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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.

Acta Cryst. (1993). D**49**, 602-603

Macromolecular crystallography with synchrotron radiation. By J. R. HELLIWELL. Pp. xx + 595. Cambridge University Press, 1992. Price £95.00, US $165.00. ISBN 0-521-33467-5.

The generation of a new scientific discipline, or advent of a new technique, is often marked by a progression from frontier scientific articles, to review articles and conference proceedings, to scholarly monographs and, finally, to graduate and undergraduate texts. John Helliwell made major contributions, through his scientific articles and conference presentations, to the birth of synchrotron-based macromolecular crystallography. This reviewer's copies of his review articles on this topic, written separately and with Trevor Greenhough, are dog-eared and battered - testimony that they are widely used and full of essential information. The present book is certain to suffer the same, surely desirable, fate! Aimed at researchers in a variety of disciplines spanning the biological and physical sciences, it reviews the theoretical and experimental foundations of conventional macromolecular crystallography before presenting a comprehensive description of the generation and nature of synchrotron radiation, of the instrumentation needed to harness the radiation and deliver it to the target crystal, and of the experimental techniques, both monochromatic and Laue, that exploit the radiation effectively and demonstrate its applicability to a wide range of problems in modern structural biology. For biochemists and biologists who conduct experiments at synchrotron sources, it answers the questions: 'what's upstream from my experiment?' and 'how do the X-rays get from the source to my crystal?' For the physicists and engineers who design the synchrotron sources or the beam lines, it answers different questions: 'just what are the structural biologists and crystallographers up to? Why

do they demand (for example) such a tightly focused, stable, rapidly tunable, monochromatic X-ray beam? Are experiments on virus crystals really brilliance-driven?' Given the diversity of interests and backgrounds of the intended readers, it is a particular strength of the author that he presents much complex material in a straightforward and generally comprehensible style. Although some topics, such as the fundamentals of crystallography, are dealt with only briefly, they are amply described in other texts, and the comprehensive reference list provides enough pointers to the research literature to satisfy the most enthusiastic reader. The numerous line drawings are of high quality, but the halftone prints seem to have suffered severely in the production process, and they are of more limited value.

Besides describing the present state of play, Helliwell offers many pointers to the next innings, so much so that a researcher looking for novel topics to pursue in the next grant application will find several here. As an example, a chapter is devoted to diffuse X-ray scattering from macromolecular crystals, where the high information content of the diffraction pattern is immediately apparent, but where the means of extracting that information in structural terms remain to be fully developed. Another chapter deals with ongoing developments in Laue diffraction, both static and time-resolved, and there are speculations on, *inter alia*, the use of ultra-short X-ray wavelengths, novel X-ray detectors, and the use of Bijvoet ratios rather than differences.

Today, conducting experiments at a synchrotron rather than in the home laboratory is always more complicated, subject to extreme time pressures and often more stressful. It is an enterprise to be undertaken only when the scientific benefits are marked. However, with the arrival of powerful and accurate multiple-wavelength anomalous dispersion (MAD) phasing techniques, where the experimental measurements are most readily made with synchrotron radiation, it seems likely that quite soon the majority of macromolecular crystallographers - not just those studying virus structure, or microcrystals, or exotic time-resolved problems - will choose to use synchrotron sources. This book will be their one essential reference.

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Time-resolved macromolecular crystallography. Edited by D. W. J. CRUICKSHANK, J. R. HELLIWELL and L. N. JOHNSON. Pp. v + 174. Oxford University Press, 1992. Price £35.00. ISBN 0-19-855781-7.

This book is a compendium of contributions presented at a discussion meeting on Laue diffraction held by the Royal Society in January 1992. All but one of them were first published in the *Philos. Trans. R. Soc. London Ser. A* (1992). **340**, 167-334. In publishing these papers separately, the editors have made available to the macromolecular crystallographic community a volume that describes the current state of the art of the Laue technique, its advantages and disadvantages, its current successful applications and its future expectations. The book gives a good overview of the problems associated with this difficult but rewarding diffraction technique, which many believe offers the key to unlock the puzzle of structure-function relationships in macromolecules.

The opening paper, by D. W. J. Cruickshank, (6 pp.) presents an interesting historical perspective to the technique. It includes extracts from letters from both Ralph Wyckoff and Linus Pauling, clearly showing that many of the problems that we face today in collecting and analyzing Laue diffraction data had already been encountered by the pioneers of the field over 70 years ago. The second paper, 'Time-resolved crystallography: principles, problems and practice', (16 pp.) by K. Moffat, Y. Chen, K. Ng, D. McRee & E. D. Getzoff, presents an overview of a modern Laue diffraction experiment. After stating the assumptions upon which proposals for time-resolved crystallography are based, the authors discuss its five major components: the X-ray source and optics, reaction initiation, reaction monitoring, X-ray data acquisition, and data reduction and analysis; using results drawn from their work on the photoactive yellow protein and a natural product, briarane B. Chapter 3, 'Time course of chemical and structural events in protein crystals measured by microspectrophotometry', (18 pp.) by G. L. Rossi, A. Mozzarelli, A. Peracchi & C. Rivetti, summarizes the use of polarized absorption spectroscopy to characterize activity in the crystalline state, with results from five protein systems. Simultaneous use of microspectrophotometry and X-ray diffraction during a time-resolved experiment will enable the crystallographer to better characterize the system of interest . In Chapter 4, H. D. Bartunik, L. J. Bartunik & H. Viehmann in 'Time-resolved X-ray diffraction studies of enzymes under cryoconditions', (12 pp.) describe the use of scanning Laue diffraction and cryocrystallography to study enzyme mechanisms. They summarize the uses and advantages of these techniques and present, for the first time, direct evidence of a covalent O—C bond between a serine protease and a productive substrate, demonstrating that cryocrystallography can yield detailed structural information on substrate intermediates. In Chapter 5, 'Synchrotron X-ray crystallography techniques: time-resolved aspects of data collection', (12 pp.) J. R. Helliwell compares the time scales for the rotation, Weissenberg and Laue data-collection methods at synchrotron sources, with particular attention to the wavelength-dependent factors in Laue diffraction. Two detector systems are presented: the three-dimensional toast rack, which maximises the number of processable spots on a Laue film by reducing the number of spatially overlapped reflections, and a charged coupled device (CCD) for monitoring changes in integrated spot intensities as a function of time, so as to check radiation damage in a protein crystal. Next, J. E. T. Corrie, Y. Katayama, G. P. Reid, M. Anson & D. R. Trentham, in 'The development and application of photosensitive caged compounds to aid time-resolved structure determination of macromolecules', (12 pp.) discuss practical and theoretical considerations when using various caged compounds for synchronous reaction initiation in the crystal.

'Time-resolved diffraction studies on glycogen phosphorylase b', (18 pp.) by E. M. H. Duke, A. Hadfield, S. Walters,