Protein structure, prediction and design

edited by John Kay, George Lunt and David Osguthorpe

The 57th annual symposium of the Biochemical Society, held at the University of Bath in April 1990, presented current attempts to determine ways of predicting protein structure and to manipulate protein structure. Some of the world's leading experts in the field presented their view of the current state of the art, and this volume recaptures some of the excitement of the symposium and serves to demonstrate that the prediction and design of protein structure and function is now an attainable goal.

Contents: An assessment of COMPOSER: a rule-based approach to modelling protein structure (Topham and others); Secondary structure prediction and protein design (Garnier and others); Inverting the protein-folding problem (Sander); Structural homology in ligand-specific transport proteins (North); Holistic approaches to receptor and channel structure and dynamics (Kosower); Modelling of binding sites of the nicotinic acetylcholine receptor and their relation to models of the whole receptor (Cockcroft and others); Monoamine neurotransmitter receptors: ligand-receptor models (Saunders and Findlay); The expert system approach to predicting protein structure (Ball and others); Basic design features of the parallel $\alpha\beta$ barrel, a ubiquitous protein-folding motif (Wodak and others); Preparation of artificial bifunctional enzymes by gene fusion (Bütow); Restructuring catalysis in the mandelate pathway (Neidhart and others); Identification and design of binding determinants in proteins (Wells and Cunningham); Antibody-combining sites: prediction and design (Gregory and others).

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