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Editor: Alton Meister
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This latest addition to the long-founded and well-received series contains four up-to-date chapters that cover diverse subjects; fibronectin and cell adhesion, dihydrofolate reductase, tyrosine hydrolase and alginate synthesis. All the chapters are well written and come from authors with considerable authority in their fields. Perhaps the chapter on fibronectin and cell adhesion, and the specificity of integrin-ligand interactions, will be of particular interest to cell biologists working in dental research. The two chapters on tyrosine hydrolase and dihydrofolate are particularly rich sources of information on these important enzymes. Those with a more clinical orientation will probably find the volume of lesser interest. It is a pity that because of its price this reviewer cannot suggest that the book will be essential for individual researchers. The volume will, however, certainly be a welcome addition to those libraries carrying the series, which has provided a fine resource on enzymological topics.

John Reynolds

Desktop Molecular Modeller Version 3.0 (1995)

Authors: M. J. C. Crabbe, J. R. Appleyard, C. R. Lay
Publisher: Oxford University Press, Oxford
Price: £295.00
ISBN: 0-19-268232-6

This package appears to be one of the best and least expensive molecular modelling software programs currently available. The latest version runs in Windows, and takes advantage of SVGA graphics and 256 colours. It is capable not only of building ionic models but also of demonstrating the structure of peptides with the relevant amino-acid sequences. In the age of ever increasing PC technology the program has fairly modest requirements: these include an IBM 386 PC or compatible, although a 486 is recommended, a minimum of 4Mb RAM, DOS version 5.0, Windows version 3.1 and a VGA or SVGA monitor.

The library structures include biomacromolecules, biochemistry, organic and inorganic chemistry and pharmacology. It is possible to change the orientation of any structure by rotating about the *x*-, *y*-, or *z*-axis. Real-time rotation, translation, and zooming of structures is available using the mouse. Structures may be projected along a specified bond or onto a specified plane, and *z*-axis clipping can be used to simplify complex displays. A 'best view' facility reorientates the structure to display the maximum number of atoms. Version 3.0 of this software provides new facilities for building and displaying peptides and proteins. Five peptide conformations are suggested: right-handed alpha-helix, Tr-helix, 3(10)-helix and parallel and antiparallel sheets. It is also possible to modify the basic structural configuration of the peptide with Psi and Phi angles.

Displays may be either printed directly or saved as BMP files. A minor irritation of the latter is that you are saving a screen dump which captures the molecule very well but leaves an irritating edge on the screen which requires editing. This does however allow integrated documents or slides to be produced of a standard suitable for publication.

DTMM reads crystal and orthogonal coordinate files in a format compatible with the Crystal Structure Search and Retrieval (CSSR) format.

Overall the package is strongly recommended for many branches of science.

Fraser McDonald