MOLECULAR BASIS OF GENE EXPRESSION pdf

1: Epistasis - Wikipedia

the one gene--one protein hypothesis. The information flow that controls protein synthesis passes from DNA to RNA to the protein synthetic machinery. The genetic code consists of codons, which are groups of 3 nucleotides along the DNA strand.

Definitions[edit] The term epigenetics in its contemporary usage emerged in the s, but for some years has been used in somewhat variable meanings. It has been used in English since the 17th century. Waddington held that cell fates were established in development canalisation much as a marble rolls down to the point of lowest local elevation. An early version was proposed, among the founding statements in embryology , by Karl Ernst von Baer and popularized by Ernst Haeckel. A radical epigenetic view physiological epigenesis was developed by Paul Wintrebert. Another variation, probabilistic epigenesis, was presented by Gilbert Gottlieb in The developmental psychologist Erik Erikson wrote of an epigenetic principle in his book Identity: Youth and Crisis , encompassing the notion that we develop through an unfolding of our personality in predetermined stages, and that our environment and surrounding culture influence how we progress through these stages. This biological unfolding in relation to our socio-cultural settings is done in stages of psychosocial development , where "progress through each stage is in part determined by our success, or lack of success, in all the previous stages. The more recent usage of the word in science has a stricter definition. For example, Adrian Bird defined epigenetics as "the structural adaptation of chromosomal regions so as to register, signal or perpetuate altered activity states. Such redefinitions however are not universally accepted and are still subject to dispute. The "epigenome" is a parallel to the word "genome", referring to the overall epigenetic state of a cell, and epigenomics refers to more global analyses of epigenetic changes across the entire genome. Taken to its extreme, the "epigenetic code" could represent the total state of the cell, with the position of each molecule accounted for in an epigenomic map, a diagrammatic representation of the gene expression, DNA methylation and histone modification status of a particular genomic region. More typically, the term is used in reference to systematic efforts to measure specific, relevant forms of epigenetic information such as the histone code or DNA methylation patterns. Molecular basis[edit] Epigenetic changes modify the activation of certain genes, but not the genetic code sequence of DNA. The microstructure not code of DNA itself or the associated chromatin proteins may be modified, causing activation or silencing. This mechanism enables differentiated cells in a multicellular organism to express only the genes that are necessary for their own activity. Epigenetic changes are preserved when cells divide. Moreover, if gene inactivation occurs in a sperm or egg cell that results in fertilization, this epigenetic modification may also be transferred to the next generation. These damages are largely repaired, but at the site of a DNA repair, epigenetic changes can remain. In one study, markers for oxidative stress, such as modified nucleotides that can result from DNA damage, were decreased by a 3-week diet supplemented with soy. Covalent modifications[edit] Covalent modifications of either DNA e. Therefore, the word "epigenetics" is sometimes used as a synonym for these processes. However, this can be misleading. Chromatin remodeling is not always inherited, and not all epigenetic inheritance involves chromatin remodeling. Because the phenotype of a cell or individual is affected by which of its genes are transcribed, heritable transcription states can give rise to epigenetic effects. There are several layers of regulation of gene expression. One way that genes are regulated is through the remodeling of chromatin. Chromatin is the complex of DNA and the histone proteins with which it associates. If the way that DNA is wrapped around the histones changes, gene expression can change as well. Chromatin remodeling is accomplished through two main mechanisms: The first way is post translational modification of the amino acids that make up histone proteins. Histone proteins are made up of long chains of amino acids. If the amino acids that are in the chain are changed, the shape of the histone might be modified. DNA is not completely unwound during replication. It is possible, then, that the modified histones may be carried into each new copy of the DNA. Once there, these histones may act as templates, initiating the surrounding new histones to be shaped in the new manner. By altering the shape of the histones around them, these modified histones would ensure that a lineage-specific transcription program is maintained after cell division. The

second way is the addition of methyl groups to the DNA, mostly at CpG sites , to convert cytosine to 5-methylcytosine. However, some areas of the genome are methylated more heavily than others, and highly methylated areas tend to be less transcriptionally active, through a mechanism not fully understood. Methylation of cytosines can also persist from the germ line of one of the parents into the zygote, marking the chromosome as being inherited from one parent or the other genetic imprinting. Mechanisms of heritability of histone state are not well understood; however, much is known about the mechanism of heritability of DNA methylation state during cell division and differentiation. Heritability of methylation state depends on certain enzymes such as DNMT1 that have a higher affinity for 5-methylcytosine than for cytosine. If this enzyme reaches a "hemimethylated" portion of DNA where 5-methylcytosine is in only one of the two DNA strands the enzyme will methylate the other half. Although histone modifications occur throughout the entire sequence, the unstructured N-termini of histones called histone tails are particularly highly modified. These modifications include acetylation , methylation , ubiquitylation , phosphorylation , sumoylation , ribosylation and citrullination. Acetylation is the most highly studied of these modifications. For example, acetylation of the K14 and K9 lysines of the tail of histone H3 by histone acetyltransferase enzymes HATs is generally related to transcriptional competence. Because it normally has a positively charged nitrogen at its end, lysine can bind the negatively charged phosphates of the DNA backbone. The acetylation event converts the positively charged amine group on the side chain into a neutral amide linkage. This removes the positive charge, thus loosening the DNA from the histone. This is the "cis" model of epigenetic function. In other words, changes to the histone tails have a direct effect on the DNA itself. In this model, changes to the histone tails act indirectly on the DNA. For example, lysine acetylation may create a binding site for chromatin-modifying enzymes or transcription machinery as well. This chromatin remodeler can then cause changes to the state of the chromatin. It may be that acetylation acts in this and the previous way to aid in transcriptional activation. The idea that modifications act as docking modules for related factors is borne out by histone methylation as well. Methylation of lysine 9 of histone H3 has long been associated with constitutively transcriptionally silent chromatin constitutive heterochromatin. It has been determined that a chromodomain a domain that specifically binds methyl-lysine in the transcriptionally repressive protein HP1 recruits HP1 to K9 methylated regions. One example that seems to refute this biophysical model for methylation is that tri-methylation of histone H3 at lysine 4 is strongly associated with and required for full transcriptional activation. Tri-methylation in this case would introduce a fixed positive charge on the tail. This enzyme utilizes a catalytically active site called the SET domain Suppressor of variegation, Enhancer of zeste, Trithorax. The SET domain is a amino acid sequence involved in modulating gene activities. This domain has been demonstrated to bind to the histone tail and causes the methylation of the histone. Also, multiple modifications may occur at the same time, and these modifications may work together to change the behavior of the nucleosome. The idea that multiple dynamic modifications regulate gene transcription in a systematic and reproducible way is called the histone code , although the idea that histone state can be read linearly as a digital information carrier has been largely debunked. Epigenetic changes of this type thus have the potential to direct increased frequencies of permanent genetic mutation. This recently identified enzyme has a catalytically active site called the Jumonji domain JmjC. The demethylation occurs when JmjC utilizes multiple cofactors to hydroxylate the methyl group, thereby removing it. JmjC is capable of demethylating mono-, di-, and tri-methylated substrates. Epigenetic control is often associated with alternative covalent modifications of histones. Small interfering RNAs can modulate transcriptional gene expression via epigenetic modulation of targeted promoters. For example, Hnf4 and MyoD enhance the transcription of many liver- and muscle-specific genes, respectively, including their own, through the transcription factor activity of the proteins they encode. RNA signalling includes differential recruitment of a hierarchy of generic chromatin modifying complexes and DNA methyltransferases to specific loci by RNAs during differentiation and development. Descendants of the cell in which the gene was turned on will inherit this activity, even if the original stimulus for gene-activation is no longer present. These genes are often turned on or off by signal transduction , although in some systems where syncytia or gap junctions are important, RNA may spread directly to other cells or nuclei by diffusion. A large amount of RNA and protein is contributed to the zygote

by the mother during oogenesis or via nurse cells , resulting in maternal effect phenotypes. A smaller quantity of sperm RNA is transmitted from the father, but there is recent evidence that this epigenetic information can lead to visible changes in several generations of offspring. Transcription from methylated CpG islands is strongly and heritably repressed. They control gene expression including virulence genes in pathogens and are viewed as new targets in the fight against drug-resistant bacteria. Their phylogenetic analyses, for example through sRNAâ€”mRNA target interactions or protein binding properties , are used to build comprehensive databases. Fungal prions Prions are infectious forms of proteins. In general, proteins fold into discrete units that perform distinct cellular functions, but some proteins are also capable of forming an infectious conformational state known as a prion. Although often viewed in the context of infectious disease , prions are more loosely defined by their ability to catalytically convert other native state versions of the same protein to an infectious conformational state. It is in this latter sense that they can be viewed as epigenetic agents capable of inducing a phenotypic change without a modification of the genome. Structural inheritance In ciliates such as Tetrahymena and Paramecium , genetically identical cells show heritable differences in the patterns of ciliary rows on their cell surface. Experimentally altered patterns can be transmitted to daughter cells. It seems existing structures act as templates for new structures. The mechanisms of such inheritance are unclear, but reasons exist to assume that multicellular organisms also use existing cell structures to assemble new ones. Nucleosome position is not random, and determine the accessibility of DNA to regulatory proteins. This determines differences in gene expression and cell differentiation. It has been shown that at least some nucleosomes are retained in sperm cells where most but not all histones are replaced by protamines. Thus nucleosome positioning is to some degree inheritable. Recent studies have uncovered connections between nucleosome positioning and other epigenetic factors, such as DNA methylation and hydroxymethylation. Predetermined epigenesis is a unidirectional movement from structural development in DNA to the functional maturation of the protein. Probabilistic epigenesis on the other hand is a bidirectional structure-function development with experiences and external molding development. Thus, as individuals develop, morphogens activate or silence genes in an epigenetically heritable fashion, giving cells a memory.

MOLECULAR BASIS OF GENE EXPRESSION pdf

2: Molecular basis of gene dosage sensitivity

The study of the molecular basis of genes and gene expression; molecular genetics.() Biology Chapter Molecular Biology of the Gene. 60 terms. Biology, Ch

Additivity[edit] This can be the case when multiple genes act in parallel to achieve the same effect. For example, when an organism is in need of phosphorus , multiple enzymes that break down different phosphorylated components from the environment may act additively to increase the amount of phosphorus available to the organism. However, there inevitably comes a point where phosphorus is no longer the limiting factor for growth and reproduction and so further improvements in phosphorus metabolism have smaller or no effect negative epistasis. Some sets of mutations within genes have also been specifically found to be additive. Alternatively the interaction may be indirect, where the genes encode components of a metabolic pathway or network , developmental pathway , signalling pathway or transcription factor network. For example, the gene encoding the enzyme that synthesizes penicillin is of no use to a fungus without the enzymes that synthesize the necessary precursors in the metabolic pathway. Epistasis within genes[edit] Just as mutations in two separate genes can be non-additive if those genes interact, mutations in two codons within a gene can be non-additive. In genetics this is sometimes called intragenic complementation when one deleterious mutation can be compensated for by a second mutation within that gene. This occurs when the amino acids within a protein interact. Due to the complexity of protein folding and activity, additive mutations are rare. Proteins are held in their tertiary structure by a distributed, internal network of cooperative interactions hydrophobic , polar and covalent. Conversely, when deleterious mutations are introduced, proteins often exhibit mutational robustness whereby as stabilising interactions are destroyed the protein still functions until it reaches some stability threshold at which point further destabilising mutations have large, detrimental effects as the protein can no longer fold. This leads to negative epistasis whereby mutations that have little effect alone have a large, deleterious effect together. For example, removing any member of the catalytic triad of many enzymes will reduce activity to levels low enough that the organism is no longer viable. This is sometimes called allelic complementation, or interallelic complementation. It may be caused by several mechanisms, for example transvection , where an enhancer from one allele acts in trans to activate transcription from the promoter of the second allele. Similarly, at the protein level, proteins that function as dimers may form a heterodimer composed of one protein from each alternate gene and may display different properties to the homodimer of one or both variants. Evolutionary consequences[edit] Fitness landscapes and evolvability[edit] The top row indicates interactions between two genes that are either additive a , show positive epistasis b or reciprocal sign epistasis c. Below are fitness landscapes which display greater and greater levels of global epistasis between large numbers of genes. Purely additive interactions lead to a single smooth peak d , as increasing numbers of genes exhibit epistasis, the landscape becomes more rugged e and when all genes interact epistatically the landscape becomes so rugged that mutations have seemingly random effects f. This is because magnitude epistasis positive and negative simply affects how beneficial mutations are together, however sign epistasis affects whether mutation combinations are beneficial or deleterious. It is frequently used as a visual metaphor for understanding evolution as the process of moving uphill from one genotype to the next, nearby, fitter genotype. The landscape is perfectly smooth, with only one peak global maximum and all sequences can evolve uphill to it by the accumulation of beneficial mutations in any order. Conversely, if mutations interact with one another by epistasis, the fitness landscape becomes rugged as the effect of a mutation depends on the genetic background of other mutations. This is referred to as a rugged fitness landscape and has profound implications for the evolutionary optimisation of organisms. If mutations are deleterious in one combination but beneficial in another, the fittest genotypes can only be accessed by accumulating mutations in one specific order. In contrast, changes in environment and therefore the shape of the fitness landscape have been shown to provide escape from local maxima. This gateway mutation alleviated the negative epistatic interactions of other individually beneficial mutations, allowing them to better function in concert. Complex environments or selections may therefore bypass local maxima found in models assuming simple positive selection. High

epistasis is usually considered a constraining factor on evolution, and improvements in a highly epistatic trait are considered to have lower evolvability. This is because, in any given genetic background, very few mutations will be beneficial, even though many mutations may need to occur to eventually improve the trait. The lack of a smooth landscape makes it harder for evolution to access fitness peaks. In highly rugged landscapes, fitness valleys block access to some genes, and even if ridges exist that allow access, these may be rare or prohibitively long. Rugged, epistatic fitness landscapes also affect the trajectories of evolution. When a mutation has a large number of epistatic effects, each accumulated mutation drastically changes the set of available beneficial mutations. Therefore, the evolutionary trajectory followed depends highly on which early mutations were accepted. Thus, repeats of evolution from the same starting point tend to diverge to different local maxima rather than converge on a single global maximum as they would in a smooth, additive landscape. Experimentally, this idea has been tested in using digital simulations of asexual and sexual populations. Over time, sexual populations move towards more negative epistasis, or the lowering of fitness by two interacting alleles. It is thought that negative epistasis allows individuals carrying the interacting deleterious mutations to be removed from the populations efficiently. This removes those alleles from the population, resulting in an overall more fit population. This hypothesis was proposed by Alexey Kondrashov , and is sometimes known as the deterministic mutation hypothesis [41] and has also been tested using artificial gene networks. Any two locus interactions at a particular gene frequency can be decomposed into eight independent genetic effects using a weighted regression. In this regression, the observed two locus genetic effects are treated as dependent variables and the "pure" genetic effects are used as the independent variables. Because the regression is weighted, the partitioning among the variance components will change as a function of gene frequency. By analogy it is possible to expand this system to three or more loci, or to cytonuclear interactions [44] Double mutant cycles[edit] When assaying epistasis within a gene, site-directed mutagenesis can be used to generate the different genes, and their protein products can be assayed e. This is sometimes called a double mutant cycle and involves producing and assaying the wild type protein, the two single mutants and the double mutant. Epistasis is measured as the difference between the effects of the mutations together versus the sum of their individual effects. The same methodology can be used to investigate the interactions between larger sets of mutations but all combinations have to be produced and assayed. For example, there are different combinations of 5 mutations, some or all of which may show epistasis Statistical coupling analysis[edit] You can help by adding to it. May Computational prediction[edit] Numerous computational methods have been developed for the detection and characterization of epistasis. Many of these rely on machine learning to detect non-additive effects that might be missed by statistical approaches such as linear regression. For example, multifactor dimensionality reduction MDR was designed specifically for nonparametric and model-free detection of combinations of genetic variants that are predictive of a phenotype such as disease status in human populations.

MOLECULAR BASIS OF GENE EXPRESSION pdf

3: An Introduction to Molecular Biology/Gene Expression - Wikibooks, open books for an open world

Regulation Of Gene Expression. Protein synthesis begins at transcription, ends at translation and involves multiple steps. Therefore, regulation of gene expression can happen at any of these steps.

RNA sugar-phosphate backbone forms. The RNA is further processed and then moves through the small nuclear pores to the cytoplasm. Transcription is the first step leading to gene expression. If the gene transcribed encodes a protein, the result of transcription is messenger RNA mRNA , which will then be used to create that protein via the process of translation. A DNA transcription unit encoding for a protein contains not only the sequence that will eventually be directly translated into the protein the coding sequence but also regulatory sequences that direct and regulate the synthesis of that protein. Transcription has some proofreading mechanisms, but they are fewer and less effective than the controls for copying DNA; therefore, transcription has a lower copying fidelity than DNA replication. Although DNA is arranged as two antiparallel strands in a double helix, only one of the two DNA strands, called the template strand, is used for transcription. The other DNA strand is called the coding strand, because its sequence is the same as the newly created RNA transcript except for the substitution of uracil for thymine. Transcription is divided into 5 stages: One gene-one enzyme hypothesis[edit] The one gene-one enzyme hypothesis is the idea that genes act through the production of enzymes, with each gene responsible for producing a single enzyme that in turn affects a single step in a metabolic pathway. The concept was proposed by George Beadle and Edward Tatum in an influential paper on genetic mutations in the mold Neurospora crassa, [3] and subsequently was dubbed the "one gene-one enzyme hypothesis" by their collaborator Norman Horowitz. It is often considered the first significant result in what came to be called molecular biology. Although it has been extremely influential, the hypothesis was recognized soon after its proposal to be an oversimplification. Even the subsequent reformulation of the "one gene-one polypeptide" hypothesis is now considered too simple to describe the relationship between genes and proteins. Neurospora crassa is a type of red bread mold of the phylum Ascomycota. The genus name, meaning "nerve spore" refers to the characteristic striations on the spores. Analysis of genetic recombination is facilitated by the ordered arrangement of the products of meiosis in Neurospora ascospores. Its entire genome of seven chromosomes has been sequenced. Beadle and Tatum exposed N. They then observed failures in metabolic pathways caused by errors in specific enzymes. This led them to propose the "one gene, one enzyme" hypothesis that specific genes code for specific proteins. Their hypothesis was later elaborated to enzyme pathways by Norman Horowitz, also working on Neurospora. One gene-one polypeptide[edit] By the early s, advances in biochemical geneticsâ€”spurred in part by the original hypothesisâ€”made the one gene-one enzyme hypothesis seem very unlikely at least in its original form. Beginning in , Vernon Ingram and others showed through protein fingerprinting that genetic variations in proteins such as sickle cell hemoglobin could be limited to differences in just a single polypeptide chain in a multimeric protein, leading to a "one gene-one polypeptide" hypothesis instead. According to geneticist Rowland H. Davis, "By â€” indeed, even by â€” one gene, one enzyme was no longer a hypothesis to be resolutely defended; it was simply the name of a research program. This splicing was discovered in by Phillip Sharp and Richard J. Operon[edit] An operon is a functioning unit of genomic material containing a cluster of genes under the control of a single regulatory signal or promoter. The genes are transcribed together into an mRNA strand and either translated together in the cytoplasm, or undergo trans-splicing to create monocistronic mRNAs that are translated separately, i. The result of this is that the genes contained in the operon are either expressed together or not at all. Several genes must be both co-transcribed and co-regulated to define an operon. Originally operons were thought to exist solely in prokaryotes but since the discovery of the first operons in eukaryotes in the early s, more evidence has arisen to suggest they are more common than previously assumed. Operons occur primarily in prokaryotes but also in some eukaryotes, including nematodes such as C. An operon is made up of several structural genes arranged under a common promoter and regulated by a common operator. It is defined as a set of adjacent structural genes, plus the adjacent regulatory signals that affect transcription of the structural genes. The regulators of a given operon, including repressors, corepressors, and activators, are not necessarily

coded for by that operon. The location and condition of the regulators, promoter, operator and structural DNA sequences can determine the effects of common mutations. Operons are related to regulons, stimulons and modulons. Whereas operons contain a set of genes regulated by the same operator, regulons contain a set of genes under regulation by a single regulatory protein, and stimulons contain a set of genes under regulation by a single cell stimulus. The promoter is recognized by RNA polymerase, which then initiates transcription. In RNA synthesis, promoters indicate which genes should be used for messenger RNA creation â€" and, by extension, control which proteins the cell manufactures. Operator â€" a segment of DNA that a regulator binds to. It is classically defined in the lac operon as a segment between the promoter and the genes of the operon. In the case of a repressor, the repressor protein physically obstructs the RNA polymerase from transcribing the genes. Structural genes â€" the genes that are co-regulated by the operon. Prokaryotic promoters[edit] In prokaryotes, the promoter consists of two short sequences at and positions upstream from the transcription start site. The Pribnow box is absolutely essential to start transcription in prokaryotes. Its presence allows a very high transcription rate. Both of the above consensus sequences, while conserved on average, are not found intact in most promoters. On average only 3 of the 6 base pairs in each consensus sequence is found in any given promoter. It should be noted that the above promoter sequences are only recognized by the sigma protein that interacts with the prokaryotic RNA polymerase. Complexes of prokaryotic RNA polymerase with other sigma factors recognize totally different core promoter sequences. They typically lie upstream of the gene and can have regulatory elements several kilobases away from the transcriptional start site enhancers. In eukaryotes, the transcriptional complex can cause the DNA to bend back on itself, which allows for placement of regulatory sequences far from the actual site of transcription. The TATA box typically lies very close to the transcriptional start site often within 50 bases. Eukaryotic promoter regulatory sequences typically bind proteins called transcription factors which are involved in the formation of the transcriptional complex. Enhancer[edit] An enhancer is a short region of DNA that can be bound with proteins namely, the trans-acting factors, much like a set of transcription factors to enhance transcription levels of genes hence the name in a gene cluster. While enhancers are usually cis-acting, an enhancer does not need to be particularly close to the genes it acts on, and need not be located on the same chromosome. In eukaryotic cells the structure of the chromatin complex of DNA is folded in a way that functionally mimics the supercoiled state characteristic of prokaryotic DNA, so that although the enhancer DNA is far from the gene in regard to the number of nucleotides, it is geometrically close to the promoter and gene. An enhancer may be located upstream or downstream of the gene that it regulates. Furthermore, an enhancer does not need to be located near to the transcription initiation site to affect the transcription of a gene, as some have been found to bind several hundred thousand base pairs upstream or downstream of the start site. Enhancers do not act on the promoter region itself, but are bound by activator proteins. These activator proteins interact with the mediator complex, which recruits polymerase II and the general transcription factors which then begin transcribing the genes. Enhancers can also be found within introns. Additionally, an enhancer may be excised and inserted elsewhere in the chromosome, and still affect gene transcription. That is the reason that intron polymorphisms are checked though they are not translated. Corepressor[edit] A corepressor is a protein that decreases gene expression by binding to a transcription factor which contains a DNA binding domain. The corepressor is unable to bind DNA by itself. The corepressor can repress transcriptional initiation by recruiting histone deacetylases which catalyze the removal of acetyl groups from lysine residues. This increases the positive charge on histones which strengthens in the interaction between the histones and DNA, making the latter less accessible to transcription. Thus, an mRNA that contains a riboswitch is directly involved in regulating its own activity, in response to the concentrations of its target molecule. The discovery that modern organisms use RNA to bind small molecules, and discriminate against closely related analogs, significantly expanded the known natural capabilities of RNA beyond its ability to code for proteins or to bind other RNA or protein macromolecules. The original definition of the term "riboswitch" specified that they directly sense small-molecule metabolite concentrations. Although this definition remains in common use, some biologists have used a broader definition that includes other cis-regulatory RNAs. However, this article will discuss only metabolite-binding riboswitches. Most known riboswitches occur in bacteria, but functional riboswitches of

one type the TPP riboswitch have been discovered in plants and certain fungi. TPP riboswitches have also been predicted in archaea, but have not been experimentally tested. It consists of three adjacent structural genes , lacZ, lacY and lacA. The lac operon is regulated by several factors including the availability of glucose and of lactose. Gene regulation of the lac operon was the first complex genetic regulatory mechanism to be elucidated and is one of the foremost examples of prokaryotic gene regulation. In its natural environment, the lac operon allows for the effective digestion of lactose. However, it would be inefficient to produce enzymes when there is no lactose available, or if there is a more readily-available energy source available such as glucose. It achieves this with the lac repressor , which halts production in the absence of lactose, and the Catabolite activator protein CAP , which assists in production in the absence of glucose. This dual control mechanism causes the sequential utilization of glucose and lactose in two distinct growth phases, known as diauxie. Similar diauxic growth patterns have been observed in bacterial growth on mixtures of other sugars as well, such as mixtures of glucose and xylose , or of glucose and arabinose , etc. The genetic control mechanisms underlying such diauxic growth patterns are known as xyl operon and ara operon , etc. The three structural genes are: Only lacZ and lacY appear to be necessary for lactose catabolism. IPTG is an allolactose analog. They were also able to isolate the portion of DNA bound by the protein by using the enzyme deoxyribonuclease, which breaks down DNA. This was later confirmed. These experiments were important, as they confirmed the mechanism of the lac operon, earlier proposed by Jacques Monod and Francois Jacob. The structure of the lac repressor protein consists of three distinct regions: This can be viewed as two dimers, with each dimer being able to bind to a single lac operator. The two subunits each bind to a slightly separated major groove region of the operator. The promoter is slightly covered by the lac repressor so RNAP cannot bind to and transcribe the operon. The DNA binding region consists of a helix-turn-helix structural motif. The lac repressor LacI operates by binding to the major groove of the operator region of the lac operon. When lactose is present, allolactose binds to the lac repressor, causing an allosteric change in its shape.

MOLECULAR BASIS OF GENE EXPRESSION pdf

4: The molecular basis of gene expression

Gene expression in eukaryotes can take place at multiple levels, where as in prokaryotes it takes palace with the help of accessory protein which is a part of an operon system.

Doctor of Philosophy Abstract Deviation of gene expression from normal levels has been associated with diseases. Both under- and overexpression of genes could lead to deleterious biological consequences. Dosage balance has been proposed to be a key issue of determining gene expression phenotype. Gene deletion or overexpression of any component in a protein complex produces abnormal phenotypes. As a result, interacting partners should be co-expressed to avoid dosage imbalance effects. The strength of transcriptional co-regulation of interacting partners is supposed to reflect gene dosage sensitivity. Although many cases of dosage imbalance effects have been reported, the molecular attributes determining dosage sensitivity remain unknown. This thesis uses a protein structure analysis protocol to explore the molecular basis of gene dosage sensitivity, and studies the post-transcriptional regulation of dosage sensitive genes. Solvent-exposed backbone hydrogen bond SEBH or called as dehydron provides a structure marker for protein interaction. Protein structure vulnerability, defined as the ratio of SEBHs to the overall number of backbone hydrogen bonds, quantifies the extent to which protein relies on its binding partners to maintain structure integrity. Genes encoding vulnerable proteins need to be highly co-expressed with their interacting partners. Protein structure vulnerability may hence serves as a structure marker for dosage sensitivity. This hypothesis is examined through the integration of gene expression, protein structure and interaction data sets. Both gene co-expression and protein structure vulnerability are calculated for each interacting subunits from human and yeast complexes. It turns out that structure vulnerability quantifies dosage sensitivity for both temporal phases yeast and tissue-specific human patterns of mRNA expression, determining the extent of co-expression similarity of binding partners. Highly dosage sensitive genes encode proteins which are vulnerable to water attack. They are subject to tight post-transcriptional regulation. In human, this extra regulation is achieved through extensive microRNA targeting of genes coding for extremely vulnerable proteins. In yeast, on the other hand, our results imply that such a regulation is likely achieved through sequestration of the extremely vulnerable proteins into aggregated states. The 85 genes encoding extremely vulnerable proteins contain the five confirmed yeast prions. It has been proposed that yeast prion protein aggregation could produce multiple phenotypes important for cell survival in some particular circumstances. These results suggest that extremely vulnerable proteins resorting to aggregation to buffer the deleterious consequences of dosage imbalance. However, a rigorous proof will require a structure-based integration of information drawn from the interactome, transcriptome and post-transcriptional regulome.

5: Molecular basis of neural-specific gene expression â€" Oregon Health & Science University

Gene expression is the process by which information from a gene is used in the synthesis of a functional gene product. These products are often proteins, but in non-protein coding genes such as ribosomal RNA (rRNA) genes or transfer RNA (tRNA) genes, the product is a functional RNA.

6: Molecular Biology | Definition of Molecular Biology by Merriam-Webster

We discussed about the definition of gene expression, levels of gene expression, transcriptional unit,operator,activator,repressor and lac operon. Sign up now to enroll in courses, follow best educators, interact with the community and track your progress.

7: Gene Structure and Expression

Abstract: DESCRIPTION: (Taken from the Application) A group of outstanding University of Missouri (MU) faculty (16

from Biochemistry, 11 from Biological Sciences, seven from Molecular Microbiology and Immunology, and eight from Genetics) propose to continue developing an interdisciplinary program in.

8: Epigenetics - Wikipedia

Our study suggests that cyclic cross-regulation of gene expression is a molecular basis for gene-gene interaction involved in disease phenotype. Advertisement www.enganchecubano.com

9: Regulation of Rhodopsin Gene Expression

Single-cell nucleosome mapping reveals the molecular basis of gene expression heterogeneity Eliza C. Small, a Liqun Xi, b Ji-Ping Wang, b Jonathan Widom, c, 1 and Jonathan D. Licht a, 2 a Division of Hematology/Oncology, Northwestern University Feinberg School of Medicine, Chicago, IL, ;.

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Heart of the Holidays The Man from the Ciguri (Dark Horse Comics) Can You? Play Like a Kitten (Copy Me Board Books) The Spanish Inquisition A guide to hardware managing maintaining Islamic Neoplatonism Western Neoplatonism. Ill tell you a tale Civil service since 1945 In Christ, my Lord Priory of Llanthony Prima and Secunda in Ireland, 1172-1541 Turners and Burners Turn South at Roswell Rainy days and reinvesting : creating peace of mind from your profit Unique solutions std 9 What is it like to be a nonracist? : Costello and Coetzee on the lives of animals and men Michael Bell Markov chain lecture notes Art and the spirit of anarchy by Brian Way Inorganic stereochemistry Information security risk assessment toolkit Beginners guide to woodturning Leonardos equestrian statuette Teach Yourself Biblical Hebrew Complete Course (Book Only (Teach Yourself) Cornwall (The Buildings of England) Lms virtual lab tutorial 2000 S Corporation Taxation Guide New Brunswick, and other poems Earth and physical science The eye of the artist. Applied Optics and Optical Engineering, Volume 5 Filming dreams The extras Dreaming features Documenting dreams Fundamentals of Agribusiness Finance Peach Fuzz, Vol. 2 Recent Developments in Muscle Relaxation Molecular biology of the cell 6th edition test bank Forest society and colonialism notes To improve relationships between the school board and the superintendent Timberland Historical Archaeology Notes Kimble InstructorS Manual (Tm to Accompany Principles of Psychology Wheres Benjy Bunny? Guia de Ciudadania/Naturalizacion en USA