Quantitation of mRNA by Polymerase Chain Reaction. Nonradioactive PCR Methods; Edited by Th. Kohler, D. Lasner, A.-K. Rost, B. Thamm, B. Pustowoit and H. Remke, Springer; Berlin–Heidelberg, 1995. xx + 165 pp. DM 68.00 (pb). ISBN 3-540-59192-3

Although the sensitivity of PCR has rendered it the method of choice in the detection of small amounts of nucleic acid targets, its utility as a quantitative tool has been slower to gain credit. The ability of PCR to make rare sequences detectable, however, makes it extremely challenging to extrapolate the amounts of initial input template molecules from the measured amounts of product molecules after many cycles of amplification. In the past few years a number of PCR strategies based on different methodological and technical approaches have been adopted for the semiquantitative or quantitative analysis of nucleic acids. Despite the development of a variety of procedures, quantitation of RT-PCR products remain difficult.

This text is an excellent comprehensive compilation of current methods for quantitation of messenger RNA. Each section of the book contains a descriptive part with one or a few illustrative figures followed by the corresponding protocols. The handbook may well serve as a laboratory manual with inspiration for both novice an experienced users. It gives the reader an overview of the most used methods together with technical hints and troubleshooting including information about possible pitfalls associated with some of these methods.

The first part of this handbook presents a short concise introduction to the general aspects of PCR, the design of PCR primers and competitor fragments to be used as internal/external standards in the assays and the use of non-isotopic labels. The contexts of the sections are presented with illustrative figures.

The second part describe both the theoretical and practical aspects of different conventional techniques for mRNA analysis. For that purpose different protocols for e.g. RNA isolation and cDNA synthesis are presented together with methods used for qualitative mRNA analysis (RT-PCR, single-tube RT-PCR) as well as methods using non-radioactive labels for detection of amplified PCR products. However, this second part could have benefitted from a brief introduction to RNase inhibitors to give the reader an opportunity for further improvement of RNA handling, isolation and reverse transcription.

The last part of the handbook concerns the quantitative analysis of mRNAs. Most PCR applications for examining gene expression can be divided into two categories, competitive and non-competitive. The described protocols for mRNA quantitation cover to a large extent the range of methods that so far have been published within this area, although this part of the book suffers from an almost complete lack of protocols for statistical validation of quantitation assays.

This handbook covers the methods used for mRNA quantitation nicely, but some experience with the techniques may be necessary to successfully achieve the goal of setting up quantitative mRNA analysis. It would therefore have been appropriate if the authors had spent a few more words discussing advantages and disadvantages of the different methods presented. Altogether this is a timely and good laboratory handbook, which covers one of the most challenging fields in molecular biology.

Niels Rüdiger

Mass Spectrometry in the Biological Sciences; Edited by A.L. Burlinghame and S.A. Carr, Humana Press; Totowa, NJ, 1995. xii + 570 pp. US$ 145.00 (hb). ISBN 0-89603-340-6

This book consists of 26 individual papers presented at the third symposium on Mass Spectrometry in the Biological Sciences by some of the leading research groups using mass spectrometry. Mass spectrometry has in recent years developed into an important tool for structural characterization of biopolymers due to the high sensitivity, speed of analysis and the quality of the structural information obtained. The book gives a detailed insight into the use of mass spectrometry (MS) for a wide array of problems in protein chemistry, immunology, glycobiology as well as studies of human pathogens, lipids, and nucleic acids.

In the first chapters the principles and future developments of time-of-flight MS and Fourier-transform MS are discussed. The next two chapters demonstrate the use of electrospray MS for elucidation of protein folding and molecular interactions. Then follows a series of very exciting chapters dealing with strategies and various approaches for microcharacterization of proteins and peptides. This includes analysis and identification of proteins separated by gel electrophoresis, partial peptide sequencing by MS/MS or by chemical and enzymatic methods, miniaturization of sample handling techniques as well as approaches to optimize the overall sensitivity. The next four chapters concern characterization of protein modifications such as glycosylation, phosphorylation, and deamidation. Then follow several chapters illustrating other applications of MS, including analysis of lipooligosaccharides, phospholipids, pharmacokinetics and quantification of drugs and metabolites. The last two chapters concern the prospects and use of MS for sequencing and characterization of oligonucleotides. In addition, the book contains eleven excellent appendices with structures and molecular masses of common residues and modifications as well as thorough explanations of common terms used in MS.

The book can be read by biochemists without experience in mass spectrometry as well as by experienced mass spectrometrists who want to keep up to date in the field. The general impression of the book is that it gives the reader a good survey of the current status of mass spectrometry as well as of potential applications and future developments. As such, the book can be a helpful source of knowledge and inspiration for scientists interested in mass spectrometry at the pre-and post-graduate levels.

Ejvind Mørtz

Molecular Biology. Current Innovations and Future Trends. Part 2; Edited by A.M. Griffin and H.G. Griffin, Horizon Scientific Press; Norfolk, 1995. 176 pp. £19.99 (pb). ISBN 1 898486 03 4

The number of technologies from which our knowledge of molecular biology stems is growing increasingly large and it must be difficult for scientists coming into the field, and indeed for practising molecular biologists, to keep abreast of current advances. This series of books, of which this volume is the second, attempts to address this by offering a variety of articles covering a number of new aspects thus hoping to keep scientists informed of recent innovations in both the theory and practice of molecular biology techniques.

This slim volume is divided into ten chapters. The first of these deals with various aspects of automated DNA sequencing, whilst high sensitivity protein sequence analysis is dealt with in the second. Chapter three deals with the introduction of DNA into prokaryotic and eukaryotic cells using electroporation techniques. Chapter four covers non-radioactive labelling and detection methods and the fifth chapter deals with PNA (peptide nucleic acids). Chapter six is concerned with magnetic bead technology and the following chapter deals with antisense technology and ribozymes (not ribosomes as the title is given in the contents and page headings). Phylogenetic tree analysis, nucleic acid analysis by HPLC, and protein analysis by NMR are described in chapters eight, nine and ten, respectively. Whilst some of these are not

strictly new topics in the true sense, since they may have been used for a number of years, they do provide a good starting point for those who want to commence any of these techniques.

Each article provides a review covering the theory and applications of the topic. In general the reviews are well written with good informative introductions. This is followed, in most cases, by useful methodology sections. Where these are given they are generally clear and explicit providing a step by step guide for the various techniques with the chapters on non-radioactive labelling and detection and peptide nucleic acid providing good examples of this. As would be expected in some chapters this section does not include detailed protocols for all the given applications and it is understandable that in a volume of this size that everything could not be included. However, all chapters are followed by a useful reference section that would point the reader in the desired direction for any given application.

In general I found this book interesting and to a large extent I thought that it fulfilled the aims that were specified for the series, at least for the majority of the techniques included in it. However, it is worthwhile to note that in most chapters the latest reference given is from 1994. Therefore the reader may need to consult further references to be completely abreast of further advances in these techniques. Nevertheless the text does provide a good helpful source for familiarisation with these topics.

Elizabeth M. Hoey

Bioinformatics: From Nucleic Acids and Proteins to Cell Metabolism; Edited by D. Schomburg and U. Lessel, VCH; Weinheim-New York, 1995. viii + 195 pp. DM 148.00 (hb). ISBN 3-527-30072-4

This book contains 14 articles on different aspects of bioinformatics, i.e. the application of computer science to biological problems. The different articles cover various aspects of bioinformatics. The articles are written as scientific publications, i.e. they are not review articles. The chapters covers the fields specified in the title: 'From Nucleic Acids and Proteins to Cell Metabolism'. They are divided into four different areas, 'Biological Databases' (one article), 'DNA and RNA' (four articles), 'Protein Sequences and Structures' (five articles) and 'From Molecules to Cell Metabolism' (four articles).

In the 'Biological Databases' section is described how a set of isolated databases can be integrated and accessed through a common interface. In the 'DNA and RNA' section different aspects of sequence analysis are discussed as well as one paper about folding landscape of RNA. These papers give some good examples of how sequence information can be used to understand how DNA has evolved. The 'Protein Sequences and Structures' section can be divided into two parts. The first three papers describes methods that can be used to identify a protein fold given its sequence. The last two papers describes two different methods for docking a ligand to a protein. The last section of the book, 'From Molecules to Cell Metabolism', contains papers that did not fit into the other sections of the book. The first paper describes a novel method to speed up the force field minimization of a macromolecule. The second paper describes a new method to compare molecular structures. The last two papers describe fluxes of substances in either micro-organisms or intra-cellular.

It is clear that most of the articles are written by computer scientists for other computer scientists as the book is too technical for biologists/chemists. However, I doubt that the book contains enough unpublished new material to be worth buying for a computer scientist in the field. For a computer scientist outside the bioinformatics field this book could be a good overview of different aspects of bioinformatics.

It can be noted that neural networks (NN) are used in three of the papers. This shows that NN has become a standard tool to solve complex problems in bioinformatics. Further, several of the papers describe how algorithms have been implemented on massively parallel computers, showing how important these computers have become.

A few considerations come to mind when reading this book. (1) Why does the book contain three articles in German? It makes these three articles completely inaccessible for the majority of the scientists in the world. (2) Reading this book you really understand the valuable work that is done by the publishing companies. Several of these articles would be much easier to read if they were formatted and not just plain manuscripts. At least it would have been nice if a similar format for references had been used throughout the book. (3) In several of the papers it seems as if the authors are more interested in the techniques, i.e. the computer science, than in the answers it can give, i.e. the biology. This makes the book less attractive for a general audience.

Arne Elofsson

Molecular Biology and Biotechnology. A Comprehensive Desk Reference; Edited by R.A. Meyers, VCH; Weinheim-New York. 1995. xxxviii + 1034 pp. DM 89.00 (pb). ISBN 1-56081-569-8

This book is a unique and valuable desk reference book of very high quality that can be recommended as a handbook in all molecular biology laboratories and libraries.

The book, which has numerous authors from the fields of molecular biology, molecular genetics, and medicine, has on its editorial board sixteen distinguished scientists of whom eight are Nobel Prize laureates. The authors, the Editorial Board and the Editor have performed an excellent job in providing a professional-level reference book that covers the molecular basis of life and the application of such knowledge in genetics, medicine and agriculture.

In contrast to other books covering similar topics this book is ordered alphabetically. This makes it an untraditional but valuable reference work. It is therefore useful that the Editor has provided a paragraph on how to use the book.

There are more than 250 articles in the 1034 page book. They cover the major areas of molecular biology and biotechnology: genetics and nucleic acid structure and processes; human genome project; molecular biology of specific organ systems and specific diseases; biotechnology techniques, applications and products; immunology and bimolecular interaction; relationships of molecular biology to pharmacology and biochemistry.

The articles fall into three categories: (1) core articles that provide a perspective on major topics (e.g. cancer); (2) satellite core articles that give a perspective on particularly active and important areas (e.g. oncogenes); (3) specific subject articles (e.g. colon cancer).

Each article is a self-contained unit. It begins with a keyword section, including definitions. This is followed by a short introduction, sections describing the different topics, and finally a section covering summary, future perspectives, an elaborate list of cross-reference keywords and a short list of relevant references. At the end of the book a list of more than 1600 keywords that are defined within the context of a given article is included. Also included is a list of the 40 most commonly used terms in molecular biology.

The book is well written and well illustrated with over 500 figures and 120 tables. Even though 378 scientists have contributed to the writing, the book has a uniform appearance. The core articles cover the subjects in a surprisingly detailed manner considering the limited amount of space available for each topic. With the included list of keywords at the end of each article and the reference list it is easy to find additional reading. The authors, Editorial Board and not least the Editor thus have succeeded in covering the very broad areas that they intended: the