the microwave oven. I particularly liked the description, written by the editor, of how to squash *Drosophila* larvae on a microscope slide by "standing on it with the ball of your foot or your heel. If using the foot method, place the slide (sandwiched in 3MED MER) on a hard clean floor, cover it carefully with a piece of wood, and stand on that".

My general impression is that this book keeps up the reputation of the 'Methods in Molecular Biology' series and I would recommend it for labs working with DNA repair, in particular for use by students and technicians.

Erik Boye

Handbook of Enzyme Inhibitors; Edited by H. Zollner, Wiley; Chichester, 1999. xi+2316 pp. (4 volumes). £ 340.00 (hc). ISBN 3-527-30103-8

The first edition of this manual was published in 1988 and listed more than 5000 inhibitors for about 1000 enzymes. The present edition, some 10 years on, details more than 19 000 inhibitors for 5000 enzymes and runs to four volumes. The work is divided into two parts, A and B. The two volumes under part A list the enzymes, alphabetically, with their inhibitors and the two volumes under part B list the inhibitors, alphabetically, with the enzymes they inhibit. Thus it is possible to search for an inhibitor of a particular enzyme and for the enzymes that are inhibited by a particular inhibitor. In part A, if available, the following data are incorporated in the columns: type of inhibition, the percentage inhibition or the K_i (inhibition constants as reported) or the I_{50} (the concentration needed for half-maximum inhibition) values, the source of the enzyme, and the substrate for which these parameters have been determined. In part B, for easy comparison of the effectiveness of the inhibitors, the type of inhibition and the effective concentration or K_i value is included. References to the literature are placed under each entry.

There are two glossaries. One gives the common names of the inhibitors as used in the handbook listed alphabetically together with the systematic names. In the other the EC numbers of enzymes covered, together with the recommended names, are given.

The enormous expansion of the work is attributed to the importance of the field of research. Inhibitors have substantially contributed to our understanding of metabolic processes and of enzyme mechanisms and have made possible the identification of the active sites of enzymes. Inhibitors are of great interest in the development of pharmaceuticals, pesticides and herbicides.

The enzyme names and EC numbers are as recommended by the IUBMB Nomenclature Committee as published in 1992. For the effective use of the publication it would be essential first to check the correct name of the enzyme of interest. As to inhibitors, the common names are frequently used in place of the systematic names since the latter are often long and cumbersome. The synonyms used are the ones recommended by the Merck Index. In all cases numerous references are given to the original literature. The spelling is British rather than American.

I looked up a few cases as examples. Captopril is correctly listed. It is an important antihypertensive drug, since it inhibits the angiotensin

converting enzyme which is not listed in this form because its proper name is peptidyl dipeptidase A, which is listed. Then I looked up the inhibitor, methionine sulphoximine, which I found listed as methionine sulphoxime, but I am glad to say that the reference given to its action was correct.

This handbook is a truly stupendous work and it is easy to understand why the previous editions have been such a success. It is splendid that Helmward Zollner has been able to bring it up to date and we are indebted to him for his labours.

Peter N. Campbell

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