Each chapter contains two types of reading lists: 'further reading' which consists primarily of monographs and review articles, and 'references' which contain more specialized reviews and primary literature references. The figures for the most part consist of very clear and simple two-colour diagrams. The figure legends also in many cases contain references to the original sources, a feature I find most helpful for students who want a starting point to pursue a specific topic further. The book contains a glossary of basic terms at the end, which will be particularly useful to neophytes to the field.

Unfortunately, as is the case for all books in rapidly evolving areas, they quickly become dated. This book, having been published in 1993 and consequently having few references after 1991, could easily fall in this trap; however, by the very nature of it being a 'generalist' overview book, it will actually become obsolete less rapidly than more specific and detailed books on the subject.

Naturally, some current areas of interest, such as techniques for predicting protein structure, protein design, and the range of protein folds and structures thus far detected, are outdated, but its overall utility as a book for the novice is little affected.

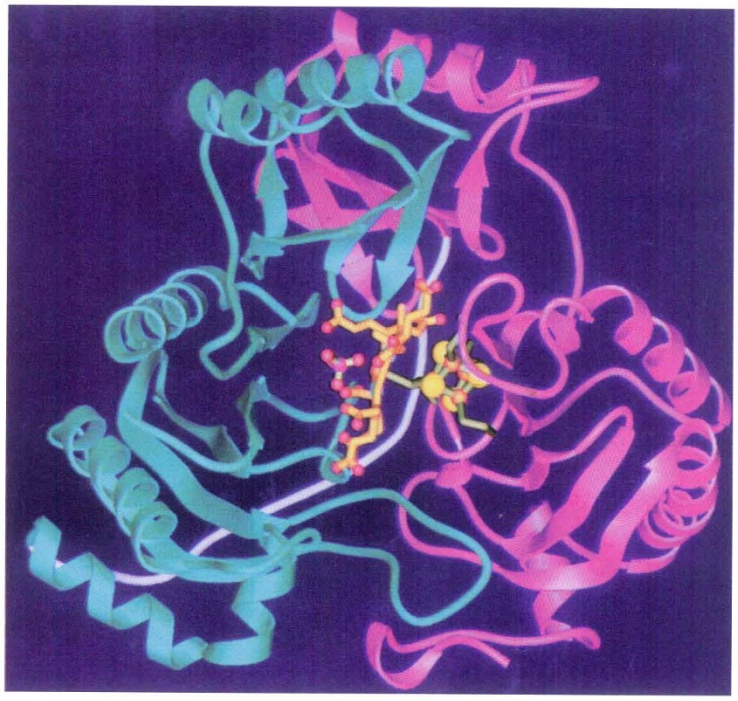
In summary, as our ability to rapidly determine one-dimensional information on proteins grows, the demand for biochemists and others to understand three-dimensional structures will increase. This should be a good introductory book for people entering or re-entering the field. Indeed, the special 'niche' of this book may be that it is such easy reading that it is best-suited for the person who wants to teach themselves about the basics of protein structure.

1. Creighton, T.E. *Proteins Structures and Molecular Properties* (W.H. Freeman and Company, N.Y.; 1993).
2. Branden, C. & Tooze, J. *Introduction to Protein Structure* (Garland Publishing, Inc., N.Y.; 1991).

B.A. Wallace is at the Department of Crystallography, Birkbeck College, University of London, London WC1E 7HX, UK.

picture story

Considering a reducing plan—The reduction of inorganic anions such as nitrite and sulphite into forms that can be used by living things is one of those phenomena that are so universal in their importance to life that they tend to be overlooked. This process invokes no fashionable or catchy features to justify its fascination; instead, the reduction of inorganic anions owes its interest to the extent to which it underlies all life. A recent paper from Brian R. Crane, Lewis M. Siegel and Elizabeth D. Getzoff (*Science* **270**, 59–67, 1995) provides a look into the heart of *E. coli* sulphite reductase haemoprotein (SiRHP), which catalyses the six-electron reduction of either nitrite to ammonia (used, for example, in amino-acid biosynthesis) or sulphite to sulphide (for incorporation into cysteine and other biomolecules). The native SiRHP exists as part of an oligomer, but a single subunit of SiRHP (shown left) can carry out its essential function when provided with a suitable electron donor. Although the sirohaem cofactor (gold bonds, brown iron, red oxygens) alone can also reduce these anions, the reaction is incomplete and inefficient.



The key to function of SiRHP lies in the way its three domains conspire to organize the sirohaem and iron-sulphur cluster (yellow sulphur, brown iron, green bonds) cofactors, which are situated near the upper surface of the protein. A phosphate anion (left centre, purple phosphorus, red oxygens) bound in the substrate-binding site at the sirohaem's distal face may serve to stabilize the active site in the substrate's absence; phosphate is displaced upon substrate binding. Positively charged residues coordinate substrate binding and polarize ligand bonds to facilitate reduction. The sirohaem and iron-sulphur cluster are linked by a shared cysteine ligand; each reduced cofactor stores at least one electron for delivery to the substrate sulphur (in the case of sulphite), which is bound to the sirohaem during catalysis. These cofactors function together as a coupled electronic system to supply electrons at low redox potentials and in fast succession to insure complete and efficient reduction to product.

Besides the evident three-domain structure, an axis of pseudo two-fold symmetry relates the N-terminal (cyan) and C-terminal (pink) portions of the protein. This structural relationship corresponds to a relationship by sequence repeat, the N-terminal repeat comprised of the front half of domain 1 (top) and all of domain 2 (bottom left) and the C-terminal repeat comprised of the remainder. Exemplifying this two-fold symmetry, a segment of the loop (white) between domains 1 and 2 occupies a position on the 'back' of this molecule that is structurally homologous to that of the sirohaem near the 'front'. The symmetry-related repeats by definition share conserved regions, which are also shared by other nitrite and sulphite reductases; this conservation may identify regions that determine appropriate fold and function within this superfamily of two-fold pseudo symmetric redox enzymes. **AF**