12 3 Rna And Protein Synthesis Answer Key

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RNA and Protein Synthesis Simon and Schuster

Methods in Enzymology, Volume 646, continues the legacy of this premier serial with quality chapters authored by leaders in the field. Chapters in this new release include Methods for Studying RNA condensation/granules in vitro, RNA Dynamics in Intracellular Condensates, Methods for Viscoelastic Characterization of Liquid and Gel Condensates, Incorporating Proteins into Complex Coacervates, Methods for Study of Liquid-Liquid Phase Coexistence in Proximity to Lipid Membranes, Preparation of and Solute Partitioning in Multiphase Coacervates, Reversible photocontrol of DNA coacervation, Enzymatic Control over Coacervation, and much more. Provides the authority and expertise of leading contributors from an international board of authors Presents the latest release in the Methods in Enzymology series

Journal of the National Cancer Institute Rodale

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.

Journal Elsevier

Targeting protein degradation using small molecules is one of the most exciting small-molecule therapeutic strategies in decades and a rapidly growing area of research. In

particular, the development of proteolysis targeting chimera (PROTACs) as potential drugs capable of recruiting target proteins to the cellular quality control machinery for elimination has opened new avenues to address traditionally 'difficult to target' proteins. This book provides a comprehensive overview from the leading academic and industrial experts on recent developments, scope and limitations in this dynamically growing research area; an ideal reference work for researchers in drug discovery and chemical biology as well as advanced students.

New Frontiers and Applications of Synthetic Biology Academic Press

Clinical DNA Variant Interpretation: Theory and Practice, a new volume in the Translational and Applied Genomics series, covers foundational aspects, modes of analysis, technology, disease and disorder specific case studies, and clinical integration. This book provides a deep theoretical background, as well as applied case studies and methodology, enabling researchers, clinicians and healthcare providers to effectively classify DNA variants associated with disease and patient phenotypes. Practical chapters discuss genomic variant interpretation, terminology and nomenclature, international consensus guidelines, population allele frequency, functional evidence transcripts for RNA, proteins, and enzymes, somatic mutations, somatic profiling, and much more. Compiles best practices, methods and sound evidence for DNA variant classification in one applied volume Features chapter contributions from international leaders in the field Includes practical examples of variant classification for common and rare disorders, and across clinical phenotypes

Protocols in Biochemistry and Clinical Biochemistry Elsevier

Transfer RNA in Protein Synthesis is a comprehensive volume focusing on important aspects of codon usage, selection, and discrimination in the genetic code. The many different functions of tRNA and the specialized roles of the corresponding codewords in protein synthesis from initiation through termination are thoroughly discussed. Variations that occur in the initiation process, in reading the genetic code, and in the selection of codons are discussed in detail. The book also examines the role of modified nucleosides in tRNA interactions, tRNA discrimination in aminoacylation, codon discrimination in translation, and selective use of termination codons. Other topics covered include the adaptation of the tRNA population to codon usage in cells and cellular organelles, the occurence of UGA as a codon for selenocysteine in the universal genetic code, new insights into translational context effects and in codon bias, and the molecular biology of tRNA in retroviruses. The contributions of outstanding molecular biologists engaged in tRNA research and prominent investigators from other scientific disciplines, specifically retroviral research, make Transfer RNA in Protein Synthesis an essential reference work for microbiologists, biochemists, molecular biologists, geneticists, and other researchers involved in protein synthesis research.

Alternative pre-mRNA Splicing John Wiley & Sons

Molecular Biology, Second Edition, examines the basic concepts of molecular biology while incorporating primary literature from today's leading researchers. This updated edition includes

Focuses on Relevant Research sections that integrate primary literature from Cell Press and focus on helping the student learn how to read and understand research to prepare them for the scientific world. The new Academic Cell Study Guide features all the articles from the text with concurrent case studies to help students build foundations in the content while allowing them to make the appropriate connections to the text. Animations provided deal with topics such as protein purification, transcription, splicing reactions, cell division and DNA replication and SDS-PAGE. The text also includes updated chapters on Genomics and Systems Biology, Proteomics, Bacterial Genetics and Molecular Evolution and RNA. An updated ancillary package includes flashcards, online self quizzing, references with links to outside content and PowerPoint slides with images. This text is designed for undergraduate students taking a course in Molecular Biology and upper-level students studying Cell Biology, Microbiology, Genetics, Biology, Pharmacology, Biotechnology, Biochemistry, and Agriculture. NEW: "Focus On Relevant Research" sections integrate primary literature from Cell Press and focus on helping the student learn how to read and understand research to prepare them for the scientific world. NEW: Academic Cell Study Guide features all articles from the text with concurrent case studies to help students build foundations in the content while allowing them to make the appropriate connections to the text. NEW: Animations provided include topics in protein purification, transcription, splicing reactions, cell division and DNA replication and SDS-PAGE Updated chapters on Genomics and Systems Biology, Proteomics, Bacterial Genetics and Molecular Evolution and RNA Updated ancillary package includes flashcards, online self quizzing, references with links to outside content and PowerPoint slides with images. Fully revised art program

The Double Helix RNA and Protein Synthesis

Medical Biochemistry, Second Edition covers the structure and physical and chemical properties of hydrocarbons, lipids, proteins and nucleotides in a straightforward and easy to comprehend language. The book develops these concepts into the more complex aspects of biochemistry using a systems approach, dedicating chapters to the integral study of biological phenomena, including particular aspects of metabolism in some organs and tissues, the biochemical bases of endocrinology, immunity, vitamins, hemostasis, autophagy and apoptosis. Additionally, the book has been updated with full-color figures, chapter summaries, and further medical examples to improve learning and illustrate the concepts described in the book. Sections cover bioenergetics and metabolic syndromes, antioxidants to treat disease, plasma membranes, ATPases and monocarboxylate transporters, the human microbiome, carbohydrate and lipid metabolism, autophagy, virology and epigenetics, non-coding, small and long RNAs, protein misfolding, signal transduction pathways, vitamin D, cellular immunity and apoptosis. Integrates basic biochemistry principles with molecular biology and molecular physiology Illustrates basic biochemical concepts through medical and physiological examples Utilizes a systems approach to understanding biological phenomena Fully updated for recent studies and expanded to include clinically relevant examples and succinct chapter summaries Academic Press

"Microbiology covers the scope and sequence requirements for a single-semester microbiology course for non-majors. The book presents the core concepts of microbiology with a focus on applications for careers in allied health. The pedagogical features of the text make the material interesting and accessible while maintaining the career-application focus and scientific rigor inherent in the subject matter. Microbiology's art program enhances students' understanding of concepts through clear and effective illustrations, diagrams, and

photographs. Microbiology is produced through a collaborative publishing agreement between OpenStax and the American Society for Microbiology Press. The book aligns with the curriculum guidelines of the American Society for Microbiology."--BC Campus website.

Practical Aspects of Vaccine Development Elsevier

This book was written for graduate and medical students, as well as clinicians and postdoctoral researchers. It describes the theory of alternative pre-mRNA splicing in twelve introductory chapters and then introduces protocols and their theoretical background relevant for experimental research. These 43 practical chapters cover: Basic methods, Detection of splicing events, Analysis of alternative pre-mRNA splicing in vitro and in vivo, Manipulation of splicing events, and Bioinformatic analysis of alternative splicing. A theoretical introduction and practical guide for molecular biologists, geneticists,clinicians and every researcher interested in alternative splicing. Website: www.wiley-vch.de/home/splicing

Spinal Muscular Atrophy Springer

Laboratory Methods in Enzymology: Protein Part B brings together a number of core protocols concentrating on protein, carefully written and edited by experts. Indispensable tool for the researcher Carefully written and edited by experts to contain step-by-step protocols In this volume we have brought together a number of core protocols concentrating on protein

Structure, Dynamics and Functional Mechanisms of the PWI Domain and the RNA-binding Domain of Rotavirus Non-structural Protein 3 Garland Science

he past fifteen years have seen tremendous growth in our understanding of T the many post-transcriptional processing steps involved in producing func tional eukaryotic mRNA from primary gene transcripts (pre-mRNA). New processing reactions, such as splicing and RNA editing, have been discovered and detailed biochemical and genetic studies continue to yield important new insights into the reaction mechanisms and molecular interactions involved. It is now apparent that regulation of RNA processing plays a significant role in the control of gene expression and development. An increased understanding of RNA processing mechanisms has also proved to be of considerable clinical importance in the pathology of inherited disease and viral infection. This volume seeks to review the rapid progress being made in the study of how mRNA precursors are processed into mRNA and to convey the broad scope of the RNA field and its relevance to other areas of cell biology and medicine. Since one of the major themes of RNA processing is the recognition of specific RNA sequences and structures by protein factors, we begin with reviews of RNA-protein interactions. In chapter 1 David Lilley presents an overview of RNA structure and illustrates how the structural features of RNA molecules are exploited for specific recognition by protein, while in chapter 2 Maurice Swanson discusses the structure and function of the large family of hnRNP proteins that bind to pre-mRNA. The next four chapters focus on pre-mRNA splicing.

Medical Biochemistry CRC Press

Spinal Muscular Atrophy: Disease Mechanisms and Therapy provides the latest information on a condition that is characterized by motoneuron loss and muscle atrophy, and is the leading genetic cause of infant mortality. Since the identification of the gene responsible for SMA in 1995, there have been important advances in the basic understanding of disease mechanisms, and in therapeutic development. This book provides a comprehensive accounting of recent advances in basic and clinical research that covers SMA clinical features and standards of care, multifaceted aspects of SMN protein functions and SMA disease pathology, various animal models, and biomarkers, as well as current therapeutic development. This title is ideal for graduate students/postdocs and principal investigators who are already in the SMA field and need to keep updated on recent findings and approaches, and for those who are new to, or would like to join, the field. Likewise, users will find an excellent source of reading for biotech/pharma scientists, clinical researchers, and practitioners, regulators, and patients and

their advocacy organizations. Furthermore, this book is a handy reference for researchers and clinicians who may want to apply the research strategies and therapeutic approaches in SMA to other rare diseases. Provides comprehensive, up-to-date reviews by leading investigators on diverse topics of SMA, including clinical features and patient care, SMN genetics and protein functions, animal models, disease pathology and mechanisms, biomarkers, current therapeutic development, and the role of non-profit organizations in therapeutic development Written to bridge multiple disciplines and promote better communications among basic scientists, clinical researchers, and health care providers on the latest developments in SMA Includes outstanding questions and perspectives for future investigations and key references for additional detailed study

RNA-protein Interactions Oxford University Press

Formulation, Development and Manufacturing of Vaccines: The Practical Aspects provides an industry perspective on vaccine product development and manufacture that covers their formulation development, manufacture and delivery/in-use considerations of vaccine production. With the increasing complexity of vaccine products in development, there is a need for a comprehensive review of the current state of the industry and its challenges. While formulation scientists working in biotherapeutic development may be familiar with proteins, vaccines present unique challenges, including the wide range of vaccine components that may comprise proteins, polysaccharides, protein-polysaccharide conjugates, adjuvants, etc. and the varying stability and behavior of solution- and suspension-based systems. This book is an essential resource for formulation scientists, researchers in vaccine development throughout medical and life sciences, and advanced students. Includes formulation considerations for various vaccine types, including proteins, polysaccharides, conjugates and live vaccines Considers process development for solution, suspension and lyophilized products Explores the future potential of vaccines, including multi-component vaccines and novel delivery mechanisms/devices

Protein Degradation with New Chemical Modalities Elsevier

Presents sixty simple and inexpensive recipes featuring canned foods, providing easy-to-follow illustrated steps in a lay-flat design and offering suggestions for such occasions as cooking for a woman and preparing a meal for the morning after. 35,000 first printing.

Encyclopedia of Biological Chemistry Academic Press

RNA and Protein Synthesis is a compendium of articles dealing with the assay, characterization, isolation, or purification of various organelles, enzymes, nucleic acids, translational factors, and other components or reactions involved in protein synthesis. One paper describes the preparatory scale methods for the reversed-phase chromatography systems for transfer ribonucleic acids. Another paper discusses the determination of adenosine- and aminoacyl adenosine-terminated sRNA chains by ion-exclusion chromatography. One paper notes that the problems involved in preparing acetylaminoacyl-tRNA are similar to those found in peptidyl-tRNA synthesis, in particular, to the lability of the ester bond between the amino acid and the tRNA. Another paper explains a new method that will attach fluorescent dyes to cytidine residues in tRNA; it also notes the possible use of N-hydroxysuccinimide esters of dansylglycine and N-methylanthranilic acid in the described method. One paper explains the use of membrane filtration in the determination of apparent association constants for ribosomal protein-RNS complex formation. This collection is valuable to bio-chemists, cellular biologists, micro-biologists, developmental biologists, and investigators working with enzymes.

Concepts of Biology Academic Press

Naturally occurring RNA always contains numerous

biochemically altered nucleotides. They are formed by enzymatic modification of the primary transcripts during the complex RNA maturation process designated RNA modification. A large number of enzymes catalyzing the formation of these modified nucleosides or converting one canonical base into another at the posttranscriptional level have been studied for many years, but only recently have systematic and comparative studies begun. The functions of individual enzymes and/or the modified/edited nucleosides in RNA, however, have remained largely ignored. This book provides advance information on RNA modification, including the associated editing machinery, while offering the reader some perspective on the significance of such modifications in fine-tuning the structure and functions of mature RNA molecules and hence the ability to influence the efficiency and accuracy of genetic expression. Outstanding scientists who are actively working on RNA modification/editing processes have provided up-to-date information on these intriguing cellular processes that have been generated over the course of millions of years in all living organisms. Each review has been written and illustrated for a large audience of readers, not only specialists in the field, but also for advanced students or researchers who want to learn more about recent progress in RNA modification and editing.

Clinical DNA Variant Interpretation John Wiley & Sons

This book is a compilation of articles on significant events in the history of biochemistry, which were published in the journal "Trends in Biochemical Sciences." Editor Witkowski has selected articles that present an insider's view of discoveries that are now seen as landmark achievements, and that relate to the central dogma of molecular biology, which is that DNA makes RNA makes protein, or, "once information has passed into protein it cannot get out again." The book begins with Albrecht Kossel and the discovery of histones, and ranges through Schrodinger and the origins of molecular biology, the double helix, DNA replication, protein synthesis, genetic code, tRNA, mRNA, early ribosome research, peptidyl transfer, and finally to the advent of rapid DNA sequencing. Annotation : 2005 Book News, Inc., Portland, OR (booknews.com)

The Inside Story Academic Press

Adenosine deaminase acting on transfer RNA (ADAT) is a human heterodimeric enzyme that catalyzes the deamination of adenosine (A) to inosine (I) at the first position of the anticodon of transfer RNAs (tRNAs) (position 34, or wobble position); one of the few essential post-transcriptional modifications on tRNAs (1-5). Inosine 34 allows the recognition of three different nucleotides: cytidine, uridine and adenosine, at the third position of the codon, thus increasing the decoding capacity of tRNAs to more than one messenger RNA (mRNA) codon (adenosine 34 can in principle only pair with codons with uridine at the third position) (6, 7). This alters the tRNA pool available for each codon and it has been proved to align the correlation between codon usage and tRNA gene copy number (8). It has also been suggested to improve fidelity and efficiency of translation (8, 9), especially for mRNAs enriched in codons translated by modified tRNAs (10, 11). Monitoring ADAT-mediated deamination is crucial for the characterization of the enzyme in terms of activity, substrates, regulation, as well as for drug discovery purposes. However, this analysis is often challenging, laborious and lacks quantitativeness. We developed an in vitro deamination assay based on restriction fragment length polymorphism (RFLP) analyses to monitor ADAT activity in an efficient, cost-effective, and semiquantitative manner (12). To overcome a limitation of the method being the need of reverse transcription and amplification of the tRNA, we designed a direct method to quantify I34 formation in vitro using the first fluorescent analogs of nucleic acids that have been reported to undergo enzymatic deaminations (13-15). ADAT has been conserved over the evolution with the acquisition of multi-substrate specificity. Whereas its bacterial homolog TadA deaminates exclusively tRN18rg (2), the human enzyme deaminates eight different tRNAs (3, 16). However, the mechanisms that drove this evolution remain unknown. While the substrate recognition in TadA has been well studied, in the eukaryotic ADAT is poorly understood. Through in vitro enzymatic activity assays with different variants of tRN18rg and tRN18la, we elucidated the most important features for efficient A34-to-I34 conversion and characterized the substrate recognition of the human enzyme. We also proposed a new potential mechanism of control of ADAT deamination activity by human tRNA-derived fragments, which provides new insights into the regulation of ADAT function and may open a

door for the development of new strategies to modulate ADAT activity. A missense mutation (V128M) in one of the two subunits of the human ADAT enzyme causes intellectual disability and strabismus, but the molecular bases of the pathology are unknown (17, 18). We characterized human ADAT in terms of kinetics and structure, and investigated the effect of the V128M mutation. We found that this substitution decreases ADAT deamination activity, and severely affects the stability of the quaternary structure of the enzyme. In this regard, we discovered small molecules with the ability to activate the enzyme, which could potentially recover the defective tRNA editing caused by the mutation. References 1.Gerber AP, Keller W. An adenosine deaminase that generates inosine at the wobble position of tRNAs. Science. 1999;286(5442):1146-9. Epub 1999/11/05. 2.Wolf J, Gerber AP, Keller W. tadA, an essential tRNA-specific adenosine deaminase from Escherichia coli. The EMBO journal. 2002;21(14):3841-51. Epub 2002/07/12. 3.Torres AG, Pineyro D, Rodriguez-Escriba M, Camacho N, Reina O, Saint-Leger A, et al. Inosine modifications in human tRNAs are incorporated at the precursor tRNA level. Nucleic acids research. 2015;43(10):5145-57. Epub 2015/04/29. 4.Zhou W, Karcher D, Bock R. Identification of enzymes for adenosine-to-inosine editing and discovery of cytidine-to-uridine editing in nucleus-encoded transfer RNAs of Arabidopsis. Plant physiology. 2014;166(4):1985-97. Epub 2014/10/16. 5.Tsutsumi S, Sugiura R, Ma Y, Tokuoka H, Ohta K, Ohte R, et al. Wobble inosine tRNA modification is essential to cell cycle progression in G(1)/S and G(2)/M transitions in fission yeast. J Biol Chem. 2007;282(46):33459-65. Epub 2007/09/19. 6.Crick FH. Codon--anticodon pairing: the wobble hypothesis. Journal of molecular biology. 1966;19(2):548-55. Epub 1966/08/01. 7.Torres AG, Pineyro D, Filonava L, Stracker TH, Batlle E, Ribas de Pouplana L. A-to-I editing on tRNAs: biochemical, biological and evolutionary implications. FEBS Lett. 2014;588(23):4279-86. Epub 2014/09/30. 8.Novoa EM, Pavon-Eternod M, Pan T, Ribas de Pouplana L. A role for tRNA modifications in genome structure and codon usage. Cell. 2012;149(1):202-13. Epub 2012/04/03. 9.Schaub M, Keller W. RNA editing by adenosine deaminases generates RNA and protein diversity. Biochimie. 2002;84(8):791-803. Epub 2002/11/30. 10.Rafels-Ybern A, Attolini CS, Ribas de Pouplana L. Distribution of ADAT-Dependent Codons in the Human Transcriptome. International journal of molecular sciences. 2015;16(8):17303- 14. Epub 2015/08/01. 11.Rafels-Ybern A, Torres AG, Grau-Bove X, Ruiz-Trillo I, de Pouplana LR. Codon adaptation to tRNAs with Inosine modification at position 34 is widespread among Eukaryotes and present in two Bacterial phyla. RNA biology. 2017:0. Epub 2017/09/08. 12.Wulff TF, Arguello RJ, Molina Jordan M, Roura Frigole H, Hauquier G, Filonava L, et al. Detection of a Subset of Posttranscriptional Transfer RNA Modifications in Vivo with a Restriction Fragment Length Polymorphism-Based Method. Biochemistry. 2017;56(31):4029-38. Epub 2017/07/14. 13.Sinkeldam RW, McCoy LS, Shin D, Tor Y. Enzymatic interconversion of isomorphic fluorescent nucleosides: adenosine deaminase transforms an adenosine analogue into an inosine analogue. Angew Chem Int Ed Engl. 2013;52(52):14026-30. Epub 2013/11/30. 14.McCoy LS, Shin D, Tor Y. Isomorphic emissive GTP surrogate facilitates initiation and elongation of in vitro transcription reactions. Journal of the American Chemical Society. 2014;136(43):15176-84. Epub 2014/09/26. 15.Rovira AR, Fin A, Tor Y. Chemical Mutagenesis of an Emissive RNA Alphabet. J Am Chem Soc. 2015;137(46):14602-5. Epub 2015/11/03. 16.Juhling F, Morl M, Hartmann RK, Sprinzl M, Stadler PF, Putz J. tRNAdb 2009: compilation of tRNA sequences and tRNA genes. Nucleic acids research. 2009;37(Database issue):D159-62. Epub 2008/10/30. 17.Alazami AM, Hijazi H, Al-Dosari MS, Shaheen R, Hashem A, Aldahmesh MA, et al. Mutation in ADAT3, encoding adenosine deaminase acting on transfer RNA, causes intellectual disability and strabismus. Journal of medical genetics. 2013;50(7):425-30. Epub 2013/04/27. 18.El-Hattab AW, Saleh MA, Hashem A, Al-Owain M, Asmari 18, Rabei H, et al. ADAT3- related intellectual disability: Further delineation of the phenotype. American journal of medical genetics Part A. 2016;170A(5):1142-7. Epub 2016/02/05.

Pre-mRNA Processing National Academies Press

The second edition of a highly acclaimed handbook and ready reference. Unmatched in its breadth and quality, around 100 specialists from all over the world share their up-to-date expertise and experiences, including hundreds of

protocols, complete with explanations, and hitherto unpublished troubleshooting hints. They cover all modern techniques for the handling, analysis and modification of RNAs and their complexes with proteins. Throughout, they bear the practising bench scientist in mind, providing quick and reliable access to a plethora of solutions for practical questions of RNA research, ranging from simple to highly complex. This broad scope allows the treatment of specialized methods side by side with basic biochemical techniques, making the book a real treasure trove for every researcher experimenting with RNA.

RNA Infrastructure and Networks Academic Press

RNA binding proteins play essential roles in many cellular processes, including structural, regulatory and catalytic roles. The molecular mechanisms by which many RNA-binding proteins recognize and interact with their targets are still unknown, and remain the subject of extensive research. The structural and functional properties of the rotavirus Non-structural Protein 3 (NSP3) and the PWI RNA binding domains are described in this study. Rotavirus is a member of the Reoviridae family of viruses and can cause severe, life threatening diarrhea in children under the age of 5. The Rotaviruses genome consists of 11 segments of double-stranded RNA, which encodes for 11-12 different proteins. Six non-structural proteins (NSPs) play regulatory roles in the replication cycle of the virus. Non-structural protein 3 (NSP3) is believed to regulate virus protein synthesis by hijacking host translation machinery and promoting viral mRNA translation using a mechanism that is analogous to Poly-Adenosine Binding Protein. The N-terminal, RNA-binding domain of NSP3 binds a conserved tetranucleotide sequence at the 3' end (---GACC) of rotavirus RNA molecules, while the C-terminal domain binds host translation initiation factor eIF4G. Gene suppression studies recently revealed that NSP3 also prevents the expression of host mRNA by preventing export from the cell nucleus using an unknown mechanism. The relative importance and the molecular mechanisms of NSP3 functions are still controversial. The aims of the study were to discover the structural features and functional mechanisms involved in NSP3 binding to RNA, and to elucidate the role of RNA binding in different protein functions. NMR spectroscopic studies of several NSP3 protein constructs revealed that the RNA binding domain contains three structurally distinct sub-domains that "hug" the RNA target during the binding mechanism. The PWI domain is named for a three amino acid residue sequence, Proline(P)-Tryptophan(W)-Isoleucine(I), that is highly conserved, and found in several proteins involved in pre-messenger RNA (pre-mRNA) processing. Pre-mRNA processing is essential in the generation of mRNA molecules that can be exported from the nucleus and translated into proteins, and can result in the formation of many different proteins from a single gene. Incorrect regulation of processing is associated with several diseases, including cancer and heart failure. The PWI domain consists of a PWI motif and an adjacent basic region that is critical for the domain's nucleic acid binding properties. The aim of the study was to investigate the mechanism by which the PWI motif and the adjacent basic region cooperatively bind to nucleic acids. Several biophysical approaches were used to investigate the nucleic acid binding mechanism of PWI domains from different proteins. Fluorescence spectroscopy was used to assess binding stoichiometry, while mobility shift assays measured binding affinity and cooperativity. PWI domains from PRP3, SRm160 and RBM25 are found to bind nucleic acids with a low micromolar binding affinity, and two or more proteins are involved in complex formation. NMR spectroscopy revealed the structural and conformationally dynamic properties of the domain.