More and more, science is dragged into politics.

In these circumstances, Stever's procedural prescriptions remain appropriate, though for reasons other than those he identifies. Procedural changes will neither produce appreciably better information nor depoliticize the issues. What they can do is to manage the political debate more effectively by granting meaningful access to all affected parties and balancing the power of competing interests. Where the substance of regulation remains ill-defined and highly politicized, the fairness of the process of regulatory decision-making assumes greater importance. Stever's prescriptions are likely to do little to reduce the vigor of the debate in arenas like Seabrook, but they may restructure the debate in ways that encourage a more even-handed treatment of the participants.

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Structures of Proteins

Protein Folding. Proceedings of a conference, Regensburg, Germany, Sept. 1979. RAINER JAENICKE, Ed. Elsevier/North-Holland, New York, 1980. 588 pp., illus. $73.25.

This proceedings volume contains a number of substantial, well-written papers that offer novel approaches to exciting problems. The question addressed is How do proteins fold up? It has been assumed, since the early experiments of Anfinsen, that the protein sequence must contain all the information needed to create the "native" structure as at least a kinetically stable state. There have been three broad approaches to protein folding.

Experimental studies of protein denaturation showed the process to be highly cooperative and led to a "two-state" model in which only "native" and "denatured" species were recognized. In the last ten years, however, various trapping procedures, fast kinetics techniques, and cryoenzymology have provided undisputable evidence that there are kinetically important intermediates. Much of this work is presented in this volume, the accounts provided by R. L. Baldwin and T. E. Creighton being exceptionally valuable. The message from the experimenters is that the folding pathway seems to be complex; intermediates with considerable tertiary structure form well before the final state Obligatory but incorrectly folded structures that must rearrange to yield the native protein have been found for trypsin inhibitor. A long-standing puzzle that emerges more forcefully on reading several of the experimental papers is that clipping a few residues from the carboxyl end of a number of proteins has a profound effect on the refolding kinetics and the stability of the native state. No general explanation is offered.

The second—some would say the major—approach has centered on the proliferation of structures determined to high resolution by x-ray crystallography. This volume is not a structural compendium, and no new structures are reported. There are, however, many papers that use the known structures as data for further analysis. The attempt to see classes of structures has a long and honorable history, beginning, in the protein field, with Pauling's insights into secondary structures. Current efforts are, on the one hand, more detailed, focusing for example on arrangements of strands in beta sheets, and, on the other, aimed at higher levels of structure, such as investigations of beta sheet stacking and domain structures. These efforts are well represented, with a well-illustrated summary of protein structures by J. S. Richardson and contributions by a number of other well-known workers. It is increasingly clear that, at least on a structural level, there are a relatively small number of domain-sized building blocks that are reused in quite similar ways from one protein to the next.

The third approach has been mathematical modeling of proteins to attempt to predict or to understand the native structure. Pioneers in this field, such as H. A. Scheraga, O. B. Ptitsyn, and V. Lim, have their latest contributions here, and there is a nice introduction and review by M. Levitt. My general impression is that the direct energy minimization efforts are still considerably short of their goal, largely, but not exclusively, because of the magnitude of the computational task. Approaches that treat only part of the problem—for instance, the combinatorial methods presented by F. M. Richards, T. J. Richmond, M. J. E. Sternberg, and F. E. Cohen—seem very promising if one wants to put a large amount of information together in a model that will produce a low-resolution "protein-like" structure.

The major omissions from the volume are considerations of protein folding in vivo and of internal motions in proteins. The latter topic has been advanced through high-resolution nuclear magnetic resonance spectroscopy, thermal parameter diffraction experiments, and calculations of molecular dynamics. Only the NMR story is offered here, through the elegant studies of K. Wuthrich, H. Roder, and G. Wagner. Fortunately this topic was covered in a recent discussion of the Biophysical Society.

In sum, this is an excellent book for all those interested in protein folding in vitro. It has enough new and thought-provoking material to serve as a source book for an advanced graduate course and certainly belongs on library shelves even in these austere days.

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