

Principles Of Protein X Ray Crystallography

An essential guide to biomolecular and bioanalytical techniques and their applications Biomolecular and Bioanalytical Techniques offers an introduction to, and a basic understanding of, a wide range of biophysical techniques. The text takes an interdisciplinary approach with contributions from a panel of distinguished experts. With a focus on research, the text comprehensively covers a broad selection of topics drawn from contemporary research in the fields of chemistry and biology. Each of the internationally reputed authors has contributed a single chapter on a specific technique. The chapters cover the specific technique's background, theory, principles, technique, methodology, protocol and applications. The text explores the use of a variety of analytical tools to characterise biological samples. The contributors explain how to identify and quantify biochemically important molecules, including small molecules as well as biological macromolecules such as enzymes, antibodies, proteins, peptides and nucleic acids. This book is filled with essential knowledge and explores the skills needed to carry out the research and development roles in academic and industrial laboratories. A technique-focused book that bridges the gap between an introductory text and a book on advanced research methods Provides the necessary background and skills needed to advance the research methods Features a structured approach within each chapter Demonstrates an interdisciplinary approach that serves to develop independent thinking Written for students in chemistry, biological, medical, pharmaceutical, forensic and biophysical sciences, Biomolecular and Bioanalytical Techniques is an in-depth review of the most current biomolecular and bioanalytical techniques in the field. Update to: Crystals, X-rays, and proteins / Dennis Sherwood. 1976.

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

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

Structural Biology Using Electrons and X-rays

Biomolecular Crystallography

Crystallography Made Crystal Clear

Protein Folding

The Molecules of Life

Physical Principles and Techniques of Protein Chemistry

University Physics is designed for the two- or three-semester calculus-based physics course. The text has been developed to meet the scope and sequence of most university physics courses and provides a foundation for a career in mathematics, science, or engineering. The book provides an important opportunity for students to learn the core concepts of physics and understand how those concepts apply to their lives and to the world around them. Due to the comprehensive nature of the material, we are offering the book in three volumes for flexibility and efficiency. Coverage and Scope Our University Physics textbook adheres to the scope and sequence of most two- and three-semester physics courses nationwide. We have worked to make physics interesting and accessible to students while maintaining the mathematical rigor inherent in the subject. With this objective in mind, the content of this textbook has been developed and arranged to provide a logical progression from fundamental to more advanced concepts, building upon what students have already learned and emphasizing connections between topics and between theory and applications. The goal of each section is to enable students not just to recognize concepts, but to work with them in ways that will be useful in later courses and future careers. The organization and pedagogical features were developed and vetted with feedback from science educators dedicated to the project. VOLUME III Unit 1: Optics Chapter 1: The Nature of Light Chapter 2: Geometric Optics and Image Formation Chapter 3: Interference Chapter 4: Diffraction Unit 2: Modern Physics Chapter 5: Relativity Chapter 6: Photons and Matter Waves Chapter 7: Quantum Mechanics Chapter 8: Atomic Structure Chapter 9: Condensed Matter Physics Chapter 10: Nuclear Physics Chapter 11: Particle Physics and Cosmology

The rational, structure-based approach has become standard in present-day drug design. As a consequence, the availability of high-resolution structures of target proteins is more often than not the basis for an entire drug development program. Protein structures suited for rational drug design are almost exclusively derived from crystallographic studies, and drug developers are relying heavily on the power of this method. Here, researchers from leading pharmaceutical companies present valuable first-hand information, much of it published for the first time. They discuss strategies to derive high-resolution structures for such important target protein classes as kinases or proteases, as well as selected examples of successful protein crystallographic studies. A special section on recent methodological developments, such as for high-throughput crystallography and

microcrystallization, is also included. A valuable companion for crystallographers involved in protein structure determination as well as drug developers pursuing the structure-based approach for use in their daily work.

This detailed, comprehensive book describes the fundamental properties of soft X-rays and extreme ultraviolet (EUV) radiation and discusses their applications in a wide variety of fields, including EUV lithography for semiconductor chip manufacture and soft X-ray biomicroscopy. The author begins by presenting the relevant basic principles such as radiation and scattering, wave propagation, diffraction, and coherence. He then goes on to examine a broad range of phenomena and applications. The topics covered include spectromicroscopy, EUV astronomy, synchrotron radiation, and soft X-ray lasers. The author also provides a wealth of useful reference material such as electron binding energies, characteristic emission lines and photo-absorption cross-sections. The book will be of great interest to graduate students and researchers in engineering, physics, chemistry, and the life sciences. It will also appeal to practising engineers involved in semiconductor fabrication and materials science.

A textbook for the student beginning a serious study of X-ray crystallography.

New Insights and Methods

An Introduction to X-ray Crystallography

Protein Crystallization

Applications in Materials, Chemistry and Biology

Principles of Protein X-ray Crystallography

History and Technical Developments

The ultra-bright femtosecond X-ray pulses provided by X-ray free electron lasers (XFELs) open up opportunities to study the structure and dynamics of a wide variety of systems beyond what is possible with synchrotron sources. This book introduces the principles and properties of currently operating and future XFELs, before outlining applications in materials science, chemistry and biology. Edited by pioneers in this exciting field, and featuring contributions from leading researchers, this book is ideal for researchers working with XFELs, synchrotron radiation, ultrafast and femtosecond crystallography and femtosecond spectroscopy.

Crystallography Made Crystal Clear is designed to meet the need for an X-ray analysis that is between brief textbook sections and complete treatments. The book provides non-crystallographers with an intellectually satisfying explanation of the principles of how protein models are gleaned from X-ray analysis. The understanding of these concepts will foster wise use of the models, including the recognition of the strengths and weaknesses of pictures or computer graphics. Since proteins comprise the majority of the mass of macromolecules in cells and carry out biologically important tasks, the book will be of interest to biologists. Provides accessible descriptions of principles of x-ray crystallography, built on simple foundations for anyone with a basic science background Leads the reader through clear, thorough, unthreatening explanations of the mathematics behind crystallography Explains how to read crystallography papers in research journals If you use computer-generated models of proteins or nucleic acids for: Studying molecular interactions Designing ligands, inhibitors, or drugs Engineering new protein functions Interpreting chemical, kinetic, thermodynamic, or spectroscopic data Studying protein folding Teaching macromolecule structure, and if you want to read new structure papers intelligently;

become a wiser user of macromolecular models; and want to introduce undergraduates to the important subject of x-ray crystallography, then this book is for you.

This book on X-ray Crystallography is a compilation of current trends in the use of X-ray crystallography and related structural determination methods in various fields. The methods covered here include single crystal small-molecule X-ray crystallography, macromolecular (protein) single crystal X-ray crystallography, and scattering and spectroscopic complimentary methods. The fields range from simple organic compounds, metal complexes to proteins, and also cover the meta-analyses of the database for weak interactions.

New textbooks at all levels of chemistry appear with great regularity. Some fields such as basic biochemistry, organic reaction mechanisms, and chemical thermodynamics are well represented by many excellent texts, and new or revised editions are published sufficiently often to keep up with progress in research. However, some areas of chemistry, especially many of those taught at the graduate level, suffer from a real lack of up to-date textbooks. The most serious needs occur in fields that are rapidly changing. Textbooks in these subjects usually have to be written by scientists actually involved in the research that is advancing the field. It is not often easy to persuade such individuals to set time aside to help spread the knowledge they have accumulated. Our goal, in this series, is to pinpoint areas of chemistry where recent progress has outpaced what is covered in any available textbooks, and then seek out and persuade experts in these fields to produce relatively concise but instructive introductions to their fields. These should serve the needs of one-semester or one-quarter graduate courses in chemistry and biochemistry. In some cases, the availability of texts in active research areas should help stimulate the creation of new courses.

Charles R. Cantor v Preface to the Second Edition Since the publication of the previous edition in 1994, X-ray crystallography of proteins has advanced by improvements in existing techniques and by addition of new techniques.

Protein Crystallography in Drug Discovery

Hydration Structures of Proteins

Principles of Medical Biochemistry E-Book

X-Ray Crystallography of Biomacromolecules

Structure Determination by X-Ray Crystallography

Principles and Applications

Physical Principles and Techniques of Protein Chemistry, Part C focuses on the effects of intermolecular interactions that are transmitted between ligands and proteins and from protein to protein. This book discusses the density and volume change measurements; direct volume change; osmotic pressure; and small-angle X-ray scattering. The theory of particulate scattering; pulsed nuclear magnetic resonance; absorption of water by diamagnetic molecules; and use of least squares in data analysis are also elaborated. This text likewise covers the iteration process; optical rotatory dispersion and the main chain conformation of proteins; and basic relations for optically active molecules. Other topics include the circular dichroism, secondary structure of proteins, visible rotatory dispersion, and peptide cotton effects. This publication is intended for protein chemists, but is also useful to biologists, medical practitioners, and students researching on protein chemistry.

Synthesizing over thirty years of advances into a comprehensive textbook, Biomolecular Crystallography describes the fundamentals, practices, and applications of protein crystallography. Deftly illustrated in full-color by the author, the text describes mathematical and physical concepts in accessible and accurate language. It distills key co

The fields of structural chemistry and biochemistry have blossomed in the last seventy years

since X-ray diffraction was discovered in 1912. Dorothy Hodgkin, who obtained a Nobel Prize in 1965 for her X-ray diffraction work wrote 'a great advantage of X-ray analysis as a method of chemical structure analysis is its power to show some totally unexpected and surprising structure with, at the same time, complete certainty.' The results of all X-ray diffraction studies are used by chemists and biochemists but these scientists need to be able to appreciate the significance and extent to which these results may be used. A number of books written for practicing crystallographers cover the theory and applications of X-ray diffraction, but few are of real practical use to non-specialists. In 'Crystal Structure Analysis for Biologists and Chemists', the general principles of crystal structure are presented in a highly readable way. The book of Glusker, who is internationally renowned, provides good coverage of theory, including data and understanding their significance.

This textbook provides an integrated physical and biochemical foundation for undergraduate students majoring in biology or health sciences. It is particularly suitable for students planning to enter the pharmaceutical industry. This new generation of molecular biologists and biochemists will harness the tools and insights of physics and chemistry to exploit the emergence of genomics and systems-level information in biology, and will shape the future of medicine.

Methods and Protocols

Biomolecular and Bioanalytical Techniques

Protein Structure and Function

First Edition

Master Lesson for Advanced Homebrewers

A Guide for Users of Macromolecular Models

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

Brewing Better Beer is a comprehensive look at technical, practical and creative homebrewing advice from Gordon Strong, three-time winner of the coveted National Homebrew Competition Ninkasi Award. Discover techniques, philosophy, recipes and tips that will help you take your

homebrew to the next level.

This volume provides methods for modern macromolecular crystallography, including all steps leading to crystal structure determination and analysis. Written in the highly successful *Methods in Molecular Biology* series format, chapters include introductions to their respective topics, lists of the necessary materials and reagents, step-by-step, readily reproducible laboratory protocols, and tips on troubleshooting and avoiding known pitfalls. Authoritative and practical, *Protein Crystallography* aims to ensure successful results in the further study of this vital field.

The prediction of the conformation of proteins has developed from an intellectual exercise into a serious practical endeavor that has great promise to yield new stable enzymes, products of pharmacological significance, and catalysts of great potential. With the application of prediction gaining momentum in various fields, such as enzymology and immunology, it was deemed time that a volume be published to make available a thorough evaluation of present methods, for researchers in this field to expound fully the virtues of various algorithms, to open the field to a wider audience, and to offer the scientific public an opportunity to examine carefully its successes and failures. In this manner the practitioners of the art could better evaluate the tools and the output so that their expectations and applications could be more realistic. The editor has assembled chapters by many of the main contributors to this area and simultaneously placed their programs at three national resources so that they are readily available to those who wish to apply them to their personal interests. These algorithms, written by their originators, when utilized on pes or larger computers, can instantaneously take a primary amino acid sequence and produce a two-or three-dimensional artistic image that gives satisfaction to one's esthetic sensibilities and food for thought concerning the structure and function of proteins. It is in this spirit that this volume was envisaged.

Membrane Biophysics

Physical Chemistry of Macromolecules

Theory, Methodology and Applications

University Physics

Atomic Details

Prediction of Protein Structure and the Principles of Protein Conformation

Protein Folding aims to collect the most important information in the field of protein folding and probes the main principles that govern formation of the three-dimensional structure of a protein from a nascent polypeptide chain, as well as how the functional properties appear. This text is organized into three sections and consists of 15 chapters. After an introductory chapter where the main problems of protein folding are considered at the cellular level in the context of protein biosynthesis, the discussion turns to the conformation of native globular proteins. Definitions and rules of nomenclature are given, including the structural organization of globular proteins deduced from X-ray crystallographic data. Folding mechanisms are tentatively deduced from the observation of invariants in the architecture of folded proteins. The next chapters focus on the energetics of protein conformation and structure, indicating the principles of thermodynamic stability of the native structure, along with theoretical computation studies of protein folding,

structure prediction, and folding simulation. The reader is also introduced to various experimental approaches; the reversibility of the unfolding-folding process; equilibrium and kinetic studies; and detection and characterization of intermediates in protein folding. This text concludes with a chapter dealing with problems specific to oligomeric proteins. This book is intended for research scientists, specialists, biochemists, and students of biochemistry and biology.

Written by one of the most significant contributors to the progress of protein crystallography, this practical guide contains case studies, a troubleshooting section and pointers on data interpretation. It covers the theory, practice and latest achievements in x-ray crystallography, such that any researcher in structural biology will benefit from this extremely clearly written book. Part A covers the theoretical basis and such experimental techniques as principles of x-ray diffraction, solutions for the phase problem and time-resolved x-ray crystallography. Part B includes case studies for different kinds of x-ray crystal structure determination, such as the MIRAS and MAD techniques, molecular replacement, and the difference Fourier technique. This volume summarises recent developments and possible future directions for small molecule X-ray crystallography. It reviews specific areas of crystallography which are rapidly developing and places them in a historical context. The interdisciplinary nature of the technique is emphasised throughout. It introduces and describes the chemical crystallographic and synchrotron facilities which have been at the cutting edge of the subject in recent decades. The introduction of new computer-based algorithms has proved to be very influential and stimulated and accelerated the growth of new areas of science. The challenges which will arise from the acquisition of ever larger databases are considered and the potential impact of artificial intelligence techniques stressed. Recent advances in the refinement and analysis of X-ray crystal structures are highlighted. In addition the recent developments in time resolved single crystal X-ray crystallography are discussed. Recent years have demonstrated how this technique has provided important mechanistic information on solid-state reactions and complements information from traditional spectroscopic measurements. The volume highlights how the prospect of being able to routinely "watch" chemical processes as they occur provides an exciting possibility for the future. Recent advances in X-ray sources and detectors that have also contributed to the possibility of dynamic single-crystal X-ray diffraction methods are presented. The coupling of crystallography and quantum chemical calculations provides detailed information about electron distributions in crystals and has resulted in a more detailed understanding of chemical bonding. The volume will be of interest to chemists and crystallographers with an interest in the synthesis, characterisation and physical and catalytic properties of solid-state materials. Postgraduate students entering the field will benefit from a historical introduction to the subject and a description of those techniques which are currently used. Since X-ray crystallography is used so widely in modern chemistry it will serve to alert senior chemists to those developments which will become routine in coming decades. It will also be of interest to the broad community of computational chemists who study chemical systems.

This textbook introduces the basics of protein structure and logically explains how to use online software to explore the information in protein structure databases. Readers will find easily understandable, step-by step exercises and video-trainings to support them in grasping the fundamental concepts. After reading this book, readers will have the skills required to independently explore and analyze macromolecular structures, will be versed in extracting information from protein databases and will be able to visualize protein structures using specialized software and on-line algorithms. This book is written for advanced undergraduates and PhD students wishing to use information from structural biology in their assignments and research and will be a valuable source of information for all those interested in applied and theoretical aspects of structural biology.

X-Ray Free Electron Lasers

Principles of X-ray Crystallography

Protein Crystallography

Soft X-Rays and Extreme Ultraviolet Radiation

Fundamentals of X-ray Crystallography

Macromolecular Crystallography

The VitalBook e-book of Introduction to Protein Structure, Second Edition is inly available in the US and Canada at the present time. To purchase or rent please visit <http://store.vitalsource.com/show/9780815323051> Introduction to Protein Structure provides an account of the principles of protein structure, with examples of key proteins in their bio

Integrating coverage of polymers and biological macromolecules into a single text, Physical Chemistry of Macromolecules is carefully structured to provide a clear and consistent resource for beginners and professionals alike. The basic knowledge of both biophysical and physical polymer chemistry is covered, along with important terms, basic structural properties and relationships. This book includes end of chapter problems and references, and also: Enables users to improve basic knowledge of biophysical chemistry and physical polymer chemistry. Explores fully the principles of macromolecular chemistry, methods for determining molecular weight and configuration of molecules, the structure of macromolecules, and their separations.

This unique and practical resource provides the most complete and concise summary of underlying principles and approaches to studying nucleic acid structure, including discussion of x-ray crystallography, NMR, molecular modelling, and databases. Its focus is on a survey of structures especially important for biomedical research and pharmacological applications. To aid novices, Principles of Nucleic Acid Structure includes an introduction to technical lingo used to describe nucleic acid structure and conformations (roll, slide, twist, buckle, etc.). This completely updated edition features expanded coverage of the latest advances relevant to recognition of DNA and RNA by small molecules and proteins. In particular, the reader will find extensive new discussions on: RNA folding, ribosome structure and antibiotic interactions, DNA quadruplexes, DNA and RNA protein complexes, and short interfering RNA (siRNA). This handy guide ends with a complete list of resources, including relevant online databases and software. Completely updated with expanded discussion of topics such as RNA folding, ribosome structure and antibiotic interactions, DNA quadruplexes, DNA and RNA protein complexes, and short interfering RNA (siRNA) Includes a complete list of resources, including relevant online databases and software Defines technical lingo for novices

FUNDAMENTALS OF X-RAY CRYSTALLOGRAPHY is based on the author's research and teaching experience over many years. Using geometric concepts and methods it systematically analyses and deduces the crystal symmetry principle and the crystal diffraction theory, establishing distinctive three-dimensional concepts which are easy to understand, grasp and apply. The whole book is divided into three parts: geometric crystallography principles, micro-space symmetry principle and basic principle of X-ray diffraction in crystal. The first and second section carry an in-depth discussion and analysis on macro-symmetry, micro-symmetry and symmetrical composition law of crystal respectively using the principle that the symmetric distribution of equivalent point in space is consistent space symmetry. The first two sections also systematically deduce the thirty two point groups and two hundred thirty micro-space symmetric combinations. Section three details Laue scattering equation and Prague

reflection equation and describes practical use of several important single crystal diffraction methods and apparatus on the basis of mutual relations between crystal lattice and its reciprocal lattice, using reciprocal lattice and reflection ball mathematical model and their interaction relation. In addition, starting from the principle that reciprocal lattice point system disappearance caused by translation vector in microscopic crystal space, it states system extinction law of diffraction, and deduces one hundred twenty diffraction groups. This book lays the foundation for study of crystallography, crystal structure analysis and protein crystallography. It is a must-have for undergraduate and postgraduate students and a very good reference for researchers engaged in relevant studies.

Introduction to Protein Structure

Exploring Protein Structure: Principles and Practice

Comprehensive Protein Crystallography

Crystal Structure Analysis for Chemists and Biologists

Molecular Biology of the Cell

Current Trends in X-Ray Crystallography

Each title in the 'Primers in Biology' series is constructed on a modular principle that is intended to make them easy to teach from, to learn from, and to use for reference.

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.

Crystallography may be described as the science of the structure of materials, using this word in its widest sense, and its ramifications are apparent over a broad front of current scientific endeavor. It is not surprising, therefore, to find that most universities offer some aspects of crystallography in their undergraduate courses in the physical sciences. It is the principal aim of this book to present an introduction to structure determination by X-ray crystallography that is appropriate mainly to both final-year undergraduate studies in crystallography, chemistry, and chemical physics, and introductory post graduate work in this area of crystallography. We believe that the book will be of interest in other disciplines, such as physics, metallurgy, biochemistry, and geology, where crystallography has an important part to play. In the space of one book, it is not possible either to cover all aspects of crystallography or to treat all the subject matter completely rigorously. In particular, certain mathematical results are assumed in order that their applications may be discussed. At the end of each chapter, a short bibliography is given, which may be used to extend the scope of the treatment given here. In addition, reference is made in the text to specific sources of information. We have chosen not to discuss experimental methods extensively, as we consider that this aspect of crystallography is best learned through practical experience, but an attempt has been made to simulate the interpretive side of experimental crystallography in both examples and exercises.

This book highlights recent advances in and diverse techniques for exploring the plasma membrane's structure and function. It starts with two chapters reviewing the history of membrane research and listing recent advances regarding membrane structure, such as the semi-mosaic model for red blood cell membranes and the protein layer-lipid-protein island model for nucleated tissue cell membranes. It subsequently focuses on the localization and interactions of membrane components, dynamic processes of membrane transport and transmembrane signal transduction. Classic and cutting-edge techniques (e.g. high-resolution atomic force microscopy and super-resolution fluorescence microscopy) used in biophysics and chemistry are presented in a very comprehensive manner, making them useful and accessible to both researchers in the field and novices studying cell membranes. This book provides readers a deeper understanding of the plasma membrane's organization at the single molecule level and opens a new way to reveal the relationship between the membrane's structure and functions, making it essential reading for researchers in various fields.

Brewing Better Beer

Outline of Crystallography for Biologists

Principles, Practice, and Application to Structural Biology

Basic Principles and Issues

Principles of Nucleic Acid Structure

Advances in Protein Molecular and Structural Biology Methods

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.

X-ray crystallography is the main method used to determine the structure of biological molecules.

X-ray crystallography is explained without maths and reading this text allows biologists to assess the quality and accuracy of biological structures.

For nearly 30 years, Principles of Medical Biochemistry has integrated medical biochemistry with molecular genetics, cell biology, and genetics to provide complete yet concise coverage that links biochemistry with clinical medicine. The 4th Edition of this award-winning text by Drs. Gerhard Meisenberg and William H. Simmons has been fully updated with new clinical examples, expanded coverage of recent changes in the field, and many new case studies online. A highly visual format helps readers retain complex information, and USMLE-style questions (in print and online) assist with exam preparation. Just the right amount of detail on biochemistry, cell biology, and genetics – in one easy-to-digest textbook. Full-color illustrations and tables throughout help students master challenging concepts more easily. Online case studies serve as a self-assessment and review tool before exams. Online access includes nearly 150 USMLE-style questions in addition to the questions that are in the book. Glossary of technical terms. Clinical Boxes and Clinical Content demonstrate the integration of basic sciences and clinical applications, helping readers make connections between the two. New clinical examples have been added throughout the text.

A Practical Guide

An Introduction for Biologists

Crystals, X-rays and Proteins

21st Century Challenges in Chemical Crystallography I