Book Reviews

Biological Membranes: Structure, Biogenesis and Dynamics; Edited by J.A.F. Op den Kamp, Springer Verlag; Berlin, Heidelberg, New York, 1994; x + 356 pages. DM 228.00. ISBN 3-540-57731-9.

This volume derives from a NATO Advanced Study Institute course held in June 1993, covering lipid dynamics, protein–lipid interactions, membrane protein structure and folding, the translocation of proteins through and their insertion into membranes, and intracellular protein traffic. There are 34 contributions in all, divided about equally amongst these topics; they vary considerably in length and format, some being overviews and others experimental reports.

'Lipid dynamics' includes a wide-ranging review of the roles of phospholipids in cellular functions (Dowhan), and shorter papers on intracellular lipid traffic and the functions of phospholipid exchange proteins. 'Protein–lipid interactions' contains a survey of the use of NMR and ESR spectroscopy in this area (Watts), followed by papers on the interaction of lipids with particular proteins, and of the role of lipid composition in protein sorting in epithelial cells. 'Protein structure' includes a brief exposition of NMR techniques as applied to membrane protein structure, and contributions on pathways of (soluble) protein folding, protein turnover, and the structures of porins and some pore-forming polypeptides. The section on protein insertion and translocation covers the familiar ground of signal peptide structure (Gierasch), topology rules (von Heijne) and bacterial protein secretion (Wickner and Leonard), as well as more specialized contributions on related topics, including the translocation and mode of action of some bacterial toxins and viral proteins. 'Intracellular traffic' is otherwise given rather short shrift, with coverage of post-translational modification in the endoplasmic reticulum. Golgi disassembly and reassembly and organelle inheritance in budding yeast, but surprisingly little on the topical areas of targetting and retention of organellar proteins, or on vesicular traffic.

In many ways this volume epitomizes the strengths and weaknesses of symposium proceedings. It is not really able to convey the multidisciplinary interaction that was clearly the object of the conference, and the participants' discussion is not included. What remains is a collection of rather formal, and sometimes apparently unrelated, contributions. Much of the work is already reported elsewhere, often in lengthier and more detailed form, and none of the papers is likely to be the definitive description of the work. An expert reader is unlikely to find anything of great novelty in his own area; on the other hand a browser may very well learn a lot, and at the very least will be provided with (fairly) up-to-date references on some specialized topics. Although one of the topics is exhaustively treated, there are illuminating contributions on all of them, and those teaching courses in membrane biochemistry at a fairly advanced level will certainly find this book a source of much useful material.

David K. Apps

The Protein Folding Problem and Tertiary Structure Prediction; Edited by K.M. Merz Jr. and Scott M. Le Grand, Birkhäuser; Boston, 1994; x + 581 pages. $99.00. ISBN 3-7643-3693-5.

Proteins, during their 'life cycle', serve multiple functions: before fulfilling their biological roles as catalysts or receptors etc., they have to fold to form their unique three-dimensional structure; finally they have to be accessible to degradation, serving as a nutrient or allowing regeneration. Next to transcription and translation, protein folding is the most important reaction in the living cell. In the overall transfer of information from the DNA to the protein level, 50 years of in vitro studies have shown that protein self-organization is an autonomous and spontaneous process which does not require either additional information or the input of energy. Due to the one-to-one relationship of an individual amino acid sequence and its specific solvent structure, one would predict that there must be a 'code of protein folding' in terms of an algorithm allowing the prediction of the three-dimensional structure from a given primary structure. In spite of the continuous efforts of physical biochemists for more than 30 years, this 'second half of the genetic code of protein translation' still awaits elucidation. The growing importance of the problem is evident, thinking of the Human Genome Project, protein design, 'synzymes', site-directed mutagenesis, etc. Correspondingly, there has been an increase in activity in the field which is reflected both by an explosion of semi-empirical and theoretical approaches and an increasing number of monographs and Conference Proceedings. It started 15 years ago with the 1st International Conference in Regensburg; in 1982 C. Ghélis and J. Yon's book 'Protein Folding' appeared, and since 1984 regular AAA Meetings have been devoted to the topic. In 1989, G.D. Fasman edited a volume of 798 pages, 'Prediction of Protein Structure and the Principles of Protein Conformation'; finally, in 1992, T.E. Creighton followed with a comprehensive collection of excellent articles covering both experimental and theoretical approaches to the protein folding problem.

The present book differs from the previous publications in three important points: (i) coming fresh from the press, it illustrates the enormous increase in the power of computers, supporting Shneior Lifson's optimistic prospect "that further creative imagination, penetrating wisdom and hard word work will finally lead to a solution of the problem"; (ii) it is focused on more specialized topics, mainly theoretical approaches, from simulated annealing and molecular dynamics to side chain packing and neural networks; (iii) most of the authors differ from those who contributed to earlier volumes, to the effect that the careful reader does not find many of the common references quoted in previous monographs. Since there is no name index, this kind of search is not trivial; names such as R.L. Baldwin, J.-R. Garel, M.E. Goldberg, P.S. Kim and F.X. Schmid occur only once or twice, others are missing altogether. One obvious reason is that the editors define 'the protein folding problem' in terms of "tertiary structure prediction". As a consequence, the topics treated, e.g. in the AAAS Selected Symposium 89 (edited by D.B. Wetlaufer) are ignored. The same holds for the 'kinetics' and 'pathways' of folding; protein 'stability' is only discussed in connection with the role of interior side chain packing (J.H. Hurley).

Instead of the traditional topics, the discussion refers to the following problems: A. Roitberg, R. Elber, S.R. Wilson and W. Cui apply simulated annealing algorithms to a number of model systems. T.N. Hart and R.J. Read discuss the docking of flexible ligands to proteins using a Monte Carlo approach. Next come S.M. Le Grand and K.M. Merz with a review of current developments in the application of the genetic algorithm, and R.E. Bruccoleri with applications of his CONGEN program. Distance geometry and molecular dynamics are covered by W.R. Taylor, A. Aszódi, A. Caflisch and M. Karplus. G.M. Crippen and V.N. Maiorov describe a contact potential function that

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