

representing proteins found abundantly in Nature. Nevertheless, my overriding impression is that the back of the problem, in part psychological, has been broken and that, after all, once armed with the appropriate detergent and a little determination, molecular biologists can overexpress (in one system or another) and crystallize membrane proteins with essentially the same techniques as used so successfully for cytosolic proteins. This volume, though not as comprehensive as I might have wished, should be a useful guide and stimulant to those laboratories now prepared to get stuck into the analysis of membrane proteins at the structural level.

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Mission impossible?

Immunoassays – A Practical Approach

edited by J.P. Gosling
Oxford University Press, 2000. £65.00 (hbk)
or £32.50 (pbk) (304 pages)
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There are now so many variations on the use of the core technology of the immunoassay, the antigen–antibody reaction, that when I opened this book I was a little sceptical as to whether James Gosling would be able to achieve the goals set for the Practical Approach series. One can be wooed by science and technology today in a way that makes it easy to lose sight of the main objectives for developing an assay. Thus, any text that sets out to provide a series of protocols to help the experimental scientist to measure a specific analyte must ensure that there is guidance on method design, optimization, calibration and validation – that is, to keep the feet on the ground! The book achieves this objective and includes useful tips and contact names and, although the latter will go out of date, it adds value.

The introductory chapter sets the scene describing some of the knowledge we have today about the chemical and three-dimensional interactions between antigen and antibody. It is a helpful

insight because it enables the experimenter to appreciate some of the issues surrounding assay optimization and calibration. We know that the antigen–antibody reaction is capable of achieving exquisite specificity, so that to ignore subtle differences in structure (e.g. caused by the effects of antigen purification, matrix or even reaction temperature) would be folly. This introduction also helps us to understand the different assay formats that can be used.

Many immunoassays are developed for antigens (or haptens), and the production (chapter 2) and selection (chapter 3) of antibodies is crucial to assay performance. However, the discussion on the choice of immunogen is also relevant when developing an antibody assay (for the choice of calibrator, see chapter 6). These chapters contain useful protocols and tips; obviously, the selection of antibodies is vital even when purchasing an antibody. Unfortunately, experience shows that you will not find an antibody with all of the information you want (or am I being too polite? – this information is often either non-existent or unreliable!)

I rubbed my hands as I approached the chapter on labels and endpoints because the choice of labels is legion, with many options being impractical for research application. However, the choice of labels described was reasonably appropriate – although I have yet to find someone with the courage to drop radioisotopes from the list! I was a little disappointed not to find a discussion of light-scattering assays because they are very simple and practical (but then I would say that because it is my interest). That apart, it was good to see more discussion on conjugation chemistry, because chemical linkage of antigen or antibody to label and to the solid phase (chapter 5) is crucial to the production of robust, stable reagents. In the chapter on solid phases (chapter 5), the emphasis was more on microtitre plates and tubes, which have a much lower surface area than spheres, and I was surprised by the limited mention of magnetic particles – surely, the most common and practical solid phase in use today.

The chapters on optimization, validation, data processing and quality assurance are crucial to the experimental scientist achieving his or her goal. There are some useful tips that I found in the chapter on optimization, warning of

potential problems that I have experienced in the past. Similarly, awareness of the pitfalls in data processing is helpful, particularly when faced with a variety of commercial data-processing packages.

This is a useful book for the analyst who needs to develop and use an immunoassay. It is also a useful text for the analyst who uses a 'commercial assay' and who has not had any part in its development, because it provides the background knowledge that will help with troubleshooting.

So it was worth taking on the mission!

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A bauhaus for biologists

An Introduction to Protein Architecture: The Structural Biology of Proteins

edited by Arthur M. Lesk
Oxford University Press, 2000. \$45.00
(347 pages)
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Architectural styles of buildings come and go, whereas the architecture of modern-day proteins has been with us for eons. In *An Introduction to Protein Architecture*, Arthur Lesk presents an insightful survey of this most fundamental topic. It is particularly timely for a new text on this subject as the current availability of extensive web-based information resources for protein sequences and structures modifies the traditional role for the textbook.

Arthur Lesk is one of the pioneers of the analysis of protein structure and its evolution. He was also one of the original developers of computerized molecular graphics for proteins in the early 1980s. So, needless to say, this book is brilliantly illustrated with an extensive array of large, clear stereo diagrams for the structures or motifs that are described in the text. Moreover, we believe that the use of stereo figures is essential for truly visualizing the complex 3D geometry of proteins. Indeed, this is a substantially illustrated graphical textbook (about half of the total

page count, discounting the structural atlas appendix, consists of figures). Presented in an uncomplicated, easy-to-read style and logically structured, the text is seldom wordy. There are brief sections describing the basic building blocks of protein structure, followed by discussions about how different proteins can be classified, with emphasis on web databases. The general discussions of protein evolution and protein motions are particularly good. Detailed studies, which stand well on their own, of immune system proteins, serine proteases and NAD-binding domains in dehydrogenases, are presented. In particular, an up-to-date introduction to structural immunology provides much information on the conformations of antibodies (with a discussion of canonical loop structures), major histocompatibility complex proteins and T-cell receptors, as well as the conformations of their interacting complexes. There is some reference at appropriate points to methods of protein

structure prediction (although there could be more about topics such as fold recognition or secondary structure prediction). A nice summary is provided of the biannual CASP (Critical Assessment of Techniques for Protein Structure Prediction) competition for assessment of prediction methods, and there is also a strong section on homology modeling.

This textbook tackles well the problem of interfacing with internet information resources. Extensive reference is made to web-based catalogs of protein structure and search tools for protein structure and sequence. The author has designed a special sort of exercise called the 'weblem'. For this, the student is asked to use web tools to solve simple tasks that aid our understanding of the links between protein structure, sequence analysis and protein structure prediction.

There are (inevitably) some omissions in the subject matter in this book. In particular, some detailed discussion of protein–nucleic acid binding and the

structural motifs involved would be welcome. Also, a section on the structure of membrane proteins would be desirable (although there is a very good opening chapter specifically describing the photosynthetic reaction center). Finally, although genomics and structural genomics are certainly mentioned, more emphasis could have been devoted to how 'global' genomic surveys of large numbers of structures are changing our view of what is typical and atypical in protein architecture.

These points aside, this text, written by a leading expert in the field, is to be highly recommended for anyone wishing to learn about protein architecture in the context of the current structure of bioinformatics information resources.

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