

Introduction To Protein Science Architecture Function And Genomics

In recent years, interest in proteins has surged. This resurgence has been driven by the expansion of the post-genomic era when structural genomics and proteomics require new techniques in protein chemistry and new applications of older techniques. Protein chemistry methods are used by nearly every discipline of biomedical research. Many techniques

Proteins in living systems carry out a great variety of specific functions, each of which depends on the precise three-dimensional structure of a particular protein.

Proteins are synthesized in the form of a flexible polypeptide chain that is capable of assuming a vast number of configurations; the transformation of this chain into a specific, relatively rigid three-dimensional structure is called folding--a remarkable process of self-

organization. It is known that the amino acid sequences of some proteins have sufficient information to determine their three-dimensional structures. There are other proteins whose folding requires additional information beyond that found in the sequence of the mature protein.

This book introduces the central problem of folding mechanisms as well as a number of other closely related issues. This book is neither a textbook nor a treatise.

Rather, it is an attempt by several investigators to convey the excitement and challenges of those aspects of the folding problem in which they are actively

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engaged. The contributors give brief introductions to protein folding from the perspectives of molecular architecture, stability and dynamics, phage genetics, DNA exons, general physiology, and natural selection. They point out emerging new directions, including the suggestion of a class of diseases that result from protein folding defects.

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.

Utilizing high speed computational methods to extrapolate to the rest of the protein universe, the knowledge accumulated on a subset of examples, protein bioinformatics seeks to accomplish what was

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impossible before its invention, namely the assignment of functions or functional hypotheses for all known proteins. The Ten Most Wanted Solutions in Protein Bioinformatics considers the ten most significant problems occupying those looking to identify the biological properties and functional roles of proteins. - Problem One considers the challenge involved with detecting the existence of an evolutionary relationship between proteins. - Two and Three studies the detection of local similarities between protein sequences and analysis in order to determine functional assignment. - Four, Five, and Six look at how the knowledge of the three-dimensional structures of proteins can be experimentally determined or inferred, and then exploited to understand the role of a protein. - Seven and Eight explore how proteins interact with each other and with ligands, both physically and logically. - Nine moves us out of the realm of observation to discuss the possibility of designing completely new proteins tailored to specific tasks. - And lastly, Problem Ten considers ways to modify the functional properties of proteins. After summarizing each problem, the author looks at and evaluates the current approaches being utilized, before going on to consider some potential approaches. Written by outstanding scientists in physics and molecular biology, this book addresses the most recent advances in the analysis of the protein folding processes and protein structure determination. Emphasis is also placed on modelling and presentation of experimental results of structural membrane bound proteins. Many color plates help to illustrate structural aspects covered

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including: Defining folds of protein domains Structure determination from sequence Distance geometry Lattice theories Membrane proteins Protein-Ligand interaction Topological considerations Docking onto receptors All analysis is presented with proven theory and experimentation. Protein Folds: A Distance-Based Approach is an excellent text/reference for biotechnologists and biochemists as well as graduate students studying in the research sciences.

Human cells produce at least 30,000 different proteins. Each has a specific function characterized by a unique sequence and native conformation that allows it to perform that function. While research in this post-genomic era has created a deluge of invaluable information, the field has lacked for an authoritative introductory text needed to inform researchers and students in all of those fields now concerned with protein research. Introduction to Peptides and Proteins brings together some of the most respected researchers in protein science to present a remarkably coherent introduction to modern peptide and protein chemistry. The first sections of the book delve into – Basic peptide and protein science from assembly through degradation Traditional and emerging research methods including those used in bioinformatics and proteomics New computational approaches and algorithms used to find patterns in the vast data collected by sequencing projects After providing a foundation in tools and methods, the authors closely examine six protein families, including representative classes such as enzymes, cell-surface receptors, antibodies, fibrous

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proteins, and bioactive peptide classes. They concentrate on biochemical mechanisms and where possible indicate therapeutic or biotechnical possibilities. Then focusing on clinical aspects, the authors investigate misfolding as found in prion diseases, miscleavage as found in Alzheimer's, and mis-sequencing as found with some cancers. Drawing from some of their own research, the authors summarize recent achievements and emerging applications. They discuss the use of proteins and peptides as drugs and the solid-phase synthesis required for drug production. They also look at the use of peptides as functional biomolecules and research tools. No longer just the domain of biologists, many key advances in protein research started in physics labs and have involved contributions from a host of fields including statistics, drug development, genetics, and chemical spectroscopy. Introduction to Peptides and Proteins provides researchers across these fields with the thorough foundation needed to explore all the potential that protein research offers.

Containing all the new as well as classical methodologies used in the investigation of amino acid and protein metabolism in human and animal models, this book is needed because of the dramatic increase in research in this field. There is no other book currently on the market that covers these methods of investigation. Methods for Investigation of Amino Acid and Protein Metabolism explores areas such as amino acid transfer across tissue membranes, past and new applications using stable isotopes, protein synthesis in organs and tissues, and more. Because of the importance of

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research methods in the field of amino acid and protein nutrition and metabolism, this book facilitates the reader's integration of the concepts involved in these investigative research methods and their corollaries. In addition to helping any nutrition investigator design and conduct appropriate research protocols in this area of nutrition, this book assists students who are planning to investigate amino acid and protein metabolism in humans or laboratory animals.

This book serves as an introduction to protein structure and function. Starting with their makeup from simple building blocks, called amino acids, the 3-dimensional structure of proteins is explained. This leads to a discussion how misfolding of proteins causes diseases like cancer, various encephalopathies, or diabetes. Enzymology and modern concepts of enzyme kinetics are then introduced, taking into account the physiological, pharmacological and medical significance of this often neglected topic. This is followed by thorough coverage of hæmoglobin and myoglobin, immunoproteins, motor proteins and movement, cell-cell interactions, molecular chaperones and chaperonins, transport of proteins to various cell compartments and solute transport across biological membranes. Proteins in the laboratory are also covered, including a detailed description of the purification and determination of proteins, as well as their characterisation for size and shape, structure and molecular interactions. The book emphasises the link between protein structure, physiological function and medical significance. This book can be used for graduate and advanced

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undergraduate classes covering protein structure and function and as an introductory text for researchers in protein biochemistry, molecular and cell biology, chemistry, biophysics, biomedicine and related courses. About the author: Dr. Buxbaum is a biochemist with interest in enzymology and protein science. He has been working on the biochemistry of membrane transport proteins for nearly thirty years and has taught courses in biochemistry and biomedicine at several universities. The second edition of *Structure in Protein Chemistry* showcases the latest developments and innovations in the field of protein structure analysis and prediction. The book begins by explaining how proteins are purified and describes methods for elucidating their sequences of amino acids and defining their posttranslational modifications. Comprehensive explanations of crystallography and of noncovalent forces—ionic interactions, hydrogen bonding, and the hydrophobic effect—act as a prelude to an exhaustive description of the atomic details of the structures of proteins. The resulting understanding of protein molecular structure forms the basis for discussions of the evolution of proteins, the symmetry of the oligomeric associations that produce them, and the chemical, mathematical, and physical basis of the techniques used to study their structures. The latter include image reconstruction, nuclear magnetic resonance spectroscopy, proton exchange, optical spectroscopy, electrophoresis, covalent cross-linking, chemical modification, immunochemistry, hydrodynamics, and the scattering of light, X-radiation, and neutrons. These procedures are applied to study the folding of polypeptides and the assembly of oligomers. Biological membranes and their proteins are also discussed. *Structure in Protein Chemistry, Second Edition*, bridges the gap between introductory biophysical chemistry

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courses and research literature. It serves as a comprehensive textbook for advanced undergraduates and graduate students in biochemistry, biophysics, and structural and molecular biology. Professionals engaged in chemical, biochemical, and molecular biological research will find it a useful reference. Not only are proteins the fundamental building blocks of all life forms, but they also have a wide range of functions - from forming enzymes acting as catalysts for specific reactions, to crucial molecules such as antibodies in the immune system, and as signalling molecules between cells. Introduction to Protein Science, 3rd edition provides a rich and broad introduction to this fascinating field by covering not only the structure and function of proteins, but also the methods and experimental techniques used to study them. The practical applications of our knowledge to diverse fields such as biotechnology and medicine are emphasized throughout, to help students appreciate the relevance of the subject to the real world.

Since the discovery of the gene for green fluorescent protein (GFP), derived from jellyfish, this protein that emits a green glow has initiated a revolution in molecular biosciences. With this tool, it is now possible to visualize nearly any protein of interest in any cell or tissue of any species. Since the publication of the first edition, there have been tremendously significant technological advances, including development of new mutant variants. Proteins are now available in yellow and blue, and Novel Fluorescent Proteins (NFPs) have expanded their utility in developing biosensors, biological markers, and other biological applications. This updated, expanded new edition places emphasis on the rise of NFPs, including new chapters on NFP properties with detailed protocols, applications of GFPs and NFPs in industry research, and biosensors. This book provides a solid theoretical framework, along with detailed, practical guidance

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on use of GFPs and NFPs with discussion of potential pitfalls. The expert contributors provide real examples in showing how to tailor GFP/NFP to specific systems, maximize expression, and enhance detection.

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A look at the methods and algorithms used to predict protein structure. A thorough knowledge of the function and structure of proteins is critical for the advancement of biology and the life sciences as well as the development of better drugs, higher-yield crops, and even synthetic bio-fuels. To that end, this reference sheds light on the methods used for protein structure prediction and reveals the key applications of modeled structures. This indispensable book covers the applications of modeled protein structures and unravels the relationship between pure sequence information and three-dimensional structure, which continues to be one of the greatest challenges in molecular biology. With this resource, readers will find an all-encompassing examination of the problems, methods, tools, servers, databases, and applications of protein structure prediction and they will acquire unique insight into the future applications of the modeled protein structures. The book begins with a thorough introduction to the protein structure prediction problem and is divided into four themes: a background on structure prediction, the prediction of structural elements, tertiary structure prediction, and functional insights. Within those four sections, the following topics are covered: Databases and resources that are commonly used for protein structure

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prediction The structure prediction flagship assessment (CASP) and the protein structure initiative (PSI) Definitions of recurring substructures and the computational approaches used for solving sequence problems Difficulties with contact map prediction and how sophisticated machine learning methods can solve those problems Structure prediction methods that rely on homology modeling, threading, and fragment assembly Hybrid methods that achieve high-resolution protein structures Parts of the protein structure that may be conserved and used to interact with other biomolecules How the loop prediction problem can be used for refinement of the modeled structures The computational model that detects the differences between protein structure and its modeled mutant Whether working in the field of bioinformatics or molecular biology research or taking courses in protein modeling, readers will find the content in this book invaluable.

The Latest Developments on the Role of Dynamics in Protein Functions Computational Approaches to Protein Dynamics: From Quantum to Coarse-Grained Methods presents modern biomolecular computational techniques that address protein flexibility/dynamics at all levels of theory. An international contingent of leading researchers in chemistry, physics, and biology show how these advanced methods provide insights into dynamic aspects of biochemical processes. A particular focus is on intrinsically disordered proteins (IDPs), which lack a well-defined three-dimensional structure and function as dynamic ensembles. The book covers a wide spectrum of dynamics, from electronic structure-based to coarse-grained techniques via multiscale at different levels. After an introduction to dynamics and historical overview of basic methodologies, the book addresses the following issues: Is there a quantitative relationship between enzymatic catalysis and protein dynamics? Which are the functionally relevant

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motions of proteins? How can structural properties and partner recognition mechanisms of IDPs be simulated? How can we speed up molecular dynamics? How can we describe conformational ensembles by the synergistic effort of computations and experiments? While dynamics is now considered essential for interpreting protein action, it is not yet an integral component in establishing structure–function relationships of proteins. Helping to reshape this classical view in biochemistry, this groundbreaking book explores advances in computational methodology and contributes to the new, ensemble way of studying proteins.

Milk proteins have nutritional value and extraordinary biological properties. Research over the last decades has provided new insight into the structure and the function of milk bioactive peptides. Some of these peptides are delivered directly into milk, and some are encrypted in major proteins such as caseins and lactoglobulins. These peptides have antimicrobial functions modulating the gut microflora. Even when milk is undisputedly the first food for mammals, milk proteins sometimes can be a health threat, either because of allergic reaction or because of toxicity. In this regard, in vitro studies showed donkey's casein and major whey proteins to be more digestible than cows' for human consumption. In this book, readers will find updated research on the major milk proteins' structure, bioactive peptides, milk protein allergy, therapeutic strategies, and chemical markers that can be used to detect cow milk intolerance in infants. This book provides the most current scientific information on milk proteins, from structure to biological properties. It will be of great benefit for those interested in milk production, milk chemistry, and human health.

Often considered the workhorse of the cellular machinery, proteins are responsible for functions ranging from molecular motors to signaling. The broad recognition of their

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involvement in all cellular processes has led to focused efforts to predict their functions from sequences, and if available, from their structures. An overview of current research directions, *Computational Protein-Protein Interactions* examines topics in the prediction of protein-protein interactions, including interference with protein-protein interactions and their design. *Explores Computational Approaches to Understanding Protein-Protein Interactions* Outlining fundamental and applied aspects of the usefulness of computations when approaching protein-protein interactions, this book incorporates different views of the same biochemical problem from sequence to structure to energetics. It covers protein-protein interaction prediction and dynamics, design, drug design for inhibition, and uses for the prediction of function. The text provides general chapters that overview the topic and also includes advanced material. The chapters detail the complexity of protein interaction studies and discuss potential caveats. *Addresses the Next Big Problem in Molecular Biology* While it is important to predict protein associations, this is a daunting task. Edited by two experts in the field and containing contributions from those at the forefront of research, the book provides a basic outline of major directions in computational protein-protein interactions research at the heart of functional genomics and crucial for drug discovery. It addresses the next big problem in molecular biology: how to create links between all the pieces of the cell jigsaw puzzle.

Our genome is the blueprint to our existence: it encodes all the information we need to develop from a single cell into a hugely complicated functional organism. But it is more than a static information store: our genome is a dynamic, tightly-regulated collection of genes, which switch on and off in many combinations to give the variety of cells from which our bodies are formed. But how do we identify the genes that

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make up our genome? How we determine their function? And how do different genes form the regulatory networks that direct the process of life? Introduction to Genomics is a fascinating insight into what can be revealed from the study of genomes: how organisms differ or match; how different organisms evolved; how the genome is constructed and how it operates; and what our understanding of genomics means in terms of our future health and wellbeing. Covering the latest techniques that enable us to study the genome in ever-increasing detail, the book explores what the genome tells us about life at the level of the molecule, the cell, the organism, the ecosystem and the biosphere. Learning features throughout make this book the ideal teaching and learning tool: extensive end of chapter exercises and problems help the student to grasp fully the concepts being presented, while end of chapter WebLems (web-based problems) and lab assignments give the student the opportunity to engage with the subject in a hands-on manner. The field of genomics is enabling us to analyze life in more detail than ever before; Introduction to Genomics is the perfect guide to this enthralling subject. Online Resource Centre: - Figures from the book available to download, to facilitate lecture preparation - Answers to odd-numbered end of chapter exercises, and hints for solving end of chapter problems, to support self-directed learning - Library of web links, for rapid access to a wider pool of additional resources

Introduction to Protein Science Architecture, Function, and Genomics Oxford University Press

In this new edition of The Membranes of Cells, all of the chapters have been updated, some have been completely rewritten, and a new chapter on receptors has been added. The book has been designed to provide both the student and researcher with a synthesis of information from a number of scientific disciplines to create a comprehensive view of the

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structure and function of the membranes of cells. The topics are treated in sufficient depth to provide an entry point to the more detailed literature needed by the researcher. Key Features * Introduces biologists to membrane structure and physical chemistry * Introduces biophysicists to biological membrane function * Provides a comprehensive view of cell membranes to students, either as a necessary background for other specialized disciplines or as an entry into the field of biological membrane research * Clarifies ambiguities in the field

Software Systems Architecture is a practitioner-oriented guide to designing and implementing effective architectures for information systems. It is both a readily accessible introduction to software architecture and an invaluable handbook of well-established best practices. It shows why the role of the architect is central to any successful information-systems development project, and, by presenting a set of architectural viewpoints and perspectives, provides specific direction for improving your own and your organization's approach to software systems architecture. With this book you will learn how to Design an architecture that reflects and balances the different needs of its stakeholders Communicate the architecture to stakeholders and demonstrate that it has met their requirements Focus on architecturally significant aspects of design, including frequently overlooked areas such as performance, resilience, and location Use scenarios and patterns to drive the creation and validation of your architecture Document your architecture as a set of related views Use perspectives to ensure that your architecture exhibits important qualities such as performance, scalability, and security The architectural viewpoints and perspectives presented in the book also provide a valuable long-term reference source for new and experienced architects alike. Whether you are an aspiring or practicing software architect,

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you will find yourself referring repeatedly to the practical advice in this book throughout the lifecycle of your projects. A supporting Web site containing further information can be found at www.viewpoints-and-perspectives.info

Introduction to Protein Science provides a broad introduction to the contemporary study of proteins in health and disease, suitable for students on biological, biochemical, and biomedical degrees internationally. The book relates the study of proteins to the context of modern high-throughput data streams of genomics and proteomics.

Offers coverage of the development of protein purification processes for large-scale commercial operations, and addresses process development, scale-up, applications and mathematical descriptions. Technologies currently used at the commercial scale are covered in depth.

Because the understanding of protein structure and function has increased remarkably in the nine years since the first edition of this volume, most of this edition needed to be entirely rewritten.

Chemical cross-linking reagents have attained great practical use in industry as well as in basic research, and an understanding of their fundamental principles of reaction is paramount to their applications. With broad coverage of the development and application of these reagents, Chemistry of Protein Conjugation and Cross-Linking discusses the mechanism of reaction and allows you to put the theory into practice. The book offers an explanation of the underlying mechanism of chemical modification, surveys all the bifunctional reagents used in bioconjugation and cross-linking, and provides a review of practical applications of these reagents in various areas of biochemistry, molecular biology, biotechnology, nucleic acid chemistry, immunochemistry, and diagnostic and biomedical disciplines. It contains numerous examples and illustrations, plus step-by-

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step explanations to reaction procedures. It is an excellent introduction and a comprehensive reference about chemical modification.

Proteins: Structure and Function is a comprehensive introduction to the study of proteins and their importance to modern biochemistry. Each chapter addresses the structure and function of proteins with a definitive theme designed to enhance student understanding. Opening with a brief historical overview of the subject the book moves on to discuss the 'building blocks' of proteins and their respective chemical and physical properties. Later chapters explore experimental and computational methods of comparing proteins, methods of protein purification and protein folding and stability. The latest developments in the field are included and key concepts introduced in a user-friendly way to ensure that students are able to grasp the essentials before moving on to more advanced study and analysis of proteins. An invaluable resource for students of Biochemistry, Molecular Biology, Medicine and Chemistry providing a modern approach to the subject of Proteins.

The Protein Reviews series serves as a publication vehicle for reviews that focus on crucial contemporary and vital aspects of protein structure, function, evolution and genetics. Volumes are published online first, prior to publication in a printed book. Chapters are selected according to their importance to the understanding of biological systems, relevance to the unravelling of issues associated with health and disease, or impact on scientific or technological advances and developments. Volume 21 presents eight review chapters authored by experts in the related fields. The first chapter covers the enzyme squalene monooxygenase and lipid levels and its relevance in health and disease. Chapter two presents a systematic analysis of the structural and functional aspects of heteromeric solute carriers. The third chapter provides a

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review of the role of CI- in type IV collagen assembly, function, and disease, including future directions for studies. This is followed by a summary in chapter four about the recent progress on defining the roles of the Slit-Robo signaling in bone metabolism and the possible roles of the interaction between Robo and neural epidermal growth factor-like proteins. Chapter five discusses recent data about the evolutionary aspects on structural differences between humans and the nematode in relation to previous knowledge of core proteins and GAG-attachment sites in Chn and CS proteoglycans of *C.elegans* and humans. The sixth chapter summarizes the immunochemical character of the IGHV1-69-derived RFs and the recognition mechanism of the IGHV1-69-derived RFs. Chapter seven covers regulated alternative translocation and its role as an emerging mechanism to regulate transmembrane proteins. Finally, chapter eight reviews current progress on IL-36 protein and biology and novel investigative tools. This volume is intended for research scientists, clinicians, physicians and graduate students in the fields of biochemistry, cell biology, molecular biology, immunology and genetics.

Praise for the first edition "This book captures, in a very accessible way, a growing body of literature on the structure, function and motion of proteins [...] [This is] a superb publication that would be very useful to undergraduates, graduate students, postdoctoral researchers, and instructors involved in structural biology or biophysics courses or in research on protein structure–function relationships." —David Sheehan, *ChemBioChem*, 2011 "Introduction to Proteins is an excellent, state-of-the-art choice for students, faculty, or researchers needing a monograph on protein structure. [...] this is an immensely informative, thoroughly researched, up-to-date text, with broad coverage and remarkable depth. Introduction to Proteins would provide an excellent basis for

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an upper-level or graduate course on protein structure, and a valuable addition to the libraries of professionals interested in this centrally important field." —Eric Martz, Biochemistry and Molecular Biology Education, 2012 Introduction to Proteins shows how proteins can be analyzed in multiple ways. It refers to the roles of proteins and enzymes in diverse contexts and everyday applications, including medical disorders, drugs, toxins, chemical warfare, and animal behavior. New features in the thoroughly-updated second edition: A brand-new chapter on enzymatic catalysis, describing enzyme biochemistry, classification, kinetics, thermodynamics, mechanisms, and applications in medicine and other industries. These are accompanied by multiple animations of biochemical reactions and mechanisms, accessible via embedded QR codes (can be viewed by smartphones) An in-depth discussion of G-protein-coupled receptors (GPCRs) A wider-scale description of biochemical and biophysical methods for studying proteins, including fully accessible internet-based resources, such as databases and algorithms Animations of protein dynamics and conformational changes, accessible via embedded QR codes Additional features Extensive discussion of the energetics of protein folding, stability and interactions A comprehensive view of membrane proteins, with emphasis on structure-function relationship Coverage of intrinsically unstructured proteins, providing a complete, realistic view of the proteome and its underlying functions Exploration of industrial applications of protein engineering and rational drug design Approximately 300 color images Downloadable solutions manual available at www.crcpress.com _ For more information, including powerpoint presentations and exercises for each chapter, please visit the author's website. High-throughputomics' projects such as genome sequencing, structural genomics and proteomics mean that there is no

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shortage of information on proteins. But the more information we have, the harder it is to make sense of it, to know where to start, and to identify the important results. This book is a clear, up to date and authoritative account of
NULL

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 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.

Protein Actions: Principles and Modeling is aimed at graduates, advanced undergraduates, and any professional who seeks an introduction to the biological, chemical, and physical properties of proteins. Broadly accessible to biophysicists and biochemists, it will be particularly useful to student and professional structural biologists and molecular biophysicists, bioinformaticians and computational biologists, biological chemists (particularly drug designers) and molecular bioengineers. The book begins by introducing the basic principles of protein structure and function. Some readers will be familiar with aspects of this, but the authors build up a more quantitative approach than their competitors. Emphasizing concepts and theory rather than experimental techniques, the book shows how proteins can be analyzed using the disciplines of elementary statistical mechanics, energetics, and kinetics. These chapters illuminate how proteins attain biologically active states and the properties of those states. The book ends with a synopsis the roles of computational biology and bioinformatics in protein science.

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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.

Since its publication in 2000, *Biochemistry & Molecular Biology of Plants*, has been hailed as a major

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contribution to the plant sciences literature and critical acclaim has been matched by global sales success. Maintaining the scope and focus of the first edition, the second will provide a major update, include much new material and reorganise some chapters to further improve the presentation. This book is meticulously organised and richly illustrated, having over 1,000 full-colour illustrations and 500 photographs. It is divided into five parts covering: Compartments: Cell Reproduction: Energy Flow; Metabolic and Developmental Integration; and Plant Environment and Agriculture. Specific changes to this edition include: Completely revised with over half of the chapters having a major rewrite. Includes two new chapters on signal transduction and responses to pathogens. Restructuring of section on cell reproduction for improved presentation. Dedicated website to include all illustrative material. Biochemistry & Molecular Biology of Plants holds a unique place in the plant sciences literature as it provides the only comprehensive, authoritative, integrated single volume book in this essential field of study.

This highly original work presents laboratory science in a deliberately skeptical way: as an anthropological approach to the culture of the scientist. Drawing on recent work in literary criticism, the authors study how the social world of the laboratory produces papers and other "texts," and how the scientific vision of reality becomes that set of statements considered, for the time being, too expensive to change. The book is based on field work done by Bruno Latour in Roger Guillemin's

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laboratory at the Salk Institute and provides an important link between the sociology of modern sciences and laboratory studies in the history of science.

As the tools and techniques of structural biophysics assume greater roles in biological research and a range of application areas, learning how proteins behave becomes crucial to understanding their connection to the most basic and important aspects of life. With more than 350 color images throughout, *Introduction to Proteins: Structure, Function, and Motion* presents a unified, in-depth treatment of the relationship between the structure, dynamics, and function of proteins. Taking a structural–biophysical approach, the authors discuss the molecular interactions and thermodynamic changes that transpire in these highly complex molecules. The text incorporates various biochemical, physical, functional, and medical aspects. It covers different levels of protein structure, current methods for structure determination, energetics of protein structure, protein folding and folded state dynamics, and the functions of intrinsically unstructured proteins. The authors also clarify the structure–function relationship of proteins by presenting the principles of protein action in the form of guidelines. This comprehensive, color book uses numerous proteins as examples to illustrate the topics and principles and to show how proteins can be analyzed in multiple ways. It refers to many everyday applications of proteins and enzymes in medical disorders, drugs, toxins, chemical warfare, and animal behavior. Downloadable questions for each chapter are available at CRC Press Online. Useful for students on biosciences degrees, this book

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provides an introduction to the study of proteins. It contains the aspects related to genomics and proteomics that have paved the way for an explosion of interest in protein structure and function.

The first full survey of statistical, topological, data-mining, and ontology-based methods for analyzing protein-protein interaction networks.

This book provides a comprehensive coverage of the basic principles of structural biology, as well as an up-to-date summary of some main directions of research in the field. The relationship between structure and function is described in detail for soluble proteins, membrane proteins, membranes, and nucleic acids. There are several books covering protein structure and function, but none that give a complete picture, including nucleic acids, lipids, membranes and carbohydrates, all being of central importance in structural biology. The book covers state-of-the-art research in various areas. It is unique for its breadth of coverage by experts in the fields. The book is richly illustrated with more than 400 color figures to highlight the wide range of structures.

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