Protein Protein Interactions A Molecular Cloning Manual

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

Given the immense progress achieved in elucidating protein-protein complex structures and in the field of protein interaction modeling, there is great demand for a book that gives interested researchers/students a comprehensive overview of the field. This book does just that. It focuses on what can be learned about protein-protein interactions from the analysis of protein-protein complex structures and interfaces. What are the driving forces for protein-protein association? How can we extract the mechanism of specific

recognition from studying protein-protein interfaces? How can this knowledge be used to predict and design protein-protein interactions (interaction regions and complex structures)? What methods are currently employed to design protein-protein interactions, and how can we influence protein-protein interactions by mutagenesis and small-molecule drugs or peptide mimetics?The book consists of about 15 review chapters, written by experts, on the characterization of protein-protein interfaces, structure determination of protein complexes (by NMR and X-ray), theory of protein-protein binding, dynamics of protein interfaces, bioinformatics methods to predict interaction regions, and prediction of protein-protein complex structures (docking and homology modeling of complexes, etc.) and design of protein-protein interactions. It serves as a bridge between studying/analyzing protein-protein complex structures (interfaces), predicting interactions, and influencing/designing interactions.

Protein-protein interactions (PPI) are at the heart of the majority of cellular processes, and are frequently dysregulated or usurped in disease. Given this central role, the inhibition of PPIs has been of significant interest as a means of treating a wide variety of diseases. However, there are inherent challenges in developing molecules capable of disrupting the relatively featureless and large interfacial areas involved. Despite this, there have been a number of successes in this field in recent years using both traditional drug discovery approaches and innovative, interdisciplinary strategies using novel chemical scaffolds. This book comprehensively covers the various aspects of PPI inhibition, encompassing small molecules, peptidomimetics, cyclic peptides, stapled peptides and macrocycles. Illustrated throughout with successful case studies, this book provides a holistic, cutting-edge view of the subject area and is ideal for chemical biologists and medicinal chemists interested in developing PPI inhibitors.

Computational and Experimental Tools

Multivalency

Proteomics for Biological Discovery

Methods, Techniques, and Practices

Identification, Computer Analysis, and Prediction

A Molecular Cloning Manual

The chapters in this book are written by a team of well-reputed international researchers. The objective is to provide advanced and updated information related to protein-protein interactions. I hope the methods, resources and approaches described here will enhance the available knowledge of the reader significantly.

The biological interactions of living organisms, and protein-protein interactions in particular, are astonishingly diverse. This comprehensive book provides a broad, thorough and multidisciplinary coverage of its field. It integrates different approaches from bioinformatics, biochemistry, computational analysis and systems biology to offer the reader a comprehensive global view of the diverse data on protein-protein interactions and protein interaction networks.

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

An In-depth Analysis of Structure, Function, and Mechanism

On Molecular Perspectives on Protein.protein Interactions 2013

Molecular Recognition of Phosphopeptides and Phosphopeptidomimetics by SH2 Domains

Protein-protein Complexes

Binding Site Detection Using Molecular Dynamics Simulations

Protein-Protein and Domain-Domain Interactions

This book provides a comprehensive overview of the fundamental aspects of protein-protein interactions (PPI), including a detailed account of the energetics and thermodynamics involved in these interactions. It also discusses a number of computational and experimental approaches for the prediction of PPI interactions and reviews their principles, advantages, drawbacks, and the recent developments. Further, it offers structural and mechanistic insights into the formation of protein-protein complexes and maps different PPIs into networks to delineate various pathways that operate at the cellular level. Lastly, it describes computational protein-protein docking techniques and discusses their implications for further experimental research. Given its scope, this

book is a valuable resource for students, researchers, scientists, entrepreneurs, and medical/healthcare professionals.

With the most comprehensive and up-to-date overview of structure-based drug discovery covering both experimental and computational approaches, Structural Biology in Drug Discovery: Methods, Techniques, and Practices describes principles, methods, applications, and emerging paradigms of structural biology as a tool for more efficient drug development. Coverage includes successful examples, academic and industry insights, novel concepts, and advances in a rapidly evolving field. The combined chapters, by authors writing from the frontlines of structural biology and drug discovery, give readers a valuable reference and resource that: Presents the benefits, limitations, and potentiality of major techniques in the field such as X-ray crystallography, NMR, neutron crystallography, cryo-EM, mass spectrometry and other biophysical techniques, and computational structural biology Includes detailed chapters on druggability, allostery, complementary use of thermodynamic and kinetic information, and powerful approaches such as structural chemogenomics and fragment-based drug design Emphasizes the need for the in-depth biophysical characterization of protein targets as well as of therapeutic proteins, and for a thorough quality assessment of experimental structures Illustrates advances in the field of established therapeutic targets like kinases, serine proteinases, GPCRs, and epigenetic proteins, and of more challenging ones like protein-protein interactions and intrinsically disordered proteins

Proteins are indispensable players in virtually all biological events. The functions of proteins are coordinated through intricate regulatory networks of transient protein-protein interactions (PPIs). To predict and/or study PPIs, a wide variety of techniques have been developed over the last several decades. Many in vitro and in vivo assays have been implemented to explore the mechanism of these ubiquitous interactions. However, despite significant advances in these experimental approaches, many limitations exist such as false-positives/false-negatives, difficulty in obtaining crystal structures of proteins, challenges in the detection of transient PPI, among others. To overcome these limitations, many computational approaches have been developed which are becoming increasingly widely used to facilitate the investigation of PPIs. This book has gathered an ensemble of experts in the field, in 22 chapters, which have been broadly categorized into Computational Approaches, Experimental Approaches, and Others.

Protein Interactions as Targets in Drug Discovery

Protein-Protein Interaction Networks

Peptides Targeting Protein-Protein Interactions: Methods and Applications

Pultusk, Poland, 25-30 May, 2013

Protein Interactions

Reflecting the various advances in the field, this book provides comprehensive coverage of protein-protein interactions. It presents a collection of the technical and theoretical issues involved in the study of protein associations, including biophysical approaches. It also offers a collection of computational methods for analyzing interactions.

The rapidly evolving field of protein science has now come to realize the ubiquity and importance of protein-protein interactions. It had been known for some time that proteins may interact with each other to form functional complexes, but it was thought to be the property of only a handful of key proteins. However, with the advent of high throughput proteomics to monitor protein-protein interactions at an organism level, we can now safely state that protein-protein interactions are the norm and not the exception. Thus, protein function must be understood in the larger context of the various binding complexes that each protein may form with interacting partners at a given time in the life cycle of a cell. Proteins are now seen as forming sophisticated interaction networks subject to remarkable regulation. The study of these interaction networks and regulatory mechanism, which I would like to term "systems proteomics," is one of the thriving fields of proteomics. The bird-eye view that systems proteomics offers should not however mask the fact that proteins are each characterized by a unique set of physical and chemical properties. In other words, no protein looks and behaves like another. This complicates enormously the design of high-throughput proteomics methods. Unlike genes, which, by and large, display similar physico-chemical behaviors and thus can be easily used in a high throughput mode, proteins are not easily amenable to the same treatment. It is thus important to remind researchers active in the proteomics field the fundamental basis of protein chemistry. This book attempts to bridge the two extreme ends of protein science: on one end, systems proteomics, which describes, at a system level, the intricate connection network that proteins form in a cell, and on the other end, protein chemistry and biophysics, which describe the molecular properties of individual proteins and the structural and thermodynamic basis of their interactions within the network. Bridging the two ends of the spectrum is bioinformatics and computational chemistry. Large data sets created by systems proteomics need to be mined for meaningful information, methods need to be designed and implemented to improve experimental designs, extract signal over noise, and reject artifacts, and predictive methods need to be worked out and put to the test. Computational chemistry faces similar challenges. The prediction of binding thermodynamics of protein-protein interaction is still in its infancy. Proteins

are large objects, and simplifying assumptions and shortcuts still need to be applied to make simulations manageable, and this despite exponential progress in computer technology. Finally, the study of proteins impacts directly on human health. It is an obvious statement to say that, for decades, enzymes, receptors, and key regulator proteins have been targeted for drug discovery. However, a recent and exciting development is the exploitation of our knowledge of protein-protein interaction for the design of new pharmaceuticals. This presents particular challenges because protein-protein interfaces are generally shallow and interactions are weak. However, progress is clearly being made and the book seeks to provide examples of successes in this area.

Protein'Protein InteractionsMethods and ApplicationsSpringer Science & Business Media

Protein Interaction - the Molecular Basis OfInteractomics

Protein-Protein Interactions in Human Disease

Targeting Protein-Protein Interactions by Small Molecules

Modeling Peptide-Protein Interactions

Structural Biology in Drug Discovery

Methods and Protocols

Protein-Protein Interactions in Human Disease, Volume 111, Part B, promotes further research and development in the protein interaction network in order to identify critical proteins involved in the etiology of human diseases and locate new protein targets for drug development. Thus, this volume is of considerable interest to protein chemists, pharmacologists, cell biologists, immunologists, structural biologists, computational biochemists and other researchers working in the field. In addition, these articles would be of great benefit to medical, biology and pharmacology students who specialize in this field. Describes advances in the application of powerful techniques in studying and analyzing protein-protein interactions Ideal for a wide audience of researchers, specialists and students Written by authorities in their field Contains a number of high quality illustrations, figures and tables that support the presented information

Written by recognized experts in the study of proteins, Proteomics for Biological Discovery begins by discussing the emergence of proteomics from genome sequencing projects and a summary of potential answers to be gained from proteome-level research. The tools of proteomics, from conventional to novel techniques, are then dealt with in terms of underlying concepts, limitations and future directions. An invaluable source of information, this title also provides a thorough overview of the current developments in post-translational modification studies, structural proteomics, biochemical proteomics, microfabrication, applied proteomics, and bioinformatics relevant to proteomics. Presents a comprehensive and coherent review of the major issues faced in terms of technology development, bioinformatics, strategic approaches, and applications Chapters offer a rigorous overview with summary of limitations, emerging approaches, questions, and realistic future industry and basic science applications Discusses higher level integrative aspects, including technical challenges and applications for drug discovery Accessible to the novice while providing experienced investigators essential information Proteomics for Biological Discovery is an essential resource for students,

postdoctoral fellows, and researchers across all fields of biomedical research, including biochemistry, protein chemistry, molecular genetics, cell/developmental biology, and bioinformatics.

Connects fundamental knowledge of multivalent interactions with current practice and state-of-the-art applications Multivalency is a widespread phenomenon, with applications spanning supramolecular chemistry, materials chemistry, pharmaceutical chemistry and biochemistry. This advanced textbook provides students and junior scientists with an excellent introduction to the fundamentals of multivalent interactions, whilst expanding the knowledge of experienced researchers in the field. Multivalency: Concepts, Research & Applications is divided into three parts. Part one provides background knowledge on various aspects of multivalency and cooperativity and presents practical methods for their study. Fundamental aspects such as thermodynamics, kinetics and the principle of effective molarity are described, and characterisation methods, experimental methodologies and data treatment methods are also discussed. Parts two and three provide an overview of current systems in which multivalency plays an important role in chemistry and biology, with a focus on the design rules, underlying chemistry and the fundamental principles of multivalency. The systems covered range from chemical/materials-based ones such as dendrimers and sensors, to biological systems including cell recognition and protein binding. Examples and case studies from biochemistry/bioorganic chemistry as well as synthetic systems feature throughout the book. Introduces students and young scientists to the field of multivalent interactions and assists experienced researchers utilising the methodologies in their work Features examples and case studies from biochemistry/bioorganic chemistry, as well as synthetic systems throughout the book Edited by leading experts in the field with contributions from established scientists Multivalency: Concepts, Research & Applications is recommended for graduate students and junior scientists in supramolecular chemistry and related fields, looking for an introduction to multivalent interactions. It is also highly useful to experienced academics and scientists in industry working on research relating to multivalent and cooperative systems in supramolecular chemistry, organic chemistry, pharmaceutical chemistry, chemical biology, biochemistry, materials science and nanotechnology.

Protein-protein Interactions

Protein-Protein Interaction Assays

Study of Protein-protein Interactions in Molecular Epigenetics

Biophysical Approaches for the Study of Complex Reversible Systems

A. Microtubule-associated Proteins Affected by Paclitaxel : B. Protein-protein Interactions Induced by Bifunctional Molecules

Protein Modules and Protein-Protein Interactions

This volume explores techniques that study interactions between proteins in different species, and combines them with context-specific data, analysis of omics datasets, and assembles individual interactions into higher-order semantic units, i.e., protein complexes and functional modules. The chapters in this book cover computational methods that solve diverse tasks such as the prediction of functional protein-protein interactions; the alignment-based comparison of interaction networks by SANA; using the RaptorX-ComplexContact webserver to predict inter-protein residue-residue contacts; the docking of alternative confirmations of proteins participating in binary interactions and the visually-guided selection of a docking model using COZOID; the detection

of novel functional units by KeyPathwayMiner and how PathClass can use such de novo pathways to classify breast cancer subtypes. Written in the highly successful Methods in Molecular Biology series format, chapters include introductions to their respective topics, lists of the necessary hardware- and software, step-by-step, readily reproducible computational protocols, and tips on troubleshooting and avoiding known pitfalls. Cutting-edge and comprehensive, Protein-Protein Interaction Networks: Methods and Protocols is a valuable resource for both novice and expert researchers who are interested in learning more about this evolving field.

Protein Interactions as Targets in Drug Discovery, Volume 121, is dedicated to the design of therapeutics, both experimental and computational, that target protein interactions. Chapters in this new release include Trends in structure based drug design with protein targets, From fragment- to peptide-protein interaction: addressing the structural basis of binding using Supervised Molecular Dynamics (SuMD), Protein-protein and protein-ligand interactions: identification of potential inhibitors through computational analysis, Aromatic-aromatic interactions in protein-drug and protein-protein interactions, Role of protein-protein interaction in allosteric drug design within the human methyltransferome, and much more. Integrates experimental and computational methods for studying protein interactions and their modulation by potential therapeutics Contains timely chapters written by well-renown authorities in their field Covers information that is well supported by a number of high quality illustrations, figures and tables Targets a very wide audience of specialists, researchers and students

This volume details protocols that cover the broad arsenal of techniques used to study a secretion system from A to Z. Chapters focus on identifying and localizing the different subunits, defining interactions within subunits, monitoring conformational changes, purifying and imaging of large complexes, defining the assembly pathway by fluorescence microscopy and the role of energy during assembly and/or secretion, identifying secreted effectors as well as reporters to follow effector transport. 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 cutting-edge, Bacterial Protein Secretion Systems: Methods and Protocol aims to provide techniques that are not restricted to the study of secretion systems but are also of specific interest for any researcher interested on multi-protein complexes of the bacterial cell envelope.

Biology, Chemistry, Bioinformatics, and Drug Design

Small Molecule Modulation of Protein-protein Interactions

Protein'Protein Interactions

Advances in Protein Molecular and Structural Biology Methods

Bacterial Protein Secretion Systems

Protein-protein Interactions and Networks

This volume covers an array of techniques available for studying peptide-protein docking and design. The book is divided into four sections: peptide binding site prediction; peptide-protein docking; prediction and design of peptide binding specificity; and the design of inhibitory peptides. The chapters in Modeling Peptide-Protein Interactions: Methods and Protocols cover topics such as the usage of ACCLUSTER and PeptiMap for peptide binding site prediction; AnchorDock and ATTRACT for blind, flexible docking of peptides to proteins; flexible peptide docking using HADDOCK and FlexPepDock; identifying loop-mediated protein-protein interactions using LoopFinder; and protein-peptide interaction design using PinaColada. Written in the highly successful Methods in Molecular Biology

series format, chapters include introductions to their respective topics, lists of the necessary details for successful application of the different approaches and step-by-step, readily reproducible protocols, as well as tips on troubleshooting and avoiding known pitfalls. Cutting-edge and thorough, Modeling Peptide-Protein Interactions: Methods and Protocols provides a diverse and unified overview of this rapidly advancing field of major interest and applicability.

This volume successfully and clearly examines how biophysical approaches can be used to study complex systems of reversibly interacting proteins. It deals with the methodology behind the research and shows how to synergistically incorporate several methodologies for use. Each chapter treats and introduces the reader to different biological systems, includes a brief summary of the physical principles, and mentions practical requirements.

The second edition covers a wide range of protein-protein interaction detection topics. Protein-Protein Interactions: Methods and Applications focuses on core technological platforms used to study protein-protein interactions and cutting-edge technologies that reflect recent scientific advances and the emerging focus on therapeutic discovery. Written in the highly successful Methods in Molecular Biology series format, chapters include introductions to their respective topics, lists of necessary materials and reagents, step-by-step laboratory protocols, and tips on troubleshooting and avoiding known pitfalls. These well-detailed protocols describe methods for identifying protein-protein interaction partners, analyzing of protein-protein interactions quantitatively and qualitatively, monitoring protein-protein interactions in live cells, and predicting and determining interaction interfaces. Authoritative and cutting-edge, Protein-Protein Interactions: Methods and Applications, Second Edition is a valuable resource that will enable readers to elucidate the mechanisms of protein-protein interactions, determine the role of these interactions in diverse biological processes, and target protein-protein interactions for therapeutic discovery.

The Protein-protein Interactions of the Molecular Chaperone, AlphaB Crystallin

Biocomputing Approaches to Protein-protein Interactions in Molecular Medicine

Methods and Applications

Modulation of Protein-protein Interactions in Signal Transduction

Principles and Techniques: Volume I

Computational Methods, Analysis and Applications

Any interactions between two protein molecules enabled by electrostatic forces like hydrophobic effect is known as protein-protein interaction. The examples of these interactions are cell metabolism, signal transduction, muscle contraction, transport across membranes, etc. The process is used in many subjects namely quantum chemistry, molecular dynamics, biochemistry, etc. This book is a compilation of chapters that discuss the most vital concepts in the field of protein-protein interactions. It discusses in detail the various applications and techniques of the subject. For someone with an interest and eye for detail, this textbook covers the most significant topics in this field. It will serve as a reference to a broad spectrum

of readers.

Gabriel Waksman Institute of Structural Molecular Biology, Birkbeck and University College London, Malet Street, London WC1E 7HX, United Kingdom Address for correspondence: Professor Gabriel Waksman Institute of Structural Molecular Biology Birkbeck and University College London Malet Street London WC1E 7H United Kingdom Email: g. waksman@bbk. ac. uk and g. waksman@ucl. ac. uk Phone: (+44) (0) 207 631 6833 Fax: (+44) (0) 207 631 6833 URL: http://people. cryst. bbk. ac. uk/?ubcg54a Gabriel Waksman is Professor of Structural Molecular Biology at the Institute of Structural Molecular Biology at UCL/Birkbeck, of which he is also the director. Before joining the faculty of UCL and Birkbeck, he was the Roy and Diana Vagelos Professor of Biochemistry and Molecular Biophysics at the Washington University School of Medicine in St Louis (USA). The rapidly evolving ?eld of protein science has now come to realize the ubiquity and importance of protein–protein interactions. It had been known for some time that proteins may interact with each other to form functional complexes, but it was thought to be the property of only a handful of key proteins. However, with the advent of hi- throughput proteomics to monitor protein–protein interactions at an organism level, we can now safely state that protein–protein interactions are the norm and not the exception.

Molecular epigenetics describe the dynamic changes of chromatin structure, consisting of histones, associated proteins and DNA, which ensure a coordinated expression of genes during cellular differentiation. In the present PhD work, we have developed tools for the analysis of protein-protein interaction and the activity of protein (histone) lysine methyltransferases. We have also studied the substrate specificities of histone lysine methyltransferases (G9a and SET7/9) and the binding specificities of reading domains (PWWP domain of Dnmt3a and ADD domain of ATRX). DNA methylation patterns are set during embryogenesis by Dnmt3a and Dnmt3b enzymes. However, the mechanisms guiding these enzymes to their target regions are not well understood. In the present study, we have shown that PWWP domain of Dnmt3a recognizes the histone 3 lysine 36 trimethylation marks and we propose that this guides the enzyme to its target regions. ATRX is a chromatin remodeling protein, which is often found to be mutated in patients having alpha-thalassemia and mental retardation X-linked syndrome (ATR-X) syndrome. Nearly half of the disease causing mutations lies in the ADD domain of ATRX. However the function of this domain is unknown. We have shown that the ADD domain of ATRX recognizes histone 3 lysine 9 trimethylation marks. Our findings provided the functional clue about the heterochromatin localization of ATRX for the first time. We have developed a general method, which we designated as Absence of Interference approach for rapid mapping of protein-protein interaction sites by using Dnmt3a and Dnmt3L yeast two hybrid interaction pair as a model system. The method is well suited for high throughput applications as well.

Proteomics and Protein-Protein Interactions

Concepts, Research and Applications

Protein-Protein Interactions

Disruption of Protein-Protein Interfaces

Inhibitors of Protein–Protein Interactions

Protein-Protein Interactions: Techniques and Applications

This book illustrates the importance and significance of the molecular (physical and chemical) and evolutionary (gene fusion) principles of protein-protein and domain-domain interactions towards the understanding of cell division, disease mechanism and target definition in drug discovery. It describes the complex issues associated with this phenomenon using cutting edge advancement in Bioinformatics and Bioinformation Discovery. The chapters provide current information pertaining to the types of protein-protein complexes (homodimers, heterodimers, multimer complexes) in context with various specific and sensitive biological functions. The significance of such complex formation in human biology in the light of molecular evolution is also highlighted using several examples. The chapters also describe recent advancements on the molecular principles of protein-protein interaction with reference to evolution towards target identification in drug discovery. Finally, the book also elucidates a comprehensive yet a representative description of a large number of challenges associated with the molecular interaction of proteins.

This book comprehensively reviews the state-of-the-art strategies developed for protein-protein interaction (PPI) inhibitors, and highlights the success stories in new drug discovery and development. Consisting of two parts with twelve chapters, it demonstrates the design strategies and case studies of small molecule PPI inhibitors. The first part discusses various discovery strategies for small molecule PPI inhibitors, such as high throughput screening, hot spot-based design, computational approaches, and fragment-based design. The second part presents recent advances in small molecule inhibitors, focusing on clinical candidates and new PPI targets. This book has broad appeal and is of significant interest to the pharmaceutical science and medicinal chemistry communities.

"Disruption of Protein-Protein Interfaces" reviews the latest developments and future perspectives in drug discovery at protein-protein interfaces. The authors detail experimental and computational tools to tackle the subject and highlight the contribution of the Italian research community to the field. Evidence shows that blocking or modulating protein-protein interactions might lead to the development of useful new drugs. Consequently, in recent years great effort has been dedicated to unveiling the molecular details of protein-protein interfaces by structural techniques e.g. X-ray diffraction, NMR spectroscopy. This book, written and edited by leaders in the field, provides examples from the literature of successes and failures to develop drug-like molecules effective in interacting at protein-protein interfaces.

Analysis, Modeling and Drug Design

Protein-protein Recognition

In Search of New Inhibitors

Computational Protein-Protein Interactions

Protein modules engage in a multitude of interactions with one another and with other cellular components, notably with DNA. These interactions are a central aspect of protein function of great relevance in the post-genomic era. This volume describes a panel of approaches for analyzing protein modules and their interactions, ranging from bioinformatics to physical chemistry, to biochemistry, with an emphasis on the structure-function relationship in protein-protein complexes involved in cellular processes including signal transduction. Comprehensive overview of different facets of macromolecule interactions Computational and bioinformatics aspects of analyzing protein modules and their interactions Emphasis on structure-function

relationship in protein–protein complexes involved in cellular processes

As the mysteries stored in our DNA have been more completely revealed, scientists have begun to face the extraordinary challenge of unraveling the int- cate network of protein–protein interactions established by that DNA fra- work. It is increasingly clear that proteins continuously interact with one another in a highly regulated fashion to determine cell fate, such as proliferation, diff- entiation, or death. These protein–protein interactions enable and exert str- gent control over DNA replication, RNA transcription, protein translation, macromolecular assembly and degradation, and signal transduction; essentially all cellular functions involve protein–protein interactions. Thus, protein–p- tein interactions are fundamental for normal physiology in all organisms. Alt- ation of critical protein–protein interactions is thought to be involved in the development of many diseases, such as neurodegenerative disorders, cancers, and infectious diseases. Therefore, examination of when and how protein–p- tein interactions occur and how they are controlled is essential for understa- ing diverse biological processes as well as for elucidating the molecular basis of diseases and identifying potential targets for therapeutic interventions. Over the years, many innovative biochemical, biophysical, genetic, and computational approaches have been developed to detect and analyze p- tein–protein interactions. This multitude of techniques is mandated by the diversity of physical and chemical properties of proteins and the sensitivity of protein–protein interactions to cellular conditions.

Protein–protein recognition is a critical event controlling in a large number of cell processes and therefore is of interest to a large section of the biological community. The purpose of this book is to bring together important concepts and systems in a single volume.