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**Protein Protein  
Interactions And  
Networks  
Identification  
Computer Analysis**

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Interactions And Networks  
**And Prediction**  
**Computational**  
**Biology**

Yeah, reviewing a book  
**protein protein interactions**  
**and networks identification**

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*An Introduction to Protein Interactions STRING: protein-protein interactions overview Introduction to Biological Network Analysis II: Protein-Protein Interaction Networks: From Graphs to Brief Introduction*

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*of Protein-Protein  
Interactions (PPIs) 14.  
Predicting Protein  
Interactions 16. Protein  
Interaction Networks  
techniques to study protein  
protein interaction Fluoppi:  
Visualizing Protein-Protein*

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*Interactions in Living Cells*

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*Protein-Protein Interactions*

*resource In-silico methods*

*for determining protein*

*interactions* **Cytoscape PPI**

**Network layouts | High**

**quality network Figures for**



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## **Publication | Bioinformatics**

Coevolutionary analysis of proteinprotein interactions

- Martin Weigt ~~What is~~

~~PROTEIN-DNA INTERACTION?~~

~~What does PROTEIN-DNA~~

~~INTERACTION mean?~~ Yeast Two

Hybrid System for Protein

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## Protein Interaction Studies

### 1. CYTOSCAPE ESSENTIALS:

Producing a SIF file for upload into CYTOSCAPE

~~Cytoscape 3 Quickstart~~

~~Tutorial — Basic Expression~~

~~Analysis Cytoscape tutorial:~~

~~How to add gene expression~~

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~~data to an interaction network~~ What is a Protein?  
Protein Ligand Interactions  
*Yeast 2 Hybrid (Y2H) system:*  
*protein protein interaction*  
*technique* ~~Fly Paper: Mapping~~  
~~the Protein Interactions of~~  
~~Our Distant Relative~~ *How to*

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*Study Protein-Ligand Interaction through Molecular Docking*  
Protein Interactions String Cytoscape

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Protein Association Network Analysis Using STRING (Part 1) Protein-Protein

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Identification Network- PART 4  
Part# 6: Protein protein interaction network Analysis Using STRING | Athar Mutahari Protein protein interaction *Strategies for Studying Protein-Protein Interactions* ~~Protein-protein~~

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## ~~Identification study: Binding analysis~~ **Protein Protein Interaction Network- PART 1** **Protein Protein Interactions And Networks**

Protein-protein interaction networks. Protein-protein interactions (PPIs) are

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essential to almost every process in a cell, so understanding PPIs is crucial for understanding cell physiology in normal and disease states. It is also essential in drug development, since drugs can

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affect PPIs. Protein-protein interaction networks (PPIN) are mathematical representations of the physical contacts between proteins in the cell.

## **Protein-protein interaction**



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## networks | Network analysis

of . . .

Protein-protein interaction (PPI) networks describe physical interactions between proteins, taking place to mediate the assembly of proteins into

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protein complexes, or e.g., mediating signaling/regulation and transport events in the cell. Genetic interaction (GI) networks deal with pairs of proteins for which there is information that

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they interact functionally (i.e., the absence or presence of both proteins has a synergetic effect on the cell physiology/phenotype).

## **Protein-Protein Interaction**

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## **Networks - an overview . . .**

Studying the topological structure (not to be confused with molecular structure) of protein-protein interaction networks is a hot topic in systems biology research. In

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such a network, proteins are represented as vertices, and interactions between protein pairs are represented as edges.

## **Protein-Protein Interaction Networks - an overview ...**

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The Protein-Protein Interactions Network (PPI-Net) is a new National Network for Protein-Protein Interactions starting April 2011. The Network was jointly funded by Engineering and Physical

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Science Research Council (EPSRC), Biotechnology and Biological Sciences Research Council (BBSRC), and the Medical Research Council (MRC) from April 2011 to November 2013.

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## **Protein-Protein Interactions Network**

This volume explores techniques that study interactions between proteins in different species, and combines them with context-specific data,



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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

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Identify diverse tasks such as the prediction of functional protein-protein interactions; the alignment-based comparison of interaction networks by SANA;

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## **Protein-Protein Interaction Networks | SpringerLink**

Protein-protein interactions (PPIs) are physical contacts of high specificity established between two or more protein molecules as a result of biochemical events

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steered by interactions that include electrostatic forces, hydrogen bonding and the hydrophobic effect. Many are physical contacts with molecular associations between chains that occur in a cell or in a living

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organism in a specific biomolecular context.

## **Protein-protein interaction - Wikipedia**

This volume explores techniques that study interactions between

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Identification 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

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Identification modules.

Analysis And Prediction  
**Protein-Protein Interaction  
Networks - Methods and...**

Protein-protein interaction  
information can already be  
retrieved from a number of  
online resources. First,

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primary interaction databases (e.g. 9–13) which are largely collaborating (14, 15) provide curated experimental data originating from a variety of biochemical, biophysical and genetic techniques.



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## **STRING v10: protein-protein interaction networks ...**

Protein-protein interactions  
in bacteria Like in  
eukaryotes, protein-protein  
interactions are essential  
in prokaryotic cells in

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which they also have a central role.

**Protein-protein interactions in bacteria: a promising and**

...

Protein-Protein Interaction Networks ... Organisms 5090;

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Proteins 24.6 mio;  
Interactions >2000 mio;  
Search ) ) ) ) ) ) ) ...  
Novo Nordisk Foundation  
Center Protein Research;  
EMBL - European Molecular  
Biology Laboratory; Credits.  
Funding; Datasources;

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**STRING: functional protein  
association networks**

STRING v10: protein-protein  
interaction networks,  
integrated over the tree of  
life Nucleic Acids Res. 2015  
Jan;43(Database

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issue):D447-52. doi:  
10.1093/nar/gku1003. Epub  
2014 Oct 28. Authors Damian  
Szkłarczyk 1 ...

**STRING v10: protein-protein  
interaction networks ...**

Protein-Protein Interaction

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Networks Proteins are vital macromolecules that facilitate diverse biological processes at both cellular and systemic levels.

## **Protein-Protein Interaction**

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## Networks - Creative Proteomics

This course provides an introduction to the theory and concepts of network analysis. It explores some of the features of protein-protein interaction networks

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and their implications for biology. Finally, the course discusses the tools and strategies that can be used to build and analyse biological networks.

## **Network analysis of protein**



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## Analysis And Prediction

The study of modules is also useful when defining intermodular interactions and proteins. These are the edges/nodes that link different communities within

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a network. They can act as switches or high-level modulators that, for example, mediate cross-talk between different complexes or pathways.

## **Properties of PPINs:**

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## transitivity | Network analysis of ...

Protein interaction networks have been used to predict the function of proteins of unknown functions. This is usually based on the assumption that

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uncharacterized proteins have similar functions as their interacting proteins (guilt by association).

## **Interactome - Wikipedia**

Genome wide protein networks have become reality in

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recent years due to high throughput methods for detecting protein interactions. Recent studies show that a networked representation of proteins provides a more accurate model of biological

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systems and processes compared to conventional pair-wise analyses.

## **Analysis of Protein-Protein Interaction Networks Using**

...

Protein-protein interactions

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(PPIs) are extremely important in orchestrating the events in a cell. They form the basis for several signal transduction pathways in a cell, as well as various transcriptional regulatory networks.

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## **Construction and analysis of protein-protein interaction**

### Computational Biology

It integrates protein-protein interaction (PPI) data from public curated databases and builds a



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complete, non-redundant protein interaction dataset for six model organisms. In particular, it provides a variety of built-in tools to filter and analyze the networks for gaining biological and functional

# Read Free Protein Protein Interactions And Networks Insights into the network. Identification Computer Analysis And Prediction Computational Biology

The biological interactions  
of living organisms, and  
protein-protein interactions  
in particular, are

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astonishingly diverse. This comprehensive book provides a broad, thorough and multidisciplinary coverage of its field. It integrates different approaches from bioinformatics, biochemistry, computational

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Identification Computer biology to offer the reader a comprehensive global view of the diverse data on protein-protein interactions and protein interaction networks.

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

The biological interactions

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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

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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

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This volume explores techniques that study interactions between proteins in different species, and combines them



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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

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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-

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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

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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

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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

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computational protocols, and tips on troubleshooting and avoiding known pitfalls.

Cutting-edge and comprehensive, Protein-Protein Interaction Networks: Methods and Protocols is a valuable

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resource for both novice and expert researchers who are interested in learning more about this evolving field.

"The goal of this book is to disseminate research results and best practices from

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cross-disciplinary computer researchers and practitioners interested in, and working on bioinformatics, data mining, and proteomics" - - Provided by publisher.



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New genomic information has revealed the crucial role that protein-protein interactions (PPIs) play in regulating numerous cellular functions. Aberrant forms of these interactions are common in numerous diseases

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and thus PPIs have emerged as a vast class of critical drug targets. Despite the importance of PPIs in biology, it has been extremely challenging to convert targets into therapeutics and targeting

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PPIs had long been considered a very difficult task. However, over the past decade the field has advanced with increasing growth in the number of successful PPI regulators. Protein-Protein Interaction

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Regulators surveys the latest advances in the structural understanding of PPIs as well as recent developments in modulator discovery.

As the mysteries stored in

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our DNA have been more completely revealed, scientists have begun to face the extraordinary challenge of unraveling the intricate network of protein-protein interactions established by that DNA fra-

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work. It is increasingly clear that proteins continuously interact with one another in a highly regulated fashion to determine cell fate, such as proliferation, differentiation, or death. These

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protein-protein interactions enable and exert stringent control over DNA replication, RNA transcription, protein translation, macromolecular assembly and degradation, and signal transduction;

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essentially all cellular functions involve protein-protein interactions. Thus, protein-protein interactions are fundamental for normal physiology in all organisms. Alt- ation of critical



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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

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protein-protein interactions occur and how they are controlled is essential for understanding diverse biological processes as well as for elucidating the molecular basis of diseases and identifying potential

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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

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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.

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The identification and mapping of protein-protein interactions (PPIs) is a major goal in systems biology. Experimental data are currently produced in large scale using a variety

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of high-throughput assays in yeast or mammalian systems. Analysis of these data using computational tools leads to the construction of large protein interaction networks, which help researchers identify novel

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protein functions. However, our current view of protein interaction networks is still limited and there is an active field of research trying to further develop this concept to include important processes: the

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topology of interactions and their changes in real time, the effects of competition for binding to the same protein region, PPI variation due to alternative splicing or post-translational modifications,



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etc. In particular, a clinically relevant topic for development of the concept of protein interactions networks is the consideration of mutant isoforms, which may be responsible for a

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pathological condition. Mutations in proteins may result in loss of normal interactions and appearance of novel abnormal interactions that may affect a protein's function and biological cycle. This

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Research Topic presents novel findings and recent achievements in the field of protein interaction networks with a focus on disease. Authors describe methods for the identification and quantification of PPIs, the

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Identification, analysis of networks, considering PPIs and protein complexes formed by mutant proteins associated with pathological conditions or genetic diseases.

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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

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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

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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

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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



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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

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Identification Computer 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

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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

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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

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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

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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

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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

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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



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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

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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.

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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-

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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.

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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

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Identification Computer Analysis And Prediction Computational Biology 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

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examines topics in the prediction of protein-protein interactions, including interference with protein-protein interactions and their design. Explores Computational Approaches to Understanding Protein-

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Outlining fundamental and applied aspects of the usefulness of computations when approaching protein-protein interactions, this book incorporates different views of the same



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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

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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.

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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

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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

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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.

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