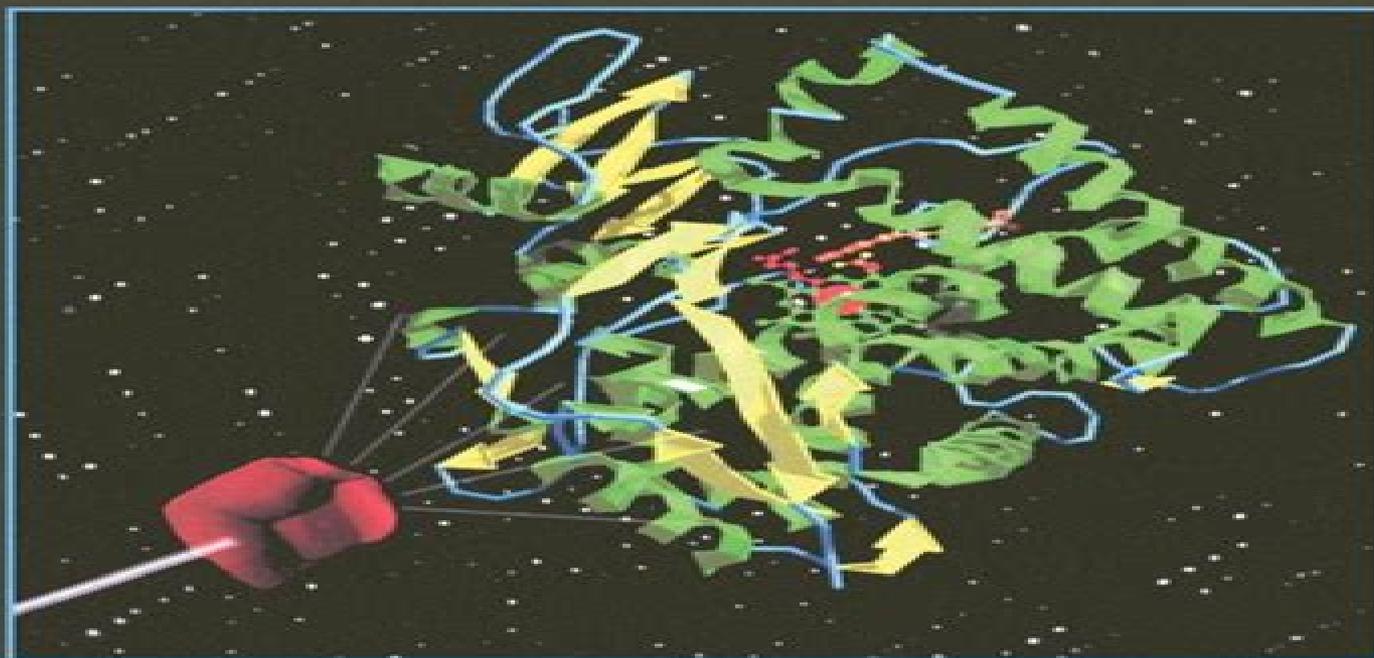




Practical Protein Crystallography

SECOND EDITION



Duncan E. McRee

Practical Protein Crystallography

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Protein Crystallography Alexander Wlodawer, Zbigniew Dauter, Mariusz Jaskolski, 2017 Structure Determination by X-ray Crystallography Mark F.C. Ladd, Rex A. Palmer, 2003-09-30 I was highly flattered when I was asked by Mark Ladd and Rex Palmer if I would write the Foreword to this Fourth Edition of their book Ladd Palmer is such a well known and classic book on the subject of crystal structure determination one of the standards in the field I did feel daunted by the prospect and wondered if I could do justice to it The determination of crystal structures by X ray crystallography has come a long way since the 1912 discoveries of von Laue and the Braggs In the intervening years great advances have been made so that today it is almost taken for granted that crystal structures can be determined in which hundreds if not thousands of separate atomic positions can be found with apparent ease In the early years the structures of relatively simple materials such as the

alkali halides were often argued over and even disputed whereas today we routinely see published structures of most complex molecular crystals including the structures of viruses and proteins

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Practical Neutron Protein Crystallography Marc-Michael Blum, Paul Langan, 2013-02-27 For the first time this promising technology is presented in a readily accessible manner The two editors a method developer and a method user have tailored the book to the needs of occasional or first time users providing ample practical advice at every stage and including a detailed walk through example of a real life protein study The result is a hands on guide starting with basic considerations of the advantages and disadvantages of this relatively new technology before going on to discuss in practical terms the course of the diffraction study from sample preparation via the actual measurement to the collection and analysis of the diffraction data For biochemists biophysicists crystallographers medicinal chemists and radiation physicists

Perspectives in Crystallography John R. Helliwell, 2015-11-16 Crystallography is one of the most multidisciplinary sciences with roots in fields as varied as mathematics physics chemistry biology materials science computation and earth and planetary science The structural knowledge gained from crystallography has been instrumental in acquiring new levels of understanding in numerous scientific areas

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Macromolecular Crystallography Mark R. Sanderson, Jane V. Skelly, 2007-08-23 Macromolecular Crystallography is the study of macromolecules proteins and nucleic acids using X ray crystallographic techniques in order to determine their

molecular structure The knowledge of accurate molecular structures is a pre requisite for rational drug design and for structure based function studies to aid the development of effective therapeutic agents and drugs The successful determination of the complete genome genetic sequence of several species including humans has recently directed scientific attention towards identifying the structure and function of the complete complement of proteins that make up that species a new and rapidly growing field of study called structural genomics There are now several important and well funded global initiatives in operation to identify all of the proteins of key model species One of the main requirements for these initiatives is a high throughput crystallization facility to speed up the protein identification process The extent to which these technologies have advanced calls for an updated review of current crystallographic theory and practice This practical reference book features the latest conventional and high throughput methods and includes contributions from a team of internationally recognized leaders and experts It will be of relevance and use to graduate students research scientists and professionals currently working in the field of conventional and high throughput macromolecular crystallography

Drug-Nucleic Acid Interactions, 2001-07-31 This volume consolidates the key methods for studying ligand nucleic acid interactions into a convenient source Techniques that are examined range from biophysical and chemical approaches to methods rooted in molecular and cell biology

Handbook of Practical Botany for the Botanical Laboratory and Private Student Eduard Strasburger, 1908

Theory and Practice of Direct Methods in Crystallography M. F. C. Ladd, R. A. Palmer, 1980-01-31

Direct methods of crystal structure determination are usually associated with techniques in which phases for a set of structure factors are determined from the corresponding experimental amplitudes by probabilistic calculations It is thus implied that such ab initio phase calculations do not require a knowledge of atomic positions and this basis distinguishes direct methods from other techniques for structure determination An acceptably wider interpretation of the term direct methods leads to other important applications involving inter alia the use of heavy atoms resolution limited phase data for large molecules rotation functions and Fourier series These topics are discussed in the later chapters of this book Although some earlier theoretical investigations were made by Harker and Kaspar direct methods may be considered to have begun around the year 1950 Important landmarks in the development of the subject include the book by Hauptmann and Karle The Centrosymmetric Crystal 1953 the definitive paper by Karle and Karle in Acta Crystallographica 1966 and the recent 1978 sophisticated program package MULTAN 78 produced mainly by Germain Main and Woolfson Woolfson's book Direct Methods in Crystallography was published in 1961 but because of the rapid progress in direct methods much of it soon became outmoded It is interesting to note that direct methods nearly came into being many years earlier Certainly the E2 relationship was used implicitly by Lonsdale in 1928 in determining the crystal structure of hexamethylbenzene

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Crystals, X-rays and Proteins Dennis Sherwood, Jon Cooper, 2010-11-05 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 Protein Crystallography T. L. Blundell,L.

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