

Daniel J. Rigden
Editor

From Protein Structure to Function with Bioinformatics

Second Edition



Springer

From Protein Structure To Function With Bioinformatics
By Springer 2009 02 13

Bertil Schmidt



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Encyclopedia of Bioinformatics and Computational Biology ,2018-08-21 Encyclopedia of Bioinformatics and Computational Biology ABC of Bioinformatics Three Volume Set combines elements of computer science information technology mathematics statistics and biotechnology providing the methodology and in silico solutions to mine biological data and processes The book covers Theory Topics and Applications with a special focus on Integrative omics and Systems Biology The theoretical methodological underpinnings of BCB including phylogeny are covered as are more current areas of focus such as translational bioinformatics cheminformatics and environmental informatics Finally Applications provide guidance for commonly asked questions This major reference work spans basic and cutting edge methodologies authored by leaders in the field providing an invaluable resource for students scientists professionals in research institutes and a broad swath of researchers in biotechnology and the biomedical and pharmaceutical industries Brings together information from computer science information technology mathematics statistics and biotechnology Written and reviewed by leading experts in the field providing a unique and authoritative resource Focuses on the main theoretical and methodological concepts before expanding on specific topics and applications Includes interactive images multimedia tools and crosslinking to further resources and databases Oligomerization in Health and Disease: From Enzymes to G Protein-Coupled Receptors

,2020-01-16 Oligomerization in Health and Disease From Enzymes to G Protein Coupled Receptors Volume 169 in the Progress in Molecular Biology and Translational Science series provides in depth reviews on topics of exceptional scientific importance Topics of note in this new release include Computational prediction and re design of aberrant oligomerization Oligomerization of G protein coupled receptors an historical overview Prediction and targeting of GPCR oligomer interfaces GPCR Oligomerization dynamics Functional consequences GPCR heteromerization in neuropsychiatric disorders Structural basis of regulation and oligomerization of human cystathionine synthase and Oligomerization of Porphobilinogen Synthase Includes comprehensive coverage of molecular biology Presents ample use of tables diagrams schemata and color figures to enhance the reader's ability to rapidly grasp the information provided Contains contributions from renowned experts in the field of molecular biology Advances in Protein Molecular and Structural Biology Methods Timir Tripathi,Vikash Kumar Dubey,2022-01-14 Advances in Protein Molecular and Structural Biology Methods offers a complete overview of the latest tools and methods applicable to the study of proteins at the molecular and structural level The book begins with sections exploring tools to optimize recombinant protein expression and biophysical techniques such as fluorescence spectroscopy NMR mass spectrometry cryo electron microscopy and X ray crystallography It then moves towards computational approaches considering structural bioinformatics molecular dynamics simulations and deep machine learning technologies The book also covers methods applied to intrinsically disordered proteins IDPs followed by chapters on protein interaction networks protein function and protein design and engineering It provides researchers with an extensive toolkit of methods

and techniques to draw from when conducting their own experimental work taking them from foundational concepts to practical application Presents a thorough overview of the latest and emerging methods and technologies for protein study Explores biophysical techniques including nuclear magnetic resonance X ray crystallography and cryo electron microscopy Includes computational and machine learning methods Features a section dedicated to tools and techniques specific to studying intrinsically disordered proteins

Biovalorisation of Wastes to Renewable Chemicals and Biofuels

Navanietha Krishnaraj Rathinam,Rajesh Sani,2019-10-25 Biovalorisation of Wastes to Renewable Chemicals and Biofuels addresses advanced technologies for converting waste to biofuels and value added products Biovalorisation has several advantages over conventional bioremediation processes as it helps reduce the costs of bioprocesses Examples are provided of several successfully commercialized technologies giving insight into developing potential processes for biovalorisation of different wastes Different bioprocess strategies are discussed for valorising the wastes coming from the leather industry olive oil industry pulp and paper winery textile and food industries as well as aquaculture A section on biorefinery for hydrocarbons and emerging contaminants is included to cover concepts on biodesulfurization of petroleum wastes leaching of heavy metals from E waste and bioelectrochemical processes for CO₂ Chapters on algal biorefinery are also included to focus on the technologies for conversion of CO₂ sequestration and wastewater utilization Biovalorisation of Wastes to Renewable Chemicals and Biofuels can be used as course material for graduate students in chemical engineering chemistry and biotechnology and as a reference for industrial professionals and researchers who want to gain a basic understanding on the subject Covers a wide range of topics from the conversion of wastes to organic acids biofuels biopolymers and industrially relevant products Bridges the gap between academics and industry Written in a lucid and self explanatory style Includes activities quiz critical questions

Bioinformatics Dev Bukhsh Singh,Rajesh Kumar Pathak,2021-10-21 Bioinformatics

Methods and Applications provides a thorough and detailed description of principles methods and applications of bioinformatics in different areas of life sciences It presents a compendium of many important topics of current advanced research and basic principles approaches easily applicable to diverse research settings The content encompasses topics such as biological databases sequence analysis genome assembly RNA sequence data analysis drug design and structural and functional analysis of proteins In addition it discusses computational approaches for vaccine design systems biology and big data analysis and machine learning in bioinformatics It is a valuable source for bioinformaticians computer biologists and members of biomedical field who needs to learn bioinformatics approaches to apply to their research and lab activities Covers basic and more advanced developments of bioinformatics with a diverse and interdisciplinary approach to fulfill the needs of readers from different backgrounds Explains in a practical way how to decode complex biological problems using computational approaches and resources Brings case studies real world examples and several protocols to guide the readers with a problem solving approach

From Protein Structure to Function with Bioinformatics Daniel John

Rigden, 2008-12-11 Proteins lie at the heart of almost all biological processes and have an incredibly wide range of activities Central to the function of all proteins is their ability to adopt stably or sometimes transiently structures that allow for interaction with other molecules An understanding of the structure of a protein can therefore lead us to a much improved picture of its molecular function This realisation has been a prime motivation of recent Structural Genomics projects involving large scale experimental determination of protein structures often those of proteins about which little is known of function These initiatives have in turn stimulated the massive development of novel methods for prediction of protein function from structure Since model structures may also take advantage of new function prediction algorithms the first part of the book deals with the various ways in which protein structures may be predicted or inferred including specific treatment of membrane and intrinsically disordered proteins A detailed consideration of current structure based function prediction methodologies forms the second part of this book which concludes with two chapters focusing specifically on case studies designed to illustrate the real world application of these methods With bang up to date texts from world experts and abundant links to publicly available resources this book will be invaluable to anyone who studies proteins and the endlessly fascinating relationship between their structure and function *Transactions Biochemical Society (Great Britain)*, 2009

Science John Michels (Journalist), 2011 **Economic plant genome and database construction and research** Gao Jihai, Mark Chapman, Shuangyang Wu, Wei Xu, Zhichao Xu, 2024-03-26 **Bioinformatics** Bertil Schmidt, 2011 A compilation of recent approaches from prominent researchers this referencediscusses how to take advantage of bioinformatics applications and algorithmson a variety of modern parallel architectures **Canadian Journal of Microbiology** , 2010 *Journal of Oil Palm Research* , 2019 *Cancer Research* , 2009-04 *Canadian Journal of Forest Research* , 2015-04 *Zoological Studies* , 2009 **Protein Function Prediction** Daisuke Kihara, 2017-05-20 This volume presents established bioinformatics tools and databases for function prediction of proteins Reflecting the diversity of this active field in bioinformatics the chapters in this book discuss a variety of tools and resources such as sequence structure systems and interaction based function prediction methods tools for functional analysis of metagenomics data detecting moonlighting proteins sub cellular localization prediction and pathway and comparative genomics databases Written in the highly successful Methods in Molecular Biology series format chapters include introductions to their respective topics step by step instructions of how to use software and web resources use cases and tips on troubleshooting and avoiding known pitfalls Thorough and cutting edge Protein Function Prediction Methods and Protocols is a valuable and practical guide for using bioinformatics tools for investigating protein function **Frontiers in Protein Structure, Function, and Dynamics** Dev Bukhsh Singh, Timir Tripathi, 2020-07-02 This book discusses a broad range of basic and advanced topics in the field of protein structure function folding flexibility and dynamics Starting with a basic introduction to protein purification estimation storage and its effect on the protein structure function and dynamics it also discusses various experimental and

computational structure determination approaches the importance of molecular interactions and water in protein stability folding and dynamics kinetic and thermodynamic parameters associated with protein ligand binding single molecule techniques and their applications in studying protein folding and aggregation protein quality control the role of amino acid sequence in protein aggregation muscarinic acetylcholine receptors antimuscarinic drugs and their clinical significances Further the book explains the current understanding on the therapeutic importance of the enzyme dopamine beta hydroxylase structural dynamics and motions in molecular motors role of cathepsins in controlling degradation of extracellular matrix during disease states and the important structure function relationship of iron binding proteins ferritins Overall the book is an important guide and a comprehensive resource for understanding protein structure function dynamics and interaction

Molecular Biology - Not Only for Bioinformaticians Wiesława Widłak, 2013-12-05 Bioinformatics which can be defined as the application of computer science and information technology to the field of biology and medicine has been rapidly developing over the past few decades It generates new knowledge as well as the computational tools to create that knowledge Understanding the basic processes in living organisms is therefore indispensable for bioinformaticians This book addresses beginners in molecular biology especially computer scientists who would like to work as bioinformaticians It presents basic processes in living organisms in a condensed manner Additionally principles of several high throughput technologies in molecular biology which need the assistance of bioinformaticians are explained from a biological point of view It is structured in the following 9 chapters cells and viruses protein structure and function nucleic acids DNA replication mutations and repair transcription and posttranscriptional processes synthesis and posttranslational modifications of proteins cell division cell signaling pathways and high throughput technologies in molecular biology

An Introduction to Protein Informatics Karl-Heinz Zimmermann, 2012-12-06 Protein informatics is a newer name for an already existing discipline It encompasses the techniques used in bioinformatics and molecular modeling that are related to proteins While bioinformatics is mainly concerned with the collection organization and analysis of biological data molecular modeling is devoted to representation and manipulation of the structure of proteins Protein informatics requires substantial prerequisites on computer science mathematics and molecular biology The approach chosen here allows a direct and rapid grasp on the subject starting from basic knowledge of algorithm design calculus linear algebra and probability theory An Introduction to Protein Informatics a professional monograph will provide the reader a comprehensive introduction to the field of protein informatics The text emphasizes mathematical and computational methods to tackle the central problems of alignment phylogenetic reconstruction and prediction and sampling of protein structure An Introduction to Protein Informatics is designed for a professional audience composed of researchers and practitioners within bioinformatics molecular modeling algorithm design optimization and pattern recognition This book is also suitable as a graduate level text for students in computer science mathematics and biomedicine

Principles of Protein Structure Georg E. Schulz, R.

Heiner Schirmer, 1988

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