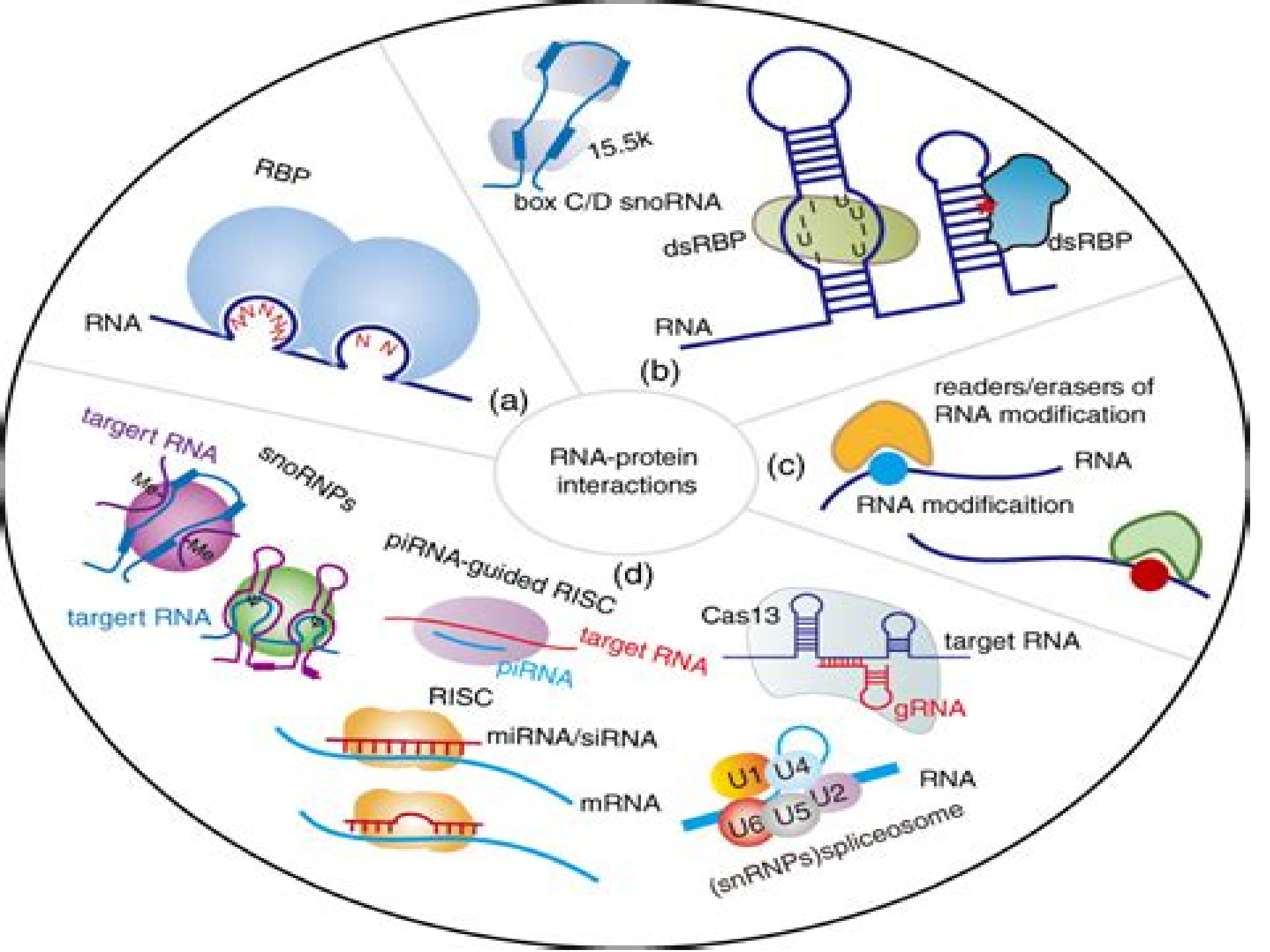
RNA-protein interactions
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U1
U4
U2
U5
U6
RNA
(snRNPs)spliceosome

Rna Protein Interactions

Gorka Lasso Cabrera,Pablo Guardado-Calvo,Rohit K. Jangra,Eva Mittler,Mercè Llabrés

Rna Protein Interactions:

RNA'Protein Interaction Protocols Susan R. Haynes,2008-02-03 The molecular characterization of RNA and its interactions with proteins is an important and exciting area of current research Organisms utilize a variety of RNA protein interactions to regulate the expression of their genes This is particularly true for eukaryotes since newly synthesized messenger RNA must be extensively modified and transported to the cytoplasm before it can be used for protein synthesis The realization that posttranscriptional processes are critical components of gene regulation has sparked an explosion of interest in both stable ribonucleoprotein RNP complexes and transient RNA protein interactions RNA is conformationally flexible and can adopt complex structures that provide diverse surfaces for interactions with proteins The fact that short RNA molecules aptamers see Chapter 16 can be selected to bind many different types of molecules is evidence of the structural variability of RNA RNA molecules are rarely entirely single or double stranded but usually contain multiple short duplexes interrupted by single stranded loops and bulges in some RNAs such as tRNAs the short duplexes stack on each other Further variability is generated by the presence of non Watson Crick base pairs modified nucleotides and more complex structures such as pseudoknots and triple strand interactions *RNA-Protein Interactions : A Practical Approach* Christopher W.J. Smith,1998-07-09 RNA protein interactions play a fundamental role in gene expression and protein synthesis Recent research into the role of RNA in cells has elucidated many more vital interactions with proteins This book provides an up to date and comprehensive guide to a wide range of laboratory procedures to investigate the interactions between RNA and proteins RNA protein interactions play a vital role in gene transcription and protein expression Interactions such as the synthesis of mRNA by RNA polymerases to the essential modification of RNA by the proteins of the spliceosome complex and the highly catalytic action of the ribosome in protein synthesis are established as being fundamental to the function of RNA Recent research into for example the role of RNA as a catalyst has elucidated many more interactions with proteins that are vital to cell function RNA Protein Interactions A Practical Approach provides a clear and comprehensive guide to the experimental procedures used in studying RNA protein interactions The approaches covered range from those initially used to detect a novel RNA protein interaction various biochemical and genetic approaches to purifying and cloning RNA binding proteins through to methods for an in depth analysis of the structural basis of the interaction The volume includes a number of procedures that have not previously been covered in this type of manual These include the production of site specifically modified RNAs by enzymatic and chemical methods and in vivo screening for novel RNA protein interactions in yeast and E coli This is the first volume to gather in one place this wide array of approaches for studying RNA protein interactions As is customary for the Practical Approach series the writing is characterized by a clear explanatory style with many detailed protocols This informative book will be a valuable aid to laboratory workers in biochemistry and molecular biology graduate students postdoctoral and senior scientists whose research encompasses this field *RNA-protein Interactions* Kiyoshi

Nagai,Iain W. Mattaj,1994 The study of RNA protein interactions is crucial to understanding the mechanisms and control of gene expression and protein synthesis The realization that RNAs are often far more biologically active than was previously appreciated has stimulated a great deal of new research in this field Uniquely in this book the world s leading researchers have collaborated to produce a comprehensive and current review of RNA protein interactions for all scientists working in this area Timely comprehensive and authoritative this new Frontiers title will be invaluable for all researchers in molecular biology biochemistry and structural biology **RNA-Protein Complexes and Interactions** Ren-Jang Lin,2023-05-11 This second edition updates complements and expands upon the first edition by providing a collection of cutting edge techniques developed or refined in the past few years along with tried and true methods Chapters explore the isolation and characterization of RNA protein complexes the analysis and measurement of RNA protein interaction and related novel techniques and strategies Written in the highly successful Methods in Molecular Biology series format the chapters include brief introductions to the material lists of necessary materials and reagents step by step readily reproducible laboratory protocols and a Notes section which highlights tips on troubleshooting and avoiding known pitfalls Authoritative and cutting edge RNA Protein Complexes and Interactions Methods and Protocols Second Edition aims to be comprehensive guide for researchers in the field Biophysics of RNA-Protein Interactions Chirlmin Joo,David Rueda,2019-09-19 RNA molecules play key roles in all aspects of cellular life but to do so efficiently they must work in synergism with proteins This book addresses how proteins and RNA interact to carry out biological functions such as protein synthesis regulation of gene expression genome defense liquid phase separation and more The topics addressed in this volume will appeal to researchers in biophysics biochemistry and structural biology The book is a useful resource for anybody interested in elucidating the molecular mechanisms and discrete properties of RNA protein complexes Included are reviews of key systems such as microRNA and CRISPR Cas that exemplify how RNA and proteins work together to perform their biological function Also covered are techniques ranging from single molecule fluorescence and force spectroscopy to crystallography cryo EM microscopy and kinetic modeling Computational Analysis and Prediction of RNA-protein Interactions Michael Uhl,2022* Abstract This dissertation is about the computational analysis and prediction of RNA protein interactions Ribonucleic acids RNAs and proteins both are essential for the control of gene expression in our cells Gene expression is the process by which a functional gene product namely a protein or an RNA is produced from a gene starting from the gene region on the DNA with the transcription of an RNA Once regarded primarily as a messenger to transmit the protein information recent years have seen RNA moving further into the biomedical spotlight thanks to its increasingly uncovered roles in regulating gene expression In addition RNA has showcased its therapeutic potential as famously demonstrated by the groundbreaking success of RNA vaccines in the COVID 19 pandemic However RNAs rarely function on their own In humans more than 1 500 different RNA binding proteins RBPs are involved in controlling the various stages of an RNA s life cycle creating a highly

complex regulatory interplay between RNAs and proteins It is therefore of fundamental importance to study these RNA protein interactions in order to deepen our understanding of gene expression Over the last decade CLIP seq has become the dominant experimental method to identify the set of cellular RNA binding sites for an RBP of interest However analysing the resulting CLIP seq data can be challenging as there are many analysis steps and CLIP seq protocol variants available each requiring specific adaptations to the analysis workflow Consequently there is a need for analysis guidelines providing easy access to tools as well as the constant improvement of tools and workflows to increase the accuracy of the analysis results The first set of works included in this thesis publications P1 P4 and P5 deals with these topics by providing a review article on CLIP seq data analysis as well as two articles on how to further improve CLIP seq data analysis Publication P1 supplies readers with an overview of tools and protocols as well as guidelines to conduct a successful analysis drawing largely from our own experience with analysing CLIP seq data Publication P4 demonstrates the issues current binding site identification tools have with CLIP seq data from RBPs that bind to processed RNAs and that the integration of RNA processing information improves the resulting binding site quality On top of this publication P5 presents Peakhood the first tool that utilizes RNA processing information in order to increase the quality of RBP binding sites identified from CLIP seq data A natural drawback of experimental methods is that a target RNA needs to be sufficiently expressed in the observed cells for an RNA protein interaction to be detected Hence since gene expression is a dynamic process that differs between cell types time points and conditions a CLIP seq experiment cannot recover the complete set of cellular RBP binding sites This creates a demand for computational methods which can learn the binding properties of an RBP from existing CLIP seq data in order to predict RBP binding sites on any given target RNA Besides interacting with proteins RNAs can also interact with other RNAs further increasing the amount of possible regulatory interactions between RNAs and proteins In this regard long non coding RNAs lncRNAs a large class of non protein coding RNAs whose functions are still vastly unexplored have become especially important as it has been shown that they can engage in RNA RNA interactions whose regulatory mechanisms also include RNA protein interactions As such mechanistic studies are typically slow and expensive computational tools that combine RNA protein and RNA RNA interaction predictions to infer potential mechanisms could be of great help e g by screening a set of target RNAs and proteins and suggesting plausible mechanisms for experimental validation The second set of works included in this thesis publications P2 and P3 thus deals with the computational prediction of RNA protein interactions RNA RNA interactions and the functional mechanisms that can be inferred from these interactions Publication P2 introduces MechRNA the first tool to infer functional mechanisms of lncRNAs based on their predicted interactions with RBPs and other RNAs as well as gene expression data We demonstrated MechRNA s capability to identify formerly described lncRNA mechanisms and experimentally validated one prediction underlining its value for functional lncRNA studies Finally publication P3 presents RNAProt a flexible and performant RBP binding site prediction tool based on recurrent neural networks Compared to other

popular deep learning methods RNAProt achieves state of the art predictive performance as well as superior runtime efficiency In addition it is more feature rich than any other available method including the support of user defined predictive features We further showed that its visualizations agree with known RBP binding preferences and demonstrated that its additional predictive features can increase the specificity of predictions RNA - Protein Interactions Symposia on RNA biology,1995 *Quantitative Modeling of RNA-Protein Interactions* Salma Sohrabi-Jahromi,2021 RNA binding proteins RBPs impact every aspect of RNA metabolism including RNA transcription maturation export localization translation and stability Specific RNA protein interactions therefore play a central role in regulating many cellular processes However most RBPs preferentially bind short often degenerate sequence motifs 3 5 bases that alone cannot explain how they target only specific subsets of transcripts in the cell In this thesis I report on the analysis and the thermodynamic modeling of RNA protein interaction datasets with the aim of cracking the code behind RBP *Protein Interactions* Volkhard Helms,Olga V. Kalinina,2022-11-15 Protein Interactions A fundamental guide to the burgeoning field of protein interactions From enzymes to transcription factors to cell membrane receptors proteins are at the heart of biological cell function Virtually all cellular processes are governed by their interactions with one another with cell bodies with DNA or with small molecules The systematic study of these interactions is called Interactomics and research within this new field promises to shape the future of molecular cell biology Protein Interactions goes beyond any existing guide to protein interactions presenting the first truly comprehensive overview of the field Edited by two leading scholars in the field of protein bioinformatics this book covers all known categories of protein interaction stable as well as transient as well as the effect of mutations and post translational modifications on the interaction behavior Protein Interactions readers will also find Introductory chapters on protein structure conformational dynamics and protein protein binding interfaces A data driven approach incorporating machine learning and integrating experimental data into computational models An outlook on the current challenges in the field and suggestions for future research Protein Interactions will serve as a fundamental resource for novice researchers who want a systematic introduction to interactomics as well as for experienced cell biologists and bioinformaticians who want to gain an edge in this exciting new field **Protein-Nucleic Acid Interactions** Phoebe A Rice,Carl C Correll,2008-04-22 The structural biology of protein nucleic acid interactions is in some ways a mature field and in others in its infancy High resolution structures of protein DNA complexes have been studied since the mid 1980s and a vast array of such structures has now been determined but surprising and novel structures still appear quite frequently High resolution structures of protein RNA complexes were relatively rare until the last decade Propelled by advances in technology as well as the realization of RNA s importance to biology the number of example structures has ballooned in recent years New insights are now being gained from comparative studies only recently made possible due to the size of the database as well as from careful biochemical and biophysical studies As a result of the explosion of research in this area it is no longer possible to

write a comprehensive review Instead current review articles tend to focus on particular subtopics of interest This makes it difficult for newcomers to the field to attain a solid understanding of the basics One goal of this book is therefore to provide in depth discussions of the fundamental principles of protein nucleic acid interactions as well as to illustrate those fundamentals with up to date and fascinating examples for those who already possess some familiarity with the field The book also aims to bridge the gap between the DNA and the RNA views of nucleic acid protein recognition which are often treated as separate fields However this is a false dichotomy because protein DNA and protein RNA interactions share many general principles This book therefore includes relevant examples from both sides and frames discussions of the fundamentals in terms that are relevant to both The monograph approaches the study of protein nucleic acid interactions in two distinctive ways First DNA protein and RNA protein interactions are presented together Second the first half of the book develops the principles of protein nucleic acid recognition whereas the second half applies these to more specialized topics Both halves are illustrated with important real life examples The first half of the book develops fundamental principles necessary to understand function An introductory chapter by the editors reviews the basics of nucleic acid structure Jen Jacobsen and Jacobsen discuss how solvent interactions play an important role in recognition illustrated with extensive thermodynamic data on restriction enzymes Marmorstein and Hong introduce the zoology of the DNA binding domains found in transcription factors and describe the combinational recognition strategies used by many multiprotein eukaryotic complexes Two chapters discuss indirect readout of DNA sequence in detail Berman and Lawson explain the basic principles and illustrate them with in depth studies of CAP while in their chapter on DNA bending and compaction Johnson Stella and Heiss highlight the intrinsic connections between DNA bending and indirect readout Horvath lays out the fundamentals of protein recognition of single stranded DNA and single stranded RNA and describes how they apply in a detailed analysis of telomere end binding proteins Nucleic acids adopt more complex structures Lilley describes the conformational properties of helical junctions and how proteins recognize and cleave them Because RNA readily folds due to the stabilizing role of its 2 hydroxyl groups Li discusses how proteins recognize different RNA folds which include duplex RNA With the fundamentals laid out discussion turns to more specialized examples taken from important aspects of nucleic acid metabolism Schroeder discusses how proteins chaperone RNA by rearranging its structure into a functional form Berger and Dong discuss how topoisomerases alter the topology of DNA and relieve the superhelical tension introduced by other processes such as replication and transcription Dyda and Hickman show how DNA transposes mediate genetic mobility and Van Duyne discusses how site specific recombinases cut and paste DNA Horton presents a comprehensive review of the structural families and chemical mechanisms of DNA nucleases whereas Li in her discussion of RNA protein recognition also covers RNA nucleases Lastly Ferr D Amar shows how proteins recognize and modify RNA transcripts at specific sites The book also emphasises the impact of structural biology on understanding how proteins interact with nucleic acids and it is intended for

advanced students and established scientists wishing to broaden their horizons **RNA-protein Interactions as Determinants of MRNA Stability in Vitro** Philip Louis Bernstein,1992 **Identifying RNA-protein Interaction Sites Throughout Eukaryotic Transcriptomes** Ian Michael Silverman,2015 Gene expression is regulated at both the transcriptional and post transcriptional levels While transcription controls only the rate of RNA production numerous and diverse mechanisms regulate the processing stability and translation of RNAs at the post transcriptional level At the heart of this regulation are RNA binding proteins RBPs and their RNA targets Thousands of RBPs are encoded in mammalian genomes each with hundreds to thousands of RNA targets Therefore cataloging these interactions represents a significant challenge Recent advances in high throughput sequencing technologies have greatly expanded the toolkit that researchers have to probe RNA protein interactions but these technologies are still in their infancy and thus new methods and applications are required to move our understanding forward We developed a novel high throughput approach to globally identify regions of RNAs that interact with proteins throughout a transcriptome of interest We applied this technique to human HeLa cells and provide evidence that our approach captures both known and novel RNA protein interaction sites We identified global patterns of RNA protein interactions found evidence for co binding of functionally related genes and revealed that disease associated single nucleotide polymorphisms are enriched within protein interaction sites We also performed detailed analysis of the RNA targets for two specific RBPs Poly A binding protein cytoplasmic 1 PABPC1 and Argonaute AGO First we used CLIP seq to generate a transcriptome wide map of PABPC1 interaction sites in the mouse transcriptome This analysis revealed that PABPC1 binds directly to the highly conserved polyadenylation signal sequence and to translation initiation and termination sites We also showed that PABPC1 binds to A rich regions in the 5 untranslated region of a subset of messenger RNAs mRNAs and negatively regulates their gene expression Finally we applied a recently developed approach to isolate and sequence AGO bound microRNA precursors pre miRNAs We uncovered widespread trimming and tailing identified novel intermediates and created an index for pre miRNA processing efficiency We discovered that numerous pre miRNA like elements are embedded within mRNAs but do not produce functional small RNAs In total these studies provide several advances in our understanding of the global landscape of RNA protein interactions and serve as a foundation for future mechanistic studies *Applications of Chimeric Genes and Hybrid Proteins, Part C: Protein-Protein Interactions and Genomics* ,2000-10-28 The critically acclaimed laboratory standard for more than forty years Methods in Enzymology is one of the most highly respected publications in the field of biochemistry Since 1955 each volume has been eagerly awaited frequently consulted and praised by researchers and reviewers alike Now with more than 300 volumes all of them still in print the series contains much material still relevant today truly an essential publication for researchers in all fields of life sciences RNA protein interactions BMB 307, *RNA-protein and Protein-protein Interactions of SRrp86* Ian Hawkins,2006 **Protein-Nucleic Acid Interactions** Phoebe A. Rice,Carl C. Correll,2008-05-22 The structural biology of

protein nucleic acid interactions is in some ways a mature field and in others in its infancy High resolution structures of protein DNA complexes have been studied since the mid 1980s and a vast array of such structures has now been determined but surprising and novel structures still appear quite frequently High resolution structures of protein RNA complexes were relatively rare until the last decade Propelled by advances in technology as well as the realization of RNA s importance to biology the number of example structures has ballooned in recent years New insights are now being gained from comparative studies only recently made possible due to the size of the database as well as from careful biochemical and biophysical studies As a result of the explosion of research in this area it is no longer possible to write a comprehensive review Instead current review articles tend to focus on particular subtopics of interest This makes it difficult for newcomers to the field to attain a solid understanding of the basics One goal of this book is therefore to provide in depth discussions of the fundamental principles of protein nucleic acid interactions as well as to illustrate those fundamentals with up to date and fascinating examples for those who already possess some familiarity with the field The book also aims to bridge the gap between the DNA and the RNA views of nucleic acid protein recognition which are often treated as separate fields However this is a false dichotomy because protein DNA and protein RNA interactions share many general principles This book therefore includes relevant examples from both sides and frames discussions of the fundamentals in terms that are relevant to both The monograph approaches the study of protein nucleic acid interactions in two distinctive ways First DNA protein and RNA protein interactions are presented together Second the first half of the book develops the principles of protein nucleic acid recognition whereas the second half applies these to more specialized topics Both halves are illustrated with important real life examples The first half of the book develops fundamental principles necessary to understand function An introductory chapter by the editors reviews the basics of nucleic acid structure Jen Jacobsen and Jacobsen discuss how solvent interactions play an important role in recognition illustrated with extensive thermodynamic data on restriction enzymes Marmorstein and Hong introduce the zoology of the DNA binding domains found in transcription factors and describe the combinational recognition strategies used by many multiprotein eukaryotic complexes Two chapters discuss indirect readout of DNA sequence in detail Berman and Lawson explain the basic principles and illustrate them with in depth studies of CAP while in their chapter on DNA bending and compaction Johnson Stella and Heiss highlight the intrinsic connections between DNA bending and indirect readout Horvath lays out the fundamentals of protein recognition of single stranded DNA and single stranded RNA and describes how they apply in a detailed analysis of telomere end binding proteins Nucleic acids adopt more complex structures Lilley describes the conformational properties of helical junctions and how proteins recognize and cleave them Because RNA readily folds due to the stabilizing role of its 2 hydroxyl groups Li discusses how proteins recognize different RNA folds which include duplex RNA With the fundamentals laid out discussion turns to more specialized examples taken from important aspects of nucleic acid metabolism Schroeder discusses how proteins

chaperone RNA by rearranging its structure into a functional form Berger and Dong discuss how topoisomerases alter the topology of DNA and relieve the superhelical tension introduced by other processes such as replication and transcription Dyda and Hickman show how DNA transposes mediate genetic mobility and Van Duyne discusses how site specific recombinases cut and paste DNA Horton presents a comprehensive review of the structural families and chemical mechanisms of DNA nucleases whereas Li in her discussion of RNA protein recognition also covers RNA nucleases Lastly Ferr D Amar shows how proteins recognize and modify RNA transcripts at specific sites The book also emphasises the impact of structural biology on understanding how proteins interact with nucleic acids and it is intended for advanced students and established scientists wishing to broaden their horizons **Influence of Protein-Protein Interactions (PPIs) on the Outcome of Viral Infections** Gorka Lasso Cabrera,Pablo Guardado-Calvo,Rohit K. Jangra,Eva Mittler,Mercè Llabrés,2022-08-02 *Mapping RNA Protein Interactions in Saccharomyces Cerevisiae* Daniel Michael Klass,2013 We are on the threshold of a new era in our understanding of that fantastic feat of regulation at the core of life itself gene expression The rapid pace of new developments in genome wide high throughput technologies has allowed us unprecedented access to observe multiple stages of the gene expression program for nearly the entire genome This has revealed a widespread discordance between mRNA abundance and protein abundance for many genes whose expression changes in response to environmental stimuli and a significant coordination of post transcriptional regulation for specific sets of related mRNAs at the levels localization translation decay and the noise in gene expression Despite this evidence suggesting the existence of a coordinated regulatory framework that potentially affects the fate of every mRNA in the cell our efforts to discern the underlying structure and regulatory themes are hindered by an incomplete understanding of RNA protein interactions To advance our comprehension of post transcriptional regulation we developed new tools to identify which proteins bind to RNA which of those bind concurrently which RNAs are bound by a given protein and where each protein binds on each RNA Using our proteomic tools we discovered hundreds unexpected RNA binding proteins uncovered new RNA binding domains identified widespread concurrent binding with several RNA binding proteins and inferred functional information from the simultaneous binding partners of several RNA binding proteins We used our genomic sequencing based tools to systematically interrogate a large set of diverse RNA binding proteins and we discerned new themes from the resulting data This revealed significant differences in function localization and regulation among the proteins encoded by the targets of a given RNA binding protein based on binding position These results suggest that the functional consequences of the RBP RNA interaction are determined not only by whether an mRNA is bound by an RBP but also by the position of the binding site within the mRNA and its relation to the other RBPs that bind the same mRNA Overall we found evidence of an extensive regulatory framework involving hundreds of RNA binding proteins encompassing nearly the entire transcriptome and extending our understanding of the RNA protein interactions at the heart of post transcriptional regulation **RNA-protein**

Interactions in Prokaryotic and Eukaryotic Ribonuclease P. Jeremy J. Day,2004 *Protein Interactions: Computational Methods, Analysis And Applications* M Michael Gromiha,2020-03-05 This book is indexed in Chemical Abstracts ServiceThe interactions of proteins with other molecules are important in many cellular activities Investigations have been carried out to understand the recognition mechanism identify the binding sites analyze the the binding affinity of complexes and study the influence of mutations on diseases Protein interactions are also crucial in structure based drug design This book covers computational analysis of protein protein protein nucleic acid and protein ligand interactions and their applications It provides up to date information and the latest developments from experts in the field using illustrations to explain the key concepts and applications This volume can serve as a single source on comparative studies of proteins interacting with proteins DNAs RNAs carbohydrates and small molecules

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