

Book Reviews

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Proteins and Proteomics: A Laboratory Manual.

R. J. SIMPSON. Cold Spring Harbor Laboratory Press. 2003. 926 pages. ISBN 0 87969 554 4. Price £129. (paperback). ISBN 0 87969 553 6. Price £185. (hardback).

The Cold Spring Harbor Press lab manual on “Proteins and Proteomics” is a highly impressive, comprehensive text. The book is very clearly written and covers all aspects of the science of protein chemistry and proteomics, including bioinformatics; protein and peptide sequence analysis; electrophoretic techniques including 2D gels and software algorithms for comparative analysis. It also includes extensive coverage of the techniques employed for preparation of (sub)cellular extracts and protein and peptide purification methods such as HPLC. The wide range of other separation techniques available, such as ion-exchange chromatography (which would fill a volume in itself) is only described for specific applications such as sample preparation for mass spectrometry and mapping of phosphorylation sites, otherwise it would have been somewhat out of the focus of the manual. The volume comprehensively covers the background, the importance of this relatively new science and illustrates all the bang up to date techniques one is likely to require.

The excellent introduction covers all aspects of the subject of protein analysis today, including protein arrays. This sets the scene for why proteomics is so essential to fully elucidate the function of proteins. The rapid development and increasing importance of “proteomics” as an independent field of study is also well elucidated, placing it as a key aspect of the “post genomic” era. There is also an excellent introduction and coverage of the growing field of Bioinformatics for protein comparisons, functional and structural predictions and comparisons. This includes homology searches and computer methodologies to link proteins functionally to particular metabolic and signalling pathways. Mass spectrometric identification of post-translational modifications is extensively covered, quite rightly with a particular focus on phosphorylation site analysis (or dare I say it, investigation of

the “phosphoproteome” or “phosphorylome”). Methods for studying protein interactions are included, which now brings us to another new “omic” science, the “interactome”. The “predictome” is also mentioned. Other topics include protein-DNA as well as protein–protein interactions and analysis of protein topology (the sites that interact) is also covered. The techniques are clearly laid out in a way that is easy to follow (and repeat in one’s own lab).

As well as covering all the essential fundamentals of protein studies, such as electrophoresis (with critical evaluation of all the commonly used staining techniques); HPLC and other separation techniques, the volume moves on to state-of-the art mass spectrometry techniques and includes a good section on protocols for preparing and printing protein arrays. Another innovative approach in this Manual that I particularly like is the fact that all relevant methods and overviews of specific topics are closely linked with the extensive Web resources that are now available. This enables the reader to readily delve into a topic in much greater depth than could be covered even in this large manual.

Mass spectrometry includes tandem (MS-MS) methods for obtaining at least partial fragmentation or sequence in order that a protein may be identified from just one peptide (invaluable if one has a complex protein mixture for example). All these techniques are comprehensively covered along with the comparative multidimensional electrophoretic techniques at the heart of proteomics.

Extensive reference tables include physical unit conversion tables; buffers and pKa and other properties; a short table of some major post-translational modifications of amino acids; non-gene encoded amino acids, their masses and properties. There is also something that will make life a lot easier and save much head scratching – a microgram to picomole conversion guide for proteins over the common range of molecular weights. Some of these listings are fairly routine but what is most valuable is to have everything under one cover in a very comprehensive tome. There are also some highly valuable and hard to find data that comprehensively cover lists of the

limits of common reagents, buffers and detergents that interfere with protein assay methods. Many of the techniques include “case studies” i.e. examples of the use of the procedures illustrating the scope and value of these protocols.

This is much more than a “lab manual” and it isn’t a spiral bound techniques handbook that would be easily ported around to sit on one’s bench top – perhaps an edition of the practical techniques alone could be published that would be invaluable for the graduate student, postdoc or senior staff attempting to follow a new method. Much of the subject matter is also now being introduced into the undergraduate curriculum.

Is there anything missing? – not a lot of major consequence but inevitably a few minor things such as protein splicing to form an intein and the mature extein protein. Someone might wish for a more comprehensive coverage of all proteases, the conditions under which they are used and their specificities. However, in the field of “proteomics” trypsin is the enzyme of choice. There is a table listing the proteases and brief conditions of use – which is certainly more than adequate and the inclusion of the commercial sources of these proteases is highly welcomed. Chemical modifications and chemical cleavage methods are also well covered. The emerging field of direct mass spectrometric identification of large protein complexes and surfaces of interaction is not fully addressed but this does require spectrometers that are installed in highly specialised research groups and may not be available even in a large mass spectrometry centre. Although there is an invaluable “bioinformatics” section that includes comprehensive coverage of structural comparisons by database algorithms, protein structure determination itself by either X-ray crystallography or NMR is rightly, in my view, outside the scope of this “Laboratory Manual”.

Proteomics will continue to be a fast developing field for some time and this volume will certainly prove to be a landmark in the field. It will be the benchmark for clarity and general usefulness in a very large number of labs for the next few years.

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Scientific and Medical Aspects of Human Reproductive Cloning. National Research Council. National Academy Press. 2002. 272 pages. ISBN 0 309 07637 4. Price £25.95. (paperback).

This book has a unique and very useful collection of papers and opinions on the subject of human

reproductive cloning, specifically dealing with the scientific and medical aspects. It arises from a meeting held in Washington in August 2001 and I must declare an interest because I believe that it was I who suggested that the meeting should be held.

In my mind the meeting was to be analogous to that held in 1975 at Asilomar in California on the subject of genetic engineering. At that time there was considerable biological uncertainty about the safety of the newly arising methods for genetic recombination in bacteria. A meeting was arranged at which eminent biologists led by Paul Berg, Maxine Singer, Sydney Brenner and David Baltimore reviewed the techniques and they concluded that there should be a moratorium until critical questions had been answered. This conclusion was published in the Proceedings of the National Academy of Sciences (P. Berg *et al.*, Proc. Natl. Acad. Sci. USA 72, 1981–1984.). My expectation was that a comparable meeting on human reproductive cloning might have a salutary effect. Events have proved that I was right in some aspects, but not others. This book summarises the information presented at the recent meeting, presents the view of the panel charged with the task of reviewing the subject and provides a clear executive summary. The panel was made up of very experienced cell, molecular and developmental biologists.

In some 70 pages in the body of the book there is a clear description of what is involved in nuclear transfer, a summary of the present outcome of nuclear transfer in mammals and of assisted reproductive techniques in humans before the conclusions and recommendations. These are all readable, precise accounts that will be very useful for those looking for accurate information on these subjects. Extremely detailed summary tables presenting most of the detailed information that was included in the original publications supplement these chapters. In addition, there is an exhaustive bibliography in which papers are collated in a single comprehensive list and then again separately by several different subjects. If you are searching for papers on the role of mitochondria, telomeres or epigenetics in cloning the papers are cited here in separate lists. In total the bibliography requires just over 100 pages!

Was the original objective met by the meeting or by this publication? Well sadly not in full because the US congress has still to decide its policy on any aspect of human nuclear transfer. However, the view of the expert panel, which is summarised at the beginning of the book, was that human reproductive cloning at present should be prohibited because of the risks to mother and child alike. In making the original suggestion I had overlooked three very important points. Those sitting in judgement on genetic engineering were also those who had the greatest influence on the awarding of grants in the USA. Hence,

when they judged it to be wise to pause for a while there was very little dissent. By contrast, the expert panel at this meeting had almost no sanction against those who might one day attempt to clone a child in the USA. Secondly, I was extremely surprised to find when I got to the meeting that three people who claim to be cloning humans were to be treated as seriously as those of us with a considerable body of published research in animal cloning. Sadly, in the USA it seems that the television cameras are accepted almost everywhere so that these people were given free publicity at our expense. Not for the first or last time, unfortunately.

Despite these reservations the meeting was very useful in making the scientific community come to a view on this subject and that view is presented clearly in this book. In addition, the book will be extremely useful for those seeking an accurate introduction to the subject.

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Quantitative Genetics, Genomics and Plant Breeding.

Edited by M. S. KANG. CABI Publishing, 2002. 400 pages. ISBN 0 851 996019. Price £75.00. (hardback).

This book is a collection of 24 papers from the “Symposium on Quantitative Genetics and Plant Breeding in the 21st Century” held at Louisiana State University on March 26–28 2001 under the auspices of the local chapter of Sigma Xi Scientific Research Society in Baton Rouge Louisiana USA. The editor, Professor Manjit Kang at Louisiana State University,

provides a preface on two research topics germane to biotechnology-driven breeding programs: 1) molecular markers in breeding programs and 2) genotype \times environment interaction. The first section opens with four general papers on quantitative genetics and genomics then proceeds in the next ten chapters with specific applications of QTL mapping, marker-aided selection practice and theory, tissue culture for crop plants and specific case studies with barley, rice and maize. The second section narrows quickly to genotype \times environment interaction ($G \times E$) and stability analysis. An additional ten chapters cover mixed model applications, data analysis and case studies related to drought resistance, nitrogen-use efficiency and photoperiod response.

The book title is grander than its contents. There is not a strong synthesis between the two parts of the book, marker-assisted breeding and $G \times E$. Authors in Chapters 1–4 build a nice foundation for the interface between quantitative genetics, genomics and plant breeding theory but there is no strong connection between the subject matter here and the rest of the volume. This volume falls short of addressing cornerstone questions within dynamic research areas of plant breeding. Perhaps discovery and applications are changing faster than an edited volume with 24 groups of authors can be expected to respond. There is little here to recommend this book for graduate student readings, classroom discussion or as a handy reference book for the researcher. At best, this is a nicely bound symposium proceedings written by some well-respected scientists.

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