

Electron Crystallography Of Biological Macromolecules

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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

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

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.

Single-particle Cryo-electron Microscopy

Joachim Frank 2018
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.

High-Resolution Electron Microscopy John C. H.

Spence 2013-09-12

Revision of:

Experimental high-resolution electron microscopy. 2nd ed. 1988.

NMR in Biological Systems K.V.R. Chary

2008-04-08 During teaching NMR to students

and researchers, we felt the need for a text-book which can cover modern trends in the application of NMR to biological systems. This book covers the entire area of NMR in Biological Sciences (Biomolecules, cells and tissues, animals, plants and drug design). As well as being useful to researchers, this is an excellent book for teaching a course on NMR in Biological Systems. *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 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.

Electron Tomography

Joachim Frank 2014-01-15

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.

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.

Crystallography in

Molecular Biology Dino

Moras 2013-04-17

Electron Crystallography of Biological

Macromolecules 1999

4D Visualization of

Matter Ahmed H Zewail

2014-09-12 Ever since the beginning of mankind's efforts to pursue scientific inquiry into the laws of nature, visualization of the very distant and the very small has been paramount. The examples are numerous. A century ago, the atom appeared mysterious, a "raisin or plum pie of no structure," until it was visualized on the appropriate length and time scales. Similarly, with telescopic observations, a central dogma of the cosmos was changed and complexity yielded to simplicity of the heliocentric structure and motion in our solar system. For matter, in over a century of developments, major advances have been made to explore the inner microscopic structures and dynamics. These advances have benefited many fields of endeavor, but visualization was incomplete; it was limited either to the 3D

spatial structure or to the 1D temporal evolution. However, in systems with myriads of atoms, 4D spatiotemporal visualization is essential for dissecting their complexity. The biological world is rich with examples, and many molecular diseases cannot be fully understood without such direct visualization, as, for example, in the case of Alzheimer's and Parkinson's. The same is true for phenomena in materials science, chemistry, and nanoscience. This anthology is an account of the collected works that have emerged over the past decade from Caltech. Through recent publications, the volume provides overviews of the principles, the electron-based techniques, and the applications made. Thanks to advances in imaging principles and technology, it is now possible with 4D electron microscopy to reach ten orders of magnitude improvement in time resolution while

simultaneously conserving the atomic spatial resolution in visualization. This is certainly a long way from Robert Hooke's microscopy, which was recorded in his 1665 masterpiece *Micrographia*.

Image Analysis Donat P. Hader 2000-08-23 Automatic image analysis has become an important tool in many fields of biology, medicine, and other sciences. Since the first edition of *Image Analysis: Methods and Applications*, the development of both software and hardware technology has undergone quantum leaps. For example, specific mathematical filters have been developed for quality enhance-

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. *Recent Advances in*

Electron Cryomicroscopy
2010-11-25 Structural genomics is the systematic determination of 3-D structures of proteins representative of the range of protein structure and function found in nature. The goal is to build a body of structural information that will predict the structure and potential function for almost any protein from knowledge of its coding sequence. This is essential information for understanding the functioning of the human proteome, the ensemble of tens of thousands of proteins specified by the human genome. While most structural biologists pursue structures of individual proteins or protein groups, specialists in structural genomics pursue structures of proteins on a genome wide scale. This implies large-scale cloning, expression and purification. One main advantage of this approach is economy of scale. Examines the three dimensional

structure of all proteins of a given organism, by experimental methods such as X-ray crystallography and NMR spectroscopy Looks at structural genomics as a foundation of drug discovery as discovering new medicines is becoming more challenging and the pharmaceutical industry is looking to new technologies to help in this mission

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

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.

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

Chemica Scripta 1979
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.

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>

Hydration Structures of Proteins Masayoshi Nakasako 2021-10-25 This book describes hydration structures of proteins by combining experimental results with theoretical considerations. It is designed to introduce graduate students and researchers to microscopic views of the interactions between

water and biological macromolecules and to provide them with an overview of the field. Topics on protein hydration from the past 25 years are examined, most of which involve crystallography, fluorescence measurements, and molecular dynamics simulations. In X-ray crystallography and molecular dynamics simulations, recent advances have accelerated the study of hydration structures over the entire surface of proteins. Experimentally, crystal structure analysis at cryogenic temperatures is advantageous in terms of visualizing the positions of hydration water molecules on the surfaces of proteins in their frozen-hydrated crystals. A set of massive data regarding hydration sites on protein surfaces provides an appropriate basis, enabling us to identify statistically significant trends in geometrical characteristics.

Trajectories obtained from molecular dynamics simulations illustrate the motion of water molecules in the vicinity of protein surfaces at sufficiently high spatial and temporal resolution to study the influences of hydration on protein motion. Together with the results and implications of these studies, the physical principles of the measurement and simulation of protein hydration are briefly summarized at an undergraduate level. Further, the author presents recent results from statistical approaches to characterizing hydrogen-bond geometry in local hydration structures of proteins. The book equips readers to better understand the structures and modes of interaction at the interface between water and proteins. Referred to as "hydration structures", they are the subject of much discussion, as they may help to answer the

question of why water is indispensable for life at the molecular and atomic level.

Cellular Electron Microscopy

J. Richard McIntosh 2011-09-02
Recent advances in the imaging technique electron microscopy (EM) have improved the method, making it more reliable and rewarding, particularly in its description of three-dimensional detail. Cellular Electron Microscopy will help biologists from many disciplines understand modern EM and the value it might bring to their own work. The book's five sections deal with all major issues in EM of cells: specimen preparation, imaging in 3-D, imaging and understanding frozen-hydrated samples, labeling macromolecules, and analyzing EM data. Each chapter was written by scientists who are among the best in their field, and some chapters provide multiple points of view on the issues they discuss. Each section of the book is

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preceded by an introduction, which should help newcomers understand the subject. The book shows why many biologists believe that modern EM will forge the link between light microscopy of live cells and atomic resolution studies of isolated macromolecules, helping us toward the goal of an atomic resolution understanding of living systems. Updates the numerous technological innovations that have improved the capabilities of electron microscopy Provides timely coverage of the subject given the significant rise in the number of biologists using light microscopy to answer their questions and the natural limitations of this kind of imaging Chapters include a balance of "how to", "so what" and "where next", providing the reader with both practical information, which is necessary to use these methods, and a sense of where the field is going
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 pre-nucleation 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.

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.

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.

Electron Microscopy John Kuo 2007 Hands-on experts describe in detail the key electron microscopy techniques used for examining cells, tissue, biological macromolecules, molecular structure, and their interactions.

Electron Microscopy

Methods and Protocols, Second Edition, offers both newcomers and established researchers across experimental biology and medicine wanting to expand their repertoire a gold-standard laboratory manual of cutting-edge electron microscopy techniques—each optimized for reproducibility and robust results—today's gold-standard laboratory manual. New to this edition are sections covering transmission electron microscopy (TEM), and scanning electron microscopy (SEM).

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

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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.

High-Resolution Transmission Electron Microscopy Peter Buseck
1989-02-02 This book provides an introduction to the fundamental concepts, techniques, and methods used for electron microscopy at high resolution in space, energy, and even in time. It delineates the theory of elastic scattering, which is most useful for spectroscopic and

chemical analyses. There are also discussions of the theory and practice of image calculations, and applications of HRTEM to the study of solid surfaces, highly disordered materials, solid state chemistry, mineralogy, semiconductors and metals. Contributors include J. Cowley, J. Spence, P. Buseck, P. Self, and M.A. O'Keefe. Compiled by experts in the fields of geology, physics and chemistry, this comprehensive text will be the standard reference for years to come.

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.

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.

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.

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.

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

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.

Imaging Life Gary C. Howard 2014-07-30 This volume provides an overview of a variety of approaches to biological image analysis, which allow for the study of living organisms at all levels of complexity and organization. These organisms range from individual macromolecules to subcellular and cellular volumes, tissues and microbial communities. Such a "systems biology" understanding of life requires the combination of a variety of imaging techniques, and with it an in-depth understanding of their respective strengths and limitations, as well as their intersection with other techniques. Howard, Brown, and Auer show us that the integration of these imaging techniques will allow us to overcome the reductionist approach to biology that dominated the twentieth century, which was aimed at

examining the physical and chemical properties of life's constituents, one macromolecule at a time. However, while based on the laws of physics and chemistry, life is not simply a set of chemical reactions and physical forces; it features an exquisite spatiotemporal organization that allows an inconceivably large number of chemical processes to coexist, refined by billions of years of evolutionary experimentation. And yet, many fundamental questions remain largely unanswered; Imaging Life argues that we are just now beginning to address the spatiotemporal organizational component of living processes. "Imaging" is needed in order to reveal the spatiotemporal relationships between components, and thus to understand organizational guiding principles of living systems. Only through imaging will we be able to decipher the mechanisms and the marvelous organization

that enable and sustain the mystery of life. Imaging Life shows us how biology is beginning to do just that.

Caught By Viruses

Michael G Rossmann
2021-11-10 The current book attempts to give a glimpse of the scientific life of Michael Rossmann. The book begins with his very interesting and moving autobiography. His enormous energy must have been evident already from early childhood when he and his mother had to emigrate from Nazi-Germany to England, via The Netherlands. Starting school with a new language was a challenge that he managed well with the assistance of understanding teachers. Crystallography soon became the tool to explore new worlds, unknown to everybody. With a skill for mathematics, he realized that the transform of a molecular structure in the diffraction pattern could be used for analysis of both

symmetry and structural relationships. This method, molecular replacement (MR, also the initials of his name) became one of his great successes of his career. The previous book by him in this series (Selected Papers by Michael G Rossmann with Commentaries) covers his main contributions in this area. With an interest in symmetry, viruses became obvious objects to study. Rossmann attacked these monstrously large molecular assemblies with his unflinching energy and his appetite for real challenges. The amazing variation of molecular arrangements with icosahedral

symmetry is truly amazing. This book includes a selection of reports of the structures of some giant viruses. As always, knowing the structure enhances the understanding of function greatly, in the case of viruses the mechanism of infection is a key problem. Rossmann has contributed many central insights in this area. Thus, this book is of interest both as an interesting personal story but also for research into viruses that repeatedly plague all living organisms on the planet, right now in the form of the corona virus pandemic.