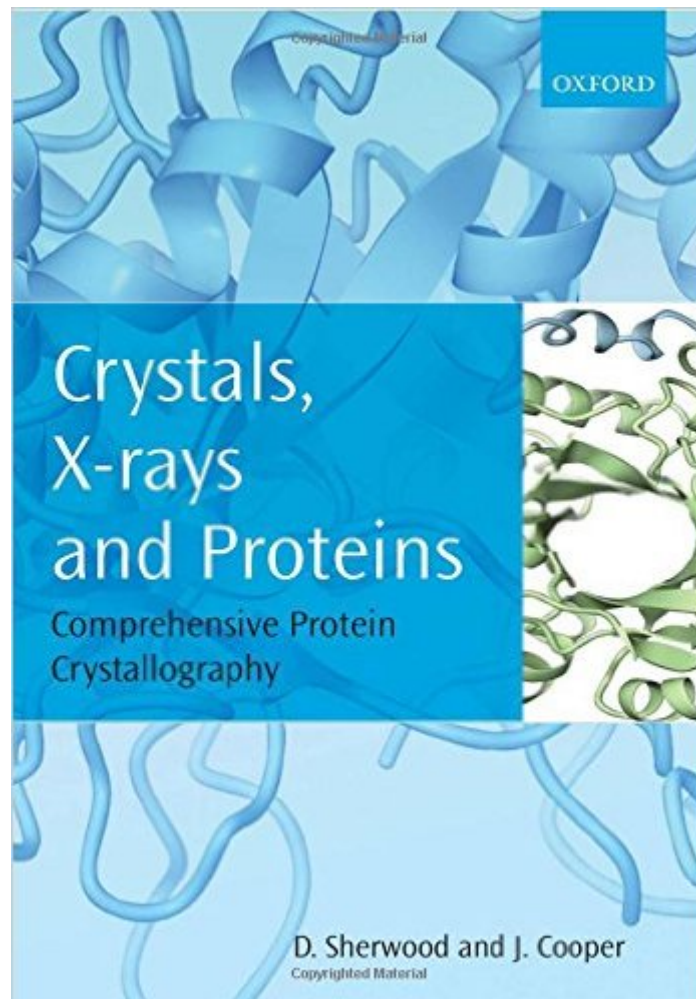


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Crystals, X-rays And Proteins: Comprehensive Protein Crystallography



Synopsis

A complete account of the theory of the diffraction of X-rays by crystals, with particular reference to the processes of determining the structures of protein molecules. This book is aimed primarily at structural biologists and biochemists but will also be valuable to those entering the field with a background in physical sciences or chemistry. It may be used at any post-school level, and develops from first principles all relevant mathematics, diffraction and wave theory, assuming no mathematical knowledge beyond integral calculus. The book covers a host of important topics in the area, including:- The practical aspects of sample preparation and X-ray data collection, using both laboratory and synchrotron sources - Data analysis at both theoretical and practical levels- The important role played by the Patterson function in structure analysis, by both molecular replacement and experimental phasing approaches - Methods for improving the resulting electron density map - The theoretical basis of methods used in refinement of protein crystal structures - In-depth explanation of the crucial task of defining the binding sites of ligands and drug molecules - The complementary roles of other diffraction methods: these reveal further detail of great functional importance in a crystal structure.

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