

Electron Crystallography Of Biological Macromolecules

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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.

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[Crystallography in Molecular Biology](#) Dino Moras 2013-04-17

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 Crystallography Thomas E. Weirich 2006-08-18 During the last decade we have been witness to several exciting achievements in electron crystallography. This includes structural and charge density studies on organic molecules complicated inorganic and metallic materials in the amorphous, nano-, meso- and quasi-crystalline state and also development of new software, tailor-made for the special needs of electron crystallography. Moreover, these developments have been accompanied by a now available new generation of computer controlled electron microscopes equipped with high-coherent field-emission sources, cryo-specimen holders, ultra-fast CCD cameras, imaging plates, energy filters and even correctors for electron optical

distortions. Thus, a fast and semi-automatic data acquisition from small sample areas, similar to what we today know from imaging plates diffraction systems in X-ray crystallography, can be envisioned for the very near future. This progress clearly shows that the contribution of electron crystallography is quite unique, as it enables to reveal the intimate structure of samples with high accuracy but on much smaller samples than have ever been investigated by X-ray diffraction. As a tribute to these tremendous recent achievements, this NATO Advanced Study Institute was devoted to the novel approaches of electron crystallography for structure determination of nanosized materials. *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 of Biological Macromolecules 1999

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

The Resolution Revolution: Recent Advances In cryoEM 2016-08-26 cryoEM, a new volume in the *Methods in Enzymology* series, continues the legacy of this premier serial with quality chapters authored by leaders in the field. This volume covers research methods and new developments in recording images, the creation, evaluation and validation of 3D maps from the images, model building into maps and refinement of the resulting atomic structures, and applications of essentially single particle methods to helical structures and to sub-tomogram averaging. Continues the legacy of this premier serial with quality chapters authored by leaders in the field Covers research methods that determine the structures of biological molecules, a vital step for understanding their function Contains the technical developments underpinning the advances of cryoEM and captures the exciting insights that have resulted

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.

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.

Small Angle X-Ray and Neutron Scattering from Solutions of Biological Macromolecules Dmitri I. Svergun 2013-08-08 Small-angle scattering of X-rays or neutrons is a technique that allows one to study the structures and interactions of disordered materials like polymers in the solid state, melt or solution or metal clusters in alloys. It is also the method of choice to characterize biological macromolecules in solution, in particular when they cannot be crystallized. A further advantage of the technique is that it can easily be combined with standard perturbation methods such as temperature and pressure jumps and stopped flow mixing thus offering useful information complementary to spectroscopic methods. The book describes all aspects of the technique: instrumentation, sample requirements, data interpretation and modelling methods in a comprehensive way and gives examples of applications in various fields of biophysics and biochemistry. Appendices describe the mathematical background and additional resources relevant to the method.

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.

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

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 lath 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.

Electron Crystallography Devinder Singh 2020-07-22 In the quantitative determination of new structures, micro-/nano-crystalline materials pose significant challenges. The different properties of materials are structure-dependent. Traditionally, X-ray crystallography has been used for the analysis of these materials. Electron diffraction is a technique that complements other techniques; for example, single crystal X-ray diffraction and powder X-ray diffraction for determination of structure. Electron diffraction plays a very important role when crystals are very small using single crystal X-ray diffraction or very complex for structure solution by powder X-ray diffraction. With the introduction of advanced methodologies, important methods for crystal structural analysis in the field of electron crystallography have been discovered, such as rotation electron diffraction (RED) and automated electron diffraction tomography (ADT). In recent years, large numbers of crystal structures have been solved using electron crystallography.

Electron Tomography Joachim Frank 2014-01-15

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.

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.

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

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.

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.

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

Liquid Cell Electron Microscopy

X-Ray Diffraction Imaging of Biological Cells Masayoshi Nakasako 2018-03-29 In this book, the author describes the development of the experimental diffraction setup and structural analysis of non-crystalline particles from material science and biology. Recent advances in X-ray free electron laser (XFEL)-coherent X-ray diffraction imaging (CXDI) experiments allow for the structural analysis of non-crystalline particles to a resolution of 7 nm, and to a resolution of 20 nm for biological materials. Now XFEL-CXDI marks the dawn of a new era in structural analysis of non-crystalline particles with dimensions larger than 100 nm, which was quite impossible in the 20th century. To conduct CXDI experiments in both synchrotron and XFEL facilities, the author has developed apparatuses, named KOTOBUKI-1 and TAKASAGO-6 for cryogenic diffraction experiments on frozen-hydrated non-crystalline particles at around 66 K. At the synchrotron facility, cryogenic diffraction experiments dramatically reduce radiation damage of specimen particles and allow tomography CXDI experiments. In addition, in XFEL experiments, non-crystalline particles scattered on thin support membranes and flash-cooled can be used to efficiently increase the rate of XFEL pulses. The rate, which depends on the number density of scattered particles and the size of X-ray beams, is currently 20-90%, probably the world record in XFEL-CXDI experiments. The experiment setups and results are introduced in this book. The author has also developed software suitable for efficiently processing of diffraction patterns and retrieving electron density maps of specimen particles based on the diffraction theory used in CXDI.

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.

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>

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.

Crystallization of Nucleic Acids and Proteins Arnaud Ducruix 1999-10-21

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 crystallogenes, 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.

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.

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.

Advances in Protein Molecular and Structural Biology Methods Timir

Tripathi 2022-01-14 *Advances in Protein Molecular and Structural Biology Methods* offers a complete overview of the latest tools and methods applicable to the study of proteins at the molecular and structural level. The book begins with sections exploring tools to optimize recombinant protein expression and biophysical techniques such as fluorescence spectroscopy, NMR, mass spectrometry, cryo-electron microscopy, and X-ray crystallography. It then moves towards computational approaches, considering structural bioinformatics, molecular dynamics simulations, and deep machine learning technologies. The book also covers methods applied to intrinsically disordered proteins (IDPs) followed by chapters on protein interaction networks, protein function, and protein design and engineering. It provides researchers with an extensive toolkit of methods and techniques to draw from when conducting their own experimental work, taking them from foundational concepts to practical application. Presents a thorough overview of the latest and emerging methods and technologies for protein study Explores biophysical techniques, including nuclear magnetic resonance, X-ray crystallography, and cryo-electron microscopy Includes computational and machine learning methods Features a section dedicated to tools and techniques specific to studying intrinsically disordered proteins

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

Advances in Imaging and Electron Physics 2014-07-17

Advances in Imaging & Electron Physics merges two long-running serials—*Advances in Electronics & Electron Physics* and *Advances in Optical & Electron Microscopy*. The series features extended articles on the physics of electron devices (especially semiconductor devices), particle optics at high and low energies, microlithography, image science and digital image processing, electromagnetic wave propagation, electron microscopy, and the computing methods used in all these domains. Contributions from leading authorities Informs and updates on all the latest developments in the field

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.

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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.

Single-particle Cryo-electron Microscopy Joachim Frank 2018

Fundamentals of Molecular Structural Biology Subrata Pal 2019-08-13

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