

Book Reviews

Works intended for notice in this column should be sent direct to the Book-Review Editor (R. F. Bryan, Department of Chemistry, University of Virginia, McCormick Road, Charlottesville, Virginia 22901, USA). As far as practicable, books will be reviewed in a country different from that of publication.

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Principles of protein X-ray crystallography. By JAN DRENTH. Pp. xiii + 305. New York: Springer-Verlag, 1994. Price \$49.50. ISBN 0-387-94091-X.

For many years after its publication in 1976, *Protein Crystallography*, by Tom Blundell and Louise Johnson (London, Academic Press), was the standard text for crystallographers interested in biological macromolecules. However, a much anticipated second edition never appeared and only recently has the void been filled by new volumes such as the specialized text *Macromolecular Crystallography Using Synchrotron Radiation*, by John Helliwell, (Oxford University Press, 1992) and the somewhat more applied text *Practical Protein Crystallography*, by Duncan McRee (New York, Academic Press, 1993). The most recent addition to the collection is this book by Jan Drenth. It is intended both for beginners wishing to understand the basic principles of the method, and as a reference for those familiar with the field.

The impression of the work gained from the first few chapters is somewhat different from that derived from the work as a whole. Drenth assumes that the reader is familiar with the basic principles of protein structure, and begins with a qualitative and somewhat anecdotal discussion of crystallization, followed by a description of crystals and symmetry. The chapter on data collection seems slightly out of place since the principles of X-ray diffraction are not discussed until the following chapter. However, Drenth's goal in the introductory chapters seems to be to make the reader feel comfortable with the subject of protein X-ray crystallography. In fact, the first two chapters are somewhat informal, and occasionally imprecise, attempting to make the reader feel a part of the experience. Only after gaining the reader's confidence does Drenth abandon the use of the second person and charge into a more mathematical treatment of the subject.

The text is centered around two mega chapters: one on the theory of X-ray diffraction and another on phase determination by isomorphous replacement. The chapter on X-ray diffraction is long and might be better divided into separate chapters on the structure factor and the Fourier series in order to emphasize the individual importance of these topics. However, Drenth presents a solid, mathematical description that is both intuitive and rigorous. The chapter on intensity distributions provides further insight into X-ray diffraction. However, the purpose of the three-page chapter on special forms of the structure factor is unclear and this material might have been better placed in an appendix.

Drenth continues by describing methods for phase determination. Once again the treatment is rigorous but might be more palatable if divided into several shorter chapters. The order of

material may also be confusing to a beginner. For example, Drenth describes how to interpret a Patterson function in terms of heavy-atom positions but waits until 40 pages later in the same chapter to show the reader why the positions of heavy atoms are useful. Succeeding chapters provide treatments of phase improvement, the use of anomalous scattering in phase determination, and molecular replacement as a method for phase determination. The three-page chapter on direct methods seems out of place and of little practical use. The remainder of the text deals with various aspects of protein X-ray crystallography such as Laue diffraction, structure refinement, phase combination and evaluation of the model.

In summary, the book fulfills its aims as a general text for the protein X-ray crystallographer. Drenth introduces the general principles and discusses most of the important new topics, including the use of synchrotron radiation, multiple-wavelength anomalous-diffraction phasing, X-ray detectors and simulated-annealing refinement, thus updating the classic work of Blundell and Johnson. However, the newer techniques are generally presented with less depth than the more familiar topics, a feature that may lessen the book's usefulness for the experienced practitioner. For example, Drenth spends eight pages on the precession method which, perhaps regrettably, is little used by the coming generation of macromolecular crystallographers, as opposed to only two pages on image plate detectors. He also presents synchrotron radiation and multiple-wavelength anomalous-diffraction phasing as difficult and challenging topics, which may tend to intimidate, rather than encourage, those who might benefit from such tools. Missing are detailed discussions of some current topics such as cryocrystallography and data-processing software. Overall, the text relies heavily on a mathematical treatment of protein X-ray crystallography and, in many cases, casual familiarity with undergraduate level mathematics may be insufficient to follow the arguments. Further, the text does not always relate the mathematical treatments to examples, thus requiring the reader to discover the practical importance of various subjects. Both of these features lessen the book's usefulness to the beginner.

Nevertheless, the text should be valuable for use in an organized course in which an experienced instructor can bring practical examples into the discussion. Notwithstanding these criticisms, Drenth's efforts are commendable and this text should be on the bookshelf of every scientist who is seriously interested in protein X-ray crystallography.

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