

Book Reviews

Green Fluorescent Protein. Methods in Enzymology, Vol. 302; Edited by P.M. Conn, Academic Press; San Diego, 1999.
xxxii+490 pp. \$ 99.95 (hb). ISBN 0-121-82203-6

GFP, the green fluorescent protein from the jellyfish, *Aequorea victoria*, has become one of the most versatile tools in biology. This remarkable protein can be used to follow cells in organisms, and to follow proteins in cells. It can be used as a reporter in promoter studies to indicate when a gene is turned on in tissue culture, or where it is turned on in a developing organism. GFP has physical properties that can be used to measure changes in pH, or to measure the distance between molecules by fluorescence resonance energy transfer (FRET). GFP can be used in any model system from bacteria to transgenic mice. Moreover, all these developments have happened in the last 5 years, and novel uses are still being discovered. Such versatility and flexibility, combined with the rapid progress in its applications, makes assembling a comprehensive guide to GFP a somewhat daunting task. Nevertheless, volume 302 of *Methods in Enzymology* and volume 58 of *Methods in Cell Biology* are both devoted to GFP, and although neither is without faults, in my judgement the *Methods in Cell Biology* volume is the more successful effort. Both are handicapped by being compiled before some novel uses of GFP were described.

What should one require from a guide to GFP? To begin with one should have a clear description of the physical and chemical properties of GFP, and its various mutant forms, because these are fundamental to understanding how to use GFP whatever the application. The way in which the protein generates its own fluorophore – an autocyclisation event which requires oxidation – should be explained, and how this is affected by the mutations that make GFP 'brighter'. Similarly, the mutations which alter the spectral properties of GFP, and, of equal importance, the means by which these can be imaged separately, should be outlined. Regrettably, this is the primary deficiency in the *Methods in Enzymology* volume. Section IV covers some of these points, with two good chapters on spectral variants and for FRET. However, two chapters are devoted to specific mutants of GFP that are not as useful as some more recent variants, and the section lacks a good description of how to choose the correct filter sets and to perform quantitative GFP imaging. In this respect *Methods in Cell Biology* is a much better guide.

After covering the basics, chapters detailing specific applications should illustrate the range of uses for GFP. In this respect, the *Methods in Enzymology* volume covers quite a lot of ground, but there are still significant omissions. In terms of probing intracellular architecture, membrane trafficking, protein secretion, microtubules and nuclear transport are all covered. The membrane trafficking chapter is also valuable because of its discussion of live cell imaging and fluorescence recovery after photobleaching (FRAP). GFP is also proving a valuable tool to assay other intracellular processes. For example, because its fluorescence disappears when GFP is degraded, GFP is an excellent marker for proteolysis in vivo. Similarly, GFP can be used to assay changes in pH because the spectral properties of its fluorophore alter in an acidic environment. There are chapters on both these aspects of GFP. GFP can also be used as a reporter gene for promoter analysis. This can be done in tissue culture cells, where new, less stable forms of GFP should prove useful. However, there are two chapters detailing these aspects of GFP that, in my view, could have been combined in favour of another chapter on promoter analysis in transgenic animals, where GFP is likely to prove most useful. The one chapter on this deals with analysis in transgenic mice; a chapter on another model systems such as *Drosophila*, *Caenorhabditis elegans* or *Xenopus* would have been valuable.

GFP as a cell marker for transfected cells, and in flow cytometry are described, but, with the exception of marking cells to follow them during metastasis, the use of GFP as a cell lineage marker (a prominent use in developmental biology) is not mentioned. Lastly, I would have liked to see a chapter on visualising GFP in tissues. There is still considerable confusion over whether any of the methods used to fix and stain tissues preserve GFP fluorescence (some do) and a chapter detailing these procedures would have helped to clarify the issues.

In all, volume 302 of *Methods in Enzymology* has some valuable chapters but would not be my first choice of a GFP manual. It is too peripheral in some areas, and too eclectic in others; one for the library, not the lab.

J. Pines

Breast Cancer. Molecular Genetics, Pathogenesis, and Therapeutics; Edited by A.M. Bowcock, Humana Press; Totowa, 1999. xiii+582 pp. \$ 145.00 (hb). ISBN 0-896-03560-3

"Breast cancer is the leading type of cancer in women in the United States. ... The financial cost is estimated to be \$ 6 billion within the United States alone. ... Unfortunately, unraveling the causes and cures for this disease is not a simple task". These excerpts from the Preface are enough to justify a review of the field of breast cancer at any time. This particular book is eclectic rather than comprehensive and aims to provide an introduction to the genetics of breast cancer with the hope that this will form a background of ideas on which to build future breast cancer research.

The book is divided into three sections; the first, entitled 'Etiology', deals with genetic changes associated with breast cancer, the second, entitled 'Biology of Tumor Progression', deals with invasion and metastasis while the third, 'Therapeutics and Diagnostics', looks at diagnosis, therapeutics, drug resistance and environmental risk factors.

Under the heading of etiology, there are eight chapters that deal with somatic mutations in breast cancer. The first five deal with growth-associated genes, focusing on the role of the estrogen receptor, on genes of the epidermal growth factor family and their receptors, on fibroblast growth factors, on transforming growth factor- β and on the

insulin-like growth factors, respectively. Then there is a chapter on 'molecular alterations in breast cancer', of which more later, one dealing with the genes involved in the control of apoptosis and one concerned with the WNT genes associated with mouse mammary tumors induced by the mouse mammary tumor virus (MMTV). Still under the heading 'Etiology' are three further chapters that consider the genes associated with hereditary breast cancer, BRCA1 and BRCA2, the function of their protein products and the psychosocial issues surrounding testing for BRCA1 and 2.

Tumor progression and metastasis account for five chapters, considering Nm23, integrins, matrix metalloproteinases (MMPs), urokinase plasminogen and angiogenesis. These chapters are aimed essentially at a description of the biology of progression, although, where appropriate, there is a gesture towards the possible utility of these research data.

Under the umbrella title of 'Therapeutics and Diagnostics', there is a single chapter on chromosome banding, and on approaches to its diagnostic use, 'approaches' because the usefulness of this technique in breast cancer is not thus far demonstrated. The therapeutics part of the section is represented by a summary chapter of the present status

of surgery and adjuvant chemotherapy, by four chapters on more speculative treatment approaches such as antibodies against EGFR, the use of MMP inhibitors, the use of MUC1 mucin as a target for immunotherapy and the use of aromatase inhibitors in hormonal therapy, and by a chapter on drug resistance. Finally, there are two chapters on potential environmental risk factors, smoking – maybe – and environmental estrogens – probably not.

Having identified the contents, what is the book? In some ways it resembles those early satellite pictures of the planets – squares filled with immense detail, some overlapping, but with many gaps. Several of the chapters have 150–250 references, a valiant attempt to cover a topic in such detail that little can be said about each reference and the work becomes a mere catalogue of (mainly American) endeavor. A notable exception is Bergstein's chapter, referred to above, in which he makes at least an attempt to do for breast cancer what Vogelstein and Kinzler did for colorectal cancer, to try to plot a pattern of molecular changes leading to its development. In general, though, one wonders whether a better picture might be obtained by an online

search of the literature. The book has the advantage of organizing the information to some degree, but the disadvantage of being some two years out of date, a major problem given the rate at which papers are published in this field. Hence, for those chapters that appear to offer the likelihood of immediate progress, it is disconcerting to realize how far back those prospects were.

So, for whom is the book written? The chapters on the psychosocial aspects of genetic testing for BRCA1/2 and on the practice of surgery and adjuvant chemotherapy point clearly to a clinical readership as do the vain hopes, expressed at the end of each chapter, that a detailed study of state of the art molecular biology will offer a target for clinical intervention. The book does offer the opportunity for an aerial reconnaissance of subjects that one might otherwise not delve into, but anyone who wishes to feel confident of having current information will still need to follow up with a literature search and to add the necessary element of judgement.

John A. Smith

Vascular Growth Factors and Angiogenesis; Edited by L. Claesson-Welsh, Springer; Heidelberg, 1999.
189 pp. DM 198.00 (hb). ISBN 3-540-64731-7

As the Editor of this book correctly points out in the preface, the subject matter of this book is likely to be of interest to a significant number of scientists. This is due to the recognition that angiogenesis and vascular remodelling play an important role in a large number of pathological processes including cancer and some cardiovascular disorders.

The book focuses on two dissimilar but interacting families of proteins which are known to play a key role in angiogenesis and vascular remodelling, namely the VEGF and the angiopoietin families.

The book contains chapters written by some of the leading workers in the field which together summarise much of what is known about VEGF-A and the related factors PIGF and the more recently discovered VEGF-B, VEGF-C and VEGF-D. Since VEGF-A has been known the longest, there is obviously the most information concerning this factor and this is reflected by the balance of the chapters in the book. Three chapters are devoted to VEGF-A and while there is some overlap between these chapters the chapter by Dvorak et al., which discusses the permeability-inducing actions of VEGF-A, is an important reminder that angiogenesis requires more than endothelial cell growth.

The chapter by Eriksson and Alitalo which describes the structure, expression and binding properties of novel VEGFs (VEGF-B, VEGF-C and VEGF-D) is a very useful summary. It describes in a detailed manner the gene structure, proteolytic processing and relationships

between these molecules and having these data summarised in a single chapter is of considerable benefit. There are also chapters describing the receptors for the VEGF family and again, to have much of the literature summarised concerning the tissue localisation, binding properties and signalling characteristics of flt-1, KDR and flt-4 (VEGF-R1, VEGF-R2 and VEGF-R3) is very useful.

The other family of genes which is discussed in the final two chapters of the book are angiopoietins and their receptors. The discovery of these factors has re-established the important pericytes and vascular smooth muscle cells in the maintenance of endothelial cells. Since the angiopoietins and the VEGFs act in a co-ordinated fashion, it is extremely appropriate that a book entitled *Vascular Growth Factors and Angiogenesis* should include both (even though strictly speaking the angiopoietins are not growth factors). Clearly the angiopoietin field is somewhat younger than the VEGF field and as Davis and Yancopoulos state in their concluding remarks, there are many challenges which lie ahead in this emerging field.

In conclusion, this book reviews in a very readable manner the most important actions of the angiopoietins and VEGFs and describes their receptors and the consequences of receptor binding in some detail. This is an important and exciting field and this book is a very useful synthesis of the key points.

D. Stephen Charnock-Jones

2-D Proteome Analysis Protocols. Methods in Molecular Biology, Vol. 112; Edited by Andrew J. Link, Humana Press; Totowa, NJ, 1999. xvii+601 pp. \$ 59.50 (hb). ISBN 0-896-03524-7

Since 1975, when O'Farrell introduced the technique, two-dimensional gel electrophoresis has proved to be the most powerful method to solve complex mixtures of proteins from different origins. The advent of computerized analysis of the gels and the high sensitivity of the methods currently used to identify the resolved polypeptides has enabled the appearance of proteomics, one of the most exciting fields in molecular biology. This is evidenced by the rapid growth in the number of proteomes published, a number that undoubtedly will greatly increase during the next years. In this context, volume 112 of the series 'Methods in Molecular Biology' has appeared entitled '2-D Proteome Analysis Protocols' consisting of 55 chapters written by 78 experts in the field and users of the techniques described. The general outline of the chapters is as usual in this series: each consists of a brief introduction to the particular topic, and a detailed enumeration of all the equipment and reagents needed to perform the experiments followed by the precise description of the protocols. A consid-

erable number of notes where the authors comment on pitfalls and give a multitude of practical hints and a list of references are always included in every chapter.

The opening chapter starts with a brief general presentation of the 2-D protein gel electrophoresis technique followed by an interesting review concerning the solubilization of proteins. Then comes a series of 11 chapters with the aim of providing a general view of the problem of sample preparation in 2-D gel electrophoresis. In this way, *Escherichia coli* (chapter 3), yeast (chapter 4), *Drosophila* (chapter 5) and *Caenorhabditis* (chapter 6) have been the biological systems selected. Eukaryotic cell labeling (chapter 7) is also described followed by two chapters in which differential detergent fractionation (chapter 8) and fractionated extraction of total tissue proteins by centrifugation (chapter 9) are considered in order to increase the number of detected proteins in the gels. Sample preparation and solubilization of some body fluids and a brief chapter on 2-D electrophoresis of

plants come next. The following two chapters consider the problem of the quantification of samples, both in the case of presence of solubilization buffers and in the case of radioactive samples.

Then comes one of the 'cores' of the book, a group of chapters, (chapters 14–28) in which the multiple methodological and technical aspects of 2-D electrophoresis are extensively documented. A brief description of ampholytes (chapter 14) comes before two chapters of unequal extension in which IEF (chapter 15) and NEPHGE (chapter 16) gels are analyzed. Both chapters analyze general aspects of sample and solution preparations as well as the technical details and the equipment needed to run gels. Then, the use of immobilized pH gradients is considered. Two chapters (chapters 19 and 20) give details concerning its advantages with a correct technical description. The use of immobilines with analytical criteria (chapter 21) and the analysis of very basic proteins (chapter 22) are considered next. Other interesting topics such as preparative 2-D electrophoresis (chapter 23), use of minigels (chapter 24), horizontal SDS-PAGE with immobilines (chapter 25), non-reducing 2-D gels (chapter 27), or 2-D diagonal gel electrophoresis (chapter 28) are equally presented. The various procedures are, in general, well described, but the multi-author modality has resulted in some overlap and redundancy between chapters with descriptions nearly identical (preparation of solutions, samples, cell labelling, etc.) and different authors giving different recommendations for solving the same problems (the time required for the equilibration of the gels, for example). Also, the quality of the gels presented in some of the chapters is far from optimal.

Ten new chapters deal with different detection systems of polypeptides resolved by 2-D gels. Phosphopeptide mapping (chapter 29), autoradiography and fluorography (chapter 31), double-label analysis (chapter 32), detection of non-radioactive samples (chapter 33), reversible metal chelate stain (chapter 37) and the specific detection of glycoproteins (chapter 38) are some of the topics considered, correctly but in a similar way to their treatment in other handbooks available. Two very clear chapters analyze the different modalities of electroblotting describing equally the methods for detecting proteins in this technique.

Then comes a series of chapters which constitute, in its entirety, probably the most original and interesting part of the book: those in which the computer appears on the scene. An introduction to the different modalities of image acquisition technology (chapter 39) gives way to the computer analysis of 2-D images (chapter 40) describing in detail how the Melanie II software for Apple power Macintosh oper-

ates. The description of other systems available (such as PDQUEST) could probably also be included in this book. Chapter 42 confronts one of the most interesting aspects, the problem of comparing 2-D gels across Internet databases. Although the problem is not absolutely solved, Java now gives us the ability to do real-time comparisons of local 2-D gel image data with gel images residing in various remote databases on the Internet. In this way, chapter 41 shows precisely how to retrieve data from the databases over the Internet and chapter 43 demonstrates how to prepare the files necessary to build a federated 2-D database in order to make it available on your own WWW server.

The last group of chapters describe methods to identify proteins in order to create an inventory of the protein products in a database. In this way, the more classic methods for the identification including comigration (chapter 45), immunoaffinity (chapter 46), analysis of amino acids with 9-fluorenylmethyl chloroformate (chapter 47), N-terminal amino acid sequencing (chapter 48) or the internal sequence analysis (chapter 49) of 2-D spots are considered first. Again, some aspects are repetitive with respect to preceding chapters.

Methods for the identification of proteins have advanced dramatically in this decade through the introduction of mass spectrometric techniques and instrumentation sensitive enough to be applicable to biological systems. The two mass spectrometric techniques that have provided these advantages are electrospray ionization mass spectrometry (ESI-MS) and matrix-assisted laser desorption/ionization mass spectrometry (MALDI-MS). In the very interesting final part of the book a group of chapters describe precisely the state of the art. In this way we can learn, for example, how to link gel electrophoresis directly to MALDI-MS, yielding masses of both intact proteins and cleavage products without electroelution or electroblotting, or the techniques for sample preparation and mass spectrometric analysis of gel isolated proteins that enable its identification by MALDI-MS, or by using LC-MS-MS.

In summary, the book covers most practical proteomics aspects, is well documented and clearly written in most of the chapters being recommended for researches in the field. This collection of protocols is an invaluable starting point for people embarking on attempts to develop new proteomes, and is moreover a good source for compilation of references.

Juan F. Santarén

D-Amino Acids in Sequences of Secreted Peptides of Multicellular Organisms; Edited by P. Jollès, Birkhäuser Verlag; Basel, 1998. viii+192 pp. DM 198.00 (hb). ISBN 3-7643-5814-9

Molecular asymmetry was recognized by Pasteur and Fischer a long time ago as essential for life and biological processes. Although proteins in living organisms are exclusively constituted of amino acids of the L configuration, the existence of gene-encoded peptides containing D-amino acids in invertebrates and vertebrates is extremely exciting and intriguing. It has been known for many years that antibiotic peptides (e.g. gramicidin, tyrocidin, etc.) produced by certain microorganisms contain D-amino acids. The biosynthesis of these molecules does not involve a ribosomal pathway but is catalyzed by multienzyme complexes. In contrast, lantibiotics, which are produced by Gram-positive bacteria, are derived from larger precursor molecules assembled on ribosomes. These molecules which contain D-amino acids in the form of a lanthionine ring structure are synthesized via a complex series of posttranslational modifications. A completely new era started in 1981 with the discovery of dermorphin, the first eukaryotic peptide containing a D-amino acid at a specific position in the sequence. Cloning cDNA encoding larger precursors provided compelling evidence for a new type of posttranslational modification, namely amino acid isomerization. Since then, D-amino acid have been identified in an increasing number of peptides from various species (frog, snails, spiders, clams, etc.). This book summarizes our current knowledge concerning the occurrence, function and biosynthesis of D-amino acid-containing peptides in multicellular organisms.

The book contains 10 chapters written by internationally recognized experts. The chapters are grouped into six main sections. In

section one, Scaloni et al. briefly recall separation methods available for the analysis of D-amino acids with special emphasis on automation and determination of chirality in the course of sequence analysis. Since amino acid isomerization is a subtle modification that cannot be detected by routine Edman sequencing, the occurrence of D-amino acid-containing peptides can be easily overlooked or underestimated. Hence there is a need for efficient analytical techniques to detect D-amino acids within peptides.

The second section, the largest of the book (four chapters) is devoted to the occurrence and function of D-amino acid-containing peptides and proteins. The first chapter of this section by Mignogna et al. deals with antimicrobial peptides found in skin secretions of frogs belonging to the genus *Bombina*. Some of these peptides were found to contain a D-alloisoleucine or a D-leucine in the second position. A number of D-amino acid containing neuropeptides including achatin-I, fulcin, fulyal, *Mytilus* FFRFamide and *Helix* CCAP-RP-III have been isolated from invertebrates. The chapter by Yasuda-Kamatani focuses on purification, structural determination, biological activities, precursor protein and localization of these peptides having D-amino acids at position 2. The X-ray crystal structures of achatin-I (D-Phe in position 2) and achatin-II (L-Phe in position 2) clearly demonstrate the increased structural diversity achievable via the introduction of D-amino acids. Opioid peptides isolated from the skin of South American frogs *Phyllomedusa* (i.e. dermorphin, dermenkephalin and deltorphins) are reviewed by Amiche et al. The authors discuss the molec-

ular mechanisms for the high selectivity of these peptides for the μ - and δ -opioid receptors in light of NMR conformational analysis. The extensive similarities between prepro regions of precursors encoding these peptides, dermaseptins and other peptides with different structure and biological activity from various amphibian species are also discussed. The authors suggest that the genes encoding these peptides are all members of the same family. The last chapter of this section by Huberman and Aguilar deals with crustacean hyperglycemic hormones. In the third section and based on their own work, Volkmann and Heck propose an attractive mechanism of action for *Agelenopsis aperta* isomerase, a novel cofactor-independent serine isomerase. Although this protein, which shares high homology with known serine proteases, is the only isomerase discovered so far, it is likely to provide important clues to explain the incorporation of single D-amino acid residues within a peptide chain. The introduction of this chapter overlaps somewhat with the previous section. Nevertheless, these two sections represent a good overview of D-amino acid-containing peptides found in a variety of animal species. As suggested by Amiche et al., the obvious question whether such peptides might exist in mammals is still left unresolved.

The following section deals with the appearance of D-amino acids during ageing. Since the original hypothesis of Kögl and Erxleben in 1940, the question of the presence of D-amino acids in tumors has remained controversial. In his chapter, G.H. Fisher relates the story of this controversy and summarizes recent data that suggest that

D-amino acids are absent in tumors. In the second chapter of this section, Ingrosso and Perna review the phenomenon of spontaneous postbiosynthetic modifications in ageing erythrocytes, also termed 'protein fatigue', which includes the formation of isomerized and/or racemized aspartyl residues. They discuss in detail the role of protein L-isoaspartyl (D-aspartyl) O-methyltransferase in the repair of ageing protein. The next brief chapter by Yamada and Kera is devoted to the proteolytic susceptibility of D-amino acid-containing peptides and D-amino acid-hydrolyzing enzymes.

The final section by Bonner comes back to homochirality and life. Why are L-amino acids present in proteins and D-sugars in nucleic acids? The author reviews in detail the various hypotheses compatible with a realistic prebiotic environment that have been proposed to account for the origin of homochirality on earth.

Although the search for novel D-amino acid-containing peptides in higher organisms and the understanding of their biosynthesis is an extremely exciting and rapidly expanding field, the literature reviewed in several chapters of this book, unfortunately, covers very few publications after 1996. Nevertheless, this book provides the reader with a large and comprehensive overview of the knowledge gained in the field of D-amino acids and D-amino acid-containing peptide in multicellular organisms.

G. Guichard

Lysozymes: Model Enzymes in Biochemistry; Edited by P. Jollès, Birkhäuser; Basel, 1996. viii+449 pp. DM 238.00 (hb). ISBN 3-764-35121-7

Reading this book, we again recognize how the technologies of protein science continue to develop through research of lysozyme as a model protein. Is there any other protein that has been investigated as extensively over as wide a range of research fields? The fields that use lysozyme are quite diverse, including evolution, chemistry, biology, biophysics and pharmacology, which are covered in 22 chapters contributed by 25 authors. Although there are several books describing a particular protein, *Lysozymes: Model Enzymes in Biochemistry and Biology* is one of the best documented books ever written by top senior researchers in the respective fields.

There are several aspects to describe lysozyme as a model protein. Topics are carefully chosen according to the key words 'Biochemistry and Biology'. One of the unique points of lysozyme is the existence of this enzyme in several species ranging from phage to mammal. The book starts by reviewing vertebrate lysozymes and then expands to the phage, bacterial, plant and insect lysozymes sufficiently to make researcher acquire an overall knowledge of these lysozymes. There are also two reviews of evolution of C-type lysozyme, enabling us to see how the function of this enzyme diverged to adapt to the surroundings from an evolutionary point of view.

This book also reminds us how X-ray crystallography has contributed to the development of the protein science field. In fact, lysozyme is one of the earliest enzymes in which the tertiary structure was determined by X-ray crystallography. The availability of the tertiary structure information was the most important factor in the study of lysozyme enzymology, protein folding, and thermal stability. In fact, many important investigations on the catalytic mechanism have been

done based on this structural information. The book summarizes how chemical modification and genetic engineering were employed to identify the role of catalytic site residues, which were interpreted by tertiary structural information using X-ray crystallography. The book also reviews how theoretical calculation using molecular dynamics simulation was first applied to understand the catalytic mechanism of an enzyme, which is one of the unique applications of the structural information of lysozyme.

From the point of view of molecular recognition, the application of X-ray crystallography to investigate the binding of lysozyme with antigen binding fragment is quite noteworthy. Two reviews cover the kinetic and thermodynamic character of the binding of lysozyme and antigen binding fragment and the determination of the epitope of lysozyme by X-ray crystallography. I believe the structural determination and thermal stability of lysozyme should have been covered in greater detail.

Very recently, lysozymes were found to possess antiviral activity against HIV, reminding us of the importance of the constant study of a protein. Conversion of the catalytic mechanism has been successful in lysozymes. Although these topics should be added in the near future, these important findings also indicate that research on lysozymes is still very active. Using lysozyme as a model protein, this book is a valuable tool in providing an overall understanding of the key techniques of protein research.

Ryota Kuroki

Biocalorimetry: Applications of Calorimetry in the Biological Sciences; Edited by John E. Ladbury and Babur Z. Chowdhry, Wiley; Chichester, 1998. xiii+345 pp. £ 70.00 (hb). ISBN 0-471-97781-0

Biocalorimetry: Applications of Calorimetry in the Biological Sciences is intended to fill a void in biochemical/biological publishing. Although texts about calorimetry are common, books devoted to biological applications of calorimetry are almost non-existent. The most recent text, A.E. Beezer's *Biological Microcalorimetry* (Academic Press, London, 1980), is out of print and may be difficult to locate even in a university library. Some general biochemistry-oriented texts

may include brief sections about calorimetry, but in general, anyone wanting information about the subject has to rely on papers and reviews. This reviewer was thus excited to find theory and practice for differential scanning calorimetry (DSC), isothermal titration calorimetry (ITC), and microphysiometry united in one volume. While serviceable, the reality did not quite measure up to expectations. This new text is too detailed for a biocalorimetry novice,

but the short chapters may not provide enough information for experts.

This book, a collection of papers presented at the 1996 conference at St. Anne's College in Oxford, UK, is logically divided into sections on ITC and DSC; each section is further subdivided into chapters. This organization allows the reader to read the text from cover to cover, or to dip into sections of interest. Every section begins with two chapters of introduction and theory, then moves onto applications of the techniques. Either by accident or by design, the two theory chapters may be separated into one of rigorous detail and another of general interest. The section on DSC also includes two chapters on instrumentation. The chapters on experimental applications of DSC and ITC cover a wide range of topics, from analyses of DNA-drug and protein-ligand interactions to synthetic polymers. With so many examples of applications of biocalorimetry, the reader has a good chance of finding mention of a topic of interest.

This book's shortcomings are those of many collections of edited papers. There is a definite lack of cohesion and continuity, an abrupt change in style from chapter to chapter. This unevenness is especially apparent in the use of units and definitions. The authors state in the Preface that they decided to allow authors to present their work using the system of units adopted by their individual countries. Conversion from joules to calories, and dm^3 to liters, can be distracting and takes the reader's attention away from the text. Different authors use different definitions and conventions in describing their subjects. For example, variables and definitions are included in Chapter 1, an introduction to ITC written by Blandamer, that are not only never encountered again in this text, but are seldom seen in any of the

literature on ITC. These definitions may be useful in giving a full theoretical treatment, but can be confusing to the thermodynamics or calorimetry novice.

Another shortcoming is the wide variation in the quality of the chapters. Most chapters are clearly taken from longer works and do not function well as stand-alone entities; the original paper (or papers) is needed for even a cursory understanding. A chapter that included simple experimental examples would have been helpful. Most of the individual chapters deal with complex interactions and/or involved analyses, particularly in the DSC section, in which most of the experiments include irreversible thermodynamics. For this reason, many of the conclusions were either preliminary or largely theoretical. Such cutting-edge results are interesting to experts (who would be better served by reading the original papers), but their complexity limits this book's use as a biocalorimetry primer. With these problems, well-written chapters really stand out. Particularly noteworthy sections include the introduction to the ITC of biomolecules by Tame, O'Brien, and Ladbury (Chapter 2), the treatment of the folding energetics of heterodimeric leucine zippers by Jelesarov and Bosshard (Chapter 8), and the introduction to DSC by Leharne and Chowdhry (Chapter 12).

The final verdict? If detailed information on biocalorimetry is desired, this book cannot replace the excellent reviews and papers already in the literature. If the reader desires a one-book source for biocalorimetry theory and practice, this volume adequately fills a void in the biological calorimetry literature.

Kimberly M. Taylor and Ronald T. Raines

Trinucleotide Diseases and Instability; Edited by B.A. Oostra, Springer; Berlin, 1998. ix+169 pp. DM 168.00 (hb). ISBN 3-540-63993-4

Interest in the field of trinucleotide diseases has rapidly increased. Since 1991, more than a dozen human genetic diseases have been demonstrated to be caused by unstable expansion of trinucleotide repeats.

The editorial introduction to this book promises to present highlights both of the mechanisms of repeat instability in these diseases and of the functions of normal and mutated genes involved.

The book contains 24 chapters by nine authors, covering four main topics. Under the first one (six chapters, 46 pages) the fragile X syndrome and other fragile site disorders are discussed. The second part (eight chapters, 30 pages) is dedicated to Huntington's disease. The other CAG repeat diseases are confined to one chapter of this part. Myotonic dystrophy is the content of the third one (six chapters, 56 pages). The last topic (four chapters, 33 pages) concerns a general overview of factors and mechanisms involved in the instabilities of triplet repeats. For each disease, clinical features, genetics and transmission, gene structure and expression, and mechanism of pathogenesis are presented. There are 692 references up to 1997. Each chapter is illustrated with diagrams, graphs, tables and photographs.

Unfortunately, the rapid growth of the knowledge in this field renders it very difficult to give up-to-date information without the risk of missing important topics. This is the case with the pathogenesis of the CAG repeat diseases. Intranuclear inclusions are now clearly observed in almost all polyglutamine disorders. Even though it remains uncertain whether these aggregates are a cause or a consequence of pathogenesis, they are considered hallmarks in these processes. No mention of aggregates in these diseases is present in the book, perhaps because they were first described in 1997.

Another weakness is the lack of a specific presentation for Friedreich's ataxia. This trinucleotide disease is cited several times, but never described in detail. Since the molecular basis of the disorder has been described in 1996, the omission of this topic is surprising.

In summary, the book could be helpful as an introduction but other sources are needed for more extensive treatment and updated references.

Sergio Cocozza

Book list No. 152

1. Rettig, W. et al. (eds.) *Applied Fluorescence in Chemistry, Biology and Medicine*. Springer; Heidelberg, 1999. xix+562 pp. DM 249.00 (hb).
2. Brown, T.A. (ed.) *Genomes*. Bios Scientific Publishers Ltd; Oxford, 1999. xxviii+472 pp. £ 29.95 (pb).
3. Hickman, J.A. and Dive, C. (eds.) *Apoptosis and Cancer Chemotherapy*. Humana Press; Totowa, 1999. xv+342 pp. \$ 99.50 (hb).
4. Henderson, B. et al. (eds.) *Cellular Microbiology. Bacteria-Host Interactions in Health and Disease*. Wiley; Chichester, 1999. xxv+452 pp. £ 29.25 (pb).
5. Gelb, M.H. (ed.) *Protein Lipidation Protocols*. Humana Press; Totowa, 1999. x+240 pp. \$ 89.50 (hb).
6. Reedijk, J. and Bouwman, E. (eds.) *Bioinorganic Catalysis. Second Edition, Revised and Expanded*. Marcel Dekker, Inc.; New York, 1999. xv+606 pp. \$ 225.00 (hb).
7. Dejana, E. and Corada, M. (eds.) *Adhesion Protein Protocols. Methods in Molecular Biology, Vol. 96*. Humana Press; Totowa, 1999. xi+229 pp. \$ 69.50 (hb).
8. Sterchi, E.E. and Stöcker, W. (eds.) *Proteolytic Enzymes. Tools and Targets*. Springer; Heidelberg, 1999. ix+366 pp. DM 129.00 (pb).
9. Famulok, M. et al. (eds.) *Combinatorial Chemistry in Biology*. Springer; Heidelberg, 1999. vi+189 pp. DM 198.00 (hb).
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