B.sc. Biochemistry (UG-sem 2)

Eukaryotic cell- An Introduction

By

Dr M. Iqbal Rather

Date: 02-05-18

Diagram of a typical animal cell

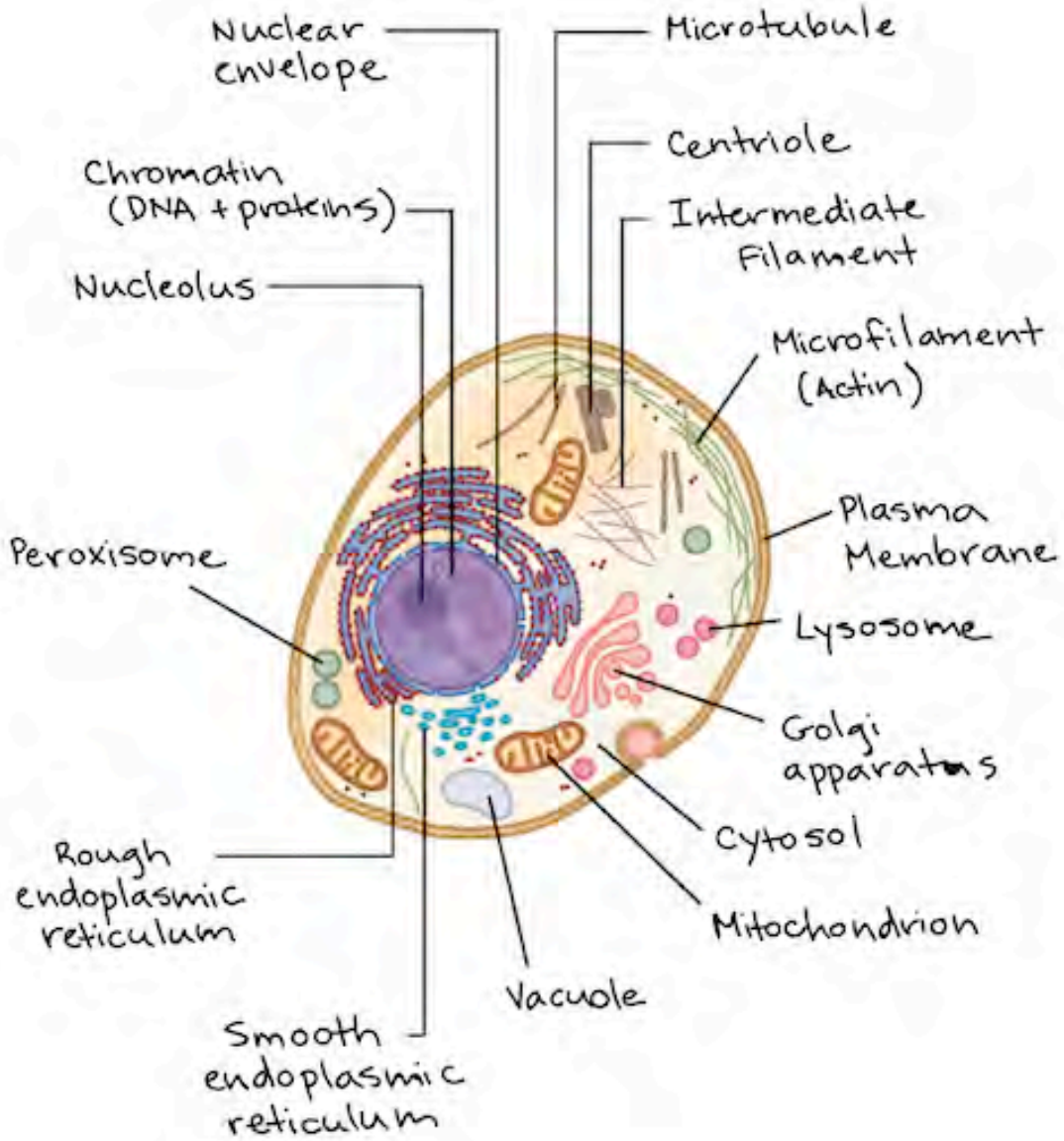
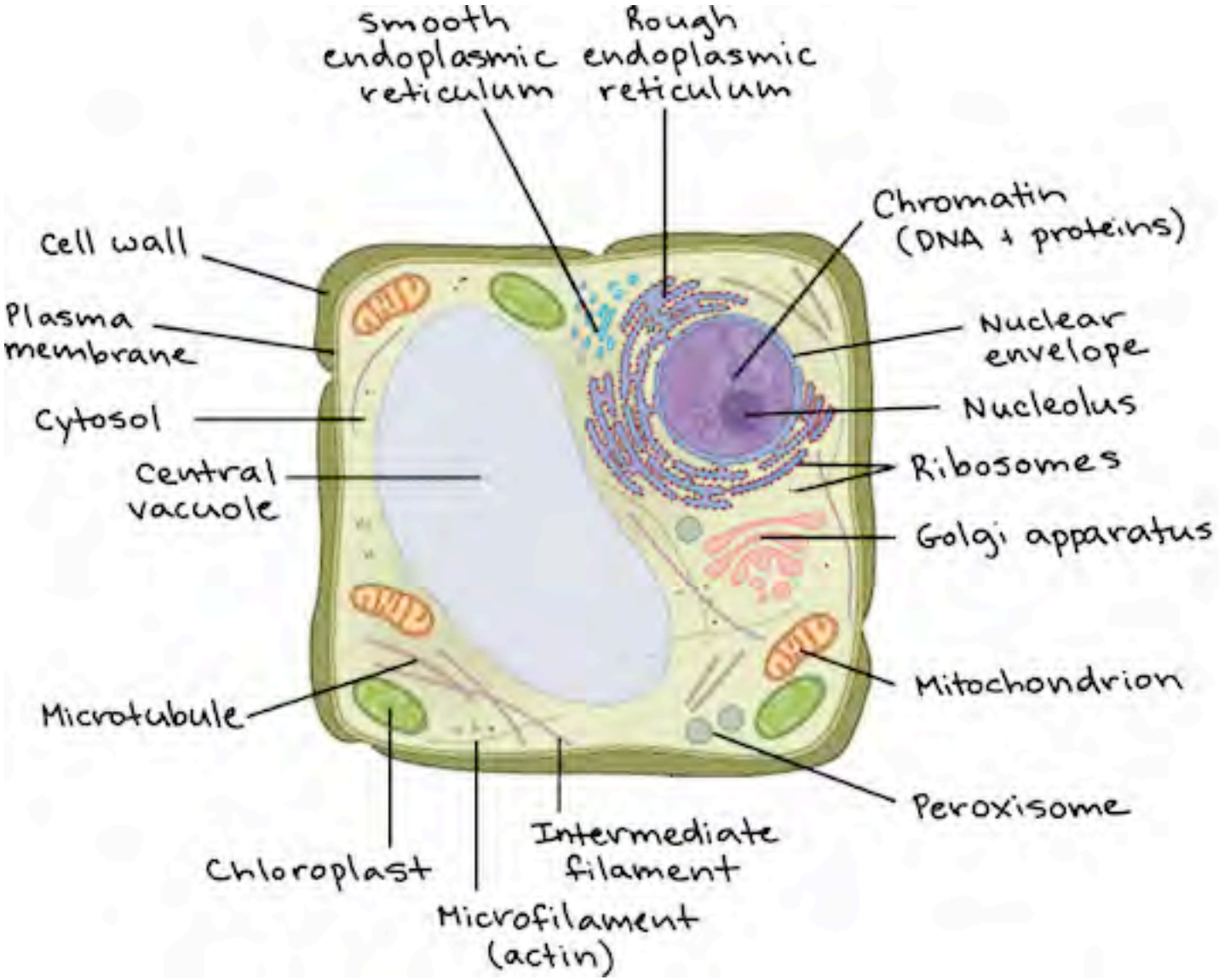
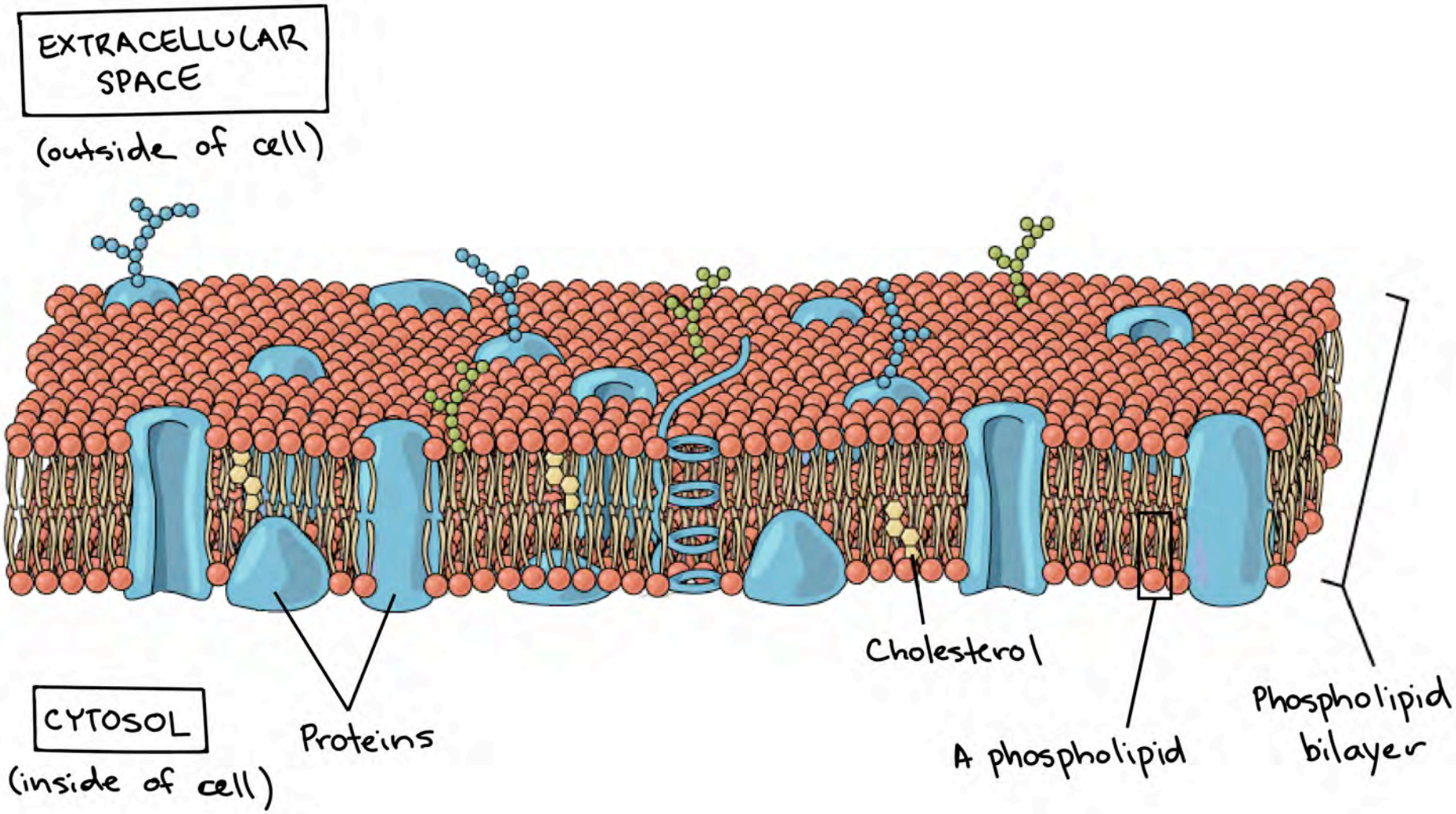


Diagram of a typical plant cell



Structure of Cell Membrane



The Cytoplasm

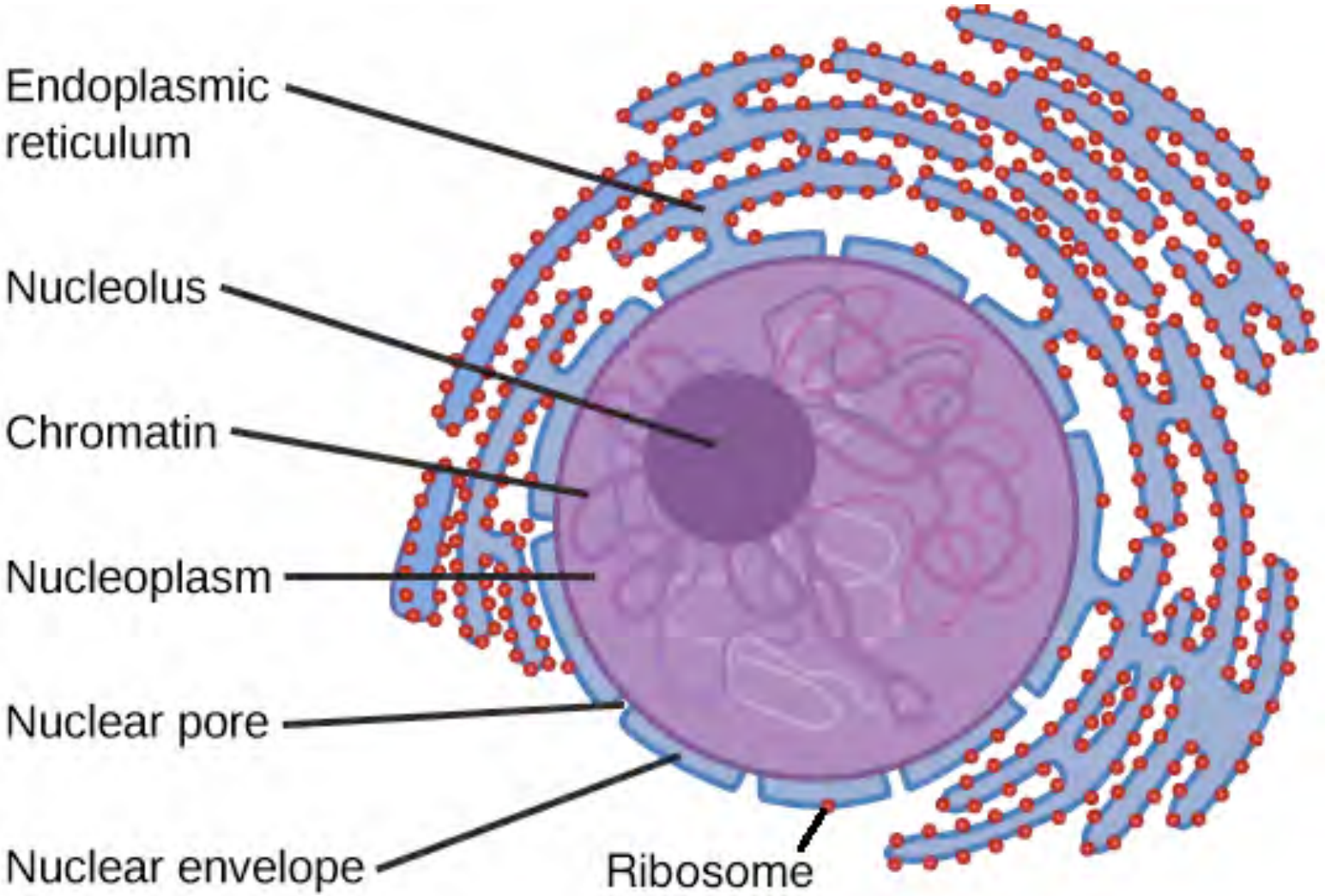
Cytoplasm of a eukaryotic cell consists not only of cytosol—a gel-like substance made up of water, ions, and macromolecules—but also of organelles and the structural proteins that make up the cytoskeleton, or "skeleton of the cell."

In eukaryotic cells, which have a nucleus, the cytoplasm is everything between the plasma membrane and the nuclear envelope. In prokaryotes, which lack a nucleus, cytoplasm simply means everything found inside the plasma membrane.

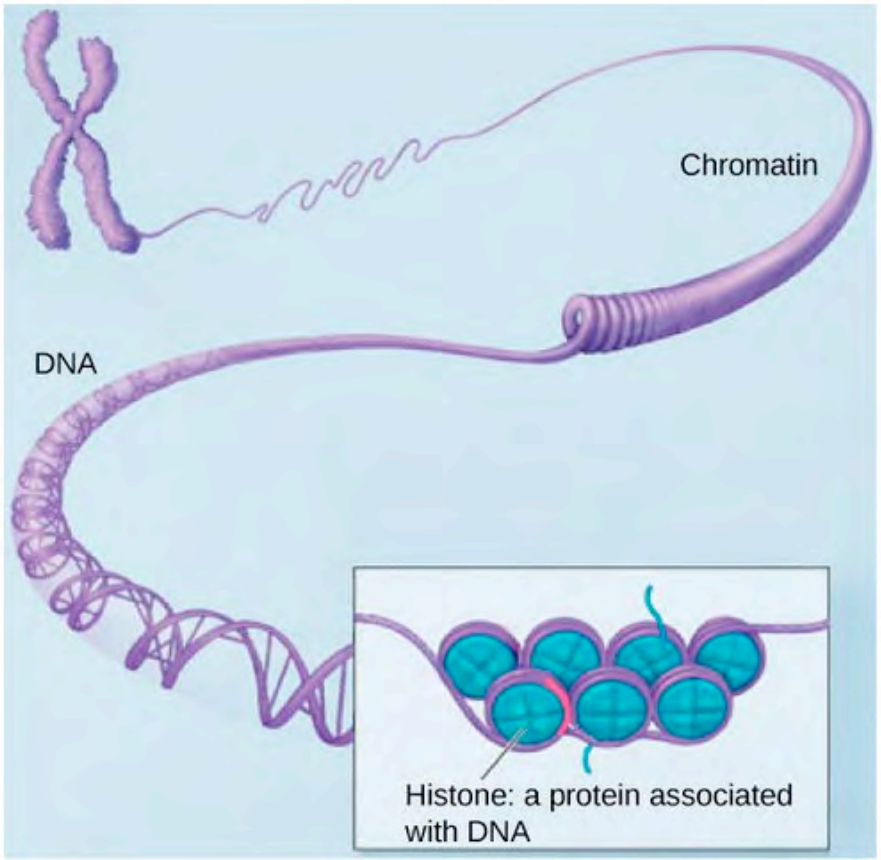
Cytoplasm Continue…..

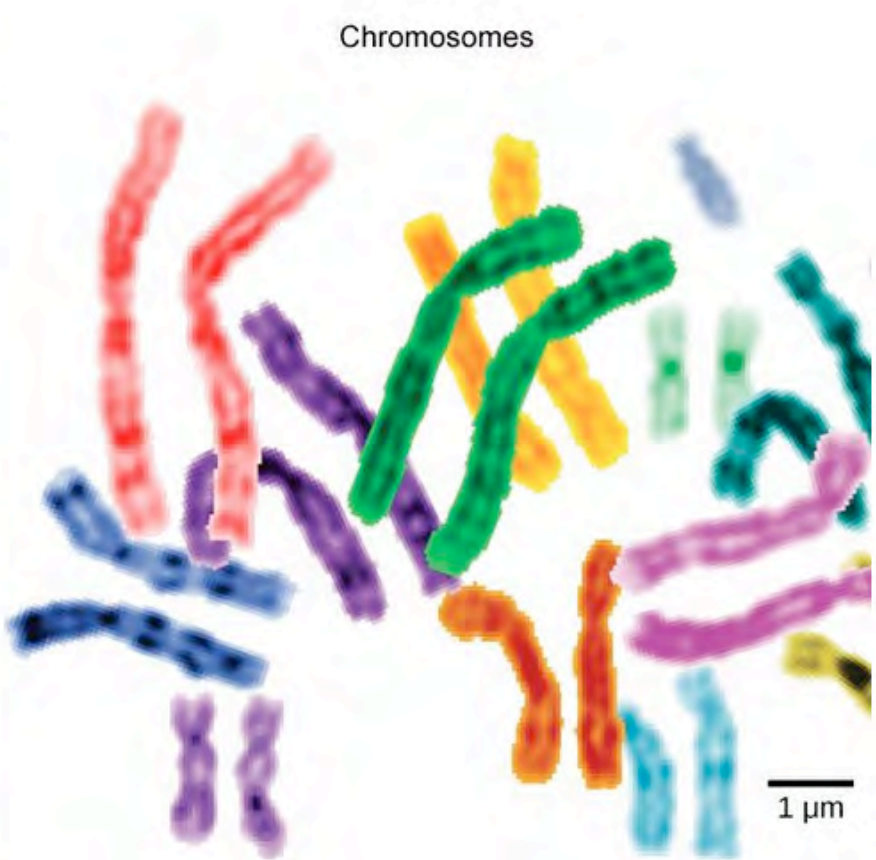
The cytosol contains a rich broth of macromolecules and smaller organic molecules, including glucose and other simple sugars, polysaccharides, amino acids, nucleic acids, and fatty acids. Ions of sodium, potassium, calcium, and other elements are also found in the cytosol. Many metabolic reactions, including protein synthesis, take place in this part of the cell.

Nucleus and Ribosomes

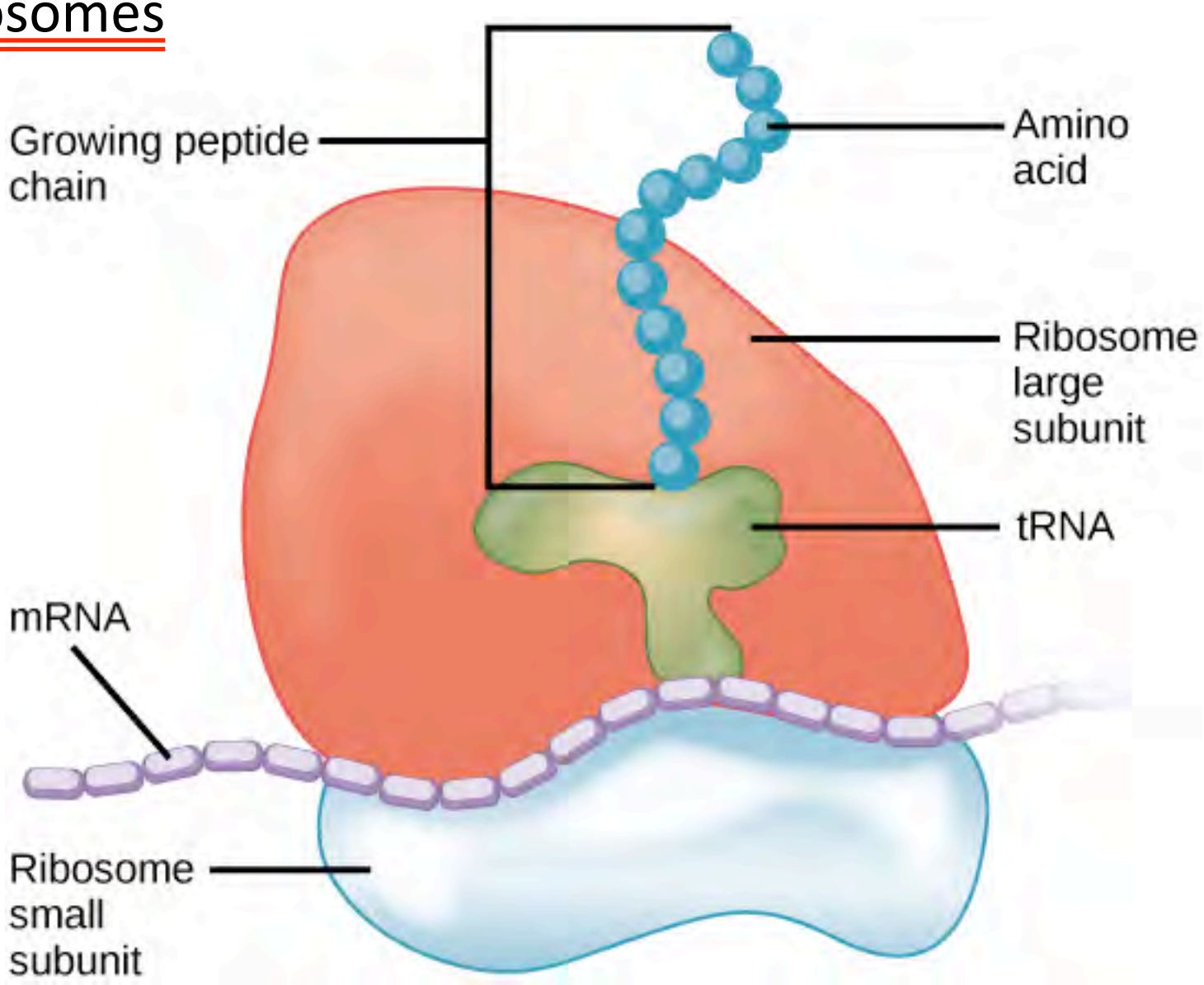


Chromosomes and DNA





Ribosomes


Growing peptide chain
Amino acid
Ribosome large subunit
tRNA
mRNA
Ribosome small subunit

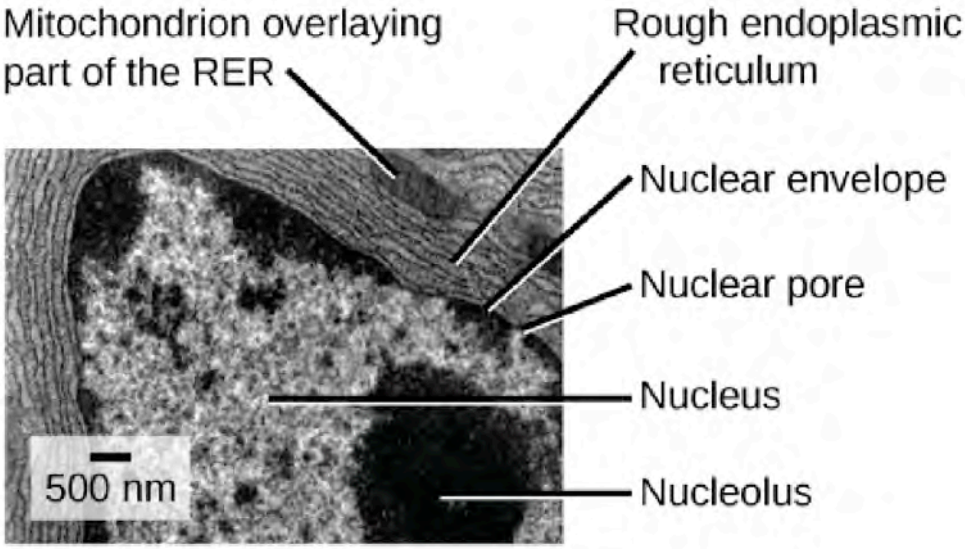
Endomembrane System?

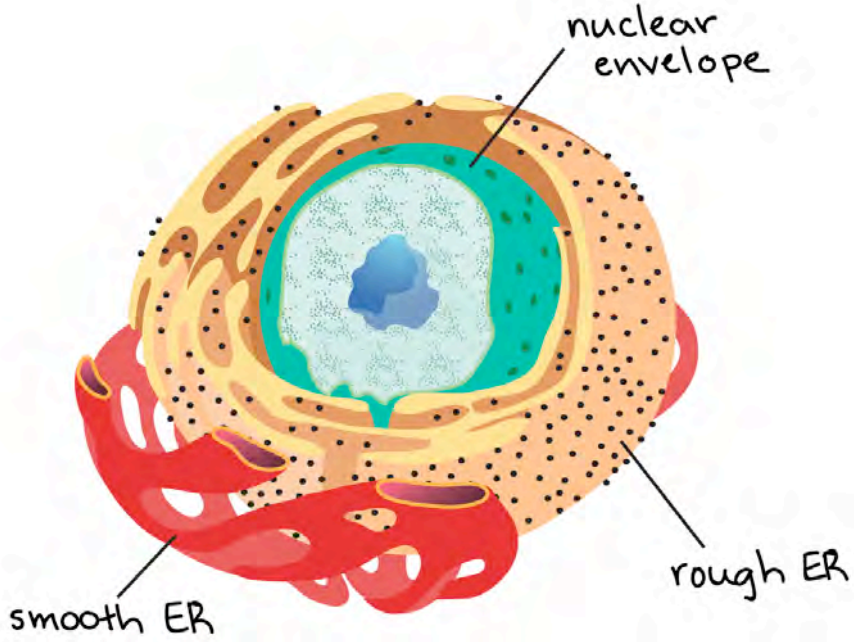
It includes a variety of organelles, such as the nuclear envelope and lysosomes, which you may already know, and the endoplasmic reticulum and Golgi apparatus.

Although it's not technically inside the cell, the plasma membrane is also part of the endomembrane system.

The endomembrane system does not include mitochondria, chloroplasts, or peroxisomes.

The Endoplasmic Reticulum





Smooth ER

- Synthesis of carbohydrates, lipids, and steroid hormones
- Detoxification of medications and poisons
- Storage of calcium ions

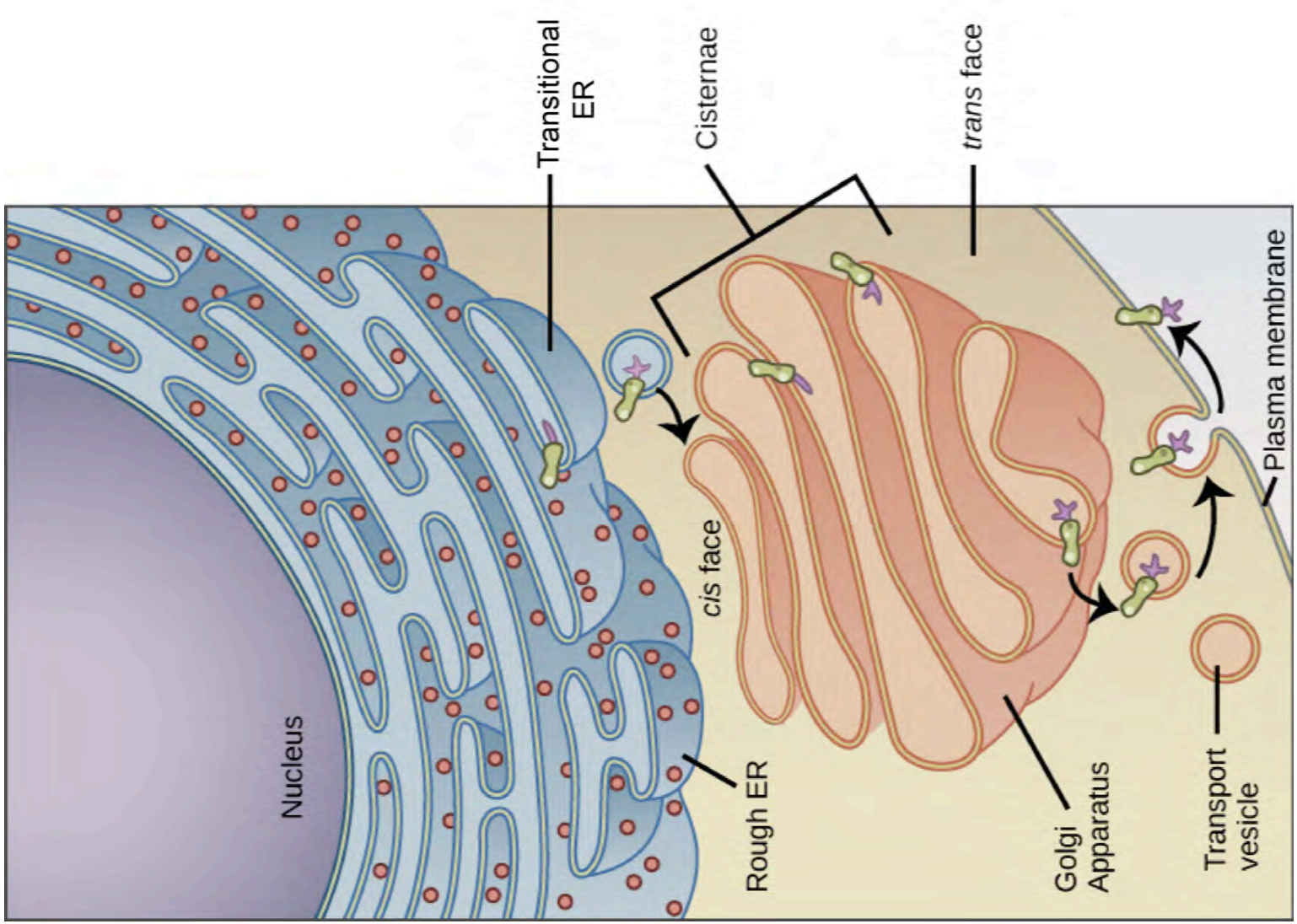
In muscle cells, a special type of smooth ER called the sarcoplasmic reticulum is responsible for storage of calcium ions that are needed to trigger the coordinated contractions of the muscle cells.

There are also tiny "smooth" patches of ER found within the rough ER. These patches serve as exit sites for vesicles budding off from the rough ER and are called transitional ER

The Golgi apparatus

When vesicles bud off from the ER, where do they go? Before reaching their final destination, the lipids and proteins in the transport vesicles need to be sorted, packaged, and tagged so that they wind up in the right place. This sorting, tagging, packaging, and distribution takes place in the Golgi apparatus (Golgi body), an organelle made up of flattened discs of membrane.

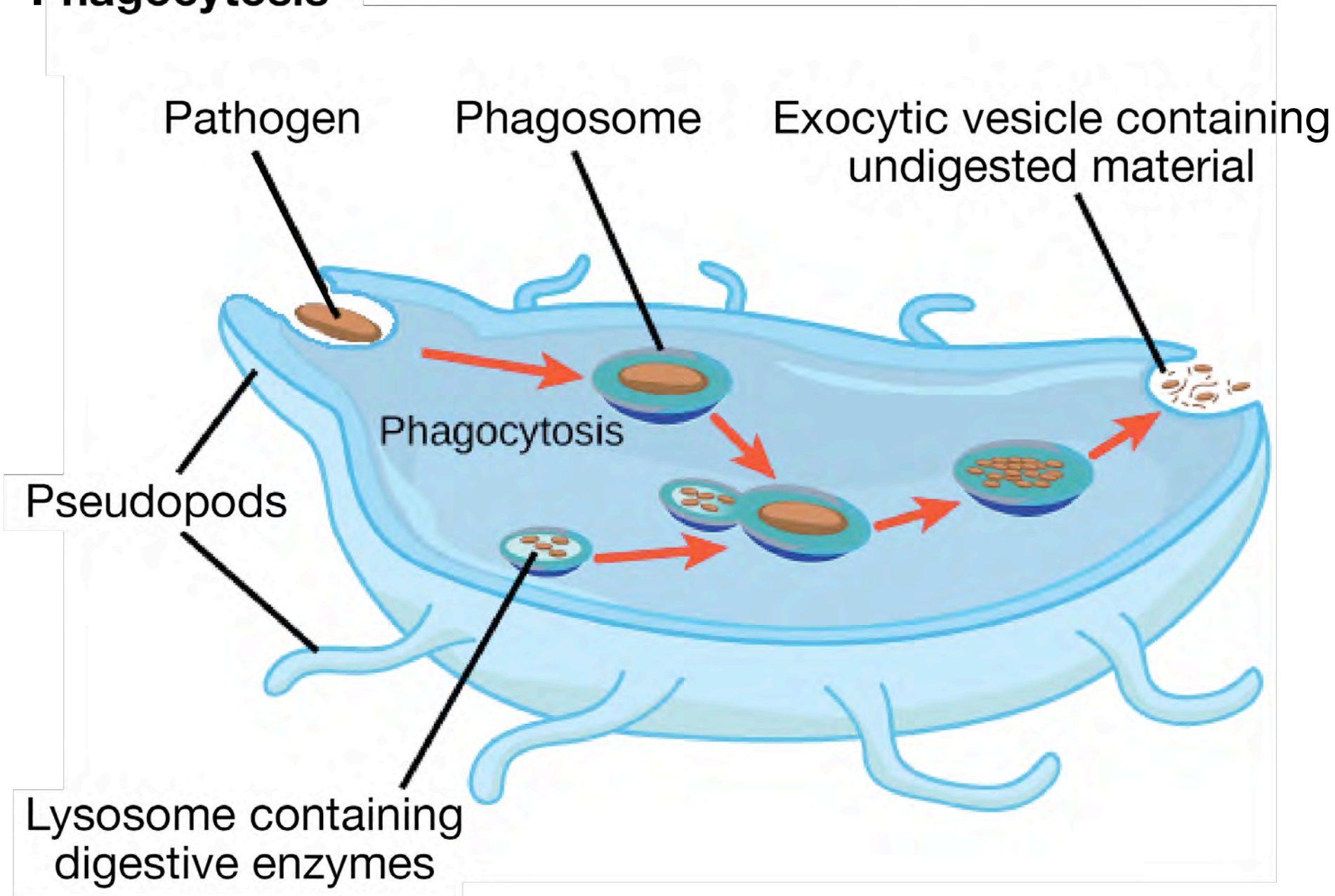
Protein Trafficking



Lysosomes

The lysosome is an organelle that contains digestive enzymes and acts as the organelle-recycling facility of an animal cell. It breaks down old and unnecessary structures so their molecules can be reused. Lysosomes are part of the endomembrane system, and some vesicles that leave the Golgi are bound for the lysosome.

Phagocytosis



Vacuoles

Plants cells do not have lysosomes. Instead, they have another type of organelle called the vacuole. The large central vacuole stores water and wastes wastes, isolates hazardous materials, and has enzymes that can break down macromolecules and cellular components, like those of a lysosome. Plant vacuoles also function in water balance and may be used to store compounds such as toxins and pigments (colored particles).

Lysosomes vs. peroxisomes

One point than can be confusing is the difference between lysosomes and peroxisomes. Both types of organelles are involved in breaking down molecules and neutralizing hazards to the cell. Also, both usually show up as small, round blobs in diagrams.

However, the peroxisome is a different organelle with its own unique properties and role in the cell. It houses enzymes involved in oxidation reactions, which produce hydrogen peroxide (H_2O_2) as a by-product. The enzymes break down fatty acids and amino acids, and they also detoxify some substances that enter the body. For example, alcohol is detoxified by peroxisomes found in liver cells.

Importantly, peroxisomes—unlike lysosomes—are are not part of the endomembrane system. That means they don't receive vesicles from the Golgi apparatus.

B.sc. Biochemistry (UG-sem 4)

Metabolism and Bioenergetics- An Introduction

By

Dr M. Iqbal Rather

Date: 10-09-18

Basic Concepts:

Metabolism: The sum of all the chemical transformations taking place in a cell or organism, occuring through a series of enzyme-catalyzed reactions

Metabolite: The precursor is converted into a product via a series of metabolic intermediates called metabolites

Intermediary Metabolism: The term intermediary metabolism is usually applied to the combined activities of all the metabolic pathways that interconvert precursors, metabolites and products of low molecular weight (often, M Wt= 1,000)

Continue…

Catabolism:

- **Catabolism** is the degradative phase of metabolism in which organic nutrient molecules (such as carbohydrates, fats, and proteins) are converted into smaller, simpler end products (such as lactic acid, H_2O, CO_2, NH_3 etc, etc)

- Catabolic pathways release energy, some of which is conserved in the formation of ATP (energy currency of cell) and reduced electron carriers (NADH, NADPH, and FADH2); the rest is lost as heat

Anabolism:

- In anabolism small, simple precursors are polymerized into larger and more complex molecules, including lipids, polysaccharides, proteins, and nucleic acids: often through a condensation reaction

- Anabolic reactions are endergonic (require an input of energy), provided by phosphoryl group transfer potential of ATP and the reducing power of NADH, NADPH, and FADH2

Bioenergetics

"A branch of biochemistry dedicated to the study of energy flow within living systems".

Why to Study Bioenergetics?

- Understanding the metabolism provides better understanding as how skeletal muscles generate energy; and how and why the body should respond to exercise the way it does.

- The study of metabolism is based on studying Bioenergetics.

- The Laws of Bioenergetics provide the rules based on which metabolism works.

Thermodynamics

"Study of energy transformations"

First Law of Thermodynamics: Energy cannot be created or destroyed but only converted from one form to other form(s), that means the energy in universe is conserved.

Second Law of Thermodynamics: Universe has always tendency to increase disorder i.e. in all natural processes the entropy of the universe increases

Implications of 2nd law of bioenergetics

1. All reactions proceed in the direction of: i) inceasing entropy and ii) a release of free energy (-ΔG)

2. The more negative the ΔG, more the release of free energy during a chemical reaction

3. Chemical reactions having a negative ΔG (-ΔG) are termed exergonic/exothermic reactions.

4. By convention, reactions that require free energy input to proceed are termed endergonic/ endothermic reactions

5. The free energy not used to do work is released as heat.

6. Reactions having no net change in substrate or product are termed equilibrium reactions, and have no change in free energy (ΔG=0).

7. All reactions have potential to be reversible.

8. The direction and free energy release of a chemical reaction can be altered by changing the substrate and product concentrations. – Increasing the products may reverse the direction of the reaction – Increasing substrates can make the ΔG more negative. Of note, if the reaction is reversed, the products are now the substrates and vice-versa

Thank You

UG-1st sem

Cell Biology-Proteins

By

Masroor Ahmad Malik

Unit II proteins

Proteins are the essential agents of biological function, and amino acids are the building blocks of proteins. The diversity of the thousands of proteins found in nature arises from the commonly occurring 20 amino acids. Proteins are polymers of amino acids, with each amino acid residue joined to its neighbour by a specific type of covalent bond. Proteins can be broken down (hydrolyzed) to their constituent amino acids. All 20 amino acids (Table 4.1) are biologically essential. Humans can synthesize 12 (nutritionally nonessential) of the 20 common amino acids from the amphibolic intermediates of glycolysis and of the citric acid cycle. Of the 12 nutritionally nonessential amino acids, nine are formed from amphibolic intermediates and three (cysteine, tyrosine and hydroxylysine) from nutritionally essential amino acids.

List of essential and nonessential amino acids

Essential	Nonessential
Histidine	Alanine
Isoleucine	Arginine
Leucine	Aspartic acid
Lysine	Cysteine
Methionine	Glutamic acid
Phenylalanine	Glutamine
Threonine	Glycine
Tryptophan	Proline
Valine	Serine
	Tyrosine

Asparagine

Selenocysteine & Pyrrolysine

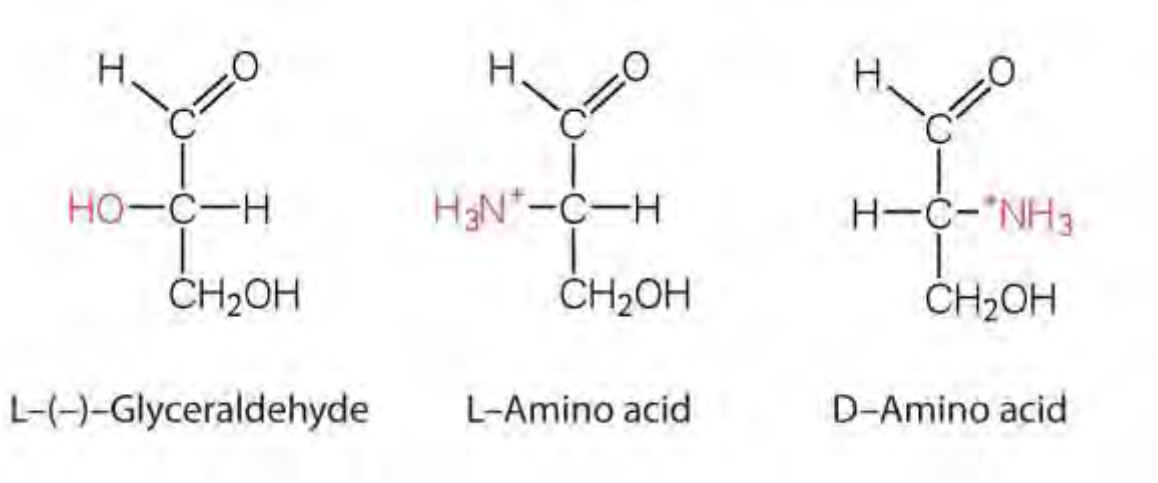
Essential amino acids are "essential" not because they are more important to life

than the others, but because the body does not synthesize them. They must be present in the diet or they will not be present in the body. In addition, the amino acids arginine, cysteine, glycine, glutamine, histidine, proline, serine and tyrosine are considered conditionally essential, meaning they are not normally required in the diet, but must be supplied exogenously to specific populations that do not synthesize them in adequate amounts. Selenocysteine, while not normally considered an amino acid present in proteins, selenocysteine occurs at the active sites of several enzymes. Examples include the human enzymes thioredoxin reductase, glutathione peroxidase, and the deiodinase that converts thyroxine to triiodothyronine. Pyrrolysine sometimes considered “the 22nd amino acid”, is not listed here as it is not used by humans.

Amino Acids are Chiral Molecules

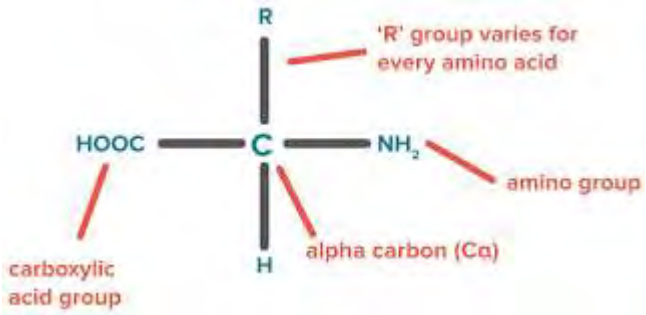
An α-amino acid consists of a central carbon atom, called the α carbon, linked to an amino group, a carboxylic acid group, a hydrogen atom, and a distinctive R group. For all the common amino acids except glycine, the α carbon is bonded to four different groups: a carboxyl group, an amino group, an R group, and a hydrogen atom(in glycine, the R group is another hydrogen atom). The α-carbon atom is thus a chiral center. Because of the tetrahedral arrangement of the bonding orbitals around the α-carbon atom, the four different groups can occupy two unique spatial arrangements, and thus amino acids have two possible stereoisomers. Since they are nonsuperimposable mirror images of each other the two forms represent a class of stereoisomers called enantiomers .The R group is often referred to as the side chain. Enantiomeric molecules display a special property called optical activity – the ability to rotate the plane of polarization of plane-polarized light. Clockwise rotation of incident light is referred to as dextrorotatory(D)behaviour &counterclockwise rotation is called levorotatory (L) behavior. Only L amino acids are constituents of proteins. The magnitude and direction of the optical rotation depend on the

nature of the amino acid side chain.



Structure of a Typical Amino Acid

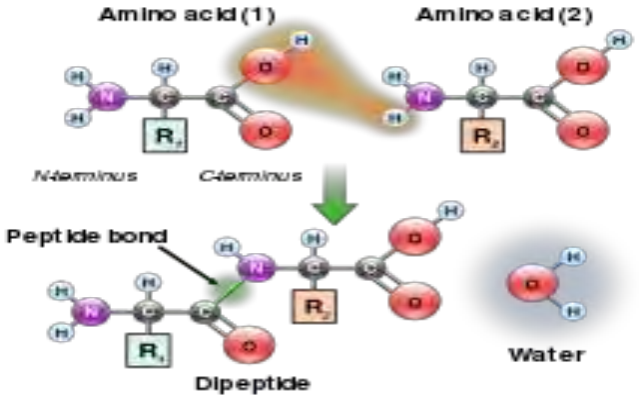
Amino acids in solution at neutral pH exist predominantly as dipolar ions (also called zwitterions). Amino acids can exist as zwitterions - substances containing equal numbers of positive and negative charge due to their carboxyl and amine groups, which can be negatively and positively charged, respectively. In the dipolar form, the amino group is protonated ($NH3^{+}$) and the carboxyl group is deprotonated (COO^{-}). The ionization state of an amino acid varies with pH. They differ from each other in their side chains, or R groups, which vary in structure, size, and electric charge, and which influence the solubility of the amino acids in water.



Amino Acids can join via Peptide Bonds

The crucial feature of amino acids that allows them to polymerize to form peptides and proteins is the existence of their two identifying chemical groups:the amino ($NH3^{+}$) and carboxyl (COO–) groups. The amino and carboxyl groups of amino acids can react in a head-

to-tail fashion, eliminating a water molecule and forming a covalent amide linkage, which, in the case of peptides and proteins, is typically referred to as a peptide bond.



CLASSIFICATION

The structures and abbreviations for the 20 amino acids commonly found in proteins are shown below. All the amino acids except proline have both free amino and free carboxyl groups. The classifications of amino acids is based on the polarity of the side chains. Thus, the structures shown below are grouped into the following categories: (1) nonpolar or hydrophobic amino acids, (2) neutral (uncharged) but polar amino acids, (3) acidic amino acids (which have a net negative charge at pH 7.0), and (4) basic amino acids (which have

a net positive charge at neutral pH).

Nonpolar Amino Acids

The nonpolar amino acids include all those with alkyl chain R groups (alanine, valine, leucine, and isoleucine), as well as proline (with its unusual cyclic structure), methionine (one of the two sulfur-containing amino acids), and two aromatic amino acids, phenylalanine and tryptophan. Tryptophan is sometimes considered a borderline member of this group because it can interact favourably with water via the N–H moiety of the indole ring. Proline, strictly speaking, is not an amino acid but rather an α-imino acid.

Polar, Uncharged Amino Acids

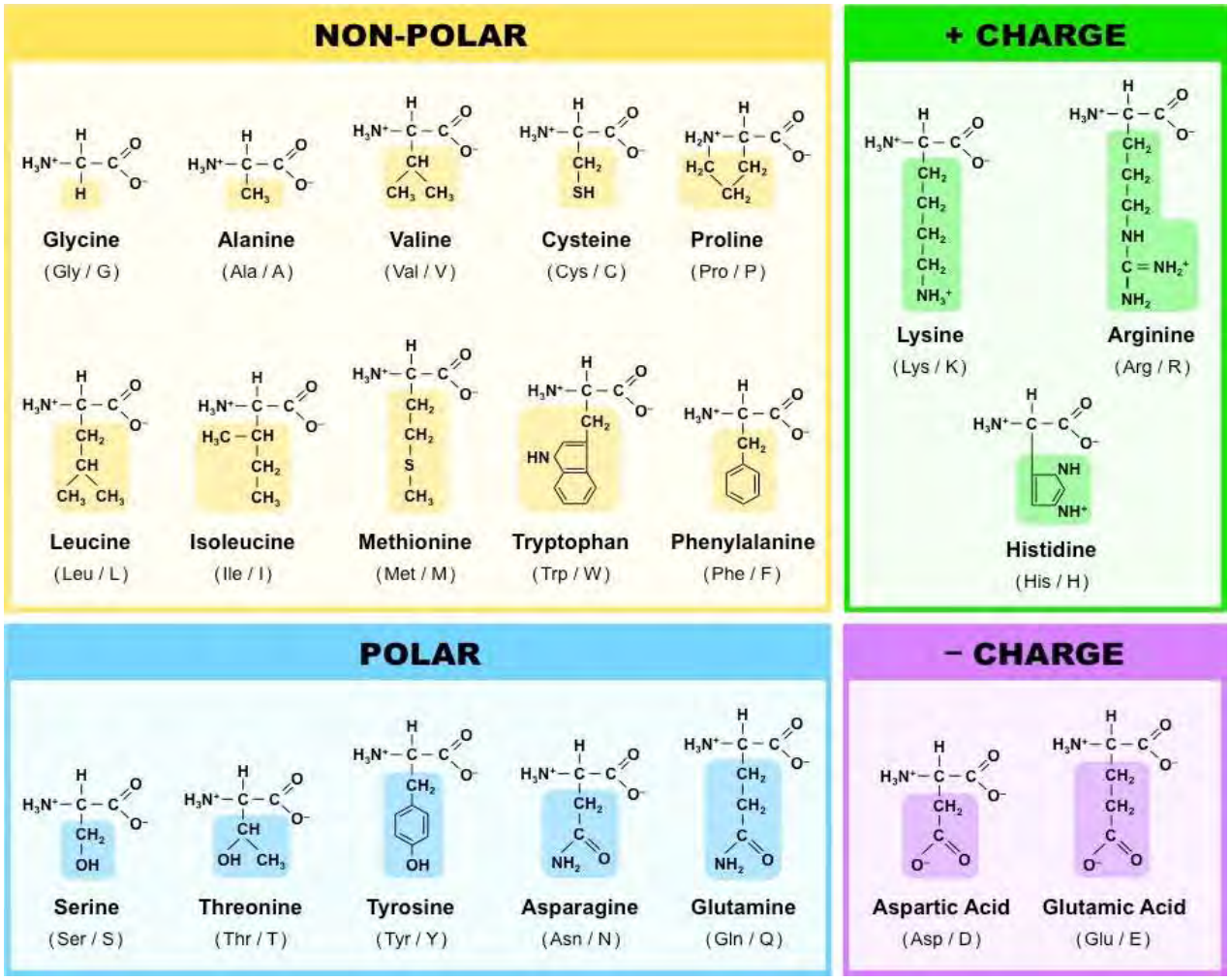
The polar, uncharged amino acids except for glycine contain R groups that can form hydrogen bonds with water. Thus, these amino acids are usually more soluble in water than the nonpolar amino acids. Tyrosine displays the lowest solubility in water of the 20 common amino acids. Glycine, the simplest amino acid, has only a single hydrogen for an R group, and this hydrogen is not a good hydrogen bond former. Glycine's solubility properties are mainly influenced by its polar amino and carboxyl groups, and thus glycine is best considered a member of the polar, uncharged group. It should be noted that tyrosine has significant nonpolar characteristics due to its aromatic ring and could arguably be placed in the nonpolar group.

Acidic Amino Acids

There are two acidic amino acids – aspartic acid and glutamic acid – whose R groups contain a carboxyl group. Aspartic acid and glutamic acid thus have a net negative charge at pH 7. Many proteins that bind metal ions for structural or functional purposes possess metal binding sites containing one or more aspartate and glutamate side chains.

Basic Amino Acids

Three of the common amino acids have side chains with net positive charges at neutral pH: histidine, arginine, and lysine. The ionized group of histidine is an imidazolium, that of arginine is a guanidinium, and lysine contains a protonated alkyl amino group. Arginine and lysine side chains, which are protonated under physiological conditions, participate in electrostatic interactions in proteins.



PROTEIN

Proteins are a diverse and abundant class of biomolecules, constituting more than 50% of the dry weight of cells. This diversity and abundance reflect the central role of proteins in virtually all aspects of cell structure and function. Biologically occurring polypeptides range in size from small to very large, consisting of two or three to thousands of linked amino acid residues. Peptides are chains of amino acids, two amino acid molecules can be covalently joined through a substituted amide linkage, termed a peptide bond to yield a dipeptide. Such a linkage is formed by removal of the elements of water (dehydration) from the α-carboxyl group of one amino acid and the α-amino group of another. Peptide bond formation is an example of a condensation reaction, a common class of reactions in living cells. Three amino acids can be joined by two peptide bonds to form a tripeptide; similarly,

amino acids can be linked to form tetrapeptides, pentapeptides, and so forth. When a few amino acids are joined in this fashion, the structure is called an oligopeptide. When many amino acids are joined, the product is called a polypeptide. Proteins may have thousands of amino acid residues. Although the terms “protein” and “polypeptide” are sometimes used interchangeably, molecules referred to as polypeptides generally have molecular weights below 10,000, and those called proteins have higher molecular weights. Proteins can be assigned to one of three global classes on the basis of shape and solubility: **fibrous, globular, or membrane.**

Fibrous proteins tend to have relatively simple, regular linear structures. These proteins often serve structural roles in cells. Typically, they are insoluble in water or in dilute salt solutions. In contrast, **globular proteins** are roughly spherical in shape. The polypeptide chain is compactly folded so that hydrophobic amino acid side chains are in the interior of the molecule and the hydrophilic side chains are on the outside exposed to the solvent, water. **Membrane proteins** are found in association with the various membrane systems of cells. For interaction with the nonpolar phase within membranes, membrane proteins have hydrophobic amino acid side chains oriented outward. As such, membrane proteins are insoluble in aqueous solutions but can be solubilized in solutions of detergents.

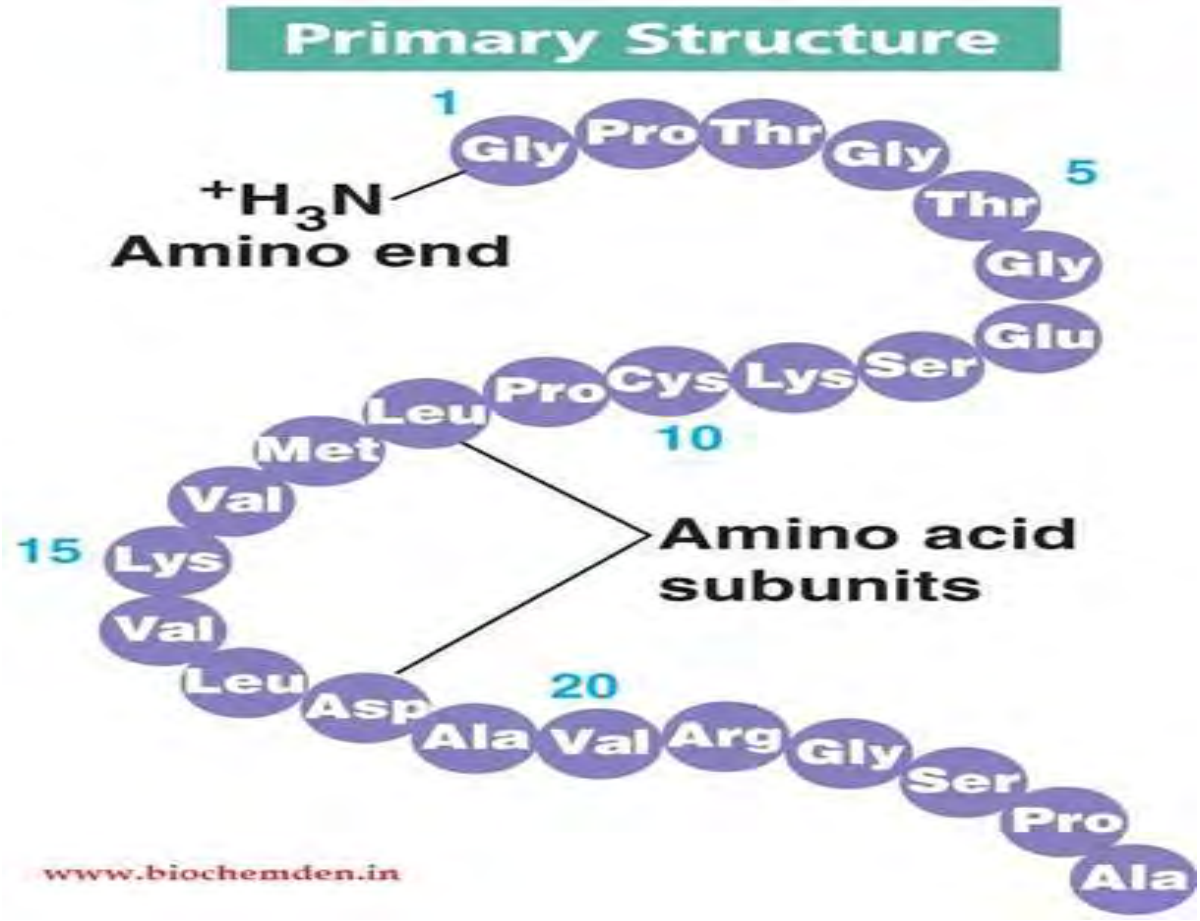
THE LEVELS OF PROTEIN STRUCTURE

The various levels of protein structural organization are defined as follows;-

Primary Structure

The primary structure of a protein refers to the sequence of amino acids in the polypeptide chain. The primary structure is held together by peptide bonds that are made during the process of protein biosynthesis. The two ends of the polypeptide chain are referred to as the carboxyl terminus (C-terminus) and the amino terminus (N-terminus) based on the nature of the free group on each extremity. Counting of residues always starts at the N-terminal end (NH2-group), which is the end where the amino group is not involved in a peptide bond. The primary structure of a protein is determined by the gene corresponding to the protein. A specific sequence of nucleotides in DNA is transcribed into mRNA, which is read by the ribosome in a process called translation. The sequence of amino acids in insulin

was discovered by Frederick Sanger, establishing that proteins have defining amino acid sequences.[3][4] The sequence of a protein is unique to that protein, and defines the structure and function of the protein. The sequence of a protein can be determined by methods such as Edman degradation or tandem mass spectrometry. Often, however, it is read directly from the sequence of the gene using the genetic code. It is strictly recommended to use the words "amino acid residues" when discussing proteins because when a peptide bond is formed, a water molecule is lost, and therefore proteins are made up of amino acid residues. Post-translational modification such as disulfide bond formation, phosphorylations and glycosylations are usually also considered a part of the primary structure, and cannot be read from the gene. For example, insulin is composed of 51 amino acids in 2 chains



Secondary Structure

Through hydrogen bonding interactions between adjacent amino acid residues the polypeptide chain can arrange itself into characteristic helical or pleated segments. These segments constitute structural conformities, so-called regular structures that extend along one dimension, like the coils of a spring. Such architectural features of a protein are designated secondary (2°) structures. Secondary structures are just one of the higher levels of structure that represent the three-dimensional arrangement of the polypeptide in space.

Tertiary Structure

When the polypeptide chains of protein molecules bend and fold in order to assume a more compact three-dimensional shape, a tertiary (3°) level of structure is generated . It is by virtue of their tertiary structure that proteins adopt a globular shape. A globular conformation gives the lowest surface to volume ratio, minimizing interaction of the protein with the surrounding environment.

Quaternary Structure

Many proteins consist of two or more interacting polypeptide chains of characteristic tertiary structure, each of which is commonly referred to as a subunit of the protein. Subunit organization constitutes another level in the hierarchy of protein structure, defined as the protein's quaternary (4°) structure. Whereas the primary structure of a protein is determined by the covalently linked amino acid residues in the polypeptide backbone, secondary and higher orders of structure are determined principally by noncovalent forces such as hydrogen bonds and ionic, van der Waals, and hydrophobic interactions.

FUNCTIONS OF PROTEINS

Proteins are the agents of biological function. Virtually every cellular activity is dependent on one or more particular proteins. Thus, a convenient way to classify the enormous number of proteins is by the biological roles they fill. The various functions of proteins are as follows.

Enzymes

By far the largest class of proteins is enzymes. More than 3000 different enzymes are listed in Enzyme Nomenclature, the standard reference volume on enzyme classification. Enzymes are catalysts that accelerate the rates of biological reactions. Each enzyme is very specific in its function and acts only in a particular metabolic reaction. Virtually every step in metabolism is catalyzed by an enzyme. Enzymes are systematically classified according to the nature of the reaction that they catalyze, such as the transfer of a phosphate group (phosphotransferase) or an oxidation–reduction (oxidoreductase). The formal names of enzymes come from the particular reaction within the class that theycatalyze, as in ATP: D-fructose-6-phosphate 1-phosphotransferase. Often, enzymes have common names in addition to their formal names. ATP: D-fructose-6-phosphate 1-phosphotransferase is more commonly known as phosphofructokinase (kinase is a common name given to ATP-dependent phosphotransferases).

Regulatory Proteins

A number of proteins do not perform any obvious chemical transformation but nevertheless can regulate the ability of other proteins to carry out their physiological functions. Such proteins are referred to as regulatory proteins. A well-known example is insulin, the hormone regulating glucose metabolism in animals. Insulin is a relatively small protein and consists of two polypeptide chains held together by disulfide cross-bridges. Other hormones that are also proteins include pituitary somatotropin and thyrotropin, which stimulates the thyroid gland.

Transport Proteins

A third class of proteins is the transport proteins. These proteins function to transport specific substances from one place to another. One type of transport protein is exemplified by the transport of oxygen from the lungs to the tissues by haemoglobin or by the transport of fatty acids from adipose tissue to various organs by the blood protein serum albumin. Membrane transport proteins take up metabolite molecules on one side of a membrane, transport them across the membrane, and release them on the other side. Examples include the transport proteins responsible for the uptake of essential nutrients into the cell, such as

glucose or amino acids.

Storage Proteins

Proteins whose biological function is to provide a reservoir of an essential nutrient are called storage proteins. Because proteins are amino acid polymers and because nitrogen is commonly a limiting nutrient for growth, organisms have exploited proteins as a means to provide sufficient nitrogen in times of need. For example, ovalbumin, the protein of egg white, provides the developing bird embryo with a source of nitrogen during its isolation within the egg. Casein is the most abundant protein of milk and thus the major nitrogen source for mammalian infants. The seeds of higher plants often contain as much as 60%

storage protein to make the germinating seed nitrogen-sufficient during this crucial period of plant development. In corn (Zea mays or maize), a family of low molecular weight proteins in the kernel called zeins serve this purpose. Ferritin is a protein found in animal tissues that binds iron, retaining this essential metal so that it is available for the synthesis of important iron containing proteins such as hemoglobin.

Contractile and Motile Proteins

Certain proteins endow cells with unique capabilities for movement. Cell division, muscle contraction, and cell motility represent some of the ways in which cells execute motion. Examples include actin and myosin, the filamentous proteins forming the contractile systems of cells, and tubulin, the major component of microtubules.

Structural Proteins

An apparently passive but very important role of proteins is their function in creating and maintaining biological structures. Structural proteins provide strength and protection to cells and tissues. Monomeric units of structural proteins typically polymerize to generate long fibers (as in hair). α-Keratins are insoluble fibrous proteins making up hair, horns, and fingernails. Collagen, another insoluble fibrous protein, is found in bone, connective tissue, tendons, and cartilage, where it forms inelastic fibrils of great strength. One-third of the total protein in a vertebrate animal is collagen. A structural protein having elastic properties is, appropriately, elastin, an important component of ligaments.Certain insects make a

structurally useful protein, fibroin (a a-keratin), the major constituent of cocoons (silk) and spider webs.

Scaffold Proteins (Adapter Proteins)

Some proteins play a recently discovered role in the complex pathways of cellular response to hormones and growth factors. These proteins, the scaffold or adapter proteins, have a modular organization in which specific parts (modules) of the protein's structure recognize and bind certain structural elements in other proteins through protein–protein interactions.

Protective and Exploitive Proteins

In contrast to the passive protective nature of some structural proteins, another group can be more aptly classified as protective or exploitive proteins because of their biologically active role in cell defense, protection, or exploitation. Prominent among the protective proteins are the immunoglobulins or antibodies produced by the lymphocytes of vertebrates. Antibodies have the remarkable ability to specifically recognize and neutralize "foreign" molecules resulting from the invasion of the organism by bacteria, viruses, or other infectious agents. Another group of protective proteins is the blood-clotting proteins, thrombin and fibrinogen, which prevent the loss of blood when the circulatory system is damaged. Arctic and Antarctic fishes have antifreeze proteins to protect their blood against freezing in the below-zero temperatures of high-latitude seas. Another class of exploitive proteins includes the toxins produced by bacteria,such as diphtheria toxin and cholera toxin. It is worth repeating that the great diversity of function in proteins, as reflected is attained using just 20 amino acids.

UG-3rd sem

Enzymology-Introduction

By

Aafia Yaseen

Contents

- Intoduction to enzymes.
- Classification of enzymes.
- Nomenclature of enzymes .
- Isoenzymes and its types.
- Enzyme specificity and its types.

ENZYMES- INTRODUCTION

- Enzymes are biological catalysts.
- Enzymes are neither consumed nor permanently altered as a consequence of their participation in a reaction.
- All enzymes are proteins but all proteins are not enzymes.
- They have high degree of specificity for their substrates, they accelerate chemical reactions tremendously and their function in aqueous solution under very mild condition of temperature and pH.

Enzyme Characteristics

1. Enzymes are used to regulate the rate (speed) of chemical reactions.

2. All enzymes are proteins, but not all proteins are enzymes.

3. Each chemical reaction in an organism requires its own specific enzyme.

4. Each chemical that is worked on by an enzyme is called a **substrate.**

5. Each enzyme can also be called an organic **calalyst.**

6. Enzymes are never changed by their reactions! They are reusable

CLASIFICATION OF ENZYMES

List of Enzymes	
Group of Enzyme	**Examples**
1. Oxidoreductases	Dehydrogenases Oxidases
2. Transferases	Transaminase Kinases
3. Hydrolases	Estrases Digestive enzymes
4. Isomerases	Phospho hexo isomerase, Fumarase
5. Lyases	Decarboxylases Aldolases
6. Ligases (Synthetases)	Citric acid synthetase

Table 5.2. IUB classification of enzymes

Major Class (Type of reaction catalyzed)	Common exmaples	Kind of reaction	Specific Example
1. ***Oxidoreductases*** *(Transfer of electrons)*	Oxidases Reductases Dehydrogenase	$A^{+3} + B^{+2} \rightarrow A^{+2} + B^{+3}$	Alcohol + NAD ↓ *Alcohol dehydrogenase* Aldehyde + $NADH_2$
2. ***Transferases*** *(Transfer of functional groups)*	Transaminase Transketolase Transaldolase	$A - X + B \rightarrow A + B - X$	Glucose + ATP ↓ *Glukokinase or hexokinase* Glucose-6-Phosphate + ADP
3. ***Hydrolases*** *(Hydrolysis Reactions)*	Amylases Lipases Proteases Nucleases	$A–B+H_2O \rightarrow A–OH + B–H$	Sucrose ↓ *Sucrase* Glucose + Fructose
4. **Lyases or *Desmolases*** *(Group elimination to form double bonds without hydrolysis)*	Aldolase Decarboxylase Fumarase Citrate synthase	$A - B \rightarrow A = B + X - Y$ X Y	Histidine ↓ *Hlstidine decarboxylase* Histidine + CO_2
5. ***Isomerases*** *(Transfer of Groups within a molecule*	Isomerase Mutase Epimerase	$A - B \rightarrow A - B$ Y X X Y	Glucose – 6-Phosphate ↓ *Isomerase* Fructose-6-Phosphate
6. ***Ligases or Synthetases*** *(Bond formation couples with ATP hydrolysis)*	Synthetases Carboxylases	$A + B + ATP \rightarrow$ $A - B + ADP + Pi$	Pyruvate + CO_2 + ATP ↓ *Pyruvate carboxylase* Oxaloacetate + ADP + Pi

NOMENCLATURE

- IUB has developed an unambiguous system of enzyme nomenclature .
- Each enzyme has a unique name and code no. that identify the type of reaction catalyzed and the substrate involved.

As per this system the name start with EC followed by 4 digits.

1st digit represent the class.

2nd digit stands for subclass.

3rd digit is sub subclass or subgroup.

4th digit give the number of particular enzyme in the list

Isoenzymes

- They are physically distinct forms of the same enzyme activity. Multiple molecular form of an enzyme is described as **isoenzymes** or **isozymes**. They synthesized from various tissues
- Ex. **Lactate dehydrogenase** has 5 forms.
- The study of isoenzymes is useful to understand diseases of different organs.

LACTATE DEHYROGENASE AND ITS ISOENZYMES

Isozymes of Lactate Dehydrogenase

Lactate dehydrogenase (LDH) functions in glucose metabolism.

Mammals have 2 versions of LDH, the H isozyme (found in heart) and the M isozyme (found in skeletal muscle) which are closely related, sharing about 75% sequence identity.

LDH functions as a tetramer, but individual tetramers can be composed of any combination of M and H isozymes. (M_4, M_3H, M_2H_2, MH_3, or H_4)

The M_4 tetramer functions optimally under anaerobic conditions, while the H_4 tetramer functions optimally under aerobic conditions.

The H_4 tetramer has higher substrate affinity and also can be allosterically inhibited by pyruvate. The M_4 tetramer has a lower affinity for substrate and is not allosterically regulated.

The mixed tetramers exhibit properties intermediate between the the H_4 and M_4 tetramers- differential expression of the two isozymes allows fine control over the LDH activity.

Isoenzymes

LDH 1	HHHH	Occurs in myocardium (aerobic tissues)
LDH 2	HHHM	In acute leukemia
LDH 3	HHHM	In acute leukemia
LDH 4	HMMM	Occurs in muscle and liver (anaerobic tissues)
LDH 5	MMMM	Occurs in muscle and liver (anaerobic tissues) in liver disease

CPK- Isoenzymes

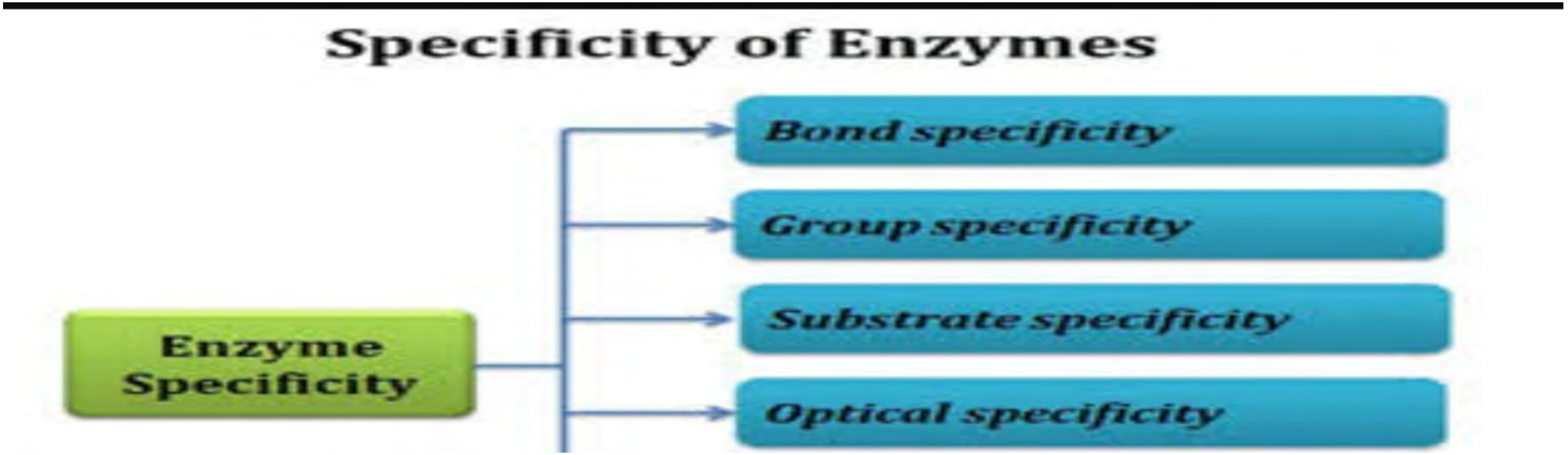
- CPK-1 (also called CPK-BB) is concentrated in the brain and lungs
- CPK-2 (also called CPK-MB) is found mostly in the heart
- CPK-3 (also called CPK-MM) is found mostly in skeletal muscle
- Because the CPK-1 isoenzyme is predominately found in the brain and lungs, injury to either of these organs (for example, stroke or lung injury due to a pulmonary embolism) are associated with elevated levels of this isoenzyme.

Liver Hexokinase and Glucokinase

- Hexokinase regulated in liver, too
  - But we cannot send glucose out of liver cell
  - Must be picked up even when liver cell does not need glucose and glycogen storage is full
  - Stored as fat
- Glucokinase: isozyme
  - Unregulated
    - Keeps activating glucose even when there is much G-6-P
    - If always active, blood sugar would crash.
    - How do we avoid depriving brain?
  - High Km
    - Only active at high [glucose]

ENZYME SPECIFICITY AND ITS TYPES

- A few enzymes exhibit absolute specificity ,i.e they catalyze only one type of particular reaction .Others will be specific for a particular type of chemical bond or functional group .
- On this basis enzymes exhibit following types of specificities

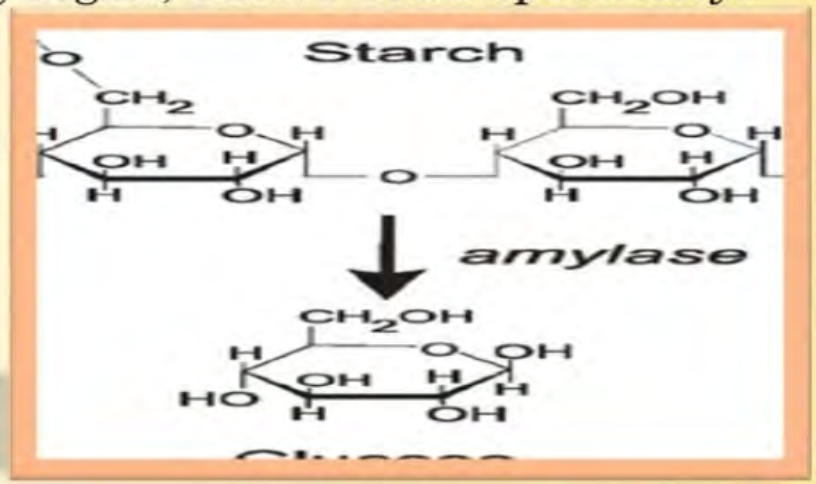


BOND SPECIFICITY

- In this type, enzyme acts on substrates that are similar in structure and contain the same type of bond.

Example :

- *Amylase* which acts on α-1-4 glycosidic ,bond in starch dextrin and glycogen, shows bond specificity.

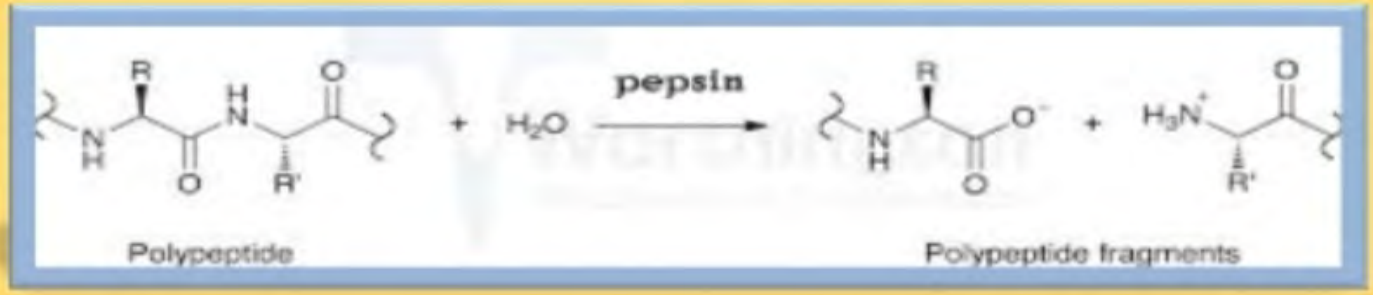


GROUP SPECIFICITY

- In this type of specificity, the enzyme is specific not only to the type of bond but also to the structure surrounding it.

Example:

- *Pepsin* is an endopeptidase enzyme, that hydrolyzes central peptide bonds in which the amino group belongs to aromatic amino acids e. g phenyl alanine, tyrosine and tryptophan.

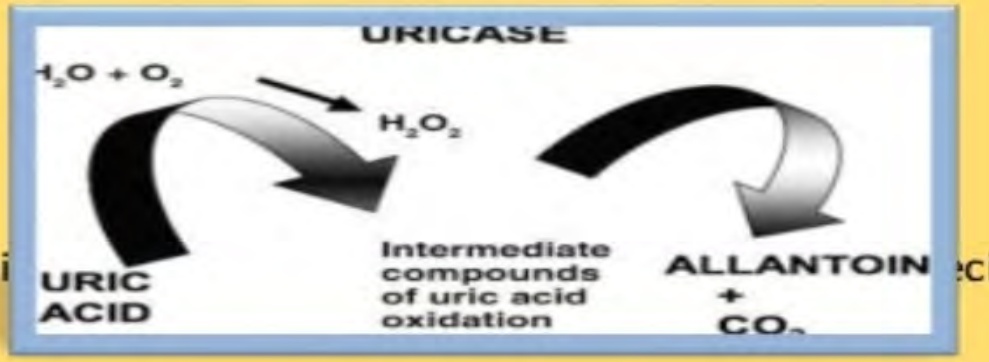


SUBSTRATE SPECIFICITY

- In this type of specificity ,the enzymes acts only on one substrate

Example :

- *Uricase* ,which acts only on uric acid, shows substrate specificity.



- *Maltase* , whi ecificity.

$$C_{12}H_{22}O_{11}(aq) + H_2O(l) \xrightarrow{\text{Maltase}} 2C_6H_{12}O_6(aq)$$

Maltose — Glucose

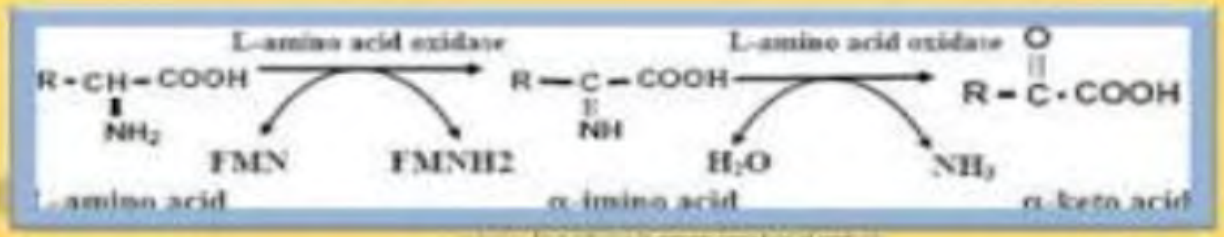
OPTICAL / STEREO-SPECIFICITY

- In this type of specificity , the enzyme is not specific to substrate but also to its optical configuration

Example:

- D amino acid oxidase acts only on D amino acids.

- L amino acid oxidase acts only on L amino acids.




Thank You