about those field exercises that, contrary to what is usually said, have shown little effect of antichemical protective posture on overall military performance? How significantly might the impact of chemical weapons be further reduced by improvements in defensive equipment, exemplified by the newer European NATO and Israeli suits and masks? And how does one assess the importance in the argument of the appreciable military and political costs and risks of maintaining and using chemical weapons?

Most countries have a defence-only policy for chemicals. Are there circumstances short of global chemical disarmament in which the United States would gain from such a policy? Relevant when Utgoff wrote, these questions are far more so today, when the Soviet threat has greatly subsided and US chemical weapons policy can spell the difference between success or failure in achieving the support of other nations for an effective chemical disarmament treaty. □

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Protein-rich menu

Richard Virden

Proteins: Form and Function. Edited by Ralph A. Bradshaw and Mary Purton. *Elsevier: 1990. Pp. 270. £21.*

Protein Engineering: Approaches to the Manipulation of Protein Folding. Edited by Saran A. Narang. *Butterworths: 1990. Pp. 262. £55.*

THE pioneer's enthusiasm for the application of recombinant DNA techniques to produce useful amounts of valuable proteins is nowadays tempered by the realization that proteins are more than derivative linear polymers. Isolation of a correctly folded recombinant protein is often a non-trivial problem which can only be tackled empirically, drawing on such experience as that gained in the experimental study of protein folding. Intelligent genetic manipulation of protein properties is a yet greater challenge, demanding a thorough understanding of protein conformation, stability and relevant interactions with other molecules. The design of improvements in protein stability by changing individual amino-acid residues is made more difficult by the fine balance of large opposing forces which define the overall, often marginal, stability of the folded state. For the most part, these properties cannot be predicted from amino-acid sequences and therefore must be determined by experiment. Such studies are necessarily broad in scope and they are being developed and applied to an ever increasing number of proteins. Both specialists and newcomers to protein science will therefore welcome collections of up-to-date, authoritative and digestible overviews of these developments; two rather different multi-author menus of protein-rich nourishment are considered here.

The first, *Proteins*, contains 16 articles first published in the July 1989 issue of *Trends in Biochemical Sciences* together with 13 more articles all grouped under four main headings: primary protein structure; protein conformation; co- and post-translational modifications; and molecular recognition.

The pivotal conformation section appropriately opens with X-ray crystallography as the mainstay of three-dimensional structure determination. There is a comprehensible and forward-looking assessment of the state of the art and well-illustrated summaries of methods of crystallization, data collection and phase determination. A more specialized account of catalytic intermediates in enzyme crystals looks to a future when high-intensity pulsed X-ray sources will permit exposure times as short as 10–100 ps. Nuclear magnetic resonance (NMR) is shown as having a distinctive place in structure determination potentially extending to proteins (and independently folding domains of larger proteins) up to a relative molecular mass of 30,000. There is an excellent introduction to experimental study of the initiation of folding in small, single-domain proteins. This shows how progress is being made towards answering a key question — is there an obligatory order in the processes of hydrophobic collapse, formation of a compact molten globule state, and formation of hydrogen-bonded secondary structure? The aspiring protein engineer, eager for accurate conformational prediction from amino-acid sequences, will find some encouragement for the fashionable practice of modelling membrane-spanning helices and optimism for the prediction of secondary structure in globular proteins. But apart from modelling based on sequence similarity with previously determined structures, success in predicting tertiary structure is evidently some way off, with "unlimited future prospects". On the other hand, progress is reported in the converse problem of designing sequences which will fold in solution to specified conformations.

Earlier chapters include reviews of recent developments in protein and peptide purification and in primary structure analysis, featuring the increasing importance of developments in sensitive techniques such as mass spectrometry. There is also a recent summary of techniques in site-directed mutagenesis. Other contributions focus on particular proteins and biological processes. Occupying both scientific and industrial high ground are the achievements of site-directed and random mutagenesis in modifying subtilisin in its catalysis, specificity, pH/rate profile and stability to some of the rigours of the wash-tub. There are further accounts of studies based on high-resolution structures, such as site-directed mutagenesis of lactate dehydrogenase and molecular recognition by helix-turn-helix DNA-binding proteins, and there is consideration of less detailed conformational information, for example in relation to the *lac* permease. Chapters on protein translocation, posttranslational modification, proteolytic processing, glycosylation and secretion give a taste of some of the complexities being confronted in identifying the significant molecular interactions of proteins in a cellular context.

Although a significant number of these articles may be found in one issue of *Trends in Biochemical Sciences*, the advantages of the enlarged collection will make this an attractive book for both advanced undergraduates and graduates, giving concise and reasonably self-contained introductions and pointers to the recent literature over a very wide range of current concerns in protein science.

The second book, *Protein Engineering*, comprises 11 chapters, several relating mainly to techniques. There are useful descriptions of a variety of techniques for study of protein folding and quite full descriptions of spectroscopic techniques including X-ray crystallography, NMR, laser-based fluorescence, and infrared spectroscopy for characterization of membrane proteins. How site-directed mutagenesis affects protein folding is the concern of one chapter, taking tryptophan synthetase α-subunits and dihydrofolate reductase as major examples. Other contributors discuss ways of identifying functional sites in a protein of unknown conformation (alanyl-tRNA synthetase), and epitope mapping of the envelope glycoprotein of the human immunodeficiency virus.

In view of the difficulties of prediction, protein engineers will probably continue for some time to come to be concerned more with the effects of mutation on the final folded conformation than on folding pathways. With its emphasis on folding, this book can therefore be recommended more for its introductions to techniques and for studies on particular proteins than as an overview of mainstream developments in protein engineering. □

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