# DOWNLOAD PDF PT. B. PROTEIN STRUCTURE AND FUNCTION ; NUCLEIC ACIDS AND GENES.

## Chapter 1 : PROTEIN MALFUNCTION AND DISEASE: The Example of Sickle Cell Anemia

*Nucleic acids Th ere are two kinds of nucleic acid: â€¢ deoxyribonucleic acid (DNA), which is located in chromosomes in the nucleus of eukaryotic cells (see fi gure ). It is the genetic material that con-tains hereditary information and is transmitted from generation to generation. â€¢ ribonucleic acid (RNA), which is formed against a template strand of DNA.*

Our models can be run directly from a browser. You only need to have Java 1. You may well have it already. If you do not, go to http: Mutations in DNA result in changes in the sequence of amino acids of a protein its primary structure. Thus, mutations may lead to changes in the way a protein functions and can become the molecular cause of illness. Students continue their exploration of the DNA coding of protein sequence. They use the Molecular Workbench model Mutations; Substitutions and Deletions to compare the effect of two different types of mutations in DNA, one caused by a nucleotide substitution and another caused by a nucleotide deletion. They reproduce a critical piece of hemoglobin structure using the Molecular Workbench: Modeling Hemoglobin model to explore changes in folding much like the change in hemoglobin in a patient with Sickle Cell disease. Finally, they take a post-test. Students will be able to: Compare the effect of nucleotide substitutions and deletions on protein structure; Reason about the molecular origin of disease; Relate the change in the structure of proteins to changes in their function and possible implications for human health. Macro to Micro Connection: Students will relate some macroscopic symptoms characteristic of human disease to microscopic changes in the primary structure of nucleic acids and proteins. Conceptual Prologue Mutations and Illness: Mutations can result from various kinds of damage to the structure of DNA. Substituting one nucleotide for another often makes no significant change in the shape of a protein, unless it occurs at a critical location. Due to the redundancy of the genetic code, in which several different codons in fact "mean" the same amino acid, many changes have no effect. Some substitutions, on the other hand, lead to change in the genetic code that brings about replacement of an hydrophilic amino acid to a hydrophobic one or vice versa. This can have a great effect. When a deleted or substituted amino acid is located in a critical position in the protein, it will affect the shape of the protein. That in turn can affect the way the protein works. Deleting a nucleotide, on the other hand, is likely to change many codons located immediately after the deletion. As the codons are read sequentially by the protein assembly line, all of the codons after the deleted nucleotide that are changed will generate the placement of "wrong" amino acids in the protein chain. Such a change typically leads to the appearance of a non-functional protein; if it was essential for the living cell protein such deletion would be a lethal mutation. A change in sequence change in shape change in activity. Such illnesses are the result either from flaws of metabolism or from damages of cellular structures, and they often originate in mutations in DNA. Sources of Mutation Mutations can either be inherited or acquired during our lifetime. Some kinds of cancer may be a combination of an inherited mutation and a mutation that we develop during our lifetime. Changes in proteins that result in disease can be the result of inborn genetic errors, so that for a certain person, DNA in every cell will always carry the mutation for the wrong protein. Changes in DNA can also result from the exposure of an organisms or any group of cells to environmental factors, such as UV rays of ionizing radiation, such as of the radiation in cosmic rays or nuclear reactions. These mutations can have different consequences for an organism, depending in what cells and tissues they occur. Mutations that occur in sperm cells or eggs can be passed to the next generation. Sickle Cell Anemia Some people inherit a specific substitution of a nucleotide in the gene that controls the sequence of amino acids in hemoglobin. These people inherit Sickle Cell Anemia. The hemoglobin molecules in people with this disease are folded in such a way that they stick to each other, making long fibers that damage red blood cells. The critical event - the formation of the fibers - occurs because the mutation replaces glutamic acid in the 6th position of the protein chain with valine, an amino acid with different properties. This replacement changes the shape of the protein: This bump fits exactly into the existing "pocket" on the surface of the adjacent

protein. The two proteins "clump" together, then the third clumps This creates a kind of domino effect leading to the formation of long fibers made of many millions of damaged hemoglobin molecules. Amino acids, charge, codon, DNA Time: There are two models in this activity, and they can be launched in one of two ways: Click the link below.:

# DOWNLOAD PDF PT. B. PROTEIN STRUCTURE AND FUNCTION ; NUCLEIC ACIDS AND GENES.

## Chapter 2 : Gene-protein relations - An Introduction to Genetic Analysis - NCBI Bookshelf

*Nucleic acids, macromolecules made out of units called nucleotides, come in two naturally occurring varieties: deoxyribonucleic acid (DNA) and ribonucleic acid (RNA). DNA is the genetic material found in living organisms, all the way from single-celled bacteria to multicellular mammals like you and me.*

One or more phosphate groups. Sequences can be complementary to another sequence in that the base on each position is complementary as well as in the reverse order. DNA is double-stranded containing both a sense strand and an antisense strand. Therefore, the complementary sequence will be to the sense strand. Image from Mao,  Solid-state structure of complexes with alkali metal ions have been reviewed. Nucleic acid secondary structure Secondary structure is the set of interactions between bases, i. The nucleotides on one strand base pairs with the nucleotide on the other strand. The secondary structure is responsible for the shape that the nucleic acid assumes. The bases in the DNA are classified as purines and pyrimidines. The purines are adenine and guanine. Purines consist of a double ring structure, a six membered and a five membered ring containing nitrogen. The pyrimidines are cytosine and thymine. It has a single ringed structure, a six membered ring containing nitrogen. A purine base always pairs with a pyrimidine base guanine G pairs with cytosine C and adenine A pairs with thymine T or uracil U. Although the two strands are aligned by hydrogen bonds in base pairs, the stronger forces holding the two strands together are stacking interactions between the bases. These stacking interactions are stabilized by Van der Waals forces and hydrophobic interactions, and show a large amount of local structural variability. The secondary structure of RNA consists of a single polynucleotide. Both single- and double-stranded regions are often found in RNA molecules. The antiparallel strands form a helical shape. Stem-loop or hairpin loop is the most common element of RNA secondary structure. Bulges and internal loops are formed by separation of the double helical tract on either one strand bulge or on both strands internal loops by unpaired nucleotides. A tetraloop is a four-base pairs hairpin RNA structure. There are three common families of tetraloop in ribosomal RNA: UNCG is the most stable tetraloop. H-type fold pseudoknots are best characterized. In H-type fold, nucleotides in the hairpin loop pairs with the bases outside the hairpin stem forming second stem and loop. This causes formation of pseudoknots with two stems and two loops. DotKnot-PW method is used for comparative pseudoknots prediction. The main points in the DotKnot-PW method is scoring the similarities found in stems, secondary elements and H-type pseudoknots.

# DOWNLOAD PDF PT. B. PROTEIN STRUCTURE AND FUNCTION ; NUCLEIC ACIDS AND GENES.

## Chapter 3 : Protein - Wikipedia

*Nucleic acids are molecules that allow organisms to transfer genetic information from one generation to the next. These macromolecules store the genetic information that determines traits and makes protein synthesis possible.*

Garland Science ;  Search term Analyzing Protein Structure and Function Proteins perform most of the work of living cells. This versatile class of macromolecule is involved in virtually every cellular process: They control cell division , metabolism , and the flow of materials and information into and out of the cell. Understanding how cells work requires understanding how proteins function. The question of what a protein does inside a living cell is not a simple one to answer. Imagine isolating an uncharacterized protein and discovering that its structure and amino acid sequence suggest that it acts as a protein kinase. Simply knowing that the protein can add a phosphate group to serine residues, for example, does not reveal how it functions in a living organism. Additional information is required to understand the context in which the biochemical activity is used. Where is this kinase located in the cell and what are its protein targets? In which tissues is it active? Which pathways does it influence? What role does it have in the growth or development of the organism? In this section , we discuss the methods currently used to characterize protein structure and function. We begin with an examination of the techniques used to determine the three-dimensional structure of purified proteins. We then discuss methods that are used to predict how a protein functions, based on its homology to other known proteins and its location inside the cell. Finally, because most proteins act in concert with other proteins, we present techniques for detecting protein-protein interactions. But these approaches only begin to define how a protein might work inside a cell. In the last section of this chapter, we discuss how genetic approaches are used to dissect and analyze the biological processes in which a given protein functions. It is presently not possible, however, to deduce reliably the three-dimensional folded structure of a protein from its amino acid sequence unless its amino acid sequence is very similar to that of a protein whose three-dimensional structure is already known. The main technique that has been used to discover the three-dimensional structure of molecules, including proteins, at atomic resolution is x-ray crystallography. X-rays, like light, are a form of electromagnetic radiation, but they have a much shorter wavelength, typically around 0. If a narrow parallel beam of x-rays is directed at a sample of a pure protein , most of the x-rays pass straight through it. A small fraction, however, is scattered by the atoms in the sample. If the sample is a well-ordered crystal, the scattered waves reinforce one another at certain points and appear as diffraction spots when the x-rays are recorded by a suitable detector Figure  Figure X-ray crystallography. A A narrow parallel beam of x-rays is directed at a well-ordered crystal B. Shown here is a protein crystal of ribulose bisphosphate carboxylase, an enzyme with a central role in CO2 fixation during photosynthesis. Some of the more The position and intensity of each spot in the x-ray diffraction pattern contain information about the locations of the atoms in the crystal that gave rise to it. Deducing the three-dimensional structure of a large molecule from the diffraction pattern of its crystal is a complex task and was not achieved for a protein molecule until  But in recent years x-ray diffraction analysis has become increasingly automated, and now the slowest step is likely to be the generation of suitable protein crystals. This requires large amounts of very pure protein and often involves years of trial and error, searching for the proper crystallization conditions. There are still many proteins, especially membrane proteins, that have so far resisted all attempts to crystallize them. Analysis of the resulting diffraction pattern produces a complex three-dimensional electron -density map. Interpreting this mapâ€”translating its contours into a three-dimensional structureâ€”is a complicated procedure that requires knowledge of the amino acid sequence of the protein. Largely by trial and error, the sequence and the electron-density map are correlated by computer to give the best possible fit. The reliability of the final atomic model depends on the resolution of the original crystallographic data: The three-dimensional structures of about 10, different proteins have now been determined by x-ray crystallography or by NMR spectroscopy see below â€”enough to begin to see families of common structures emerging. These structures or protein folds

often seem to be more conserved in evolution than are the amino acid sequences that form them see Figure  X-ray crystallographic techniques can also be applied to the study of macromolecular complexes. In a recent triumph, the method was used to solve the structure of the ribosome , a large and complex cellular machine made of several RNAs and more than 50 proteins see Figure  The determination required the use of a synchrotron, a radiation source that generates x-rays with the intensity needed to analyze the crystals of such large macromolecular complexes. This technique is now also increasingly applied to the study of small proteins or protein domains. Unlike x-ray crystallography, NMR does not depend on having a crystalline sample; it simply requires a small volume of concentrated protein solution that is placed in a strong magnetic field. Certain atomic nuclei, and in particular those of hydrogen, have a magnetic moment or spin: The spin aligns along the strong magnetic field, but it can be changed to a misaligned, excited state in response to applied radiofrequency RF pulses of electromagnetic radiation. When the excited hydrogen nuclei return to their aligned state, they emit RF radiation, which can be measured and displayed as a spectrum. The nature of the emitted radiation depends on the environment of each hydrogen nucleus , and if one nucleus is excited, it influences the absorption and emission of radiation by other nuclei that lie close to it. It is consequently possible, by an ingenious elaboration of the basic NMR technique known as two-dimensional NMR, to distinguish the signals from hydrogen nuclei in different amino acid residues and to identify and measure the small shifts in these signals that occur when these hydrogen nuclei lie close enough together to interact: In this way NMR can give information about the distances between the parts of the protein molecule. By combining this information with a knowledge of the amino acid sequence, it is possible in principle to compute the three-dimensional structure of the protein Figure  Figure NMR spectroscopy. A An example of the data from an NMR machine. This two-dimensional NMR spectrum is derived from the C-terminal domain of the enzyme cellulase. The spots represent interactions between hydrogen atoms that are near neighbors in the protein more For technical reasons the structure of small proteins of about 20, daltons or less can readily be determined by NMR spectroscopy. Resolution is lost as the size of a macromolecule increases. But recent technical advances have now pushed the limit to about , daltons, thereby making the majority of proteins accessible for structural analysis by NMR. The NMR method is especially useful when a protein of interest has resisted attempts at crystallization, a common problem for many membrane proteins. Because NMR studies are performed in solution, this method also offers a convenient means of monitoring changes in protein structure, for example during protein folding or when a substrate binds to the protein. NMR is also used widely to investigate molecules other than proteins and is valuable, for example, as a method to determine the three-dimensional structures of RNA molecules and the complex carbohydrate side chains of glycoproteins. Some landmarks in the development of x-ray crystallography and NMR are listed in Table  Sequence Similarity Can Provide Clues About Protein Function Thanks to the proliferation of protein and nucleic acid sequences that are catalogued in genome databases, the function of a gene â€”and its encoded proteinâ€”can often be predicted by simply comparing its sequence with those of previously characterized genes. Because amino acid sequence determines protein structure and structure dictates biochemical function, proteins that share a similar amino acid sequence usually perform similar biochemical functions, even when they are found in distantly related organisms. At present, determining what a newly discovered protein does therefore usually begins with a search for previously identified proteins that are similar in their amino acid sequences. Searching a collection of known sequences for homologous genes or proteins is typically done over the World-Wide Web, and it simply involves selecting a database and entering the desired sequence. A sequence alignment programâ€”the most popular are BLAST and FASTAâ€”scans the database for similar sequences by sliding the submitted sequence along the archived sequences until a cluster of residues falls into full or partial alignment Figure  The results of even a complex searchâ€”which can be performed on either a nucleotide or an amino acid sequenceâ€”are returned within minutes. Such comparisons can be used to predict the functions of individual proteins, families of proteins, or even the entire protein complement of a newly sequenced organism. Sequence databases can be searched to find similar amino acid or nucleic acid sequences. In the end, however,

the predictions that emerge from sequence analysis are often only a tool to direct further experimental investigations. Proteins that travel from the cytoplasm to the nucleus when a cell is exposed to a growth factor , for example, may have a role in regulating gene expression in response to that factor. A protein often contains short amino acid sequences that determine its location in a cell. Most nuclear proteins, for example, contain one or more specific short sequences of amino acids that serve as signals for their import into the nucleus after their synthesis in the cytosol discussed in Chapter  These special regions of the protein can be identified by fusing them to an easily detectable protein that lacks such regions and then following the behavior of this surrogate protein in a cell. Such fusion proteins can be readily produced by the recombinant DNA techniques discussed previously. Another common strategy used both to follow proteins in cells and to purify them rapidly is epitope tagging. The fusion protein can therefore be specifically detected, even in the presence of a large excess of the normal protein, using the anti-epitope antibody and a labeled secondary antibody that can be monitored by light or electron microscopy Figure  Figure Epitope tagging allows the localization or purification of proteins. Using standard genetic engineering techniques, a short epitope tag can be added to a protein of interest. The resulting protein contains the protein being analyzed plus a short peptide more Today large numbers of proteins are being tracked in living cells by using a fluorescent marker called green fluorescent protein GFP. Tagging proteins with GFP is as simple as attaching the gene for GFP to one end of the gene that encodes a protein of interest. In most cases, the resulting GFP fusion protein behaves in the same way as the original protein, and its movement can be monitored by following its fluorescence inside the cell by fluorescence microscopy. The GFP fusion protein strategy has become a standard way to determine the distribution and dynamics of any protein of interest in living cells. We discuss its use further in Chapter 9. GFP , and its derivatives of different color, can also be used to monitor protein -protein interactions. In this application, two proteins of interest are each labeled with a different fluorochrome, such that the emission spectrum of one fluorochrome overlaps the absorption spectrum of the second fluorochrome. If the two proteinsâ€”and their attached fluorochromesâ€”come very close to each other within about 1â€”10 nm , the energy of the absorbed light will be transferred from one fluorochrome to the other. The energy transfer, called fluorescence resonance energy transfer FRET , is determined by illuminating the first fluorochrome and measuring emission from the second Figure  By using two different spectral variants of GFP as the fluorochromes in such studies, one can monitor the interaction of any two protein molecules inside a living cell. Fluorescence resonance energy transfer FRET. To determine whether and when two proteins interact inside the cell, the proteins are first produced as fusion proteins attached to different variants of GFP. A In this example, protein X is coupled to more Affinity Chromatography and Immunoprecipitation Allow Identification of Associated Proteins Because most proteins in the cell function as part of a complex with other proteins, an important way to begin to characterize their biological roles is to identify their binding partners. If an uncharacterized protein binds to a protein whose role in the cell is understood, its function is likely to be related. For example, if a protein is found to be part of the proteasome complex, it is likely to be involved somehow in degrading damaged or misfolded proteins. Protein affinity chromatography is one method that can be used to isolate and identify proteins that interact physically.

# DOWNLOAD PDF PT. B. PROTEIN STRUCTURE AND FUNCTION ; NUCLEIC ACIDS AND GENES.

## Chapter 4 : Analyzing Protein Structure and Function - Molecular Biology of the Cell - NCBI Bookshelf

*Start studying Carbohydrates,Proteins,Lipids Nucleic Acids. Learn vocabulary, terms, and more with flashcards, games, and other study tools.*

Adam Cloe has been published in various scientific journals, including the "Journal of Biochemistry. Grilled piece of steak on a cutting board. The main substances found in every cell are a combination of lipids, carbohydrates, nucleic acids and proteins. Each of these substances plays a different role in the body, and all of them must either come from the diet or be manufactured using other chemicals in the body. Video of the Day Lipid Function in the Body Lipids, also known as fats, play multiple roles in the body. Fats are broken down in the digestive tract to form individual fatty acids and cholesterol molecules. Fatty acids and cholesterol are key components of the membranes that surround all cells. Cholesterol can also be used to make many other compounds in the body, such as steroid hormones. Finally, fatty acids represent an important source of energy, particularly for the purposes of long-term storage. Carbohydrates as Energy Carbohydrates are the preferred source of energy for most of the tissues in the body, including the nervous system and the heart. Carbohydrates from the diet are converted into glucose, which can either be immediately used as a source of energy or stored in the form of glycogen. The body cannot digest all carbohydrates in the diet, however; indigestible carbohydrates, also known as fiber, travel through the intestines and can help maintain proper digestive health. Nucleic Acids for Storing Information Nucleic acids consist of three different types of molecules joined together: The main role of nucleic acids is to store information that is used to make proteins. Nucleic acids come in two main forms: The main function of DNA is to store the genetic information that cells in the body need to function. RNA, on the other hand, plays an important role in converting the information from DNA into proteins. Proteins as Workhorses of the Body Proteins are large and fairly complex molecules that are responsible for doing most of the work that occurs in cells. The body uses the information stored in DNA to create proteins, which are made up of subunits called amino acids. Enzymes, which help speed chemical reactions in cells, are a specialized type of protein. Protein also plays a crucial role in maintaining muscle tissue, since muscle tissue has large amounts of protein. For muscles to increase in size and strength, more protein must be made to expand the muscle fibers.

## Chapter 5 : # Nucleic acids and protein synthesis - Syllabus - | Biology Notes for A level

*The Structure and Function of Nucleic Acids organism is stored in the form of genes in a cell and how these genes are 2 Nucleic acids:structure and function.*

Only proline differs from this basic structure as it contains an unusual ring to the N-end amine group, which forces the COâ€”NH amide moiety into a fixed conformation. Once linked in the protein chain, an individual amino acid is called a residue, and the linked series of carbon, nitrogen, and oxygen atoms are known as the main chain or protein backbone. The other two dihedral angles in the peptide bond determine the local shape assumed by the protein backbone. The words protein, polypeptide, and peptide are a little ambiguous and can overlap in meaning. Protein is generally used to refer to the complete biological molecule in a stable conformation , whereas peptide is generally reserved for a short amino acid oligomers often lacking a stable three-dimensional structure. However, the boundary between the two is not well defined and usually lies near 20â€”30 residues. Interactions Proteins can interact with many types of molecules, including with other proteins , with lipids , with carboyhydrates , and with DNA. Smaller bacteria, such as Mycoplasma or spirochetes contain fewer molecules, on the order of 50, to 1 million. By contrast, eukaryotic cells are larger and thus contain much more protein. For instance, yeast cells have been estimated to contain about 50 million proteins and human cells on the order of 1 to 3 billion. For instance, of the 20, or so proteins encoded by the human genome, only 6, are detected in lymphoblastoid cells. Eukaryotes, bacteria, archaea and viruses have on average , , and 42 proteins respectively coded in their genomes. Protein biosynthesis Proteins are assembled from amino acids using information encoded in genes. Each protein has its own unique amino acid sequence that is specified by the nucleotide sequence of the gene encoding this protein. The genetic code is a set of three-nucleotide sets called codons and each three-nucleotide combination designates an amino acid, for example AUG adenine - uracil - guanine is the code for methionine. Because DNA contains four nucleotides, the total number of possible codons is 64; hence, there is some redundancy in the genetic code, with some amino acids specified by more than one codon. Most organisms then process the pre-mRNA also known as a primary transcript using various forms of Post-transcriptional modification to form the mature mRNA, which is then used as a template for protein synthesis by the ribosome. In prokaryotes the mRNA may either be used as soon as it is produced, or be bound by a ribosome after having moved away from the nucleoid. In contrast, eukaryotes make mRNA in the cell nucleus and then translocate it across the nuclear membrane into the cytoplasm , where protein synthesis then takes place. The rate of protein synthesis is higher in prokaryotes than eukaryotes and can reach up to 20 amino acids per second. The mRNA is loaded onto the ribosome and is read three nucleotides at a time by matching each codon to its base pairing anticodon located on a transfer RNA molecule, which carries the amino acid corresponding to the codon it recognizes. The growing polypeptide is often termed the nascent chain. Proteins are always biosynthesized from N-terminus to C-terminus. The average size of a protein increases from Archaea to Bacteria to Eukaryote , , residues and 31, 34, 49 kDa respecitvely due to a bigger number of protein domains constituting proteins in higher organisms. Peptide synthesis Short proteins can also be synthesized chemically by a family of methods known as peptide synthesis , which rely on organic synthesis techniques such as chemical ligation to produce peptides in high yield. Chemical synthesis is inefficient for polypeptides longer than about amino acids, and the synthesized proteins may not readily assume their native tertiary structure. Most chemical synthesis methods proceed from C-terminus to N-terminus, opposite the biological reaction. A single protein subunit is highlighted. Chaperonins assist protein folding. Three possible representations of the three-dimensional structure of the protein triose phosphate isomerase. All-atom representation colored by atom type. Simplified representation illustrating the backbone conformation, colored by secondary structure. Solvent-accessible surface representation colored by residue type acidic residues red, basic residues blue, polar residues green, nonpolar residues white. The shape into which a protein naturally folds is known as its native conformation. A protein is

a polyamide. Because secondary structures are local, many regions of different secondary structure can be present in the same protein molecule. Tertiary structure is generally stabilized by nonlocal interactions, most commonly the formation of a hydrophobic core , but also through salt bridges , hydrogen bonds, disulfide bonds , and even posttranslational modifications. The term "tertiary structure" is often used as synonymous with the term fold. The tertiary structure is what controls the basic function of the protein. Proteins are not entirely rigid molecules. In addition to these levels of structure, proteins may shift between several related structures while they perform their functions. In the context of these functional rearrangements, these tertiary or quaternary structures are usually referred to as " conformations ", and transitions between them are called conformational changes. In solution proteins also undergo variation in structure through thermal vibration and the collision with other molecules. From left to right are: Proteins can be informally divided into three main classes, which correlate with typical tertiary structures: Almost all globular proteins are soluble and many are enzymes. Fibrous proteins are often structural, such as collagen , the major component of connective tissue, or keratin , the protein component of hair and nails. Membrane proteins often serve as receptors or provide channels for polar or charged molecules to pass through the cell membrane. Protein domain Many proteins are composed of several protein domains , i. Domains usually also have specific functions, such as enzymatic activities e. Sequence motif Short amino acid sequences within proteins often act as recognition sites for other proteins. Cellular functions Proteins are the chief actors within the cell, said to be carrying out the duties specified by the information encoded in genes. The enzyme hexokinase is shown as a conventional ball-and-stick molecular model. To scale in the top right-hand corner are two of its substrates, ATP and glucose. The chief characteristic of proteins that also allows their diverse set of functions is their ability to bind other molecules specifically and tightly. The region of the protein responsible for binding another molecule is known as the binding site and is often a depression or "pocket" on the molecular surface. Extremely minor chemical changes such as the addition of a single methyl group to a binding partner can sometimes suffice to nearly eliminate binding; for example, the aminoacyl tRNA synthetase specific to the amino acid valine discriminates against the very similar side chain of the amino acid isoleucine. When proteins bind specifically to other copies of the same molecule, they can oligomerize to form fibrils; this process occurs often in structural proteins that consist of globular monomers that self-associate to form rigid fibers. Proteinâ€”protein interactions also regulate enzymatic activity, control progression through the cell cycle , and allow the assembly of large protein complexes that carry out many closely related reactions with a common biological function. Proteins can also bind to, or even be integrated into, cell membranes. The ability of binding partners to induce conformational changes in proteins allows the construction of enormously complex signaling networks. Enzyme The best-known role of proteins in the cell is as enzymes , which catalyse chemical reactions. Enzymes are usually highly specific and accelerate only one or a few chemical reactions. Some enzymes act on other proteins to add or remove chemical groups in a process known as posttranslational modification. About 4, reactions are known to be catalysed by enzymes. Although enzymes can consist of hundreds of amino acids, it is usually only a small fraction of the residues that come in contact with the substrate, and an even smaller fractionâ€”three to four residues on averageâ€”that are directly involved in catalysis. Dirigent proteins are members of a class of proteins that dictate the stereochemistry of a compound synthesized by other enzymes. Some proteins, such as insulin , are extracellular proteins that transmit a signal from the cell in which they were synthesized to other cells in distant tissues. Others are membrane proteins that act as receptors whose main function is to bind a signaling molecule and induce a biochemical response in the cell. Many receptors have a binding site exposed on the cell surface and an effector domain within the cell, which may have enzymatic activity or may undergo a conformational change detected by other proteins within the cell. Antibodies can be secreted into the extracellular environment or anchored in the membranes of specialized B cells known as plasma cells. Whereas enzymes are limited in their binding affinity for their substrates by the necessity of conducting their reaction, antibodies have no such constraints. These proteins must have a high binding affinity when their ligand is present in high

concentrations, but must also release the ligand when it is present at low concentrations in the target tissues. The canonical example of a ligand-binding protein is haemoglobin , which transports oxygen from the lungs to other organs and tissues in all vertebrates and has close homologs in every biological kingdom. Lectins typically play a role in biological recognition phenomena involving cells and proteins. Transmembrane proteins can also serve as ligand transport proteins that alter the permeability of the cell membrane to small molecules and ions. The membrane alone has a hydrophobic core through which polar or charged molecules cannot diffuse. Membrane proteins contain internal channels that allow such molecules to enter and exit the cell. Many ion channel proteins are specialized to select for only a particular ion; for example, potassium and sodium channels often discriminate for only one of the two ions. Most structural proteins are fibrous proteins ; for example, collagen and elastin are critical components of connective tissue such as cartilage , and keratin is found in hard or filamentous structures such as hair , nails , feathers , hooves , and some animal shells. Other proteins that serve structural functions are motor proteins such as myosin , kinesin , and dynein , which are capable of generating mechanical forces. These proteins are crucial for cellular motility of single celled organisms and the sperm of many multicellular organisms which reproduce sexually. They also generate the forces exerted by contracting muscles [42] and play essential roles in intracellular transport. Methods of study Main article: Protein methods The activities and structures of proteins may be examined in vitro , in vivo , and in silico. In vitro studies of purified proteins in controlled environments are useful for learning how a protein carries out its function: By contrast, in vivo experiments can provide information about the physiological role of a protein in the context of a cell or even a whole organism. In silico studies use computational methods to study proteins. Protein purification Main article: Protein purification To perform in vitro analysis, a protein must be purified away from other cellular components. The resulting mixture can be purified using ultracentrifugation , which fractionates the various cellular components into fractions containing soluble proteins; membrane lipids and proteins; cellular organelles , and nucleic acids. Precipitation by a method known as salting out can concentrate the proteins from this lysate. Various types of chromatography are then used to isolate the protein or proteins of interest based on properties such as molecular weight, net charge and binding affinity. Additionally, proteins can be isolated according to their charge using electrofocusing. To simplify this process, genetic engineering is often used to add chemical features to proteins that make them easier to purify without affecting their structure or activity. Here, a "tag" consisting of a specific amino acid sequence, often a series of histidine residues a " His-tag " , is attached to one terminus of the protein. As a result, when the lysate is passed over a chromatography column containing nickel , the histidine residues ligate the nickel and attach to the column while the untagged components of the lysate pass unimpeded. A number of different tags have been developed to help researchers purify specific proteins from complex mixtures. Although many intracellular proteins are synthesized in the cytoplasm and membrane-bound or secreted proteins in the endoplasmic reticulum , the specifics of how proteins are targeted to specific organelles or cellular structures is often unclear.

# DOWNLOAD PDF PT. B. PROTEIN STRUCTURE AND FUNCTION ; NUCLEIC ACIDS AND GENES.

## Chapter 6 : Nucleic acid - Wikipedia

*And proteins control cell function and provide structure. So, the basis of life happens in each and every cell. Whenever a new cell is made in an organism, the genetic material is reproduced and put into the new cell.*

Nucleic Acid Nucleotides Possibly the first biomolecules to support life, nucleic acids store and transfer cellular information and transfer energy in all living organisms. Deoxyribonucleic acid, better known as DNA, stores hereditary information in small segments called genes inside long polymer strands. Other RNA molecules are active, three-dimensional products that provide enzymatic or regulatory functions inside cells. Nucleic acids are polymers of individual nucleotide monomers. Each nucleotide is composed of three parts: Only two 5-carbon sugars are found in nature: Deoxyribose is a ribose derivative in which an oxygen atom is missing from one carbon; the carbon was deoxygenated. A 5-carbon sugar ribose or deoxyribose forms the central molecule in a nucleotide. A nitrogenous base is an organic molecule containing both carbon and nitrogen atoms. The name nitrogenous base signifies that several nitrogen atoms act as bases in solution. In nucleic acids, nitrogenous bases contain either one ring or two fused rings. Purines are double-ring nitrogenous bases found in nature and include adenine and guanine. Thymine, cytosine and uracil are pyrimidines, single-ring nitrogenous bases found in nature. The sugar and nitrogenous base present in a nucleotide define the nucleotide and its functional role. Because the sugar and phosphate are similar structural components in all nucleotides, scientists frequently use a shorthand notation to identify a nucleotide by naming only the unique nitrogenous base present. Like monosaccharides, nucleotides and short nucleotide chains perform important cellular functions. Adenosine triphosphate ATP is an important energy carrier in living organisms. ATP is composed of adenine, a ribose sugar, and three phosphate groups bonded sequentially. The bonding of three anionic phosphate groups in a row forces several negative ions into close proximity, an unfavorable state. Reactions that remove the outermost phosphate group forming adenosine diphosphate, or ADP release energy for use in other chemical reactions. Building Nucleotides In this activity, you will select components of a nucleotide and place them in the correct position to form covalent bonds. Please enable iFrames to view this content or visit Interactive Activity. The unique structure of a DNA polymer provides a template for identification and delivery of the information inside each gene and for accurate replication of DNA during cell division. RNA polymers perform a variety of cellular functions, including delivering DNA messages to synthesize proteins and acting as enzymes or regulatory molecules in many cellular processes. Although less complex than protein structure, RNA polymers frequently form three-dimensional structures specific to their function. Interactions between the nitrogenous bases in DNA and RNA polymers form the basis for the structure, function, and accurate replication of nucleic acids. Nucleic acids are formed by repeated dehydration synthesis reactions between nucleotides. During dehydration synthesis, a phosphodiester linkage forms between the phosphate group of one nucleotide and the sugar of another nucleotide. Phosphodiester linkages form between the phosphate and sugar segments of each nucleotide, leaving the nitrogenous bases free to interact with one another. Because some nitrogenous bases contain oxygen in addition to nitrogen, hydrogen bonds easily form between separate bases in a specific pattern. DNA polymers form paired strands in which the nitrogenous bases act like a zipper, binding the two strands together. Structurally, nitrogenous bases in a polymer tend to pair in an anti-parallel pattern, meaning that two paired strands of nucleic acid sit in opposite directions. The nucleotide pairs on opposing strands that form hydrogen bonds are frequently called base pairs. In DNA, polymers are almost exclusively found in long, paired anti-parallel strands forming the famous double helix. All DNA nucleotides contain the sugar deoxyribose and one of four different nitrogenous bases: With only four different nucleotides, it seems impossible that DNA could encode enough information to produce the millions of different proteins and functional RNA molecules that yield such a vast diversity of living organisms. However, the order and choice of nucleotides allows an almost infinite number of possible sequences. Imagine creating a 5-nucleotide chain

using only the 4 DNA nucleotides. With these parameters, up to 1, possible polymers exist. Imagine how many different polymer sequences are possible for the shortest human chromosome, which is fifty million nucleotides long! RNA nucleotides are defined by the sugar ribose, and contain a slightly different set of nitrogenous bases: RNA molecules do not contain thymine. Many single-stranded RNA molecules bend and twist into a three-dimensional structure that includes some hydrogen bonding between nucleotides in the same strand. As with protein structure, the three-dimensional structure of an RNA molecule specifies a unique function in cells, including enzyme catalysis.

# DOWNLOAD PDF PT. B. PROTEIN STRUCTURE AND FUNCTION ; NUCLEIC ACIDS AND GENES.

## Chapter 7 : Functions of Lipids, Carbohydrates, Nucleic Acids & Proteins | www.nxgvision.com

*Virtually all enzymes are proteins, and thus we must review the basic facts of protein structure to follow the next step in the study of gene function. Protein structure In simple terms, a protein is a macromolecule composed of amino acids attached end to end in a linear string.*

Figure Electron micrograph of the enzyme aspartate transcarbamylase. Note the quaternary structure: Photograph from Jack D. Many proteins are compact structures; such proteins are called globular proteins. Enzymes and antibodies are among the important globular proteins. Other, unfolded proteins, called fibrous proteins, are important components of such structures as hair and muscle. This configuration creates specific sites to which substrates bind and at which catalytic reactions take place. The three-dimensional structure of a protein, which is crucial for its function, is determined solely by the primary structure linear sequence of amino acids. Therefore, genes can control enzyme function by controlling the primary structure of proteins. Protein motifs Often, several elements of secondary structure combine to produce a pattern, or motif, that is found in numerous other proteins. We can recognize motifs sometimes by their amino acid sequence pattern and other times by observing the three-dimensional structure. Figure shows two examples. The helix-loop-helix motif is found in calcium binding proteins, and a variant of it is found in regulatory proteins that bind DNA. The zinc-binding motif, also found in DNA binding proteins, is termed the zinc finger, because of the way that the residues protrude outward, like a finger. Figure Secondary structure motifs. Determining protein sequence If we purify a particular protein, we find that we can specify a particular ratio of the various amino acids that make up that specific protein. But the protein is not formed by a random hookup of fixed amounts of the various amino acids; each protein has a unique, characteristic sequence. For a small polypeptide , the amino acid sequence can be determined by clipping off one amino acid at a time and identifying it. Frederick Sanger worked out a brilliant method for deducing the sequence of large polypeptides. There are several different proteolytic enzymesâ€”enzymes that can break peptide bonds only between specific amino acids in proteins. Proteolytic enzymes can break a large protein into a number of smaller fragments, which can then be separated according to their migration speeds in a solvent on chromatographic paper. Because different fragments will move at different speeds in various solvents, two-dimensional chromatography can be used to enhance the separation of the fragments Figure  When the paper is stained, the polypeptides appear as spots in a characteristic chromatographic pattern called the fingerprint of the protein. Each of the spots can be cut out, and the polypeptide fragments can be washed from the paper. Because each spot contains only small polypeptides, their amino acid sequences can be easily determined. Figure Two-dimensional chromatographic fingerprinting of a polypeptide fragment mixture. A protein is digested by a proteolytic enzyme into fragments that are only a few amino acids long. A piece of chromatographic filter paper is then spotted with this mixture more Using different proteolytic enzymes to cleave the protein at different points, we can repeat the experiment to obtain other sets of fragments. The fragments from the different treatments overlap, because the breaks are made in different places with each treatment. The problem of solving the overall sequence then becomes one of fitting together the small-fragment sequencesâ€”almost like solving a tricky jigsaw or crossword puzzle Figure  Figure Alignment of polypeptide fragments to reconstruct an entire amino acid sequence. Different proteolytic enzymes can be used on the same protein to form different fingerprints, as shown here. The amino acid sequence of each fragment can be determined rather more Using this elegant technique, Sanger confirmed that the sequence of amino acids as well as the amounts of the various amino acids is specific to a particular protein. In other words, the amino acid sequence is what makes insulin insulin. Relation between gene mutations and altered proteins We now know that the change of just one amino acid is sometimes enough to alter protein function. This was first shown in by Vernon Ingram, who studied the globular protein hemoglobinâ€”the molecule that transports oxygen in red blood cells. As shown in Figure d , hemoglobin is made up of four polypeptide chains: Ingram compared

hemoglobin A HbA , the hemoglobin from normal adults, with hemoglobin S HbS , the protein from people homozygous for the mutant gene that causes sickle-cell anemia , the disease in which red blood cells take on a sickle-cell shape see Figure  Sequencing that spot from the two kinds of hemoglobin, Ingram found that only one amino acid in the fragment differs in the two kinds. Unless patients with HbS receive medical attention, this single error in one amino acid in one protein will hasten their death. Figure shows how this gene mutation ultimately leads to the pattern of sickle-cell disease.

# DOWNLOAD PDF PT. B. PROTEIN STRUCTURE AND FUNCTION ; NUCLEIC ACIDS AND GENES.

## Chapter 8 : Nucleic acid structure - Wikipedia

*Nucleic Acid Building Blocks â€¢ For nucleic acids, tertiary structure refers to the Nucleic Acids and Protein Production.*

Your answer sheet with your name on it. Your bluebook with your name on it. Your copy of the exam with your name on it. If more than one response is selected, the answer will be marked as an incorrect answer. Choose the molecular definition of a gene that includes all of DNA elements that may be part of the DNA sequence of a gene: The DNA sequence of a gene includes only exons. The DNA sequence of a gene includes only exons and introns. The DNA sequence of a gene includes exons, introns and noncoding regulatory control regions. The DNA sequence of a gene includes exons, introns, noncoding regulatory control regions, and intergenic regions. Crick considered the crucial point in his hypothesis to be the idea that information transfer is not allowed in which one of the following conditions? Transfer from RNA to protein. Transfer from protein back to RNA. Choose the answer that correctly names both of these processes: Reverse transcription and protein folding B. DNA replication and protein folding C. Translation and protein folding D. Reverse transcription and transposon jumping 4. Watson and Crick proposed a molecular structure or model of double helical DNA in which contains a helical turn every 10 base paris and adjacent base pairs 0. This form of DNA is now one of several forms known to exist. Triple helical DNA 5. It is useful to think about gene expression in eukaryotic cells in relation of the cell cycle. In which phase of the cell cycle is gene expression almost completely shut down? Which one of the following classes of molecules is not encoded in genes? Here is a nucleotide sequence: Choose the answer that correctly gives the most important change in the structure of cellular DNA for allowing the initiation of transcription as the first step in gene expression: Proteins bind to specific sequences in the DNA often resulting in both the bending and unwinding of the double helix to expose unpaired purine and pyrimidine bases. DNA has the ability to undergo denaturation at the appropriate temperature and ionic strength of its solution environment and then to reversible renature into a double helix again. Double-stranded DNA has extensive secondary structure that is melted out by proteins binding to specific regulatory sequences. The nitrogen bases in double helical DNA are reversibly crossed linked by covalent bonds and these cross links are removed when regulatory proteins bind thus allowing strand separation and the initiation of transcription. Identify the experimental condition that does not favor DNA denaturation: Increased ionic concentration of solution. Addition of formamide or urea. Alkaline basic pH conditions. Choose the pair of macromolecules that are most alike in their secondary structures: Single stranded RNA and proteins D. Single stranded DNA and proteins  One of the rules was that the monomers are added one at a time. Select the answer that correctly lists all of the steps in gene expression to which this rule applies: Replication and transcription only C. Replication, transcription and translation. Synthesis requires a cellular supply of nucleoside triphosphates. New chains are produced using an exisiting or parental strand as a template. RNA polymerases can begin a new RNA chain with the addition of the first nucleoside triphosphate but not DNA polymerase which requires a primer sequence. In which process of information transfer would you find at work helicases, topoisomerases, ligases and a primase? Choose the response that correctly identifies the cells in which genes may be clustered into a tendem arrangement of genes all under control of the same regulatory sequence, i. Both prokaryotic and eukaryotic cells D. Neither prokaryotic nor eukaryotic cells  Choose the answer that correctly names all three of the molecules that must be bound to amino acyl-tRNA synthetase as part of the two-step decoding process: Position 3 only D. Positions 2 and 3. Which one of the following amino acids is frequently found both at the N-terminus of a polypeptide chain in eukaryotic cells as a consequence of the initiation of translation and also internally in the polypeptide chain? Initiation of eukaryotic protein synthesis depends on the formation of a crucial complex called the ternary complex. Choose the answer that correctly lists the components of the ternary complex: Identify the mechanism by a complex eukaryotic transcription unit produces a primary transcript that can be processed into two or more different mRNAs: Alternative splice sites D. Internal ribosome entry sites  What do we call a set

of eukaryotic genes that encode proteins with similar but nonidentical amino acid sequences? Moderately repeated DNA D. Simple sequence DNA  Reassociation experiments revealed that eukaryotic DNA does not renature uniformly. These experiments are performed by fragmenting total DNA from an organism into pieces about base pairs long. The DNA is then melted into single strands and allowed to reform complementary base-paired double helices. Which class of DNA would be expected to have the most rapid rate of renaturation reassociation?

## Chapter 9 : Nucleic acids (article) | Khan Academy

*Transfer RNA (tRNA) is a small type of stable RNA that carries an amino acid to the corresponding site of protein synthesis in the ribosome. It is the base pairing between the tRNA and mRNA that allows for the correct amino acid to be inserted in the polypeptide chain being synthesized.*