and the final year of degree courses will be grateful to Professor Sheppard and the other contributors for producing this excellent hybrid between text book and practical manual. The seven chapters include full descriptions of the techniques of cytogenetics and the culture methods for a wide range of organisms with detailed practical guides to exercises in basic genetics using Drosophila, fungi, bacteria and bacteriophage. Other chapters outline exercises in population, ecological and quantitative genetics and provide clearer accounts of biometrical genetics and elementary statistics than are found in most textbooks. Perhaps the chapter of most general value is the one concerned with higher organisms where a mine of information on the use and availability of teaching material emphasises that practicals in genetics need not be restricted to the few organisms commonly used in research.

Some of the suggested exercises can each be carried out by individuals in a single practical session, whereas others require the cooperative efforts of a number of students over a full term. All of the authors have provided a useful list of altruistic university departments and commercial suppliers that can provide suitable materials.

The editing is lenient, allowing some useful repetition, but the legend to plate 4.7 underlines the role of practicals in encouraging students in critical observation: those who follow the instructions and prepare slides of meiosis in locust species, might question whether the plate depicts diakinesis in *Schistocerca gregaria* or diplotene in some other species. JOHN GIBSON

Protein in stereo

Atlas of Molecular Structures in Biology. 1, Ribonuclease-S. Prepared by F. M. Richards and H. W. Wyckoff; edited by D. C. Phillips and F. M. Richards; figured by J. L. Mouning and J. W. Schilling. Pp ix+75. (Clarendon: Oxford; Oxford University; London, 1973.) £3.50.

PRESENTING the structure of a protein molecule is perhaps as immense a problem as solving the structure. In this volume on ribonuclease-S the editors and authors present a workable format for this task. It is the intention of the series to present structure unencumbered by interpretation. A short description of what the enzyme does, giving appropriate references to more detailed reviews and primary source material, starts the pleasantly brief text. After all, it is the pictures which are important in this book. Following is a series of tables and figures giving such items as physical properties, amino acid sequences, Cartesian coordinates, hydrogen and ionic bonds, and various contact and angular properties of the chain. Some of the measured coordinates and angles are presented in several different forms, thus eliminating some conversion by the reader and making the work more usable.

The heart of the volume is the computer-generated drawings of the molecule. Forty-three red-green stereo drawings depict the main chain and all non-hydrogen side chain atoms from three mutually perpendicular directions. Four of these are specially devoted to the environment around the UpcA inhibitor complex. Many of the others are taken in ordered slices through the molecule. The publishers did an excellent job in the alignment of the stereo pairs but there was a slight shadow effect caused by an incorrect match of the green ink with the green filter in the stereo glasses provided. This effect became more pronounced as one moved closer to the diagram to read the small residue labels. From normal viewing distance the three-dimensional effect was quite good.

The last section contains the electron density maps for the apo-protein, This section should give the non-crystallographer the opportunity to see how a complete electron density map looks. The electron density of each section of the map is printed in green, and superimposed on it are all the atoms involved in that section with their Van der Waals radii drawn in red. By closing one eye and using the stereo glasses, one can see either the map or model. This section is excellent in its concept and execution. Unfortunately there is no index as to which sections on the map a residue will appear in, so the coordinate list must be used.

In general, the volume provides an excellent source for the structure of ribonuclease-S. Distances between residues of interest can easily be calculated from the coordinate lists and environment relationships can be found by consulting the many stereo diagrams. The major fault of the series is not in this volume, but perhaps in future volumes. Ribonuclease-S is approximately one-fifteenth the size of the larger multi-component proteins now being studied. The inclusion of the necessary diagrams to fully depict the subunit structure and the important subunit–interactions of one of these large proteins would not only make the volumes larger, but more expensive to produce and to purchase. Unfortunately, there seems to be no simple solution to the problem of disseminating all the structural information of a molecule as large as a protein, and this volume presents a good compromise solution. STEVEN J. STEINDEL