The book starts with a short but imaginative chapter, ambitiously titled "The 'Zen' of Bacterial Pathogenicity", setting the scene for what follows, suggesting the way the subject is likely to change, and emphasizing the importance of the host. There is a chapter on relevant population genetics, and the remaining 18 chapters are divided into three sections: 'Surfaces and Colonization', 'Invasion and Intracellular Growth', and 'Toxins'. They vary in the width of their coverage: from detailed chapters on specific factors, such as iron acquisition in *E. coli* and other organisms, to more general chapters covering a whole field, for example *Salmonella* pathogenesis.

This is a book which will prove valuable to those already conversant with the outline of the subject. It deals authoritatively and interestingly with many systems not well reviewed elsewhere. Those who need it will highly value it.

S. van Heyningen

Modern Methods in Protein- and Nucleic Acid Research: Review Articles; Edited by H. Tschesche; Walter de Gruyter; Berlin, 1990; ix + 446 pages; DM 330.00

This is a rather diverse mixture of 20 articles of which the overall aim is to allow chemists and molecular biologists the opportunity to evaluate a series of methods used in protein and nucleic acid research. The variety of contributions is extensive, both in area and quality, and this detracts from its usefulness to the individual as no-one will have such a wide range of interests. A second point that identifies this volume for library purchase only is the price. I would have thought that a book containing several articles promoting methodology being commercially advertised might have been subsidised by the interested companies.

Some of the papers are simply research articles and, for example, the final article on the NMR analysis of ribonuclease T1 would have been much better had it included an explanation of the background, potential and limitations of the method. In contrast, the paper on CD spectral analysis describes not only its range of application and advantages over other methods but also gives an outline of the theory, instrumentation and applications.

It is this latter type of contribution which gives this book its value. There is an interesting article on DNA diagnostics which explains nucleic acid hybridization and the use and limitations of radioactive probes in clinical laboratories. This is followed by a consideration of several, alternative probes and here the contrast with the opening article, which considers digoxigenin-dUTP labelled probes exclusively, is significant.

There are other, specialized articles on free-flow electrophoresis, tentacle-type ion exchangers, ion-spray mass spectrometry, analysis of racemization of amino acids and the raising of antibodies to thymosins. While these areas may be of value to the specialist, they are treated in a manner which reduces their interest to the more general reader.

And yet it is difficult to be critical on these grounds as I found equally specialized articles on C-terminal sequencing of proteins and the use of spin-labelling techniques in the study of membrane proteins to be of interest. Nevertheless I feel that the best of this collection were the articles on protein crystallization and protein structure modelling which are excellent reviews that I would be happy to recommend to the graduate or even undergraduate students. Also in this category, though more specialized, were the articles on photoaffinity labelling and the erudite and comprehensive essay concerning the prediction of what might form a good epitope for generating anti-peptide antibodies.

For the molecular biologist there are valuable articles on methods of construction of oligonucleotide-directed mutations and on the problems encountered during the isolation and refolding of fusion proteins. It is a pity that these are not linked with the presentation on the construction and use of columns containing immobilized metal ions for isolation of fusion proteins with histidine tails as this is a potentially valuable technique. As it is, the latter article appears earlier in the book, distinct from the other two on a similar topic.

I would have liked to have seen more editorial input into this volume to provide a theme to tie the articles together, to correct the English and to insert Greek symbols where appropriate. Despite these criticisms, and the price, I would think this book should be on the library shelves for the half dozen or so very valuable reviews that it contains.

R.L.P. Adams

Protein Structural Analysis, Folding and Design; Edited by M. Hatano; Japan Scientific Societies Press, Tokyo/Elsevier, Amsterdam, 1990; viii + 237 pages; Dfl. 185.00, $ 97.25

The combination of site-specific mutagenesis of proteins with experimental data obtained by physico-chemical techniques, particularly X-ray crystallography, has greatly extended our understanding of the features of protein molecules that are responsible for their 3-dimensional structures, functional properties, stabilities and, above all, their exquisite

specificities. With notable exceptions, Japanese scientists have not been in the forefront of recent advances in this field. One can only guess that the principal aim of the Editor and Publishers of this book has been to bring attention to Japanese work, all but one of the 14 articles coming from Japanese laboratories. As the book has been prepared from camera-ready copy with a variety of typefaces and reference styles, one might suppose that it represented the proceedings of a conference, but there is no statement to this effect. The book is, however, typical of many conference proceedings in having little coherence and no evidence of firm editorial guidance.

There are three sections. The first, on protein structure analysis and folding, starts with chapters on conformational energy analysis and theoretical studies of protein folding. As with most of the book, these chapters make no attempt to review the current state of work in these fields. Simulations of protein vibration modes start from published X-ray coordinates, but make no comment on the precision of the starting values, the difficulties of establishing appropriate force fields or the relationship between the conclusions from the theoretical work and experimental observations by crystallography and spectroscopy. The chapter on prediction seems dated and naive. Other chapters in this section have no pattern; they include one on folding-intermediates of hen-egg lysozyme, bovine α-lactalbumin and on equine lysozyme, recently found to have a calcium-binding site like that of lactalbumin; these observations throw some light on the curious differences in folding behaviour of lysozyme and lactalbumin, two highly homologous proteins, but it is remarkable that the authors manage to avoid any reference to the work of Creighton. Other chapters are on the relationship between neurotoxin flexibility and receptor binding, on cytochrome *c* flexibility and its susceptibility to protease digestion and on the crystal structure of a plant-type ferredoxin.

The second section of the book, with chapters on subunit organization in fatty acid synthetase, on the denaturation of trans-membrane proteins and on the tendency of bovine serum albumin molecules to form clusters in a velocity gradient, is concerned with higher-order structure of protein systems.

The third section, the most coherent, covers mutation and the structural design of proteins. Three papers on haemoglobin show the value of having substantial evidence from crystallography on which to base interpretation of the effects of mutations - natural, in the case of haemoglobin M's, or synthetic. By far the most informative chapter in the book (incidentally, the only one not from a Japanese laboratory) is that on the role of the distal residues of haemoglobin on the kinetics and thermodynamics of oxygen-binding, on discrimination between O and CO and on protection from auto-oxidation.

The final chapters, on the membrane-bound eukaryotic cytochrome P450d and on tryptophan synthase, confirm the value of site-directed mutagenesis in attempting to understand functional properties, but show how much less informative such studies are in the absence of firm 3-D structural information.

The book covers much ground but often superficially, and only in the three chapters on haemoglobin is there any coherence. It is difficult to suggest its intended readership and it presents little information that is not available elsewhere.

A.C.T. North

Arachidonate Related Lipid Mediators (Methods in Enzymology, Vol. 187); Edited by R.C. Murphy and F.A. Fitzpatrick; Academic Press; San Diego, New York and London, 1990; xxxviii + 628 pages; $ 85.00

The series 'Methods in Enzymology' is now in its 35th year since its founding by Colowick and Kaplan and occupies an essential place in all serious biological science libraries. In this sense, therefore, it is rather presumptuous of me to attempt to place a value judgement on this book by means of a short review. Indeed, it is rather like being asked to review the Bible or a large telephone directory.

Perhaps I could start by saying that this volume is the second in the series dealing with the lipid metabolites of arachidonic acid (prostaglandins, thromboxanes, leukotrienes etc). The first was Methods in Enzymology Volume 86, published in 1982, and ably edited by Lands and Smith. This is now a classic reference source for research workers in the field, and was written "to provide *in one source* a detailed description of the major techniques currently available for the study of *significant* arachidonic acid metabolites" (my italics). Their objective certainly succeeded. How does the present volume compare?

Well, it is fatter (5.4 cm vs 3.8 cm) and heavier (1.4 kg vs 1.1 kg), presumably on account of the thicker acid-free paper as there are actually fewer pages (628 vs 667). This expansionist trend is underlined by the authorship: the present volume has 67 chapters by 159 authors (2.4 authors per chapter), whereas in 1982 the figures were 76 chapters by just 100 authors (1.3 authors per chapter). Of the authors, Europeans account for 23% both times - probably a fair reflection of the status of research in this area.

Statistics aside, I must congratulate everyone on this book. It is well presented and the coverage dovetails very nicely with that in the earlier volume. Thus in 1982 the emphasis was on, *inter alia*, enzyme purification and assay (surely the bedrock on which this series is founded), RIA for various arachidonate metabolites, chemical synthesis of eicosanoids, TLC and HPLC separation and GC-MS analysis. Of these topics, newer methods using GC-MS, HPLC for more recently identified metabolites are introduced, including epoxyeicosanoids, as well as areas which did not receive much attention previously, viz. phospholipase assays, receptor binding assays, platelet activating factor methodologies and cloning of various enzymes. A new and useful section comprises details of various different cell type preparations which have underpinned much valuable recent research (e.g.