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Book Review

Works intended for notice in this column should be sent direct to the Book-Review Editor (R. O. Gould, Department of Chemistry, University of Edinburgh, West Mains Road, Edinburgh EH9 3JJ, Scotland). As far as practicable books will be reviewed in a country different from that of publication.

Acta Cryst. (1988). B**44**, 544

Protein structure and design. Edited by Dale L. Oxender. **(UCLA symposia on molecular and cellular biology, New series,** Volume 69.) Pp. x + 576. Alan R. Liss, New York, 1987. Price US $110.

In a brief essay on protein crystallography and its new revolution, Dodson surveyed the impact that the technique is having on modern biochemistry [*Trends Biochem. Sci.* (1986), **11**, 309]. Not only is the technique itself developing rapidly through advances in synchrotron X-ray sources, supercomputers, interactive graphics and, less directly, site-directed mutagenesis, but also it is being applied to an ever-widening range of exciting biological problems. The insight afforded from a detailed knowledge of molecular architecture has long been appreciated by crystallographers, and it is refreshing to see this appreciation flooding into the field of biology. This book is the proceedings of a Du Pont–UCLA conference, and it provides ample evidence of the impact protein crystallography is having on biology and, in particular, protein engineering. Further, the significant company participation shows that there is considerable commercial interest in the subject. However, it must be said that this is not a book from which to learn directly of specific techniques, rather it is in the results obtained from nine topical areas that the reader is immersed. Also, the results are not obtained from X-ray diffraction alone, although that could be said to have provided the basis of much of what is described.

The first section has eight papers on the structure and interactions of DNA-binding proteins: those involved in processing, or controlling the processing, of DNA. The next section on protein structural analysis comprises 11 papers including X-ray determinations, solution studies by nuclear magnetic resonance and circular dichroism and modelling studies based on existing coordinates. Energy considerations and molecular dynamics, the third section, provide a basis for studying binding of ligands to proteins, whilst the seven papers on enzyme catalysis include some beautiful examples of how site-directed mutagenesis (SDM) can help elucidate enzyme mechanisms. That a given polypeptide chain folds up to produce a unique tertiary structure has generated much speculation as to the nature of the pathway by which this occurs. Protein folding forms the fifth section in which SDM is shown to be a powerful tool for studying the problem and the seventh part is concerned with peptide and protein design: how the 'rules' so far extracted from analyses of protein structure can be put into practice. This section also includes a discussion of the strategies best suited to maximizing the production of a protein once the gene has been cloned. The previous section deals with mutagenesis of the cloned gene. Section 8 is short and deals with the interactions between antibody and antigen. The final part has two papers on viruses. The first links back to the previous section by considering the surface peptides of the poliovirus which are responsible for the host immune response and so may help in vaccine development. The second, all too brief, abstract refers to a crystallographic *tour de force,* the structures of several icosahedral viruses, their assembly and function.

The book is well produced from camera-ready typescript, though one or two of the stereo diagrams have been reproduced on too small a scale. There is a fairly full, if somewhat idiosyncratic, subject index but no author index. The reviewer found the book contained much of value but, as with many conference proceedings, was left with the feeling that it was aimed primarily at the participants.

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