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GTPase Protocols Ed Manser 2002-06-05 In the last 10 years researchers have firmly established key roles for R- related GTPases in almost every aspect of cell biology. In the 1980s the pro-oncogene Ras itself was the focus of interest, though in the 1990s this shifted to the increasing variety of Ras-related proteins. In this new decade much yet needs to be done to establish the role for all the small GTPases now uncovered by the human genome project. In particular, these GTPases need to be und- stood in the appropriate biochemical and cellular contexts. In the process of trying to uncover the role of these versatile proteins, a variety of novel te- niques and methodologies has been developed. These now enable investi- tors to move easily within a diversity of fields ranging from structural studies to real-time in vivo analysis of a GTPase. In recognition of the need for access to key background methodologies, GTPase Protocols: The Ras Superfamily is devoted to techniques that are pr- ently widely used and that will continue to be the standard for researchers worldwide. Each chapter is aimed at supplying detailed methodologies to allow reproduction in any laboratory, while also providing the general pr- ciples on which the methods are based. Some of the techniques grouped in the first section apply broadly to small GTPases, whereas others in Part II are more applicable within each GTPase subfamily.
The Role of the Small GTPase Ran During Assembly of a Mitotic Spindle Christoph Schatz 2003

ARF Family GTPases Richard A. Kahn 2004-02-29 For the first time experts in the area of signalling research with a focus on the ARF family have contributed to the production of a title devoted to ARF biology. A comprehensive phylogenetic analysis of the ARF family, tables of the ARF GEFs and ARF GAPs, and more than a dozen chapters describing them in detail are provided. The impact of the ARF proteins on widely diverse aspects of cell biology and cell signalling can be clearly seen from the activities described; including membrane traffic, lipid metabolism, receptor desensitization, mouse development, microtubule dynamics, and bacterial pathogenesis. Anyone interested in understanding the complexities of cell signalling and the integration of signalling networks will benefit from this volume.
Yeast Horst Feldmann 2012-09-06 Finally, a stand-alone, all-inclusive textbook on yeast biology. Based on the feedback resulting from his highly successful monograph, Horst Feldmann has totally rewritten he contents to produce a comprehensive, student-friendly textbook on the topic. The scope has been widened, with almost double the content so as to include all aspects of yeast biology, from genetics via cell biology right up to biotechnology applications. The cell and molecular biology sections have been vastly expanded, while information on other yeast species has been added, with contributions from additional authors. Naturally, the illustrations are in full color throughout, and the book is backed by a complimentary website. The

resulting textbook caters to the needs of an increasing number of students in biomedical research, cell and molecular biology, microbiology and biotechnology who end up using yeast as an important tool or model organism.

Cell Biology E-Book Thomas D. Pollard 2007-04-26 A masterful introduction to the cell biology that you need to know! This critically acclaimed textbook offers you a modern and unique approach to the study of cell biology. It emphasizes that cellular structure, function, and dysfunction ultimately result from specific macromolecular interactions. You'll progress from an explanation of the "hardware" of molecules and cells to an understanding of how these structures function in the organism in both healthy and diseased states. The exquisite art program helps you to better visualize molecular structures. Covers essential concepts in a more efficient, reader-friendly manner than most other texts on this subject. Makes cell biology easier to understand by demonstrating how cellular structure, function, and dysfunction result from specific macromole¬cular interactions. Progresses logically from an explanation of the "hardware" of molecules and cells to an understanding of how these structures function in the organism in both healthy and diseased states. Helps you to visualize molecular structures and functions with over 1500 remarkable full-color illustrations that present physical structures to scale. Explains how molecular and cellular structures evolved in different organisms. Shows how molecular changes lead to the development of diseases through numerous Clinical Examples throughout. Includes STUDENT CONSULT access at no additional charge, enabling you to consult the textbook online, anywhere you go · perform quick searches · add your own notes and bookmarks · follow Integration Links to related bonus content from other STUDENT CONSULT titles—to help you see the connections between diverse disciplines · test your knowledge with multiple-choice review questions · and more! New keystone chapter on the origin and evolution of life on earth probably the best explanation of evolution for cell biologists available! Spectacular new artwork by gifted artist Graham Johnson of the Scripps Research Institute in San Diego. 200 new and 500 revised figures bring his keen insight to Cell Biology illustration and further aid the reader's understanding. New chapters and sections on the most dynamic areas of cell biology - Organelles and membrane traffic by Jennifer Lippincott-Schwartz; RNA processing (including RNAi) by David Tollervey., updates on stem cells and DNA Repair. ,More readable than ever. Improved organization and an accessible new design increase the focus on understanding concepts and mechanisms. New guide to figures featuring specific organisms and specialized cells paired with a list of all of the figures showing these organisms. Permits easy review of cellular and molecular mechanisms. New glossary with one-stop definitions of over 1000 of the most important terms in cell biology.

Strukturelle und funktionale Analyse der acetylierten kleinen GTPase Ran 2015 The nucleus is the most prominent feature of every eukaryotic cell. Since the nucleus contains virtually all the genetic information it separates the transcription and translation. This separation requires a bidirectional process divided into import and export of macromolecules through the nuclear pore complex (NPC) the nuclear transport. This process is largely mediated by receptors of the karyopherin-[beta] superfamily. The driving force behind the nuclear transport is a gradient of the small GTPase Ran across the nuclear envelope. This protein and its gradient simultaneously form an important...

Handbook of Cell Signaling Ralph A. Bradshaw 2009-11-03 Handbook of Cell Signaling, Three-Volume Set, 2e, is a comprehensive work covering all aspects of intracellular signal processing, including extra/intracellular membrane receptors, signal transduction, gene expression/translation, and cellular/organotypic signal responses. The second edition is an up-to-date, expanded reference with each section edited by a recognized expert in the field. Tabular and well illustrated, the Handbook will serve as an in-depth reference for this complex and evolving field. Handbook of Cell Signaling, 2/e will appeal to a broad, cross-disciplinary audience interested in the structure, biochemistry, molecular biology and pathology of cellular

effectors. Contains over 350 chapters of comprehensive coverage on cell signaling Includes discussion on topics from ligand/receptor interactions to organ/organism responses Provides user-friendly, well-illustrated, reputable content by experts in the field

Nuclear-Cytoplasmic Transport Weidong Yang 2018-07-27 Dysfunction of nuclear-cytoplasmic transport systems has been associated with many human diseases. Thus, understanding of how functional this transport system maintains, or through dysfunction fails to maintain remains the core question in cell biology. In eukaryotic cells, the nuclear envelope (NE) separates the genetic transcription in the nucleus from the translational machinery in the cytoplasm. Thousands of nuclear pore complexes (NPCs) embedded on the NE selectively mediate the bidirectional trafficking of macromolecules such as RNAs and proteins between these two cellular compartments. In this book, the authors integrate recent progress on the structure of NPC and the mechanism of nuclear-cytoplasmic transport system in vitro and in vivo.

The Small Nuclear GTPase Ran Mark G. Rush 1996*

Nuclear Pore Complexes and Nucleocytoplasmic Transport - Methods 2014-05-20 Volume 122 of Methods in Cell Biology describes modern tools and techniques used to study nuclear pore complexes and nucleocytoplasmic transport in diverse eukaryotic model systems (including mammalian cells, Xenopus, C. elegans, yeast). The volume enables investigators to analyze nuclear pore complex structure, assembly, and dynamics; to evaluate protein and RNA trafficking through the nuclear envelope; and to design in vivo or in vitro assays appropriate to their research needs. Beyond the study of nuclear pores and transport as such, these protocols will also be helpful to scientists characterizing gene regulation, signal transduction, cell cycle, viral infections, or aging. The NPC being one of the largest multiprotein complexes in the cell, some protocols will also be of interest for people currently characterizing other macromolecular assemblies. This book is thus designed for laboratory use by graduate students, technicians, and researchers in many molecular and cellular disciplines. Describes modern tools and techniques used to study nuclear pore complexes and nucleocytoplasmic transport in diverse eukaryotic model systems (mammalian cells, Xenopus, C. elegans, yeast) Chapters are written by experts in the field Cutting-edge material

RNA Exosome Torben Heick Jensen 2011-06-29 The diversity of RNAs inside living cells is amazing. We have known of the more “classic” RNA species: mRNA, tRNA, rRNA, snRNA and snoRNA for some time now, but in a steady stream new types of molecules are being described as it is becoming clear that most of the genomic information of cells ends up in RNA. To deal with the enormous load of resulting RNA processing and degradation reactions, cells need adequate and efficient molecular machines. The RNA exosome is arising as a major facilitator to this effect. Structural and functional data gathered over the last decade have illustrated the biochemical importance of this multimeric complex and its many co-factors, revealing its enormous regulatory power. By gathering some of the most prominent researchers in the exosome field, it is the aim of this volume to introduce this fascinating protein complex as well as to give a timely and rich account of its many functions. The exosome was discovered more than a decade ago by Phil Mitchell and David Tollervey by its ability to trim the 3’end of yeast, S. cerevisiae, 5. 8S rRNA. In a historic account they laid out the events surrounding this identification and the subsequent birth of the research field. In the chapter by Kurt Januszyk and Christopher Lima the structural organization of eukaryotic exosomes and their evolutionary counterparts in bacteria and archaea are discussed in large part through presentation of structures.

The Role of the Small GTPase Ran in Assembly of a Bipolar Mitotic Spindle Christoph Schatz 2003

Functional Investigation of Arabidopsis Long Coiled-coil Proteins and Subcellular Localization of Plant Rangap1 Sun Yong Jeong 2004 Abstract: Only a few long alpha-helical coiled-coil proteins have been investigated in plants. Here, two such plant proteins were investigated in detail, MAR-binding filament-like protein1 (MFP1) and the

putative Arabidopsis homolog of Tpr (translocated promoter region). MFP1 is a nuclear-encoded, long coiled-coil protein that is targeted to plastids. It accumulates to comparable levels in all tissues of Arabidopsis which contain green chloroplasts, regardless of age and organ identity, but is much less abundant in roots of both light-grown and dark-grown seedlings. MFP1 protein accumulation parallels chloroplast development during the greening of seedlings shifted from dark to light, suggesting that MFP1 expression is regulated in a tissue-specific and light-dependent manner. MFP1 is localized in chloroplasts both in suspension culture cells and in leaves, and it is associated with the stromal side of thylakoid membranes of mature chloroplasts. It is co-purified with nucleoids, suggesting a function at the interface of the chloroplast genome and the photosynthetic membranes. MFP1 comprises a major DNA-binding activity in Arabidopsis chloroplasts and binds to several regions of the chloroplast DNA with equal affinity. Several thylakoid proteins are phosphorylated by a protein kinase CKII-like activity, and the alpha subunit of a chloroplast-located CKII has been identified as a component of the chloroplast transcription complex. Chloroplast-localized MFP1 is phosphorylated in vivo, and in vitro by CKII and phosphorylation inhibits its DNA-binding activity. A tandem CKII site in the DNA-binding domain of MFP1 was identified which is involved in the phosphorylation-dependent loss of DNA-binding activity. These features of MFP1 make CKII-dependent phosphorylation a possible mode of regulating the DNA-binding activity of the protein in vivo. Together, these data suggest that MFP1 is an interesting candidate for an architectural protein, possibly involved in anchoring nucleoids to thylakoid membranes. Tpr is a long coiled-coil protein associated with the nuclear surface of the nuclear pore in animals and yeast, where it is involved in mRNA export. A putative Arabidopsis Tpr homolog was identified. A T-DNA insertion mutant in its gene has a pleiotropic phenotype including early flowering, reduced apical dominance and morphological alterations of leaves and inflorescences. The connection between the predicted function of Tpr and its mutant phenotype is currently being investigated. In animals and yeast, the small GTPase Ran is involved in nucleocytoplasmic transport, spindle formation, and nuclear envelope formation, functions controlled by a RanGTPase-activating protein (RanGAP) and a guanine nucleotide exchange factor (RCC1). Vertebrate RanGAP1 is conjugated with the ubiquitin-like protein SUMO. SUMOylation of RanGAP1 is required for nuclear envelope-association in interphase and for spindle and centromere association in mitosis. Plant RanGAP lacks the SUMOylated C-terminal domain of vertebrate RanGAP, but contains instead a plant-specific N-terminal WPP domain, which is necessary and sufficient for targeting the protein to the nuclear rim. By examining the localization of Arabidopsis RanGAP1 during the cell cycle in stably transformed tobacco BY-2 cells expressing AtRanGAP1-GFP, we found that AtRanGAP1 localizes to the nuclear rim during interphase and to the cell plate during cytokinesis. A WPP domain-GFP fusion behaves like full-length AtRanGAP1-GFP, while WPP-domain deletion abolishes all targeting, demonstrating that the WPP domain is necessary and sufficient for both targeting events. Point mutations in conserved residues of the WPP domain abolish targeting to the nuclear rim and the cell plate, suggesting that the same mechanism is involved in anchoring RanGAP1 in both locations. These results imply a novel function of AtRanGAP1 during cell cycle and suggest a role of the Ran cycle in controlling cell plate formation in plant cytokinesis.

Sumoylation of Nuclear Transport Receptors and the Small GTPase Ran 2012 Sumoylation has been linked to nucleocytoplasmic transport since the discovery of SUMO as a modifier of vertebrate RanGAP1, which is targeted to the nuclear pore complex (NPC) after sumoylation. The link between sumoylation and nucleocytoplasmic transport has been strengthened even more with the discovery that the major component of NPC cytoplasmic filaments, RanBP2, acts as a SUMO E3 ligase. RanBP2 is in stable complex with Ubc9 and sumoylated RanGAP1, and it was recently discovered that it is the RanBP2 complex which acts as a multisubunit E3 ligase in cells. One fascinating feature of th...

GTPase Protocols Edward J. Manser 2002 Small

GTPase binding proteins (GTPases) are an ancient group of proteins that play key roles in almost every aspect of cell biology, from cell proliferation to nuclear transport. In GTPase Protocols: The Ras Superfamily, Edward J. Manser and Thomas Leung have collected the key techniques currently in use to probe the function of these ubiquitous proteins both in vitro and in vivo. Presented in a format that ensures ready reproducibility by accomplished experimentalists who have refined the various methods in their laboratories, each technique includes step-by-step instructions, tips on avoiding pitfalls and troubleshooting, and ancillary notes explaining how to adapt each procedure in the event of problems. The methods cover the spectrum of core techniques required for the five major GTPase subfamilies (Ras, Rho, Rab, Arf, and Ran) and permit a diversity of applications ranging from structural studies on a GTPase to real time in vivo analysis. Timely and highly practical, GTPase Protocols: The Ras Superfamily illuminates the powerful techniques used by investigators today to study this special family of proteins that plays such important roles in human health and disease.

Interactions of Nuclear Carriers with the Nuclear Pore Complex and the Small GTPase Ran Ian Cushman 2004

The Role of Small GTPase Rac1 in Cell Senescence, Apoptosis and Proliferation Ran You 2006

Ras Signaling Lorenza Trabalzini 2014-01-28 Featuring experimental approaches that shed light on the complexity of Ras GTPase biological functions, Ras Signaling: Methods and Protocols contains general overviews and detailed applications of both well-established and recently developed research techniques, including biochemical, biophysical, molecular biology, genetic and behavioral approaches, advanced high resolution fluorescence and electron microscopy imaging and “omics” technologies. Through this, the detailed volume provides information on expression, post-translational modifications, subcellular localization and dynamics, regulatory mechanisms of upstream and downstream signaling pathways and ultimately, biological activities and functions of Ras GTPases in different model systems, including high and low eukaryotic organisms. Written in the highly successful Methods in Molecular Biology series format, chapters include brief introductions, lists of the necessary materials and reagents, step-by-step, readily reproducible laboratory protocols and tips on troubleshooting and avoiding known pitfalls. Wide-ranging and authoritative, Ras Signaling: Methods and Protocols serves as an aid for investigators of different backgrounds and interests related to the multiple physiological and pathological functions of the large superfamily of Ras GTPases.

Modulation of the Small GTPase Ran by Legionella RCC1 Repeat Proteins Anna Leoni Swart 2019

GTPase Protocols Ed Manser 2008-02-03 In the last 10 years researchers have firmly established key roles for R- related GTPases in almost every aspect of cell biology. In the 1980s the pro-oncogene Ras itself was the focus of interest, though in the 1990s this shifted to the increasing variety of Ras-related proteins. In this new decade much yet needs to be done to establish the role for all the small GTPases now uncovered by the human genome project. In particular, these GTPases need to be und- stood in the appropriate biochemical and cellular contexts. In the process of trying to uncover the role of these versatile proteins, a variety of novel te- niques and methodologies has been developed. These now enable investi- tors to move easily within a diversity of fields ranging from structural studies to real-time in vivo analysis of a GTPase. In recognition of the need for access to key background methodologies, GTPase Protocols: The Ras Superfamily is devoted to techniques that are pr- ently widely used and that will continue to be the standard for researchers worldwide. Each chapter is aimed at supplying detailed methodologies to allow reproduction in any laboratory, while also providing the general pr- ciples on which the methods are based. Some of the techniques grouped in the first section apply broadly to small GTPases, whereas others in Part II are more applicable within each GTPase subfamily.

Ras Superfamily Small G Proteins: Biology and Mechanisms 2 Alfred Wittinghofer 2014-09-26 This second of two volumes discusses subfamily proteins which function in molecular and vesicular transport mechanisms inside the cell.

In this volume the focus lies on the Rab, Ran and Arf subfamily members. As in Volume 1, the book is written by international renowned scientists in the field of small G-proteins. In elaborate reviews, biochemistry, structure, function and G-protein - effector interactions are described. Together with Volume 1 this book provides an comprehensive state-of-the-art work on small G-proteins (GTPases). It is written for Graduates and Professors in Biochemistry and Cell Biology interested in the mechanism and function of small G-proteins but are extremely valuable for those who want to move into the field.

Encyclopedia of Cancer Manfred Schwab 2008-09-23 This comprehensive encyclopedic reference provides rapid access to focused information on topics of cancer research for clinicians, research scientists and advanced students. Given the overwhelming success of the first edition, which appeared in 2001, and fast development in the different fields of cancer research, it has been decided to publish a second fully revised and expanded edition. With an A-Z format of over 7,000 entries, more than 1,000 contributing authors provide a complete reference to cancer. The merging of different basic and clinical scientific disciplines towards the common goal of fighting cancer makes such a comprehensive reference source all the more timely.

Dissection of Mitotic Ran Pathway Function Using the Small Molecule Importazole Stephen Lucien Bird 2012 The faithful and proper segregation of the genome between dividing cells is of paramount importance to all organisms. In order to maintain the integrity of the genetic information during division, cells make use of an extremely complex and highly regulated set of processes known collectively as mitosis. A key aspect of mitosis is the generation and maintenance of the mitotic spindle, a large and complex microtubule based structure that is responsible for organizing and transporting the chromosomes to the daughter cells. The mitotic spindle is of vital importance to the life of the cell, and multiple partially redundant pathways have evolved to regulate its assembly and operation. The small GTPase Ran governs one such pathway functioning in the vicinity of the chromosomes to control the activation of a variety of proteins that contribute to mitotic spindle assembly. However, in addition to promoting spindle assembly, the Ran pathway also regulates a number of other essential processes during the cell cycle such as nucleocytoplasmic transport and nuclear envelope dynamics. Due to this fact, studying the mitotic roles of the Ran pathway in vivo is challenging, as mitosis comprises only a small portion of the cell cycle. In order to overcome this obstacle, we took a small molecule inhibitor based approach, and sought to identify a compound capable of disrupting Ran pathway function with great temporal precision in living cells. In the following dissertation, we first provide an introduction to the cellular processes regulated by mitotic Ran pathway function, and then follow with descriptions of our efforts to develop and improve an inhibitor of RanGTP/importin-[beta] function. Finally, we describe how we made use of this inhibitor to gain insight into a newly discovered role for Ran in the regulation of mitotic spindle positioning. First we set out to develop a small molecule inhibitor capable of disrupting Ran pathway function. During interphase, the transport receptor importin-[beta] carries cargoes into the nucleus, where RanGTP releases them. A similar mechanism operates in mitosis to generate a gradient of active spindle assembly factors around mitotic chromosomes. We implemented a FRET-based, high-throughput small molecule screen for compounds that interfere with the interaction between RanGTP and importin-[beta] and identified importazole, a 2,4-diaminoquinazoline. We found that importazole specifically blocked importin-[beta]-mediated nuclear import both in Xenopus egg extracts and cultured cells, without disrupting transportin-mediated nuclear import or CRM1-mediated nuclear export. When added during mitosis, importazole impaired the release of an importin-[beta] cargo FRET probe and caused both predicted and novel defects in spindle assembly. Together, our results identified importazole as a compound suitable for study of the Ran pathway in mitosis that specifically inhibits importin-[beta] function, and suggest a possible molecular mechanism for importazole in which it alters importin-[beta] interaction with RanGTP. With an inhibitor of the pathway in hand, we

attempted to improve importazole as a tool for study of mitotic Ran pathway function by elucidating its mechanism of action and devloping more potent analogues to maximize compound specificity. In order to gain further insight into importazole's molecular mechanism, we made use of surface plasmon resonance to directly measure the in vitro association between RanGTP and importin-[beta] in the presence of importazole. In concordance with our previous observations, these experiments suggested that importazole does not destabilize the RanGTP/importin-[beta] complex. However, the data was ultimately not reproducible enough to provide additional information about importazole function. In an effort to produce more potent inhibitors of RanGTP/importin-[beta] function, we developed small molecule analogues based on the structure of importazole. One of these second generation compounds was capable of disrupting nucleocytoplasmic transport and mitotic spindle assembly, though it was not shown to be a significantly more potent inhibitor than importazole. Thus, we determined that importazole remains the best currently available tool for study of the Ran pathway in mitosis. Finally, we took advantage of importazole to explore RanGTP/importin-[beta] involvement in regulating mitotic spindle positioning, a mitotic function of the Ran pathway that has only recently been discovered. Proper positioning of the spindle is required to ensure correct segregation of the chromosomes during mitosis, and is mediated through pulling forces exerted on the astral microtubules by dynein/dynactin complexes linked to the cell cortex with G[alpha]i, LGN, and the importin-[beta] cargo protein NuMA. We found that importazole treatment disrupted mitotic spindle positioning in living cells without preventing formation of astral microtubules, and that it affected the cortical localization of both LGN and NuMA. These results demonstrated a role for RanGTP/importin-[beta] function in spindle positioning, and our data suggest a model in which Ran may control this process through regulation of the stability of cortical positioning factors. A great deal remains to be learned about the role of the Ran pathway in mitotic spindle positioning, but importazole provides a promising avenue of study for this and other Ran mediated cellular processes.

GTPases Alan Hall 2000 GTPases are molecular switches that are used to control biochemical pathways. This book describes the properties and cellular roles of all the major families of GTPases: the G proteins, Ras, Rho, Rab, Arf, and Ran. All cells use GTPases to regulate the delivery of amino acids to the ribosomeduring protein synthesis, but eukaryotes, with their complex and compartmentalized environment, have exploited the versatility of GTPases to a much greater extent. The roles of two further families of GTPases in protein localization and protein tanslocation are discussed in chapter 8. Chapter 9covers the huge amount of structural data accumulated for all families of GTPases and the proteins with which they interact. The final chapter describes the modification of GTPases by numerous bacterial toxins. It is not surprising, therefore, that GTPases have become a centre of attention forthose studying the control of proliferation, differentiation, cell polarity, cell movement and vesicle and protein trafficking. GTPases: Frontiers in Molecular Biology provides a complete guide to this area and should be essential reading for cell and molecular biologists, biochemists andgeneticists interested in these contemporary problems.

Cloning and Characterization of Nuclear Transport Receptor Importin Beta7 Gina Dee Visser 2000 A family of receptor proteins has emerged as the pathways and mechanisms of nucleocytoplasmic transport have been revealed. Importin beta1 (Impbeta1), the founding member of this family, Importin alpha (Impalpha) and the small GTPase Ran are all essential to the classical nuclear protein import pathway. Studies of Impbeta1 led to the identification of a 116 kDa Impbeta1-associated protein. A cDNA encoding this protein was cloned. Based on sequence analysis and binding studies with Ran-GTP and the Nuclear Pore Complex (NPC), this protein was placed in the Importin beta-related family. As a solo receptor, p116 is capable of in vitro ribosomal protein import. Identified as a functional receptor of nuclear protein import, p116 was named Importin beta7 (Impbeta7). Complexed with Impbeta1, Impbeta7 also promotes histone H1 nuclear accumulation. Impbeta7, a Importin beta family member, maintains two distinctive

properties: it forms a heterodimer with another member of this receptor family (Impbeta1), and it is a serine phosphoprotein. Binding studies were undertaken to investigate the character of the Impbeta7-Impbeta1 complex. Domain mapping revealed the corresponding binding regions of Impbeta1 and Impbeta7. Full length recombinant Impbeta7 and Impbeta1 localize to the nuclear envelope (NE) of digitonin permeabilized cells. Impbeta7 cannot localize to the NE through its association with Impbeta1, as shown by using truncated protein constructs. In exploring the second distinctive property of Impbeta7, two predicted Casein Kinase II (CKII) serine phosphorylation sites were targeted. A serine to alanine mutant was not phosphorylated when incubated with reticulocyte lysate as a kinase source, but a wild type form of Impbeta7 was phosphorylated under these conditions. Cells transfected with wild type and mutant Impbeta7-EGFP showed differential nuclear and cytoplasmic localization. The translocation of many nuclear import and export cargoes is regulated by phosphorylation in the vicinity of signaling sequences or by association of the cargo with other proteins. It is possible that in the case of Impbeta7 the cell can also modulate transport at the receptor level via regulation of Impbeta7 binding to Impbeta1 or via Impbeta7 phosphorylation.

Molecular Biology of the Cell Bruce Alberts 2004

Nucleocytoplasmic Transport Reiner Peters 2012-12-06

Nuclear Transport Karsten Weis 2002

Bidirectional traffic of macromolecules across the nuclear envelope is an active and essential transport process in all eukaryotic cells. Work on various model systems has led to a tremendous increase in our understanding of nuclear transport in recent years. This volume summarizes our current knowledge of protein and RNA transport into and out of the nucleus. It contains nine up-to-date reviews which cover various aspects of nucleocytoplasmic transport, including the structure and function of the nuclear pore complex, the role of soluble transport factors in protein and RNA transport, and the regulation of protein transport through the nuclear pore.

Rho Gtpases: Molecular Biology In Health And Disease Fort Philippe 2017-12-12 Rho GTPases control many aspects of cell physiology. This includes polarity, endo/exocytosis, adhesion, motility, transcriptional activation, cell cycle progression or apoptosis. In view of such pleiotropic activities, Rho-controlled signaling has proven to be of medical relevance, especially in tumorigenesis, disease-associated bone remodeling and infectiology. This book is divided into three parts. Part 1 gives an evolutionary perspective of the Rho family, its atypical members, and an overview of how Rho activity is regulated. Part 2 addresses two important aspects of multicellularity controlled by Rho-dependent pathways, namely, cell-cell interactions and mechanotransduction. It also describes how post-translational modifications control Rho activity and how this is exploited by pathogenic bacteria. Part 3 explores several examples of the variety of pathophysiological processes controlled by Rho signaling, and gives a successful example of translational research, from the inhibition of Rho activation to the development of new molecules against osteoporosis. This updated review on the biology of Rho GTPases is an essential read for molecular and cell biologists. It is also an invaluable guide to post-graduate and medical students who wish to deepen their knowledge in cell biology. Contents: An Historical and Evolutionary PerspectiveAtypical Rho GTPases in Health and DiseaseRegulators of Rho SignalingRho GTPases in Cadherin-Based Cell-Cell InteractionsRho Signaling in MechanotransductionPost-Translational modifications of Rho GTPasesRhoA Mutations in Cancer: Oncogenes or Tumor-SuppressorsModulation of Osteoclast Differentiation and Function by Rho GTPasesRhoGEFs as Therapeutic TargetsEndothelial-Specific Rho GTPase Signaling During Leukocyte Extravasation Readership: Molecular and cell biologists, post-graduate and medical students interested in cell biology. Keywords: Rho GTPases;Signaling Oathways;F-actin;Cytoskeleton;Adhesion;Migration;CancerReview: Key Features: Different integration levels for a better understanding of biological and pathological implications of Rho signalingChapters cover updated and original Rho-controlled aspects of cell

biologyContributors are leaders in their fields of research

The Small GTPase Ran and [beta]-importins Tnpo-SR and Cadmus Promote Ovarian Cyst Formation in Drosophila Allison Nicole Beachum 2021 Germ cells follow a precise and coordinated molecular timeline to produce a viable oocyte. While undergoing mitotic expansion via incomplete cytokinesis, cysts of undifferentiated cells form and remain interconnected prior to meiotic initiation, through mechanisms that are not well-defined. In somatic cells, Ras-related nuclear protein (Ran) spatiotemporally regulates mitotic spindle assembly, cleavage furrow formation and abscission. Here, we identify Ran and [beta]-importins as critical regulators of cyst development in the Drosophila ovary. Depletion of Ran or the [beta]-importins Tnpo-SR and Cadmus results in egg chambers with variable numbers of germ cells, suggesting abnormal cyst development and cyst fragmentation, and consequently disrupts oocyte selection. We demonstrate that Ran, Tnpo-SR, and Cadmus regulate key cellular processes during cyst formation, including cell cycle dynamics, fusome biogenesis, and ring canal stability, all independently of mitotic spindle assembly. Further, Tnpo-SR and Cadmus control cyclin accumulation and suppress cytokinesis, suggesting that [beta]-importins sequester protein cargos that normally promote the mitotic-to-meiotic transition. Our data demonstrates that Ran and [beta]-importins are critical for the cell fate decisions of germ cells, a role that is likely conserved in other organisms.

Textbook of Neural Repair and Rehabilitation Michael Selzer 2014-04-24 Volume 1 of the Textbook of Neural Repair and Rehabilitation covers the basic sciences relevant to recovery of function following injury to the nervous system.

Encyclopedia of Signaling Molecules 19??

Origin and spatiotemporal dynamics of the peroxisomal endomembrane system Vladimir I Titorenko 2015-03-05 The peroxisome is an organelle with essential roles in lipid metabolism, maintenance of reactive oxygen species homeostasis, and anaplerotic replenishment of tricarboxylic acid cycle intermediates destined for mitochondria. Peroxisomes constitute a dynamic endomembrane system. The homeostatic state of this system is upheld via two pathways for assembling and maintaining the diverse peroxisomal compartments constituting it; the relative contribution of each pathway to preserving such system may vary in different organisms and under various physiological conditions. One pathway begins with the targeting of certain peroxisomal membrane proteins to an endoplasmic reticulum template and their exit from the template via pre-peroxisomal carriers; these carriers mature into metabolically active peroxisomes containing the entire complement of membrane and matrix proteins. Another pathway operates via growth and maturation of pre-existing peroxisomal precursors that do not originate from the endoplasmic reticulum; mature peroxisomes proliferate by undergoing fission. Recent studies have uncovered new roles for the peroxisomal endomembrane system in orchestrating important developmental decisions and defining organismal longevity. This Frontiers Special Topic Issue is focused on the advances in our understanding of how evolutionarily distant organisms coordinate the formation, maturation, proliferation, maintenance, inheritance and quality control of the peroxisomal endomembrane system and how peroxisomal endomembranes communicate with other cellular compartments to orchestrate complex biological processes and various developmental programs from inside the cell.

The Journal of Cell Biology 2007 No. 2, pt. 2 of November issue each year from v. 19 (1963)-47 (1970) and v. 55 (1972)- contain the Abstracts of papers presented at the Annual Meeting of the American Society for Cell Biology, 3d (1963)-10th (1970) and 12th (1972)-

Regulation of the Assembly and Function of the Nuclear Pore Valerie Anne Delmar 2008 The nucleus is the defining structure of eukaryotic cells. The nuclear envelope acts as a barrier between nucleus and cytoplasm. Nuclear pore complexes perforating the envelope control all traffic into and out of the nucleus, and thus act to regulate transcription, translation, and other essential cellular processes. During mitosis, the nuclear envelope from flies to mammals disassembles into its component parts, with the

nuclear pore breaking into multiple subunits. The pore then reassembles in a step-wise process as the nuclear envelope reforms in late anaphase. The major focus of this thesis has been to better understand the assembly and function of the nuclear pore. It has resulted in three published papers and one paper in preparation. First, I participated, with postdoc Dr. Corine Lau, in a study of the novel vertebrate transmembrane nucleoporin, Ndc1. I resolved the topology of yeast Ndc1p and identified conserved amino acids to target for future functional studies (Chapter 1). In a second study, I participated in a collaboration with the laboratory of Dr. Pamela Silver at Harvard Medical School in identifying a new role for the vertebrate nuclear pore in the regulation of transcription. We found that in vertebrates, specific chromosomal regions move to the nuclear pore complexes during transcriptional activation (Chapter 2). Key work next centered on the mechanism of action of importin beta in negatively regulating nuclear membrane fusion and pore assembly. (The small GTPase, Ran, positively regulates both these processes.) A major unanswered question has been, which specific steps in nuclear pore assembly are regulated by importin beta or RanGTP. I determined, using Xenopus constructs, that importin beta is an authentic regulator of nuclear pore assembly and that, contrary to previously published results, Ran reverses this negative regulation (Chapter 3). Finally, a fourth study, done with Dr. Corine Lau, established that the distant importin beta relative, transportin, also negatively regulates nuclear membrane and pore assembly (Chapter 4). I showed that both transportin and importin beta act early to control the initial step of pore assembly: the binding of the pore-targeting protein ELYS to chromatin, which sets in motion the specific targeting of nuclear pores to the nuclear surface.

GTPases in Biology I 2012-12-06 The GTPase switch appears to be almost as old as life itself, and nature has adapted it to a variety of purposes. This two-volume work surveys the major classes of GTPases, including their role in ensuring accuracy during protein translation, a new look at the trimeric G-protein cycle, the molecular function of ARF in vesicle coating, the emerging role of the dynamin family in vesicle transfer, GTPases which activate GTPases during nascent protein translocation, and the many roles of ras-related proteins in growth, cytoskeletal polymerization, and vesicle transfer. 80 chapters contain much previously unpublished data and, at the rate the extended family of GTPases is growing, it is unlikely that it will again sit for a group portrait such as this. Thus, this could well become the standard reference work.

Proteins interacting with Ran/TC4, a small Ras-related GTPase involved in nucleo-cytoplasmic transport Elena Smirnova 1996

Lewin's CELLS Lynne Cassimeris 2011-03-25 Completely revised and updated to incorporate the latest data in the field, Lewin's CELLS, Second Edition is the ideal resource for advanced undergraduate and graduate students entering the world of cell biology. Redesigned to incorporate new learning tools and elements, this edition continues to provide readers with current coverage of the structure, organization, growth, regulation, movements, and interaction of cells, with an emphasis on eukaryotic cells. Under the direction of three expert lead editors, new chapters on metabolism and general molecular biology have been added by subject specialist. All chapters have been carefully edited to maintain consistent use of terminology and to achieve a homogenous level of detail and rigor. A new design incorporates many new pedagogical elements, including Concept & Reasoning Questions, Methods boxes, Clinical Applications boxes, and more.

Regulation of Assembly of the Vertebrate Nucleus Rene Che-Ling Chan 2005

The Small GTPase Ran Mark Rush 2012-12-06 The Ras-related nuclear protein Ran is a member of the so-called Ras-superfamily of small GTP-binding proteins and hydrolyzing proteins. A variety of edited anthologies related to the Ras-superfamily have appeared over the last decade, but Ran has been under-represented in all of them. This under-representation is not due to the fact that Ran is unimportant or non-abundant. It is almost certainly because Ran was discovered and its functions elucidated only recently, and that some of these functions may not follow the typical Ras-superfamily paradign. Even workers in the field have difficulty keeping

up with the Ran literature, and most outsiders rarely try even though they may be aware that major breakthroughs regarding the mechanisms of nuclear-cytosolic transport, mitosis and the maintenance of nuclear structure have depended upon an understanding of Ran function. The Small GTPase Ran is meant to provide specialists with a concise summary of some of the recent research in this area, along with background describing its initial identification and early characterization.

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Table of Contents Small Gtpase Ran

11. Cultivating a Reading Routine Small Gtpase Ran

- Setting Reading Goals Small Gtpase Ran
- Carving Out Dedicated Reading Time

12. Sourcing Reliable Information of Small Gtpase Ran

- Fact-Checking eBook Content of Small Gtpase Ran
- Distinguishing Credible Sources

13. Promoting Lifelong Learning

- Utilizing eBooks for Skill Development
- Exploring Educational eBooks

14. Embracing eBook Trends

- Integration of Multimedia Elements
- Interactive and Gamified eBooks

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