

Electron Crystallography Of Biological Macromolecules

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Cryo-EM Part A: Sample Preparation and Data Collection
2010-09-30 Cryo-EM Part A: Sample Preparation and Data Collection is dedicated to a description of the instruments, samples, protocols, and analyses that belong to cryo-

EM. It emphasizes the relatedness of the ideas, instrumentation, and methods underlying all cryo-EM approaches, which allow practitioners to easily move between them. Within each section, the articles are ordered according to the most common

symmetry of the sample to which their methods are applied. Includes time-tested core methods and new innovations applicable to any researcher. Methods included are useful to both established researchers and newcomers to the field. Relevant background and reference information given for procedures can be used as a guide.

High-Resolution Electron Microscopy John C. H. Spence
2013-09-12 Revision of:
Experimental high-resolution electron microscopy. 2nd ed. 1988.

Fundamentals of Molecular Structural Biology Subrata Pal
2019-09-02 Fundamentals of Molecular Structural Biology reviews the mathematical and physical foundations of molecular structural biology. Based on these fundamental concepts, it then describes molecular structure and explains basic genetic mechanisms. Given the increasingly interdisciplinary nature of research, early career researchers and those shifting into an adjacent field often

require a "fundamentals" book to get them up-to-speed on the foundations of a particular field. This book fills that niche. Provides a current and easily digestible resource on molecular structural biology, discussing both foundations and the latest advances. Addresses critical issues surrounding macromolecular structures, such as structure-based drug discovery, single-particle analysis, computational molecular biology/molecular dynamic simulation, cell signaling and immune response, macromolecular assemblies, and systems biology. Presents discussions that ultimately lead the reader toward a more detailed understanding of the basis and origin of disease.

Modeling Nanoscale Imaging in Electron Microscopy Thomas Vogt
2012-03-02 This book presents advances in nanoscale imaging capabilities of scanning transmission electron microscopes, along with superresolution techniques, special denoising methods,

application of mathematical/statistical learning theory, and compressed sensing.

Molecular Biology of Assemblies and Machines

Alasdair C. Steven 2016-02-18
Molecular Biology of Assemblies and Machines presents a comprehensive narrative describing the structures of macromolecular complexes and how they assemble and interact. Richly illustrated, it is written for advanced undergraduates, graduate students, and researchers in biochemistry, structural biology, molecular biology, biophysics, cell biology, and microbiology, and will also appeal to those in chemistry, immunology, and medicine. Essentially all major biological activities are performed by assemblies of macromolecules (proteins, RNA, and DNA) acting in concert. These assemblies are dynamic and many are endowed with machine-like properties. This unique book explores the molecular mechanisms employed at the critical level between individual

macromolecules and cells and organelles.

Bioimaging: Current Concepts in Light & Electron Microscopy

Douglas E Chandler 2009
The development of microscopy revolutionized the world of cell and molecular biology as we once knew it and will continue to play an important role in future discoveries. Bioimaging: Current Concepts in Light and Electron Microscopy is the optimal text for any undergraduate or graduate bioimaging course, and will serve as an important reference tool for the research scientist. This unique text covers, in great depth, both light and electron microscopy, as well as other structure and imaging techniques like x-ray crystallography and atomic force microscopy. Written in a user-friendly style and covering a broad range of topics, Bioimaging describes the state-of-the-art technologies that have powered the field to the forefront of cellular and molecular biological research. Important Notice: The digital edition of this book is missing

some of the images or content found in the physical edition.

Electron Crystallography of Biological Macromolecules 1999

Biological Small Angle Scattering: Techniques, Strategies and Tips Barnali Chaudhuri 2017-12-07 This book provides a clear, comprehensible and up-to-date description of how Small Angle Scattering (SAS) can help structural biology researchers. SAS is an efficient technique that offers structural information on how biological macromolecules behave in solution. SAS provides distinct and complementary data for integrative structural biology approaches in combination with other widely used probes, such as X-ray crystallography, Nuclear magnetic resonance, Mass spectrometry and Cryo-electron Microscopy. The development of brilliant synchrotron small-angle X-ray scattering (SAXS) beam lines has increased the number of researchers interested in solution scattering. SAS is especially useful for studying

conformational changes in proteins, highly flexible proteins, and intrinsically disordered proteins. Small-angle neutron scattering (SANS) with neutron contrast variation is ideally suited for studying multi-component assemblies as well as membrane proteins that are stabilized in surfactant micelles or vesicles. SAS is also used for studying dynamic processes of protein fibrillation in amyloid diseases, and pharmaceutical drug delivery. The combination with size-exclusion chromatography further increases the range of SAS applications. The book is written by leading experts in solution SAS methodologies. The principles and theoretical background of various SAS techniques are included, along with practical aspects that range from sample preparation to data presentation for publication. Topics covered include techniques for improving data quality and analysis, as well as different scientific applications of SAS. With abundant illustrations and practical tips, we hope the clear

explanations of the principles and the reviews on the latest progresses will serve as a guide through all aspects of biological solution SAS. The scope of this book is particularly relevant for structural biology researchers who are new to SAS. Advanced users of the technique will find it helpful for exploring the diversity of solution SAS methods and applications. Chapter 3 of this book is available open access under a CC BY 4.0 license at link.springer.com.

Nature structural biology

[Anonymus AC03909881] 1994 Presents information on "Nature Structural Biology," an international monthly journal publishing original research in all fields relating to the structure of biological macromolecules as determined by X-ray crystallography and electron microscopy. Posts contact information for the editorial office in New York City via mailing address, telephone and fax numbers, and e-mail. Includes the tables of contents for past issues. Highlights author's guidelines and

subscription information. Links to structural biology resources. *Neutron Protein Crystallography* Nobuo Niimura 2011-02-17 One of the first books dedicated to the emerging field of neutron protein crystallography (NPC). It covers all of the practical aspects of NPC and demonstrates how NPC can explore protein features such as hydrogen bonds, protonation and deprotonation of amino acid residues, and hydration structures.

Electron Crystallography

Xiaodong Zou 2011-08-18 Includes bibliographical references and index.

Molecular Machines in Biology

Joachim Frank 2011-12-19 The concept of molecular machines in biology has transformed the medical field in a profound way. Many essential processes that occur in the cell, including transcription, translation, protein folding and protein degradation, are all carried out by molecular machines. This volume focuses on important molecular machines whose architecture is known and whose functional principles

have been established by tools of biophysical imaging (X-ray crystallography and cryo-electron microscopy) and fluorescence probing (single-molecule FRET). This edited volume includes contributions from prominent scientists and researchers who understand and have explored the structure and functions of these machines. This book is essential for students and professionals in the medical field who want to learn more about molecular machines.

Single-particle Cryo-electron Microscopy Joachim Frank 2018

International Tables for Crystallography, Crystallography of Biological Macromolecules Michael G. Rossmann 2001-09-12 International Tables for Crystallography is the definitive resource and reference work for crystallography and structural science. Each of the eight volumes in the series contains articles and tables of data relevant to crystallographic research and to applications of

crystallographic methods in all sciences concerned with the structure and properties of materials. Emphasis is given to symmetry, diffraction methods and techniques of crystal-structure determination, and the physical and chemical properties of crystals. The data are accompanied by discussions of theory, practical explanations and examples, all of which are useful for teaching. Volume F, Crystallography of Biological Macromolecules is an expert guide to macromolecular crystallography for the modern 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, and to the growing field of structural genomics. The volume covers all stages of a crystallographic analysis, from the preparation of samples using the techniques of molecular

biology, through crystallization, diffraction data collection, phase determination, structure validation, and structure analysis. Although the book 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 the availability of useful programs and databases, including the Protein Data Bank. Each chapter is written by an internationally recognized expert.

Optics in Our Time Mohammad D. Al-Amri 2016-12-12 Light and light based technologies have played an important role in transforming our lives via scientific contributions spanned over thousands of years. In this book we present a vast collection of articles on various aspects of light and its applications in the contemporary world at a

popular or semi-popular level. These articles are written by the world authorities in their respective fields. This is therefore a rare volume where the world experts have come together to present the developments in this most important field of science in an almost pedagogical manner. This volume covers five aspects related to light. The first presents two articles, one on the history of the nature of light, and the other on the scientific achievements of Ibn-Haitham (Alhazen), who is broadly considered the father of modern optics. These are then followed by an article on ultrafast phenomena and the invisible world. The third part includes papers on specific sources of light, the discoveries of which have revolutionized optical technologies in our lifetime. They discuss the nature and the characteristics of lasers, Solid-state lighting based on the Light Emitting Diode (LED) technology, and finally modern electron optics and its relationship to the Muslim golden age in science.

The book's fourth part discusses various applications of optics and light in today's world, including biophotonics, art, optical communication, nanotechnology, the eye as an optical instrument, remote sensing, and optics in medicine. In turn, the last part focuses on quantum optics, a modern field that grew out of the interaction of light and matter. Topics addressed include atom optics, slow, stored and stationary light, optical tests of the foundation of physics, quantum mechanical properties of light fields carrying orbital angular momentum, quantum communication, and Wave-Particle dualism in action.

Macromolecular

Crystallography Maria Armenia Carrondo 2011-12-01 This volume is a collection of the contributions presented at the 42nd Erice Crystallographic Course whose main objective was to train the younger generation on advanced methods and techniques for examining structural and dynamic aspects of biological macromolecules. The papers

review the techniques used to study protein assemblies and their dynamics, including X-ray diffraction and scattering, electron cryo-electron microscopy, electro nanospray mass spectrometry, NMR, protein docking and molecular dynamics. A key theme throughout the book is the dependence of modern structural science on multiple experimental and computational techniques, and it is the development of these techniques and their integration that will take us forward in the future.

Introduction to Macromolecular Crystallography

Alexander McPherson 2011-09-20 A comprehensive and approachable introduction to crystallography — now updated in a valuable new edition The Second Edition of this well-received book continues to offer the most concise, authoritative, and easy-to-follow introduction to the field of crystallography. Dedicated to providing a complete, basic presentation of the subject that does not assume a background

in physics or math, the book's content flows logically from basic principles to methods, such as those for solving phase problems, interpretation of Patterson maps and the difference Fourier method, the fundamental theory of diffraction and the properties of crystals, and applications in determining macromolecular structure. This new edition includes a vast amount of carefully updated materials, as well as two completely new chapters on recording and compiling X-ray data and growing crystals of proteins and other macromolecules. Richly illustrated throughout to clarify difficult concepts, this book takes a non-technical approach to crystallography that is ideal for professionals and graduate students in structural biology, biophysics, biochemistry, and molecular biology who are studying the subject for the first time.

**International Tables for
Crystallography,
Crystallography of
Biological Macromolecules**

Eddy Arnold 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>

[Three-Dimensional Electron Microscopy of Macromolecular](#)

[Assemblies](#) Joachim Frank
2006-02-02 Cryoelectron microscopy of biological molecules is among the hottest growth areas in biophysics and structural biology at present, and Frank is arguably the most distinguished practitioner of this art. CryoEM is likely over the next few years to take over much of the structural approaches currently requiring X-ray crystallography, because one can now get good and finely detailed images of single molecules down to as little as 200,000 MW, covering a substantial share of the molecules of greatest biomedical research interest. This book, the successor to an earlier work published in 1996 with Academic Press, is a natural companion work to our forthcoming book on electron crystallography by Robert Glaeser, with contributions by six others, including Frank. A growing number of workers will employ CryoEM for structural studies in their own research, and a large proportion of biomedical researchers will have a growing interest in

understanding what the capabilities and limits of this approach are.

Electron Crystallography of Biological Macromolecules

Robert M. Glaeser 2007 This is a complete introduction to all major topics needed in order to use electron microscopy as a research tool in structural biology.

4D Electron Microscopy Ahmed H. Zewail 2010 Structural phase transitions, mechanical deformations, and the embryonic stages of melting and crystallization are examples of phenomena that can now be imaged in unprecedented structural detail with high spatial resolution, and ten orders of magnitude as fast as hitherto. No monograph in existence attempts to cover the revolutionary dimensions that EM in its various modes of operation nowadays makes possible. The authors of this book chart these developments, and also compare the merits of coherent electron waves with those of synchrotron radiation. They judge it prudent to recall some

important basic procedural and theoretical aspects of imaging and diffraction so that the reader may better comprehend the significance of the new vistas and applications now afoot. This book is not a vade mecum - numerous other texts are available for the practitioner for that purpose.

Fungal Cell Wall and Immune Response J.P. Latge 2014-01-13

Recent findings on the role of the cell wall of pathogenetic fungi in the pathogenic processes of both vertebrates and invertebrates are presented. The fungal cell wall not only gives shape to the fungus, but it is a dynamic structure allowing fungal growth and survival of fungi in both friendly and adverse environments. It acts as a living sieve controlling the entry of nutrients and the secretion of metabolic products. In terms of fungal pathogenesis, the fungal wall may be responsible for eliciting the defense response of their respective invertebrate or vertebrate hosts or conversely it may provide protection against the host

defense system during the pathogenic process.

Small Angle X-Ray and Neutron Scattering from Solutions of Biological Macromolecules

Dmitri I. Svergun 2013-08-08

This book describes all aspects of the technique of small-angle scattering of X-rays and neutrons, including instrumentation, sample requirements, data interpretation and modelling methods, in a comprehensive way and gives examples of applications in various fields of biophysics and biochemistry.

Chemica Scripta 1979

Crystallography in Molecular Biology Dino Moras 2013-04-17

Biological Field Emission Scanning Electron Microscopy

Roland A. Fleck 2019-02-06

The go-to resource for microscopists on biological applications of field emission gun scanning electron microscopy (FEGSEM) The evolution of scanning electron microscopy technologies and capability over the past few years has revolutionized the biological imaging capabilities of the microscope—giving it the

capability to examine surface structures of cellular membranes to reveal the organization of individual proteins across a membrane bilayer and the arrangement of cell cytoskeleton at a nm scale. Most notable are their improvements for field emission scanning electron microscopy (FEGSEM), which when combined with cryo-preparation techniques, has provided insight into a wide range of biological questions including the functionality of bacteria and viruses. This full-colour, must-have book for microscopists traces the development of the biological field emission scanning electron microscopy (FEGSEM) and highlights its current value in biological research as well as its future worth. Biological Field Emission Scanning Electron Microscopy highlights the present capability of the technique and informs the wider biological science community of its application in basic biological research. Starting with the theory and history of FEGSEM, the book offers chapters

covering: operation (strengths and weakness, sample selection, handling, limitations, and preparation); Commercial developments and principals from the major FEGSEM manufacturers (Thermo Scientific, JEOL, HITACHI, ZEISS, Tescan); technical developments essential to bioFEGSEM; cryobio FEGSEM; cryo-FIB; FEGSEM digital-tomography; array tomography; public health research; mammalian cells and tissues; digital challenges (image collection, storage, and automated data analysis); and more. Examines the creation of the biological field emission gun scanning electron microscopy (FEGSEM) and discusses its benefits to the biological research community and future value Provides insight into the design and development philosophy behind current instrument manufacturers Covers sample handling, applications, and key supporting techniques Focuses on the biological applications of field emission gun scanning electron microscopy (FEGSEM),

covering both plant and animal research Presented in full colour An important part of the Wiley-Royal Microscopical Series, Biological Field Emission Scanning Electron Microscopy is an ideal general resource for experienced academic and industrial users of electron microscopy—specifically, those with a need to understand the application, limitations, and strengths of FEGSEM.

Single-particle Cryo-EM of Biological Macromolecules
GLAESER 2021-05-19 This edited book is written for students, postdocs and established investigators who want to enter the field of single-particle cryo-EM. This is a recently developed method to determine high-resolution structures of biological macromolecules. A major strength is the fact that cryo-EM does not require prior crystallization of protein complexes. It is especially well suited for larger complexes and molecular machines. This book, provides a comprehensive, accessible and authoritative introduction to the field. It

covers all necessary background, ranging from the underlying concepts to practical aspects such as specimen preparation, data-collection, data analysis, and the final validation of results. Key features Written for students, postdocs and established investigators who want to enter the field of single-particle cryo-EM Provides a comprehensive, accessible and authoritative introduction to the field of high-resolution structure analysis by single-article cryo-EM Covers all necessary background, ranging from the underlying concepts to practical aspects such as specimen preparation, data-collection, data analysis, and the final validation of results Authors of individual sections of this book have been recruited from among the most authoritative leaders in each topic

Crystallization of Nucleic Acids and Proteins Arnaud Ducruix 1992 Crystallography is the major method of determining structures of biological macromolecules yet crystallization techniques are

still regarded as difficult to perform. This new edition of *Crystallization of Nucleic Acids and Proteins: A Practical Approach* continues in the vein of the first edition by providing a detailed and rational guide to producing crystals of proteins and nucleic acids of sufficient quantity and quality for diffraction studies. It has been thoroughly updated to include all the major new techniques such as the uses of molecular biology in structural biology (maximizing expression systems, sequence modifications to enable crystallization, and the introduction of anomalous scatterers); diagnostic analysis of prenucleation and nucleation by spectroscopic methods; and the two-dimensional electron crystallography of soluble proteins on planar lipid films. As well as an introduction to crystallogenesis, the other topics covered are: Handling macromolecular solutions, experimental design, seeding, proceeding from solutions to crystals Crystallization in gels Crystallization of nucleic acid

complexes and membrane proteins Soaking techniques Preliminary characterization of crystals in order to tell whether they are suitable for diffraction studies. As with all Practical Approach books the protocols have been written by experienced researchers and are tried and tested methods. The underlying theory is brought together with the laboratory protocols to provide researchers with the conceptual and methodological tools necessary to exploit these powerful techniques.

Crystallization of Nucleic Acids and Proteins: A Practical Approach 2e will be an invaluable manual of practical crystallization methods to researchers in molecular biology, crystallography, protein engineering, and biological chemistry.

Structural Biology Using Electrons and X-rays Michael F Moody 2011-03-03 Structural Biology Using Electrons and X-Rays discusses the diffraction and image-based methods used for the determination of complex biological

macromolecules. The book focuses on the Fourier transform theory, which is a mathematical function that is computed to transform signals between time and frequency domain. Composed of five parts, the book examines the development of nuclear magnetic resonance (NMR), which allows the calculation of the images of a certain protein. Parts 1 to 4 provide the basic information and the applications of Fourier transforms, as well as the different methods used for image processing using X-ray crystallography and the analysis of electron micrographs. Part 5 focuses entirely on the mathematical aspect of Fourier transforms. In addition, the book examines detailed structural analyses of a specimen's symmetry (i.e., crystals, helices, polyhedral viruses and asymmetrical particles). This book is intended for the biologist or biochemist who is interested in different methods and techniques for calculating the images of proteins using nuclear magnetic

resonance (NMR). It is also suitable for readers without a background in physical chemistry or mathematics. Emphasis on common principles underlying all diffraction-based methods Thorough grounding in theory requires understanding of only simple algebra Visual representations and explanations of challenging content Mathematical detail offered in short-course form to parallel the text

Electron Microscopy John J. Bozzola 1999 New edition of an introductory reference that covers all of the important aspects of electron microscopy from a biological perspective, including theory of scanning and transmission; specimen preparation; darkroom, digital imaging, and image analysis; laboratory safety; interpretation of images; and an atlas of ultrastructure. Generously illustrated with bandw line drawings and photographs. Annotation copyrighted by Book News, Inc., Portland, OR
High Resolution Electron Crystallography of Protein

Molecules 1993 Electron diffraction data and high resolution images can now be used to obtain accurate, three-dimensional density maps of biological macromolecules. These density maps can be interpreted by building an atomic-resolution model of the structure into the experimental density. The Cowley-Moodie formalism of dynamical diffraction theory has been used to validate the use of kinematic diffraction theory, strictly the weak phase object approximation, in producing such 3-D density maps. Further improvements in the preparation of very flat specimens and in the retention of diffraction to a resolution of 0.2 nm or better could result in electron crystallography becoming as important a technique as x-ray crystallography currently is for the field of structural molecular biology.

Electron Tomography
Joachim Frank 2014-01-15
Macromolecular Crystallography Charles W. Carter 1997 Annotation

Accurate molecular structures is vital for rational drug design and for structure based functional studies directed toward the development of effective therapeutic agents and drugs. Crystallography can reliably predict structure, both in terms of folding and atomic details of bonding. * Phases * Map interpretation and refinement * Analysis and software.

Three-Dimensional Electron Microscopy of Macromolecular Assemblies

Joachim Frank 2006-02-02
Cryoelectron microscopy of biological molecules is among the hottest growth areas in biophysics and structural biology at present, and Frank is arguably the most distinguished practitioner of this art. CryoEM is likely over the next few years to take over much of the structural approaches currently requiring X-ray crystallography, because one can now get good and finely detailed images of single molecules down to as little as 200,000 MW, covering a substantial share of the

molecules of greatest biomedical research interest. This book, the successor to an earlier work published in 1996 with Academic Press, is a natural companion work to our forthcoming book on electron crystallography by Robert Glaeser, with contributions by six others, including Frank. A growing number of workers will employ CryoEM for structural studies in their own research, and a large proportion of biomedical researchers will have a growing interest in understanding what the capabilities and limits of this approach are.

Liquid Cell Electron Microscopy
Physical Biology Ahmed H. Zewail 2008
Addresses significant problems in physical biology and adjacent disciplines. This volume provides a perspective on the methods and concepts at the heart of chemical and biological behavior, covering the topics of visualization; theory and computation for complexity; and macromolecular function, protein folding, and protein misfolding

Electron Tomography

Joachim Frank 2008-03-05 This definitive work provides a comprehensive treatment of the mathematical background and working methods of three-dimensional reconstruction from tilt series. Special emphasis is placed on the problems presented by limitations of data collection in the transmission electron microscope. The book, extensively revised and updated, takes the reader from biological specimen preparation to three-dimensional images of the cell and its components.

Membrane Proteins: Structures, Interactions and Models A.

Pullman 2012-12-06 The 25th Jerusalem Symposium represents a most significant highlight in the development and history of these meetings. Living within the decimal system we have celebrated with much pleasure the 15th and the 20th Jerusalem Symposia. With this one we experience a feeling of particular satisfaction because 25 years is different from, is more than, two decades and a

half. It is a quarter of a century. It seems thus as if we have changed the dimension of our endeavour. In no way do we lose the sense of modesty with respect to the significance of these meetings. For the organizers, however, they do represent a continuity of efforts which we feel happy to have been able to carry out. At this occasion it seems useful to say a few words about the origin of the Jerusalem Symposia and to recall the name of a colleague who played an essential role in their creation and has been a most efficient and devoted co-organizer of the seven first of them. This was Professor Ernst Bergmann, one of the most distinguished founders of Israeli Science and a world famous physico-organic chemist.

Three-Dimensional Electron Microscopy of Macromolecular Assemblies

Frank Joachim 1996-01-24 Three-Dimensional Electron Microscopy of Macromolecular Assemblies is the first systematic introduction to single-particle methods of reconstruction. It covers correlation alignment,

classification, 3D reconstruction, restoration, and interpretation of the resulting 3D images in macromolecular assemblies. It will be an indispensable resource for newcomers to the field and for all using or adopting these methods. Key Features * Presents methods that offer an alternative to crystallographic techniques for molecules that cannot be crystallized * Describes methods that have been instrumental in exploring the three-dimensional structure of * the nuclear pore complex *

the calcium release channel; * the ribosome * chaperonins
Crystals, X-rays and Proteins Dennis Sherwood
2011 Information derived from X-ray crystal structures of biological molecules allows us to explain their functions in living organisms in extraordinary detail, and to develop drugs to treat disease. This book describes the principles and practice of X-ray diffraction as a key technique at the forefront of new discoveries in biology and medicine.