Directed The Structure Of Dna Answers

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Directed Enzyme Evolution ScholarlyEditions

Proceedings of the NATO Advanced Study Institute on Genome Structure and Function, held in Marciana Marina, Elba, Italy, 13-23 June 1996

Cancer Genomics Springer Science & Business Media

The classic personal account of Watson and Crick’s groundbreaking discovery of the structure of DNA, now with an introduction by Sylvia Nasar, author of A Beautiful Mind. By identifying the structure of DNA, the molecule of life, Francis Crick and James Watson revolutionized biochemistry and won themselves a Nobel Prize. At the time, Watson was only twenty-four, a young scientist hungry to make his mark. His uncompromisingly honest account of the heady days of their thrilling sprint against other world-class researchers to solve one of science’s greatest mysteries gives a dazzlingly clear picture of a world of brilliant scientists with great gifts, very human ambitions, and bitter rivalries. With humility unspoiled by false modesty, Watson relates his and Crick’s desperate efforts to beat Linus Pauling to the Holy Grail of life sciences, the identification of the basic building block of life. Never has a scientist been so truthful in capturing in words the flavor of his work.

Measuring Distances Between Nucleotides Using CW- EPR and Dual Site-directed Spin Labels to Distinguish Parallel Quadruplexes from B-DNA Benjamin-Cummings Publishing Company

"The proper identification of DNA secondary structure is paramount for determining possible factors that can influence rates of genomic transcription. Structures such as DNA quadruplexes (QPX), which are found in guanine-rich regions of DNA, can have a significant effect on an organism, due to their ability to influence transcription rates under certain conditions. Aside from NMR and X-ray crystallography, Circular Dichroism (CD) has been shown to be an easy and effective method to distinguish between classical double helical A, B, and Z DNA, and other secondary structures. However, complications have arisen from this technique, due to the similarities in B DNA and parallel QPX spectra, because both have positive CD peaks at 260 nm, negative at 245 nm and a positive peak around 210 nm and 205 nm, respectively. Currently, a G-C rich duplex DNA oligonucleotide, G21, which contains sequences found in the promoter region of the ChAT gene, has shown both B-DNA and parallel quadruplex spectra. However, under different salts and salt concentrations, changes of peak intensities were observed. This could be due to the formation of different secondary structures that are not distinguishable under CD. To address this, a continuous wave electron paramagnetic resonance (CW-EPR) technique was used. This technique utilizes a pair of site-directed spin labels (SDSL) attached via phosphorothioate bonds to two different modified nucleotides, to determine the distances between them. Variations in the measured distance will be used to distinguish between B-DNA or parallel QPX, as either structure could be possible from the CD spectrum alone."--Abstract from author supplied metadata.

Springer Science & Business Media

Exonuclease I (ExoI) from Escherichia coli is a monomeric enzyme that processively degrades single stranded DNA in the 3' to 5' direction and has been implicated in DNA recombination and repair. It functions in numerous genome maintenance pathways, with particularly well defined roles in methyl-directed mismatch repair (MMR). The Escherichia coli MMR pathway can be reconstituted in vitro with the activities of eight proteins (8). MutS, MutL and MutH are involved in initiation of repair including mismatch recognition and generation of a nick at a nearby GATC sequence (53, 54, 55, 56). The hemimethylated state of GATC sequences immediately following replication serves as a signal to direct repair to the nascent strand of the DNA duplex (57, 58). DNA helicase II and one of several exonucleases (Exonucleas I, Exonuclease VII and RecJ) are required to excise the error-containing DNA strand beginning at the nicked GATC site (34, 35). Restoration of the correct DNA sequence by repair synthesis involves DNA polymerase III holoenzyme and SSB, and the final nick is sealed by DNA ligase (34). To identify interactions with ExoI involved in MMR repair system, we used the yeast two-hybrid system with ExoI as bait. By screening an E.coli genomic library, E. coli DNA helicase II (UvrD) was identified as a potential interacting protein. UvrD has been shown to be required for DNA excision repair, methyl-directed mismatch repair and has some undefined, role in DNA replication and recombination. In this report, in vitro experiments confirm that UvrD and ExoI make a direct physical interaction that may be required for function of the methyl-directed mismatch repair. Werner Syndrome is a rare autosomal recessive disease characterized by a premature aging phenotype, genomic instability and a dramatically increased incidence of cancer and heart disease. Mutations in a single gene encoding a 1,432 amino-acid helicase/exonuclease (hWRN) have been shown to be responsible for the development o

Advances in Photochemistry Molecular Biology of the CellMolecular Biology of the Gene

On first consideration, acute myeloid leukemia (AML) represents a nearly insurmountable challenge in terms of understanding it at the molecular level in large part because of its immense heterogeneity as well as its variability across different age groups. In addition, while significant progress has been made in the overall survival of subsets of patients with AML, many continue to show little progress in terms of positive treatment outcomes. Cytogenetic and initial molecular studies have resulted in the ability to stratify patients into specific risk categories that predict favorable-, intermediate- and poor-risk outcomes. However, these categories are limited in their ability to predict accurately how individual patients will respond to therapy and have not resulted in the ability to treat effectively patients with specific treatments. They have, however, resulted in excluding hematopoietic stem cell transplantation for patients with favorable-risk disease. Genome-wide analysis promises to improve both treatment and outcomes. The initial studies using whole-exon or whole-genome sequencing identified mutations in several novel genes that surprisingly were involved in regulating DNA methylation and chromatin structure. Subsequently, mutations were found in genes encoding transcription factors, signaling pathway modulators and genes involved in RNA splicing. Further analyses have identified mutations in key elements of miRNAs. Genome-wide methylation studies have highlighted key patterns that track with specific cytogenetic and gene mutations. Such epigenetic studies have led to the use of treatments directed to altering chromatin structure and DNA methylation. These treatments remain targeted specifically at specific enzymatic components of chromatin structure and function, but their key molecular consequences remain unclear and clinical responses unpredictable. RNA sequencing has led to the identification of both novel pathways of leukemia cell survival and unexpected fusion transcripts, which may ultimately be therapeutically targeted.

Research Awards Index Springer Science & Business Media

There has been a sea change in how we view genetic recombination. When germ cells are produced in higher organisms, genetic recombination assures the proper segregation of like chromosomes. In the course of that process, called meiosis, recombination not only assures segregation of one chromosome of each type to progeny germ cells, but also further shuffles the genetic deck, contributing to the unique inheritance of individuals. In a nutshell, that is the classical view of recombination. We have also known for many years that in bacteria recombination plays a role in horizontal gene transfer and in replication itself, the latter by establishing some of the replication forks that are the structural scaffolds for copying DNA. In recent years, however, we have become increasingly aware that replication, which normally starts without any help from recombination, is a vulnerable process that frequently leads to broken DNA. The enzymes of recombination play a vital role in the repair of those breaks. The recombination enzymes can function via several different pathways that mediate the repair of breaks, as well as restoration of replication forks that are stalled by other kinds of damage to DNA. Thus, to the classical view of recombination as an engine of inheritance we must add the view of recombination as a vital housekeeping function that repairs breaks suffered in the course of replication. We have also known for many years that genomic instability--including mutations, chromosomal rearrangements, and aneuploidy--is a hallmark of cancer cells. Although genomic instability has many contributing causes, including faulty replication, there are many indications that recombination, faulty or not, contributes to genome instability and cancer as well. The (Nas colloquium) Links Between Recombination and Replication: Vital Roles of Recombination was convened to broaden awareness of this evolving area of research. Papers generated by this colloquium are published here. To encourage the desired interactions of specialists, we invited some contributions that deal only with recombination or replication in addition to contributions on the central thesis of functional links between recombination and replication. To aid the nonspecialist and specialist alike, we open the set of papers with a historical overview by Michael Cox and we close the set with a commentary on the meeting and the field by Andrei Kuzminov.

Virology & AIDS Abstracts John Wiley & Sons

Directed evolution comprises two distinct steps that are typically applied in an iterative fashion: (1) generating molecular diversity and (2) finding among the ensemble of mutant sequences those proteins that perform the desired fu- tion according to the specified criteria. In many ways, the second step is the most challenging. No matter how cleverly designed or diverse the starting library, without an effective screening strategy the ability to isolate useful clones is severely diminished. The best screens are (1) high throughput, to increase the likelihood that useful clones will be found; (2) sufficiently sen- tive (i. e. , good signal to noise) to allow the isolation of lower activity clones early in evolution; (3) sufficiently reproducible to allow one to find small improvements; (4) robust, which means that the signal afforded by active clones is not dependent on difficult-to-control environmental variables; and, most importantly, (5) sensitive to the desired function. Regarding this last point, almost anyone who has attempted a directed evolution experiment has learned firsthand the truth of the dictum “you get what you screen for. ” The protocols in Directed Enzyme Evolution describe a series of detailed p- cedures of proven utility for directed evolution purposes. The volume begins with several selection strategies for enzyme evolution and continues with assay methods that can be used to screen enzyme libraries. Genetic selections offer the advantage that functional proteins can be isolated from very large libraries s- ply by growing a population of cells under selective conditions.

DNA Directed Self-assembly of Plasmonic Nanoparticles ScholarlyEditions

Evolution - both the fact that it occurred and the theory describing the mechanisms by which it occurred - is an intrinsic and central component in modern biology. Theodosius Dobzhansky captures this well in the much-quoted title of his 1973 paper 'Nothing in biology makes sense except in the light of evolution'. The correctness of this assertion is even more obvious today: philosophers of biology and biologists agree that the fact of evolution is undeniable and that the theory of evolution explains that fact. Such a theory has far-reaching implications. In this volume, eleven distinguished scholars address the conceptual, metaphysical and epistemological richness of the theory and its ethical and religious impact, exploring topics including DNA barcoding, three grand challenges of human evolution, functionalism, historicity, design, evolution and development, and religion and secular humanism. The volume will be of great interest to those studying philosophy of biology and evolutionary biology.

DNA polymerases in Biotechnology Springer Science & Business Media

Now completely up-to-date with the latest research advances, the Seventh Edition retains the distinctive character of earlier editions. Twenty-two concise chapters, co-authored by six highly distinguished biologists, provide current, authoritative coverage of an exciting, fast-changing discipline.

Exploring the Structure and Function of Bacterial Cytosine Specific DNA Methyltransferases Using Site-directed Mutagenesis Cambridge University Press

The series Topics in Current Chemistry Collections presents critical reviews from the journal Topics in Current Chemistry organized in topical volumes. The scope of coverage is all areas of chemical science including the interfaces with related disciplines such as biology, medicine and materials science. The goal of each thematic volume is to give the non-specialist reader, whether in academia or industry, a comprehensive insight into an area where new research is emerging which is of interest to a larger scientific audience. Each review within the volume critically surveys one aspect of that topic and places it within the context of the volume as a whole. The most significant developments of the last 5 to 10 years are presented using selected examples to illustrate the principles discussed. The coverage is not intended to be an exhaustive summary of the field or include large quantities of data, but should rather be conceptual, concentrating on the methodological thinking that will allow the non-specialist reader to understand the information presented. Contributions also offer an outlook on potential future developments in the field. The chapter "DNA-Programmed Chemical Synthesis of Polymers and Inorganic Nanomaterials" is available open access under a CC BY 4.0 License via link.springer.com.

Evolutionary Biology Academic Press

Advances in RNA-Directed DNA Polymerase Research and Application / 2012 Edition is a ScholarlyBrief™ that delivers timely, authoritative, comprehensive, and specialized information about RNA-Directed DNA Polymerase in a concise format. The editors have built Advances in RNA-Directed DNA Polymerase Research and Application / 2012 Edition on the vast information databases of ScholarlyNews.™ You can expect the information about RNA-Directed DNA Polymerase in this eBook to be deeper than what you can access anywhere else, as well as consistently reliable, authoritative, informed, and relevant. The content of Advances in RNA-Directed DNA Polymerase Research and Application / 2012 Edition has been produced by the world’s leading scientists, engineers, analysts, research institutions, and companies. All of the content is from peer-reviewed sources, and all of it is

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Cambridge Scientific Biochemistry Abstracts Simon and Schuster

Deoxyribonucleic acid (DNA), a biopolymer well known for its role in preserving genetic information in biology, is now drawing great deal of interest from material scientists. Ease of synthesis, predictable molecular recognition via Watson-Crick base pairing, vast numbers of available chemical modifications, and intrinsic nanoscale size makes DNA a suitable material for the construction of a plethora of nanostructures that can be used as scaffold to organize functional molecules with nanometer precision. This dissertation focuses on DNA-directed organization of metallic nanoparticles into well-defined, discrete structures and using them to study photonic interaction between fluorophore and metal particle. Presented here are a series of studies toward this goal. First, a novel and robust strategy of DNA functionalized silver nanoparticles (AgNPs) was developed and DNA functionalized AgNPs were employed for the organization of discrete well-defined dimeric and trimeric structures using a DNA triangular origami scaffold. Assembly of 1:1 silver nanoparticle and gold nanoparticle heterodimer has also been demonstrated using the same approach. Next, the triangular origami structures were used to co-assemble gold nanoparticles (AuNPs) and fluorophores to study the distance dependent and nanogap dependencies of the photonic interactions between them. These interactions were found to be consistent with the full electrodynamic simulations. Further, a gold nanorod (AuNR), an anisotropic nanoparticle was assembled into well-defined dimeric structures with predefined inter-rod angles. These dimeric structures exhibited unique optical properties compared to single AuNR that was consistent with the theoretical calculations. Fabrication of otherwise difficult to achieve 1:1 AuNP- AuNR hetero dimer, where the AuNP can be selectively placed at the end-on or side-on positions of anisotropic AuNR has also been shown. Finally, a click chemistry based approach was developed to organize sugar modified DNA on a particular arm of a DNA origami triangle and used them for site-selective immobilization of small AgNPs.

The Double Helix Stanford University Press

Thousands of methods have been developed in the various biomedical disciplines, and those covered in this book represent the basic, essential and most widely used methods in several different disciplines.

DNA Nanostructures for Biotechnological Applications Elsevier

This volume, written by experts in the field, discusses the current understanding of the biophysical principles that govern RNA folding, with featured RNAs including the ribosomal RNAs, viral RNAs, and self-splicing introns. In addition to the fundamental features of RNA folding, the central experimental and computational approaches in the field are presented with an emphasis on their individual strengths and limitations, and how they can be combined to be more powerful than any method alone; these approaches include NMR, single molecule fluorescence, site-directed spin labeling, structure mapping, comparative sequence analysis, graph theory, course-grained 3D modeling, and more. This volume will be of interest to professional researchers and advanced students entering the field of RNA folding.

New Approaches in Eukaryotic DNA Replication Springer

Advances in RNA-Directed DNA Polymerase Research and Application: 2013 Edition is a ScholarlyBrief™ that delivers timely, authoritative, comprehensive, and specialized information about ZZZAdditional Research in a concise format. The editors have built Advances in RNA-Directed DNA Polymerase Research and Application: 2013 Edition on the vast information databases of ScholarlyNews.™ You can expect the information about ZZZAdditional Research in this book to be deeper than what you can access anywhere else, as well as consistently reliable, authoritative, informed, and relevant. The content of Advances in RNA-Directed DNA Polymerase Research and Application: 2013 Edition has been produced by the world's leading scientists, engineers, analysts, research institutions, and companies. All of the content is from peer-reviewed sources, and all of it is written, assembled, and edited by the editors at ScholarlyEditions™ and available exclusively from us. You now have a source you can cite with authority, confidence, and credibility. More information is available at http://www.ScholarlyEditions.com/.

Biomedical Index to PHS-supported Research Springer Nature

DNA polymerases are core tools for molecular biology including PCR, whole genome amplification, DNA sequencing and genotyping. Research has focused on discovery of novel DNA polymerases, characterization of DNA polymerase biochemistry and development of new replication assays. These studies have accelerated DNA polymerase engineering for biotechnology. For example, DNA polymerases have been engineered for increased speed and fidelity in PCR while lowering amplification sequence bias. Inhibitor resistant DNA polymerase variants enable PCR directly from tissue (i.e. blood). Design of DNA polymerases that efficiently incorporate modified nucleotide have been critical for development of next generation DNA sequencing, synthetic biology and other labeling and detection technologies. The Frontiers in Microbiology Research Topic on DNA polymerases in Biotechnology aims to capture current research on DNA polymerases and their use in emerging technologies.

Nanocomposite Structures and Dispersions Nova Publishers

One of the promises of nanotechnology is the ability to create a bulk, designer material with its structure programmed at each length scale using deterministic control over the placement of each nanoscale component. Self-assembled nanoparticle colloids, particularly those directed by sequence-specific DNA hybridizations, have emerged as a promising building block for producing these designer materials from nanoparticles that arrange themselves into precise symmetries through mechanisms analogous to atomic crystallization. However, DNA-directed colloids and other self-assembled nanoparticle systems still struggle to realize the goal of arbitrary structure control at length scales larger than a few microns due to the complexity of forces impacting different scales simultaneously. Utilizing existing atomic analogues for inspiration, this work extends the structure-defining nature of these programmable building blocks by imposing lithographic boundary conditions and devising processing techniques resembling those of atomic thin films and powders. Crystallization at an interface is explored, and preferential grain growth from a substrate is demonstrated to control large scale crystal texture. Full crystal orientation control is achieved by using standard nano-fabrication techniques to construct a lithographically-defined template for epitaxial growth that can define arbitrary macroscale shapes over millimeters. The resulting crystallization platform exhibits remarkable resiliency to lattice mismatch due to the 'soft' nature of the DNA ligands binding nanoparticles together. The understanding garnered from the DNA-grafted nanoparticle as a model system is extended to a colloid synthesized from a more scalable and robust directing polymer, polystyrene. The unique advantages of this new building block enable the fabrication of truly bulk, 3D materials with arbitrary macroscale shape on the centimeter scale via sintering and post-processing of nanoparticle-based crystallites. The results of this work are nanoparticle-based materials with dictated structure from the nanoscale (crystallographic unit cell), through the microscale (crystallite size and orientation), to the macroscale (lithographically defined shape).

Bowker's Complete Video Directory 2001 Frontiers Media SA

The purpose of this book is to highlight some of latest developments and applications of CRISPR, RNA, and DNA to treat diseases ranging from cancers to cardiovascular and degenerative disorders. It also features innovations of the delivery methods for nucleic acids ranging from nanodevices made from DNA and pseudo amino acids to viral vectors. This is an ideal book for academics, clinicians, and students interested in gene therapy.

Study Protein-protein Interaction in Methyl-directed DNA Mismatch Repair in E. Coli: Exonuclease I (Exo I) and DNA Helicas II (UvrD) & A Minimal Exonuclease Domain of WRN Forms a Hexamer on DNA and Possesses Both 3'-5' Exonuclease and 5'-Protruding Strand Endonuclease Activities & Solving the Structure of the Ligand-Binding Domain of the Pregnane-Xenobiotic-Receptor with 17? Estradiol and Springer Nature

DNA replication in eukaryotes is an important field, particular ly because of its direct impact on the study of cancer. The under standing of molecular mechanisms of replication and their regulation should allow a better comprehension of the alterations that lead to the proliferation of tumor cells and to error-prone repair in cells exposed to radiation or chemical carcinogens. During the last several years, many enzymes and proteins which participate in replication of DNA in eukaryotic cells have been identified, isolated and characterized. New concepts in chromatin structure have refocused attention on the study of replication of DNA complexed with his tones and non-histone chromosomal proteins. However, progress has been noticeably slower than for prokaryotes, essentially because of the difficulty in genetic analysis of eukaryo tic DNA replication. In June 1980, a workshop was organized in Cargese, Corsica (France) to facilitate exchanges of information between workers spe cializing in prokaryotes and those specializing in eukaryotes, and to allow discussion of new experimental approaches. With this in mind, special interest has been taken in the origin and termination of chromosome cycles and how they are controlled.

Molecular Biology of the Cell Springer Science & Business Media

RNA exists at the heart of many important questions in biology today. Its diverse functionality is rooted in the wide range of structures RNA is able to form. The nucleotides in an RNA sequence possess the ability to form bonds with each other. Such bonding allows a strand of RNA to fold onto itself. In contrast to the iconic double helix structure of DNA, this results in intricate 3D conformations that vary with RNA sequence and in part allow the RNA to perform its cellular functions. The study of RNA's 2D folding pattern between bases in the sequence serves as an intermediate step to deciphering its complex final 3D formation. Determining this folding pattern, also called the secondary structure, remains a challenging task. In recent years, the advancement in DNA sequencing technology has popularized a number of chemical and enzymatic experiments that probe RNA molecules in a massively parallel fashion. These structure probing experiments can be performed both in vitro and in vivo and provide a wealth of information on RNA structure. The data coming from these experiments are typically quantified into a measure of reactivity per nucleotide. This reactivity is correlated with structure and thus this data is used to infer RNA structure. Combined with sequence information, these experimental datasets are typically incorporated into computational secondary structure prediction algorithms. Another class of psoralen-facilitated cross-linking experiments make use of psoralen's ability to form cross-links at interacting regions of RNA to directly probe base-pairing interactions in an RNA structure. These experiments provide direct structural information on an RNA and the resulting data have been particularly useful in uncovering alternative folding patterns for long RNA sequences. Despite the richness in experimental data, current data-driven secondary structure prediction methods suffer from major inaccuracies. In fact, while experimental protocols have been refined over the years, less progress has been made towards statistical characterization of structure probing data. This is even more true for the relatively new psoralen-facilitated cross-linking experiments. Further, most computational methods for structure prediction aim to predict a single optimal structure, whereas it is well-established that the same RNA sequence can exist in multiple conformations in nature. Thus, studying the entire Boltzmann ensemble of possible secondary structures for a given RNA can help uncover important underlying structures that would otherwise remain unknown. Additionally, prediction accuracy improves when abstract representations of RNA structures are used. The work done in this dissertation focuses on the development of computational tools to better utilize data coming from both types of experiments in the context of secondary structure prediction. First, we explored methods for improved signal extraction of structure probing data using signal processing techniques. We then developed a probabilistic model for characterization of structure probing data by analyzing statistical properties of such data. This model was incorporated into thermodynamics based secondary structure prediction algorithms for improved structure prediction. Finally, we studied the use of psoralen-facilitated cross-linking data to recover the structural landscape for a given RNA. We introduced a probabilistic model for these data and provide an extension of the previously developed structural landscape explorer, SLEQ. As these experiments are aimed at probing long RNAs, this extension makes use of abstract structural elements to help cluster similar structures and aggregate similar structural motifs.