



تَوِير

BIOLOGY

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File Title: Chapter 5

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Campbell
Biology



Summary
Chapter Five

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Chapter Five Summary

The structure and function of large biological molecules

The most important large molecules:

- 1) carbohydrates →
- 2) nucleic acids →
- 3) proteins →
- 4) lipids →

Macromolecules/Polymer

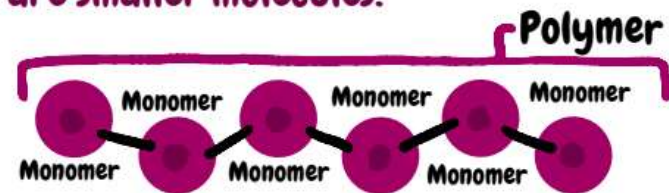
↳ All four classes of large biological molecules

Macromolecules are large molecules composed of thousands of covalently connected atoms.

▶ Molecular structure and function are inseparable

A Polymer is a long molecule consisting of many similar or identical building blocks linked by covalent bonds.

A Monomers is the repeating units that serve as the building blocks of a polymer are smaller molecules.



▶ Carbohydrates, proteins, nucleic acids are polymers

The Synthesis and Breakdown of Polymers

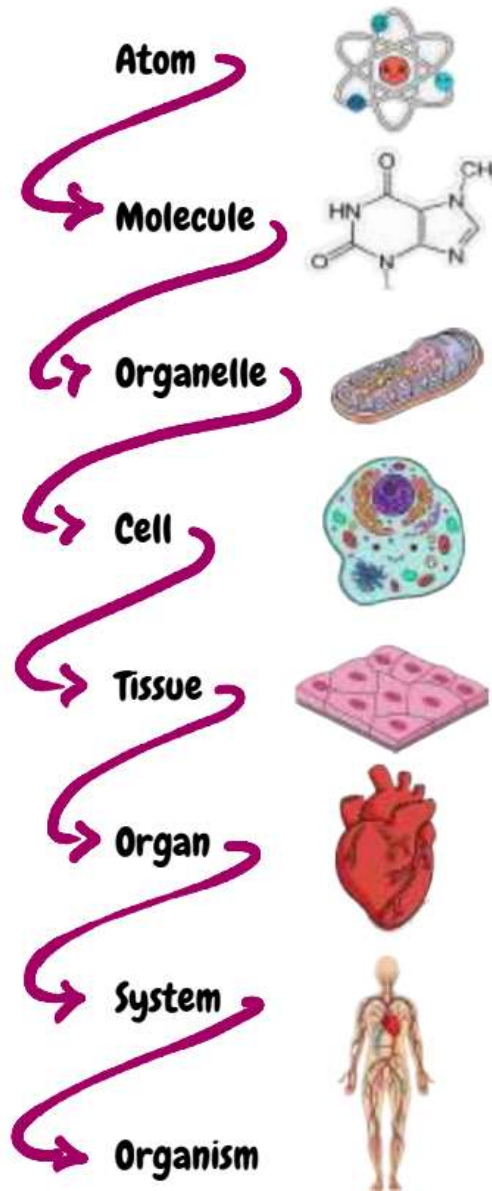
Dehydration reaction (polymerization) is a reaction in which two molecules are covalently bonded to each other with the loss of a water molecule.

Each monomer contributes part of the water molecule that is released during the reaction: One monomer provides a hydroxyl group (-OH), while the other provides a hydrogen (-H).

Hydrolysis (water breakage) is a reaction when the bond between monomers is broken by the addition of a water molecule.

A hydrogen from water attaching to one monomer and the hydroxyl group attaching to the other

▶ Number of H₂O molecules = number of links
The number of links in a polymer = The number of monomers - 1



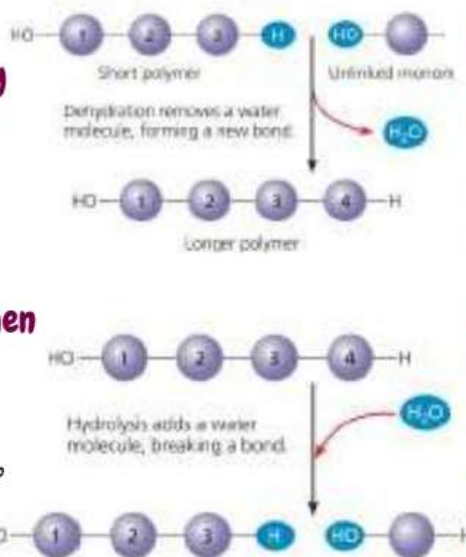
- 1-Mono-uni-one
- 2-Di-Bi-two
- 3-Tri-three
- 4-Tetra-four
- 5-Penta-five
- 6-Hexa-six
- 7-Hepta-seven
- 8-Octa-eight

Vitamins are Micro molecule. The body needs macro molecules more than its need for micro molecule.

Types of chemical bonds :-

1. Hydrophobic (weak, in a small space)
2. Ionic (losing or gaining electrons)
3. Hydrogen bond (dissolving in water)
4. Covalent (sharing electrons, it can be polar or nonpolar)

مفیش وقت للأخبار دأكر
وانت بصيغ



Dehydration reactions and hydrolysis can also be involved in the formation and breakdown of molecules that are not polymers, such as some lipids.

The difference in monomers makes difference in polymers. Each cell has thousands of different macromolecules. Macromolecules vary among cells of an organism, vary more within a species, and vary even more between species. An immense variety of polymers can be built from a small set of monomers.

Carbohydrates serve as fuel and building material

1) Monosaccharide

The simplest carbohydrates (Single sugars)

Molecular formulas $(CH_2O)_x$

Difference between monosaccharides:

-Location of the carbonyl group

Aldoses (Aldehyde Sugars)

Carbonyl group at end of carbon skeleton

Ketoses (Ketone Sugars)

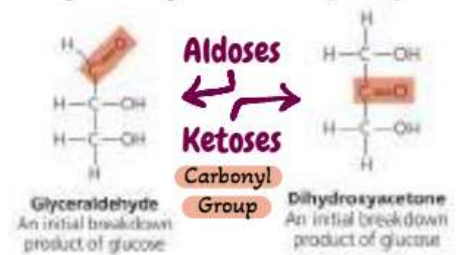
Carbonyl group within carbon skeleton

-Length of the carbon skeleton:

1) Trioses: three-carbon sugars $(C_3H_6O_3)_x$

A) Glyceraldehyde

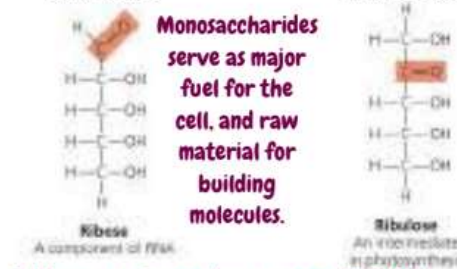
B) Dihydroxyacetone



2) Pentoses: five-carbon sugars $(C_5H_{10}O_5)_x$

A) Ribose.

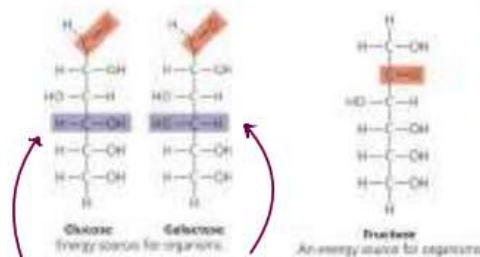
B) Ribulose



3) Hexoses: six-carbon sugars $(C_6H_{12}O_6)_x$

A) Glucose B) Galactose

C) Fructose



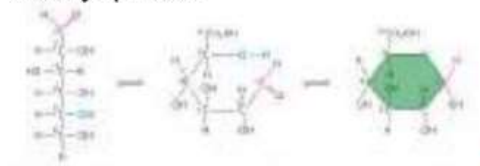
-The arrangement of different atoms

(Isomers)

Molecules that have the same molecular formula but different structural formulas

-The Linear and Ring forms.

Monosaccharides change from linear form into ring form when they're put in water.



Chitin, Structural Polysaccharides used by arthropods

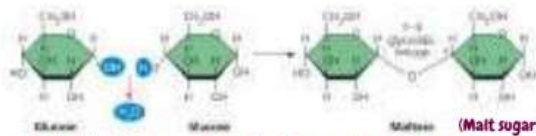
An exoskeleton is a hard case that surrounds the soft parts of an animal. Made up of chitin embedded in a layer of proteins, the case is leathery and flexible at first, but becomes hardened when the proteins are chemically linked to each other. Chitin is also found in fungi, which use this polysaccharide rather than cellulose as the building material for their cell walls. Chitin is similar to cellulose, with β linkages, except that the glucose monomer of chitin has a nitrogen containing attachment.

2) Disaccharide

A disaccharide consists of two monosaccharides joined by a glycosidic linkage, a covalent bond formed between two monosaccharides by a dehydration reaction.

Difference between Disaccharides:

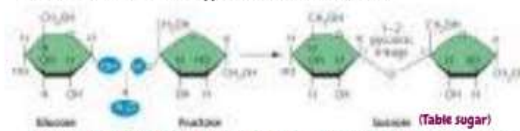
-Disaccharides differ according to the monosaccharides that build them



Dehydration reaction in the synthesis of maltose.

The bonding of two glucose units forms maltose. The 1-4 glycosidic linkage joins the number 1 carbon of one glucose to the number 4 carbon of the second glucose.

Joining the glucose monomers in a different way would result in a different disaccharide.



Dehydration reaction in the synthesis of sucrose.

Sucrose is a disaccharide formed from glucose and fructose. Notice that fructose forms a five-sided ring, though it is a hexose like glucose.

Plants generally transport carbohydrates from leaves to roots and other nonphotosynthetic organs in the form of sucrose.

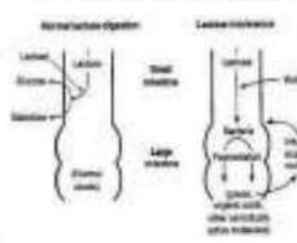
Lactose, the sugar present in milk (disaccharide).

Lactose forms when glucose molecule joined to a galactose molecule.

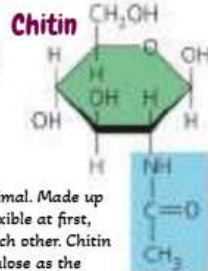
Disaccharides must be broken down into monosaccharides to be used for energy by organisms.



Lactose intolerance is a common condition in humans who lack lactase, the enzyme that breaks down lactose. The sugar is instead broken down by intestinal bacteria, causing formation of gas and subsequent cramping. The problem may be avoided by taking the enzyme lactase when eating or drinking dairy products or consuming dairy products that have already been treated with lactase to break down the lactose.



Almost all animals, including humans, do not digest cellulose. Some microorganisms can digest cellulose, breaking it down into glucose monomers. A cow harbors cellulose digesting prokaryotes and protists in its gut. These microbes hydrolyze the cellulose of hay and grass and convert the glucose to other compounds that nourish the cow. Similarly, a termite, which is unable to digest cellulose by itself, has prokaryotes or protists living in its gut that can make a meal of wood. Some fungi can also digest cellulose in soil and elsewhere.



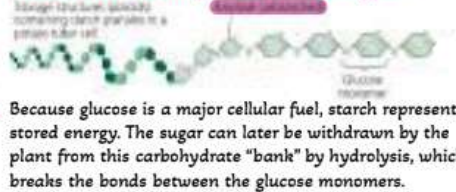
3) Polysaccharide

Polysaccharides are macromolecules, polymers with a few hundred to a few thousand monosaccharides joined by glycosidic linkages

The architecture and function of a polysaccharide are determined by its sugar monomers and by the positions of its glycosidic linkages.

Storage Polysaccharides

Starch stored in plant cells (2 types)



Glycogen stored in muscle cells

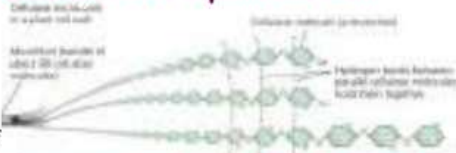


Vertebrates (animals) store glycogen mainly in liver and muscle cells. The extensively branched structure of glycogen fits its function: More free ends are available for hydrolysis. This stored fuel cannot sustain an animal for long. In humans glycogen stores are depleted in about a day. This is an issue of concern in low-carbohydrate diets, which can result in weakness and fatigue.

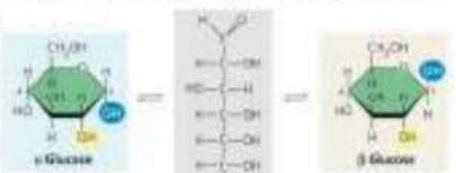
Most of the glucose monomers in starch are joined by 1-4 linkages (like maltose). The simplest form of starch, amylose, is unbranched. Amylopectin and glycogen are branched polymers with 1-6 linkages at the branch points.

Structural Polysaccharides

Cellulose fibers in plant cell walls



Cellulose is a polymer of glucose with 1-4 glycosidic linkages, but the linkages in these two polymers differ.



In cellulose the upside down beta glucose makes the structure stronger and helps to build hydrogen bond between each strand for more stronger material.

In starch the Alfa glucose is weaker than beta so it function its need, the need of easy access for energy and easier breakdown.

Enzymes that digest starch by hydrolyzing its α linkages are unable to hydrolyze the β linkages of cellulose due to the different shapes of these two molecules. Cellulose abrades the wall of the digestive tract and stimulates the lining to secrete mucus, which aids in the smooth passage of food through the tract. So cellulose is not a nutrient for humans, but it is an important part of a healthful diet.

Lipids hydrophobic

1) Fats The major function of fats is energy storage.

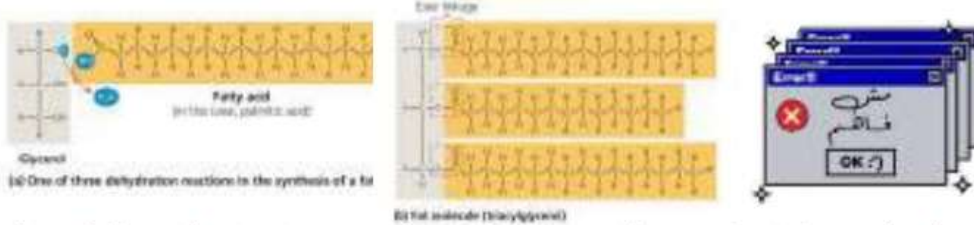
Fats are large molecules assembled from smaller molecules by dehydration reactions

A fat is constructed from two kinds of smaller molecules: glycerol and fatty acids

Glycerol is an alcohol; each of its three carbons bears a hydroxyl group

Fatty acid has a long carbon skeleton, usually 16 or 18 carbon atoms in length. The carbon at one end of the skeleton is part of a carboxyl group, the functional group that gives these molecules the name fatty acid.

The rest of the skeleton consists of a hydrocarbon chain. The relatively nonpolar C - H bonds in the hydrocarbon chains of fatty acids are the reason fats are hydrophobic.



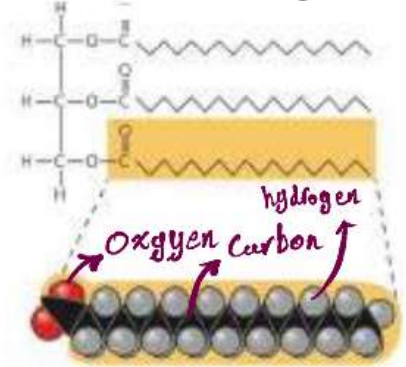
Three fatty acid molecules are each joined to glycerol by an ester linkage, a bond formed by a dehydration reaction between a hydroxyl group and a carboxyl group. The resulting fat, also called a triacylglycerol (triglyceride).

Three water molecules are produced by dehydration reaction & three ester bonds is formed.

A fat made from saturated fatty acids is called a saturated fat. Most animal fats are saturated. The hydrocarbon chains of their fatty acid (tails) lack double bonds, and their flexibility allows the fat molecules to pack together tightly. Saturated fats are solid at room temperature. The fats of plants and fishes are generally unsaturated, meaning that they are built of one or more unsaturated fatty acids. Usually liquid at room temperature, plant and fish fats are referred to as oils. The kinks where the cis double bonds are located prevent the molecules from packing together closely enough to solidify at room temperature. Hydrogenated vegetable oils means that unsaturated fats have been synthetically converted to saturated fats by adding hydrogen, allowing them to solidify.

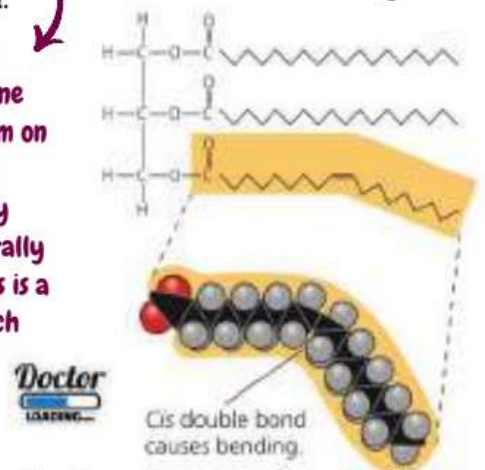
There is one or more double bonds, with one fewer hydrogen atom on each double bonded carbon. Nearly every double bond in naturally occurring fatty acids is a cis double bond, which creates a kink in the hydrocarbon chain wherever it occurs.

Saturated fatty acid



There are no double bonds between carbon atoms composing a chain. As many hydrogen atoms as possible are bonded to the carbon skeleton. Such a structure is said to be saturated with hydrogen

Unsaturated fatty acid



A diet rich in saturated fats is one of several factors that may contribute to the cardiovascular disease known as atherosclerosis. In this condition, deposits called plaques develop within the walls of blood vessels, causing inward bulges that impede blood flow and reduce the resilience of the vessels. The process of hydrogenating vegetable oils produces unsaturated fats with trans double bonds.

Trans fats can contribute to coronary heart disease. The hydrocarbon chains of fats are similar to gasoline molecules and just as rich in energy. A gram of fat stores more than twice as much energy as a gram of a polysaccharide. Humans and other mammals stock their long-term food reserves in adipose cells, which swell and shrink as fat is deposited and withdrawn from storage. In addition to storing energy, adipose tissue also cushions such vital organs as the kidneys, and a layer of fat beneath the skin insulates the body.

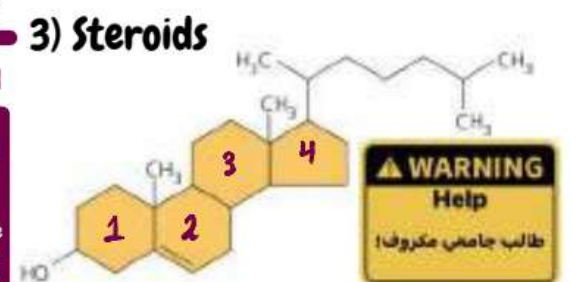
2) Phospholipids أنا بروع الجامعة بمخسر علامات وصحة وفلوس وحسنات ورجع 3) Steroids

Phospholipids are essential for cells because they are major constituents of cell membranes.

(a) Structural formula (b) Space-filling model (c) Phospholipid symbol (d) Phospholipid bilayer

The two ends of phospholipids show different behaviors with respect to water. The hydrocarbon tails are hydrophobic and are excluded from water. However, the phosphate group and its attachments form a hydrophilic head that has an affinity for water. When phospholipids are added to water, they self-assemble into a double-layered sheet called a "bilayer" that shields their hydrophobic fatty acid tails from water.

At the surface of a cell, phospholipids are arranged in a similar bilayer. The hydrophilic heads of the molecules are on the outside of the bilayer, in contact with the aqueous solutions inside and outside of the cell. The hydrophobic tails point toward the interior of the bilayer, away from the water. The phospholipid bilayer forms a boundary between the cell and its external environment and establishes separate compartments within eukaryotic cells; in fact, the existence of cells depends on the properties of phospholipids.



Steroids are lipids characterized by a carbon skeleton consisting of four fused rings. Different steroids are distinguished by the particular chemical groups attached to this ensemble of rings. Cholesterol, a type of steroid, is a crucial molecule in animals. It is a common component of animal cell membranes and is also the precursor from which other steroids, such as the vertebrate sex hormones, are synthesized. In vertebrates, cholesterol is synthesized in the liver and is also obtained from the diet. A high level of cholesterol in the blood may contribute to atherosclerosis.

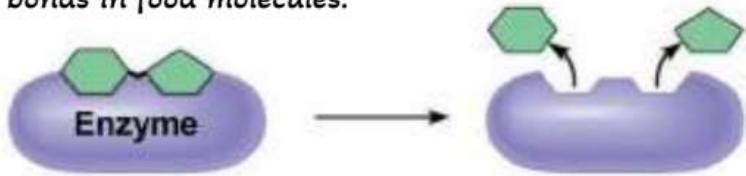
Proteins account for more than 50% of the dry mass of most cells

Enzymes are a type of protein that acts as a catalyst to speed up chemical reactions. Enzymes can perform their functions repeatedly, functioning as workhorses that carry out the processes of life.

Functions of proteins

-Enzymatic proteins

Function: Selective acceleration of chemical reactions
Example: Digestive enzymes catalyze the hydrolysis of bonds in food molecules.



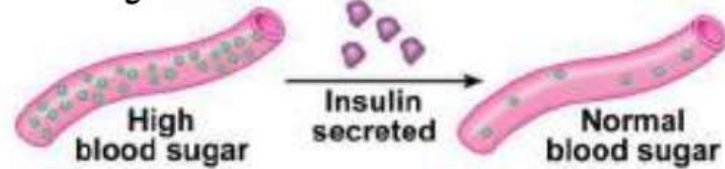
-Storage proteins

Function: Storage of amino acids
Examples: Casein, the protein of milk, is the major source of amino acids for baby mammals. Plants have storage proteins in their seeds. Ovalbumin is the protein of egg white, used as an amino acid source for the developing embryo.



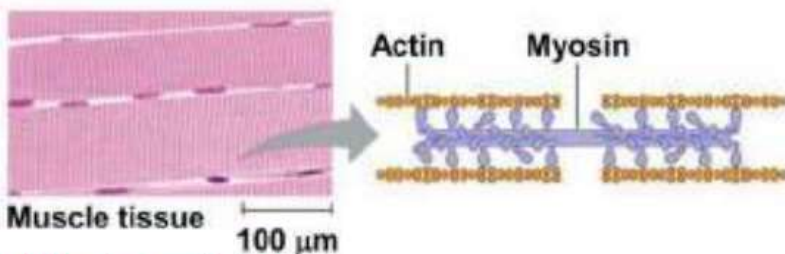
-Hormonal proteins

Function: Coordination of an organism's activities
Example: Insulin, a hormone secreted by the pancreas, causes other tissues to take up glucose, thus regulating blood sugar concentration.



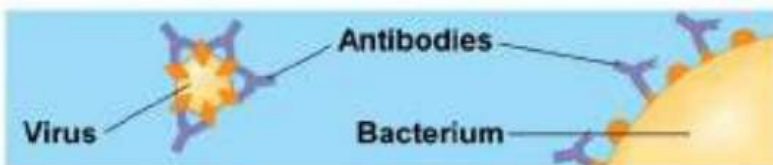
-Contractile and motor proteins

Function: Movement
Examples: Motor proteins are responsible for the undulations of cilia and flagella. Actin and myosin proteins are responsible for the contraction of muscles.



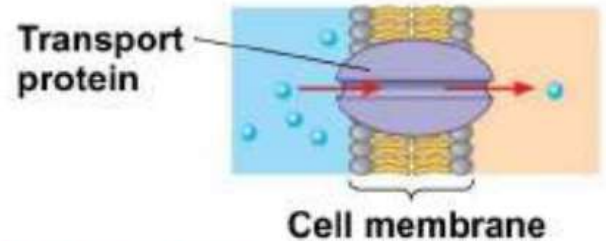
-Defensive proteins

Function: Protection against disease
Example: Antibodies inactivate and help destroy viruses and bacteria.



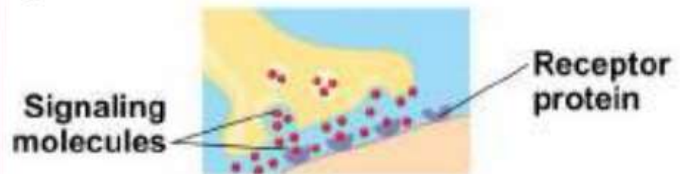
-Transport proteins

Function: Transport of substances
Examples: Hemoglobin, the iron-containing protein of vertebrate blood, transports oxygen from the lungs to other parts of the body. Other proteins transport molecules across membranes, as shown here.



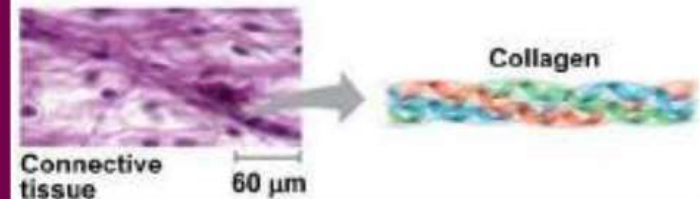
-Receptor proteins

Function: Response of cell to chemical stimuli
Example: Receptors built into the membrane of a nerve cell detect signaling molecules released by other nerve cells.



-Structural proteins

Function: Support
Examples: Keratin is the protein of hair, horns, feathers, and other skin appendages. Insects and spiders use silk fibers to make their cocoons and webs, respectively. Collagen and elastin proteins provide a fibrous framework in animal connective tissues.

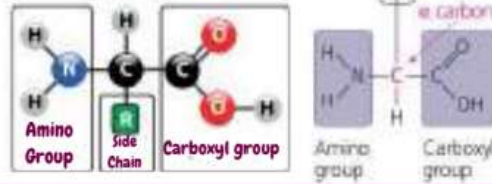


Proteins are all constructed from the same set of 20 amino acids, linked in unbranched polymers. The bond between amino acids is called a peptide bond, so a polymer of amino acids is called a polypeptide. A protein is a biologically functional molecule made up of one or more polypeptides, each folded and coiled into a specific three-dimensional structure. A human has tens of thousands of different proteins, each with a specific structure and function; proteins, in fact, are the most structurally sophisticated molecules known.

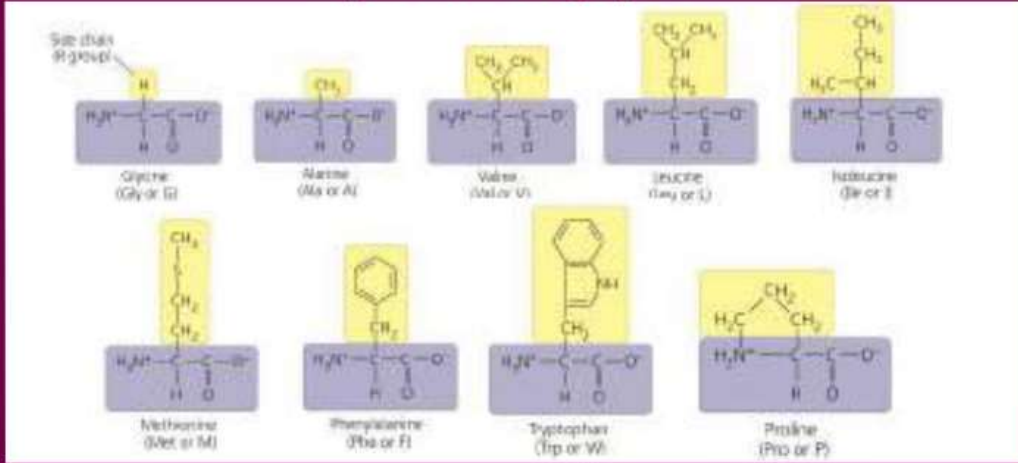
Amino Acid Monomers

An amino acid is an organic molecule with both an amino group and a carboxyl group.

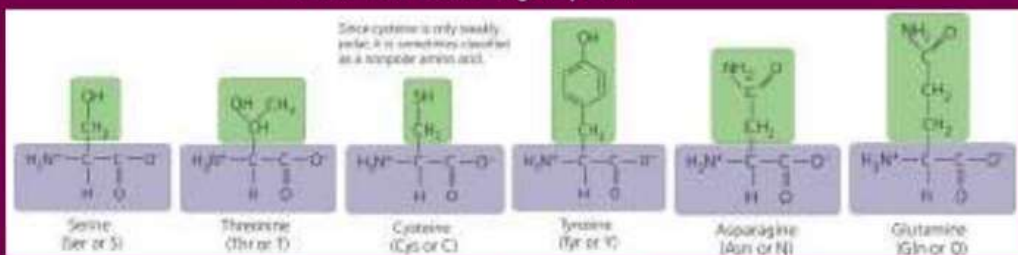
At the center of the amino acid is an asymmetric carbon atom called the alpha (α) carbon. Its four different partners are an amino group, a carboxyl group, a hydrogen atom, and a variable group symbolized by R. The R group, also called the side chain, differs with each amino acid.



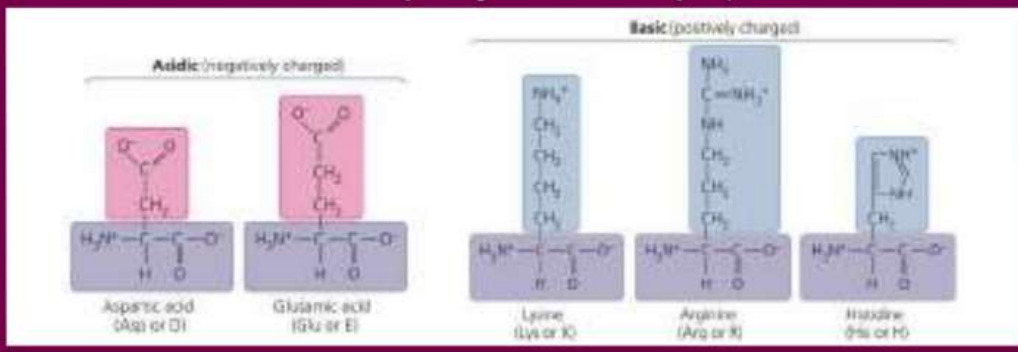
Nonpolar side chains (Hydrophobic)



Polar side chains (Hydrophilic)



Electrically charged side chains (Hydrophilic)



Protein Structure and Function

A functional protein is not just a polypeptide chain, but one or more polypeptides precisely twisted, folded, and coiled into a molecule of unique shape.

It is the amino acid sequence of each polypeptide that determines what three-dimensional structure the protein will have under normal cellular conditions.

A protein's structure determines its function.

Many proteins are roughly spherical (globular proteins), while others are shaped like long fibers (fibrous proteins).



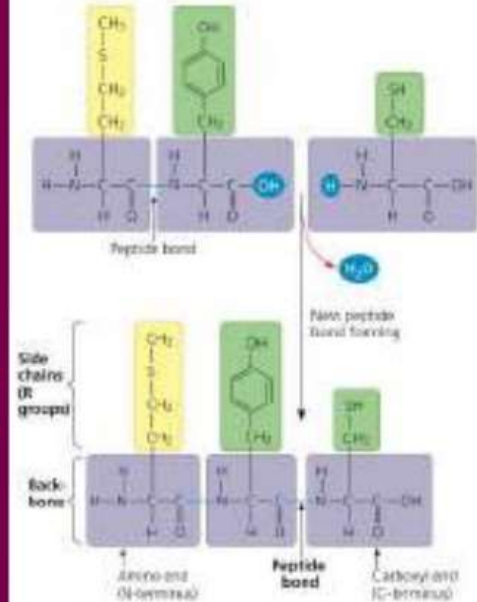
The function of a protein depends on its ability to recognize and bind to some other molecule. In an especially striking example of the marriage of form and function. When a cell synthesizes a polypeptide, the chain may fold spontaneously, assuming the functional structure for that protein. This folding is driven and reinforced by the formation of various bonds between parts of the chain, depending on the sequence of amino acids.

Polypeptides

(Amino Acid Polymers)

When two amino acids are positioned so that the carboxyl group of one is adjacent to the amino group of the other, they can become joined by a dehydration reaction, with the removal of a water molecule.

Polypeptides range in length from a few amino acids to 1,000 or more.



The chemical nature of the molecule as a whole is determined by the kind and sequence of the side chains, which determine how a polypeptide folds and thus its final shape and chemical characteristics.

Primary Structure
 Linear chain of amino acids

Secondary Structure
 Regions stabilized by hydrogen bonds between atoms of the polypeptide backbone

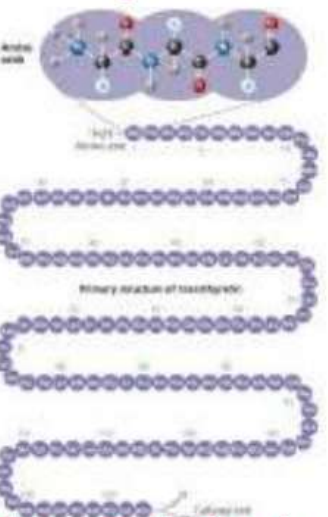
Tertiary Structure
 Three-dimensional shape stabilized by interactions between side chains (Protein)

Quaternary Structure
 Association of two or more polypeptides (some proteins only)



Four Levels of Protein Structure

Primary Structure Secondary Structure Tertiary Structure Quaternary Structure



The primary structure of a protein is its sequence of amino acids.

Transthyretin is a globular blood protein that transports vitamin A and one of the thyroid hormones throughout the body. Transthyretin is made up of four identical polypeptide chains, each composed of 127 amino acids. Each of the 127 positions along the chain is occupied by one of the 20 amino acids. The primary structure is like the order of letters in a very long word. The precise primary structure of a protein is determined not by the random linking of amino acids, but by inherited genetic information. The primary structure in turn dictates secondary and tertiary structure, due to the chemical nature of the backbone and the side chains (R groups) of the amino acids along the polypeptide.

Sickle-Cell Disease

Even a slight change in primary structure can affect a protein's shape and ability to function. Sickle-cell disease, an inherited blood disorder, is caused by the substitution of one amino acid (valine) for the normal one (glutamic acid) at the position of the sixth amino acid in the primary structure of hemoglobin, the protein that carries oxygen in red blood cells. Normal red blood cells are disk-shaped, but in sickle-cell disease, the abnormal hemoglobin molecules tend to aggregate into chains, deforming some of the cells into a sickle shape. A person with the disease has periodic "sickle-cell crises" when the angular cells clog tiny blood vessels, impeding blood flow. The toll taken on such patients is a dramatic example of how a simple change in protein structure can have devastating effects on protein function.

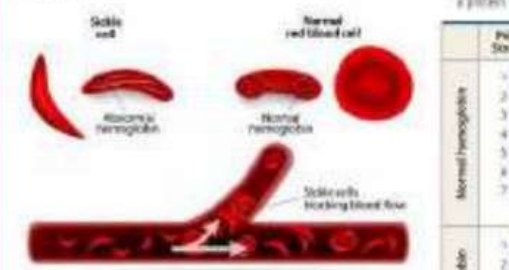


Most proteins have segments of their polypeptide chains repeatedly coiled or folded in patterns that contribute to the protein's overall shape.

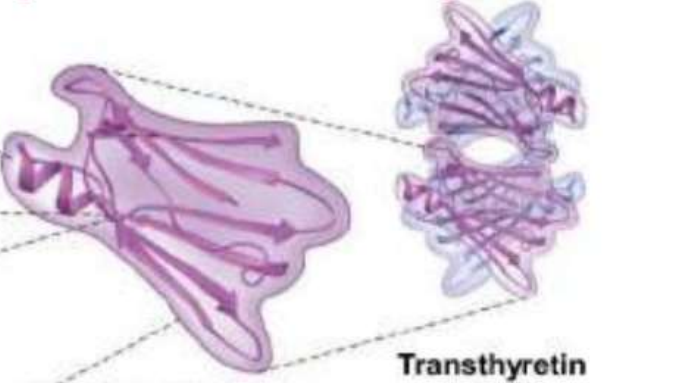
Secondary structure are the result of hydrogen bonds between the repeating constituents of the polypeptide backbone (not the amino acid side chains). Within the backbone, the oxygen atoms have a partial negative charge (-), and the hydrogen atoms attached to the nitrogens have a partial positive charge (+), hydrogen bonds can form between these atoms. Hydrogen bonds are weak, but because they are repeated many times over a relatively long region of the polypeptide chain, they can support a particular shape for that part of the protein.

α helix, a delicate coil held together by hydrogen bonding between every fourth amino acid (1-4/2-5/3-7/4-8/...). Each transthyretin polypeptide has only one α helix region, other globular proteins have multiple stretches of α helix separated by nonhelical regions. Some fibrous proteins, such as α-keratin, the structural protein of hair, have the α helix formation over most of their length.

β pleated sheet. In this structure two or more segments of the polypeptide chain lying side by side (called β strands) are connected by hydrogen bonds between parts of the two parallel segments of polypeptide backbone. β pleated sheets make up the core of many globular proteins, and dominate some fibrous proteins, including the silk protein of a spider's web. The teamwork of so many hydrogen bonds makes each spider silk fiber stronger than a steel strand of the same weight.



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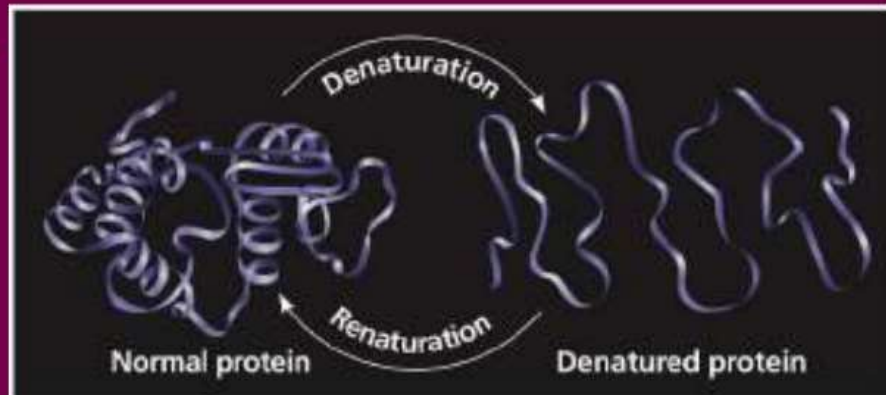
Secondary structure involves interactions between backbone constituents. tertiary structure is the overall shape of a polypeptide resulting from interactions between the side chains (R groups) of the various amino acids.

One type of interaction that contributes to tertiary structure is a hydrophobic interaction. As a polypeptide folds into its functional shape, amino acids with hydrophobic (nonpolar) side chains usually end up in clusters at the core of the protein, out of contact with water. Hydrophobic interaction is actually caused by the exclusion of nonpolar substances by water molecules. Once nonpolar amino acid side chains are close together, van der Waals interactions help hold them together. Hydrogen bonds between polar side chains and ionic bonds between positively and negatively charged side chains also help stabilize tertiary structure. These are all weak interactions in the aqueous cellular environment, but their cumulative effect helps give the protein a unique shape. Covalent bonds called disulfide bridges may further reinforce the shape of a protein. Disulfide bridges form where two cysteine monomers, which have sulfhydryl groups (SH) on their side chains are brought close together by the folding of the protein. All of these different kinds of interactions can contribute to the tertiary structure of a protein.



	Primary Structure	Secondary and Tertiary Structures	Quaternary Structure	Function	Red Blood Cell Shape
Normal hemoglobin	Linear sequence of amino acids	Normal α subunit	Normal hemoglobin	Normal hemoglobin carries oxygen (it associates with one another, each carries oxygen)	Normal red blood cell with biconcave hemoglobin proteins
Sickle-cell hemoglobin	Linear sequence of amino acids	Sickle-cell β subunit	Sickle-cell hemoglobin	Hydrophobic interactions between sickle-cell hemoglobin proteins lead to their aggregation into a fiber, causing the red blood cell to become rigid and sticky	Fibers of sickle-cell hemoglobin deform red blood cell into sickle shape

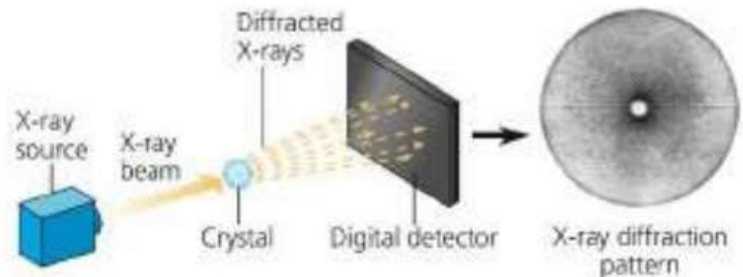
A polypeptide chain of a given amino acid sequence can be arranged into a three-dimensional shape determined by the interactions responsible for secondary and tertiary structure. This folding normally occurs as the protein is being synthesized in the crowded environment within a cell, aided by other proteins. However, protein structure also depends on the physical and chemical conditions of the protein's environment. If the pH, salt concentration, temperature, or other aspects of its environment are altered, the weak chemical bonds and interactions within a protein may be destroyed, causing the protein to unravel and lose its native shape, a change called denaturation. Because it is misshapen, the denatured protein is biologically inactive. Most proteins become denatured if they are transferred from an aqueous environment to a nonpolar solvent, the polypeptide chain refolds so that its hydrophobic regions face outward toward the solvent. Other denaturation agents include chemicals that disrupt the hydrogen bonds, ionic bonds, and disulfide bridges that maintain a protein's shape. Denaturation can also result from excessive heat, which agitates the polypeptide chain enough to overpower the weak interactions that stabilize the structure. The white of an egg becomes This also explains why excessively high fevers can be fatal: Proteins in the blood tend to denature at very high body temperatures. When a protein in a test-tube solution has been denatured by heat or chemicals, it can sometimes return to its functional shape when the denaturing agent is removed. (Sometimes this is not possible: For example, a fried egg will not become liquefied when placed back into the refrigerator!) We can conclude that the information for building specific shape is intrinsic to the protein's primary structure; this is often the case for small proteins. The sequence of amino acids determines the protein's shape—where an α helix can form, where β pleated sheets can exist, where disulfide bridges are located, where ionic bonds can form, and so on.



Protein Folding in the Cell

Application Scientists use X-ray crystallography to determine the three-dimensional (3-D) structure of macromolecules such as nucleic acids and proteins.

Technique Researchers aim an X-ray beam through a crystallized protein or nucleic acid. The atoms of the crystal diffract (bend) the X-rays into an orderly array that a digital detector records as a pattern of spots called an X-ray diffraction pattern, an example of which is shown here.



Results Using data from X-ray diffraction patterns and the sequence of monomers determined by chemical methods, researchers can build a 3-D computer model of the macromolecule being studied, such as the four-subunit protein transthyretin



Biochemists now know the amino acid sequence for about 65 million proteins, with roughly 1.5 million added each month, and the three-dimensional shape for almost 35,000. Researchers have tried to correlate the primary structure of many proteins with their three-dimensional structure to discover the rules of protein folding. Unfortunately, however, the protein-folding process is not that simple. Most proteins probably go through several intermediate structures on their way to a stable shape, and looking at the mature structure does not reveal the stages of folding required to achieve that form. However, biochemists have developed methods for tracking a protein through such stages and learning more about this important process.

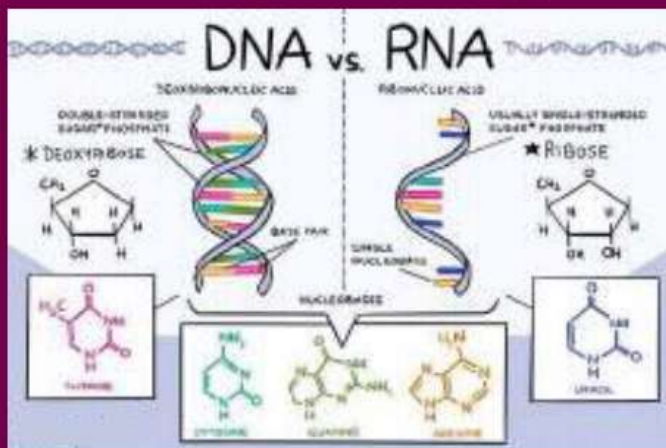
Misfolding of polypeptides in cells is a serious problem that has come under increasing scrutiny by medical researchers. Many disease such as cystic fibrosis, Alzheimer's, Parkinson's, and mad cow disease are associated with an accumulation of misfolded proteins. In fact, misfolded versions of the transthyretin protein have been implicated in several diseases, including one form of senile dementia.

Even when scientists have a correctly folded protein in hand, determining its exact three-dimensional structure is not simple, for a single protein has thousands of atoms. The method most commonly used to determine the 3-D structure of a protein is X-ray crystallography, which depends on the diffraction of an X-ray beam by the atoms of a crystallized molecule. Using this technique, scientists can build a 3-D model that shows the exact position of every atom in a protein molecule. Nuclear magnetic resonance (NMR) spectroscopy and bioinformatics are complementary approaches to understanding protein structure and function. The structure of some proteins is difficult to determine for a simple reason: A growing body of biochemical research has revealed that a significant number of proteins, or regions of proteins, do not have a distinct 3-D structure until they interact with a target protein or other molecule. Their flexibility and indefinite structure are important for their function, which may require binding with different targets at different times. These proteins, which may account for 20–30% of mammalian proteins, are called intrinsically disordered proteins and are the focus of current research.

Nucleic acids store, transmit, and help express hereditary information.

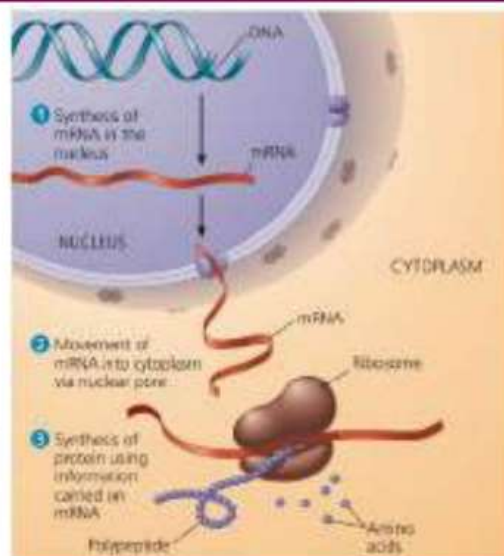
The amino acid sequence of a polypeptide is programmed by a discrete unit of inheritance known as a gene. Genes consist of DNA, which belongs to the class of compounds called nucleic acids. Nucleic acids are polymers made of monomers called nucleotides.

The two types of nucleic acids, deoxyribonucleic acid (DNA) and ribonucleic acid (RNA), enable living organisms to reproduce their complex components from one generation to the next. Unique among molecules, DNA provides directions for its own replication. DNA also directs RNA synthesis and, through RNA, controls protein synthesis (this entire process is called gene expression).



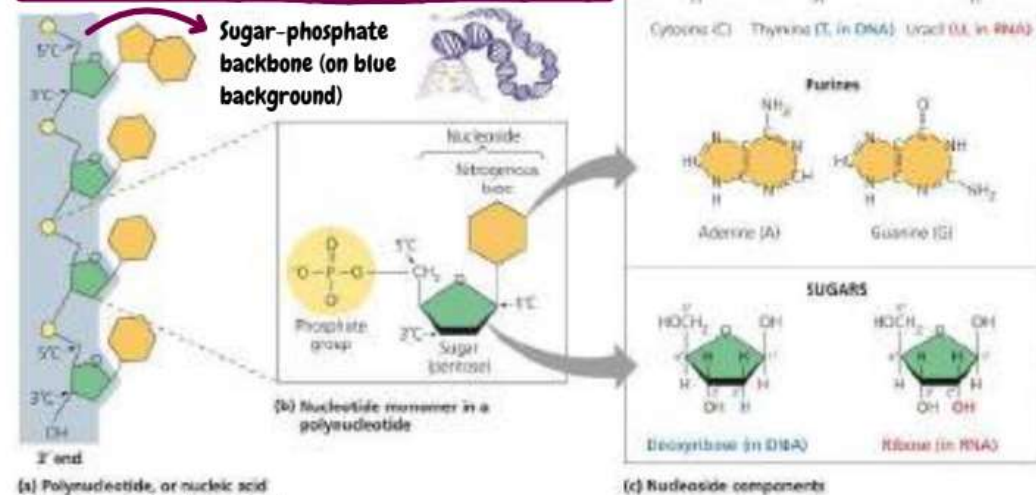
DNA is the genetic material that organisms inherit from their parents. Each chromosome contains one long DNA molecule, usually carrying several hundred or more genes. When a cell reproduces itself by dividing, its DNA molecules are copied and passed along from one generation of cells to the next. The information that programs all the cell's activities is encoded in the structure of the DNA.

A given gene along a DNA molecule can direct synthesis of a type of RNA called messenger RNA (mRNA). The mRNA molecule interacts with the cell's protein synthesizing machinery to direct production of a polypeptide, which folds into all or part of a protein. We can summarize the flow of genetic information as DNA > RNA > protein. The sites of protein synthesis are cellular structures called ribosomes. In a eukaryotic cell, ribosomes are in the cytoplasm, the region between the nucleus and the plasma membrane, the cell's outer boundary, but DNA resides in the nucleus. Messenger RNA conveys genetic instructions for building proteins from the nucleus to the cytoplasm. Prokaryotic cells lack nuclei but still use mRNA to convey a message from the DNA to ribosomes and other cellular equipment that translate the coded information into amino acid sequences.



The Components of Nucleic Acids

Nucleic acids are macromolecules that exist as polymers called polynucleotides. As indicated by the name, each polynucleotide consists of monomers called nucleotides. A nucleotide, in general, is composed of three parts: a five-carbon sugar (a pentose), a nitrogen-containing (nitrogenous) base, and one to three phosphate groups.



The beginning monomer used to build a polynucleotide has three phosphate groups, but two are lost during the polymerization process. The portion of a nucleotide without any phosphate groups is called a nucleoside. Each nitrogenous base has one or two rings that include nitrogen atoms. (They are called nitrogenous bases because the nitrogen atoms tend to take up H⁺ from solution, thus acting as bases.) There are two families of nitrogenous bases: pyrimidines and purines. A pyrimidine has one six-membered ring of carbon and nitrogen atoms. The members of the pyrimidine family are cytosine (C), thymine (T), and uracil (U). Purines are larger, with a six-membered ring fused to a five-membered ring. The purines are adenine (A) and guanine (G). The specific pyrimidines and purines differ in the chemical groups attached to the rings. Adenine, guanine, and cytosine are found in both DNA and RNA; thymine is found only in DNA and uracil only in RNA.

In DNA the sugar is deoxyribose; in RNA it is ribose. The only difference between these two sugars is that deoxyribose lacks an oxygen atom on the second carbon in the ring, hence the name deoxyribose. One to three phosphate groups is attached to the 5' carbon of the sugar. With one phosphate, this is a nucleoside monophosphate, more often called a nucleotide.

Nucleotide Polymers

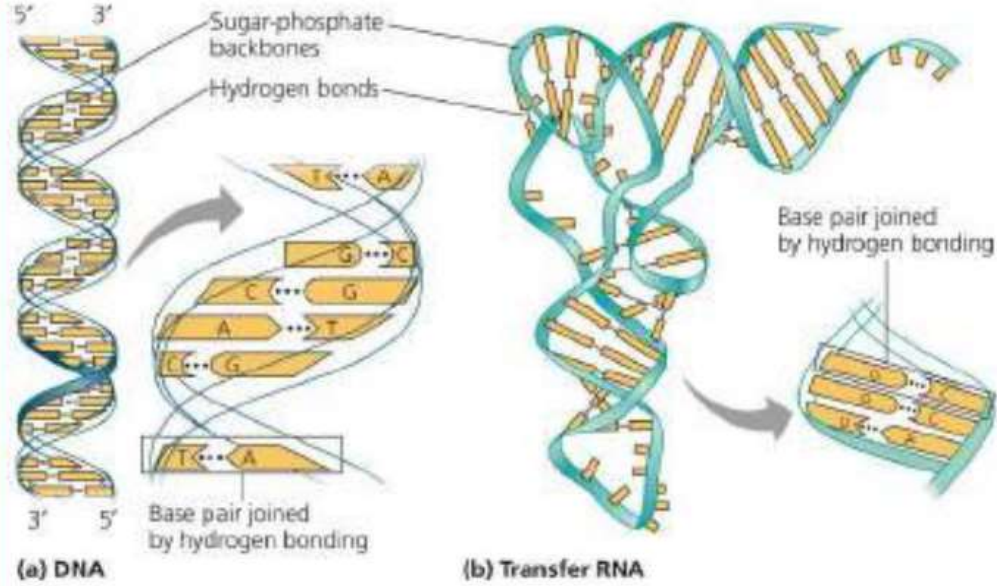
The linkage of nucleotides into a polynucleotide involves a dehydration reaction. In the polynucleotide, adjacent nucleotides are joined by a phosphodiester linkage, which consists of a phosphate group that links the sugars of two nucleotides. This bonding results in a repeating pattern of sugar-phosphate units called the sugar-phosphate backbone. The two free ends of the polymer are distinctly different from each other. One end has a phosphate attached to a 5' carbon, and the other end has a hydroxyl group on a 3' carbon, referred as the 5' end and the 3' end. Polynucleotide has a built-in directionality along its sugar-phosphate backbone, from 5' to 3'. The bases are attached all along the sugar-phosphate backbone.

The sequence of bases along a DNA (or mRNA) polymer is unique for each gene and provides very specific information to the cell. Because genes are hundreds to thousands of nucleotides long, the number of possible base sequences is effectively limitless. The information carried by the gene is encoded in its specific sequence of the four DNA bases. For example, the sequence 5'-AGGTAAGT-3' means one thing, whereas the sequence 5'-CGCTTAAAC-3' has a different meaning. (Entire genes, of course, are much longer.) The linear order of bases in a gene specifies the amino acid sequence—the primary structure—of a protein, which in turn specifies that protein's 3-D structure, thus enabling its function in the cell.

The Structures of DNA and RNA Molecules

DNA molecules have two polynucleotides, or "strands," that wind around an imaginary axis, forming a double helix. The two sugar phosphate backbones run in opposite 5' to 3' directions from each other; this arrangement is referred to as antiparallel. The sugar phosphate backbones are on the outside of the helix, and the nitrogenous bases are paired in the interior of the helix. The two strands are held together by hydrogen bonds between the paired bases. Most DNA molecules are very long, with thousands or even millions of base pairs. The one long DNA double helix in a eukaryotic chromosome includes many genes, each one a particular segment of the molecule.

In base pairing, only certain bases in the double helix are compatible with each other. Adenine (A) in one strand always pairs with thymine (T) in the other, and guanine (G) always pairs with cytosine (C). Reading the sequence of bases along one strand of the double helix would tell us the sequence of bases along the other strand. If a stretch of one strand has the base sequence 5'-AGGTCCG-3', then the base-pairing rules tell us that the same stretch of the other strand must have the sequence 3'-TCCAGGC-5'. The two strands of the double helix are complementary. It is this feature of DNA that makes it possible to generate two identical copies of each DNA molecule in a cell that is preparing to divide. When the cell divides, the copies are distributed to the daughter cells, making them genetically identical to the parent cell.



The structure of DNA accounts for its function of transmitting genetic information whenever a cell reproduces. RNA molecules exist as single strands. Complementary base pairing can occur between regions of two RNA molecules or even between two stretches of nucleotides in the same RNA molecule. In fact, base pairing within an RNA molecule allows it to take on the particular three-dimensional shape necessary for its function. The type of RNA called transfer RNA (tRNA), which brings amino acids to the ribosome during the synthesis of a polypeptide. A tRNA molecule is about 80 nucleotides in length. Its functional shape results from base pairing between nucleotides where complementary stretches of the molecule can run antiparallel to each other. In RNA, adenine (A) pairs with uracil (U); thymine (T) is not present in RNA. Another difference between RNA and DNA is that DNA almost always exists as a double helix, whereas RNA molecules are more variable in shape.

ملاحظة

هذا التلخيص يشمل المادة كاملة وانصح بدراسة الكتاب قبل الدراسة من التلخيص بشكل أساسي، هذا التلخيص اشتمل كل المعلومات المهمة والتي تمكن الطالب من الحصول على العلامة الكاملة في الإمتحان، لقد استنيت الأمثلة والمعلومات الغير مهمة للطالب، ويمكن لأي طالب الإعتداد على هذا التلخيص بشكل كامل ولكن انصح بالاطلاع على الكتاب ولو مرة واحدة.

سوف استمر بعمل التلاخيص لمراد الطب الأساسية، ولكن مثل هذا التلخيص استهلك من وقتي اسبوعا كاملا من تجميع المعلومات والتفريغ والتلخيص والترتيب، وأحب أن اشارك هذا المجهود مع طلاب الطب في المملكة كاملة، ولأن هذا المجهود سوف يقتصر على جميع مواد الطب فسوف اجمع تالاخيصي كاملة بعد الإنتهاء من كل مادة في دوريات للأجيال القادمة، ولكن في الوقت الحالي سوف انشر تالاخيصي بشكل مجاني، وفي المستقبل بعد جمع مجموعة من التلاخيص وتحويلها لدوريات سوف اتم نشرها باسعار زهيدة في جميع أنحاء الاردن حتى يتمكن من الأستمرار في هذا المجهود. سوف اسمي هذه التلاخيص **تالاخيص الفرائشة للطب**.

وتوجد مجموعة خاصة لهذه التلاخيص لجميع طلاب الطب في المملكة، وسوف انشر تالاخيصي بشكل اساسي في هذه المجموعة حينما اتمها.
رابط المجموعة:



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