



Direct Methods for Solving Macromolecular Structures

Edited by

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Direct Methods For Solving Macromolecular Structures

Charles W. Carter, Robert M. Sweet



Direct Methods For Solving Macromolecular Structures:

Direct Methods for Solving Macromolecular Structures S. Fortier, 2013-06-29 This book of the proceedings of the 1997 NATO Advanced Study Institute ASI on Direct Methods for Solving Macromolecular Structures was assembled from the lecturers contributions and represents a comprehensive and in depth overview of crystallographic structure determination methods for macromolecules While having a focus based on the direct methods the Institute adopted an inclusive and broad perspective Thus both direct and experimental phasing techniques are presented in this book highlighting their complementarities and synergies As well methodologies spanning the full crystallographic image reconstruction process from low resolution envelope definition to high resolution atomic refinement are discussed The first part of the book introduces the array of tools currently used in structure determination whether originating from a mathematical computational or experimental framework This section of the book displays the variety and ingenuity of old and new phasing approaches developed to solve increasingly complex structures Some of the contributions focus on recent developments and or implementations that have given older approaches a new life A case in point is the re implementation of Buerger s superposition approach which is now solving protein structures Another beautiful example is found in the introduction to the traditional multiple isomorphous replacement approach where new techniques such as site directed mutagenesis and the use of inert gases in the preparation of heavy atom derivatives are described Equally impressive are the presentations of newer approaches which take advantage of advances on the experimental front e g

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

[International Tables for Crystallography, Volume F](#) Eddy Arnold, Daniel M. Himmel, Michael G. Rossmann, 2012-03-05 International Tables for Crystallography Volume F is an expert

guide to macromolecular crystallography for the structural biologist It was commissioned by the International Union of Crystallography in recognition of the extraordinary contributions that knowledge of macromolecular structure has made and will make to the analysis of biological systems from enzyme catalysis to the workings of a whole cell The volume covers all stages of a crystallographic analysis from the preparation of recombinant proteins through crystallization diffraction data collection phase determination structure validation and structure analysis Although the volume is written for experienced scientists it is recognized that the reader is more likely to be a biologist interested in structure than a classical crystallographer interested in biology Thus there are chapters on the fundamentals history and current perspectives of macromolecular crystallography as well as on useful programs and databases such as the Protein Data Bank Each chapter is written by one or more internationally recognized experts This second edition features 19 new articles and many articles from the first edition have been revised The new articles cover topics such as standard definitions for quality indicators expression of membrane proteins protein engineering high throughput crystallography radiation damage merohedral twinning low resolution ab initio phasing robotic crystal loading whole cell X ray diffraction imaging and halogen interactions in biological crystal structures There are also new articles on relevant software including software for electron microscopy These enhancements will ensure that Volume F continues to be a key reference for macromolecular crystallographers and structural biologists More information on the series can be found at <http://it.iucr.org>

Direct Methods of Solving Crystal Structures Henk Schenk, 1991 Proceedings of the 18th course of the International School of Crystallography held April 1990 in Erice Italy Annotation copyrighted by Book News Inc Portland OR

International Tables for Crystallography, Volume B Uri Shmueli, 2008-08-27 International Tables for Crystallography are no longer available for purchase from Springer For further information please contact Wiley Inc follow the link on the right hand side of this page Volume B presents accounts of the numerous aspects of reciprocal space in crystallographic research After an introductory chapter Part 1 presents the reader with an account of structure factor formalisms an extensive treatment of the theory algorithms and crystallographic applications of Fourier methods and fundamental as well as advanced treatments of symmetry in reciprocal space In Part 2 these general accounts are followed by detailed expositions of crystallographic statistics the theory of direct methods Patterson techniques isomorphous replacement and anomalous scattering and treatments of the role of electron microscopy and diffraction in crystal structure determination including applications of direct methods to electron crystallography Part 3 deals with applications of reciprocal space to molecular geometry and best plane calculations and contains a treatment of the principles of molecular graphics and modelling and their applications A convergence acceleration method of importance in the computation of approximate lattice sums is presented and the part concludes with a discussion of the Ewald method Part 4 contains treatments of various diffuse scattering phenomena arising from crystal dynamics disorder and low dimensionality liquid crystals and an exposition of the underlying theories and or experimental evidence

Polymer crystallography and reciprocal space images of aperiodic crystals are also treated Part 5 of the volume contains introductory treatments of the theory of the interaction of radiation with matter dynamical theory as applied to X ray electron and neutron diffraction techniques The simplified trigonometric expressions for the structure factors in the 230 three dimensional space groups which appeared in Volume I of International Tables for X ray Crystallography are now given in Appendix 1 4 3 to Chapter 1 4 of this volume Volume B is a vital addition to the library of scientists engaged in crystal structure determination crystallographic computing crystal physics and other fields of crystallographic research Graduate students specializing in crystallography will find much material suitable for self study and a rich source of references to the relevant literature

Biocrystallography Mr. Rohit Manglik, 2024-04-06 EduGorilla Publication is a trusted name in the education sector committed to empowering learners with high quality study materials and resources Specializing in competitive exams and academic support EduGorilla provides comprehensive and well structured content tailored to meet the needs of students across various streams and levels

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Proteins in Solution and at Interfaces Juan M. Ruso, Ángel Piñeiro, 2013-01-31 Explores new applications emerging from our latest understanding of proteins in solution and at interfaces Proteins in solution and at interfaces increasingly serve as the starting point for exciting new applications from biomimetic materials to nanoparticle patterning This book surveys the state of the science in the field offering investigators a current understanding of the characteristics of proteins in solution and at interfaces as well as the techniques used to study these characteristics Moreover the authors explore many of the new and emerging applications that have resulted from the most recent studies Topics include protein and protein aggregate structure computational and experimental techniques to study protein structure aggregation and adsorption proteins in non standard conditions and applications in biotechnology Proteins in Solution and at Interfaces is divided into two parts Part One introduces concepts as well as theoretical and experimental techniques that are used to study protein

systems including X ray crystallography nuclear magnetic resonance small angle scattering and spectroscopic methods Part Two examines current and emerging applications including nanomaterials natural fibrous proteins and biomolecular thermodynamics The book s twenty three chapters have been contributed by leading experts in the field These contributions are based on a thorough review of the latest peer reviewed findings as well as the authors own research experience Chapters begin with a discussion of core concepts and then gradually build in complexity concluding with a forecast of future developments Readers will not only gain a current understanding of proteins in solution and at interfaces but also will discover how theoretical and technical developments in the field can be translated into new applications in material design genetic engineering personalized medicine drug delivery biosensors and biotechnology

Methods and Applications in Crystallographic Computing Sydney R. Hall,Tamaichi Ashida,1984 Thirty five international authorities offer comprehensive review of current computing techniques in crystal structure analysis The volume contains sections on data measurement and processing solution techniques refinement techniques accurate electron density analysis computer software and hardware data base techniques and computer graphics There are also contributions on powder methods and electron diffraction and microscopy

Macromolecular Crystallography, Part A Charles W. Carter,Robert M. Sweet,1997-02-12 The critically acclaimed laboratory standard for more than forty years Methods in Enzymology is one of the most highly respected publications in the field of biochemistry Since 1955 each volume has been eagerly awaited frequently consulted and praised by researchers and reviewers alike More than 270 volumes have been published all of them still in print and much of the material is relevant even today truly an essential publication for researchers in all fields of life sciences Crystal Growth Phase Determination Instrumentation and Data Collection Model Building Refinement

Principles of X-ray Crystallography Li-ling Ooi,2010 With an understanding of three dimensional structure being so central to the understanding of molecular function Principles of X ray Crystallography is the perfect guide for anyone needing to gain a working insight into X ray crystallography Book Jacket

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Components, Packaging and Manufacturing Technology Yanwen Wu,2011-01-20 Selected peer reviewed paper from 2010 International Conference on Components Packaging and Manufacturing Technology ICCPMT 2010 Sanya China December 9 10 2010

Crystallographic Computing 5 Dino Moras,1991 This is the latest entry in a series of volumes based on lectures given at the International School of Computational Crystallography This is the fifth volume published by OUP Of particular interest to molecular biologists and computing scientists this book provides a timely state of the art account of current research

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Protein Engineering Saran A. Narang,1990 Addresses the theoretical implication of the protein problem and outlines new genetic tools to synthesize gene coding for novel proteins site directed mutagenesis gene transposition and

phenotype selection procedure Also described are various physiochemical tools such as x ray crystallography *New Trends in Materials Chemistry* Charles Richard Arthur Catlow, A. K. Cheetham, 1997 Aspires to a coherent survey of the field by considering all the major aspects of the current study of the chemistry of materials Some of the 18 papers emphasize basic techniques such as new synchrotron sources in crystallography new computational techniques in simulation studies of complex materials and crystallographic microscopic spectroscopic and other characterization methods Others explore principles such as atomic transport reactivity and catalysis Still others focus on specific classes of materials including solid state ionics ceramics and microporous and molecular materials Reproduced from typescripts some double spaced Annotation copyrighted by Book News Inc Portland OR

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