ZO503 ANIMAL PHYSIOLOGY AND PHYSIOLOGICAL CHEMISTRY

BLOCK – III: PHYSIOLOGICAL CHEMISTRY

Proteins

Dr.Shyam S.Kunjwal
Department of Zoology
Uttarakhand Open University
Haldwani

PROTEINS

Content

12.1 OBJECTIVES

1. The objective of this chapter is to understand about proteins.
2. To understand structures and classification of proteins.
3. To understand the properties of proteins.
4. Understanding the metabolism of proteins.
5. Major sources of proteins.
6. Biological significance and deficiency diseases of proteins.

12.2 INTRODUCTION TO PROTEINS

Proteins are the highly complex chemical compounds present in all living organism. These are the high molecular weight polypeptides, composed of carbon, hydrogen, oxygen, nitrogen, sulpher and phosphorus. Proteins are the most abundant and essential constituents of living cells. All the basic functions of life depend upon specific proteins. The term protein was first suggested by Swedish chemist Berzalius in 1938 and derived from the Greek word "proteios" meaning 'first'. Geradus Mulder for the first time used the term in 1840 and referred it to the complex organic nitrogenous substance found in the cells of living organisms. Proteins are the most significant compound in living beings depending upon their chemical and physical structures they are involved in wide variety of functions i.e. catalysis, conduction, contraction, structure, nutrition, binding and defense.

Chemical Structure of Proteins

Proteins are the linear polymers of amino acids. Proteins can be very long polypeptide chains of hundred to several thousand amino acids. When a large number of amino acids join together they form polypeptides chains. The amino acids molecules in a polypeptide chains are linked by polypeptide bonds.

$$[\text{Amino Acid}]_n \rightarrow \text{Peptide} \rightarrow \text{Polypeptide} \rightarrow \text{Protein}$$

Peptide Bond: The amino acids of a protein are joined to one another by their respective amino and carboxyl groups i.e. the carboxyl group of one amino acid is joined to the amino group of the next amino acid to form a peptide bond or peptide linkage with the release of one molecule of water.

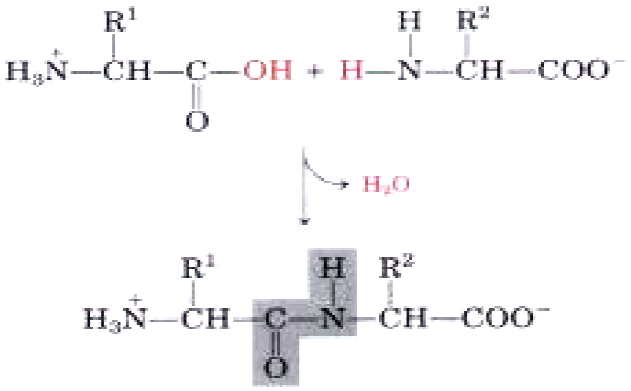


Fig.12.1. Formation of a peptide bond

12.3 CLASSIFICATION OF PROTEINS

Proteins can be classified according to their functions, shape, structures and complexity. On the basis of their conformation the proteins can be classified into two major classes:

1. Fibrous proteins
2. Globular Proteins

1. Fibrous proteins

In fibrous proteins polypeptide chains are arranged in a parallel manner along a single axis producing long fibers or sheet like structures. Fibrous proteins Fibrous proteins are insoluble in water or dilute salt solution. These are the basic structural elements in animal tissues. Keratin of hair and skin, elastin of ligament and collagen of tendons and bone matrix all are examples of fibrous proteins.

2. Globular Proteins

Polypeptide chains are tightly folded into compact spherical or globular shapes. Most of the globular proteins are soluble in water example of globular proteins are all the enzymes, certain hormones, and antibodies etc.

On the basis of their structure and complexity proteins are classified into three major classes:

1. Simple proteins
2. Conjugated or Complex proteins
3. Derived proteins

1. Simple proteins: Proteins which consist solely of amino acid are called simple proteins. These are further classified into the following subclasses

Albumins: They are soluble in water and coagulate on heating. They are precipitated by dilute acids and alkalis. Albumins are widely distributed in nature stored as food reserved e.g. egg albumin, serum albumin, legumelin (legumes), lactalbumin (milk), lecucosin (cereals), gliadin (wheat).

Protamins: They are basic proteins highly soluble in water, dilute acids and ammonium hydroxide. Protamins are not coagulated by heat. These are simplest of all the naturally occurring proteins, isolated from mature sperms e.g. Sturine and salmine.

Histones: These are soluble in water and dilute acids but insoluble in ammonia. They are not coagulated by heat. Histones occur as part of nucleoproteins.

Scleroproteins: These are also known as albuminoids. Scleroproteins are soluble in water and solutions of neutral salts. They are found exclusively in animals e.g. keratin, collagen, elastin and fibroin.

Globulins: These are insoluble in water but are soluble in dilute neutral salt solution such as NaCl. On heating globulin get coagulated. They are precipitated by half saturated with ammonium sulphate examples of globulins are fibrinogen (blood plasma), egg globulin, myogen (muscles), legumin (peas), tuberin (potato) etc.

Glutelins: They are insoluble in water but are soluble in dilute acids and alkalies, Glutelin get coagulate on heating. These are found exclusively in seeds of cereal grains e.g. glutenin (wheat) and oxyzenin (rice).

Prolamins: These are insoluble in water but are soluble in dilute alkalies and 50-80% of alcohol. They are not coagulated by heat and found in plants only e.g. hordein (barley), gliadin (wheat) and zein (maize).

2. Conjugated Proteins: These proteins are composed of not only amino acids but also some non-protein components. This non-protein substance linked to proteins is called “prosthetic group”. Conjugated proteins are further classified into the following subclasses on the basis of their prosthetic group.

Glycoproteins: In glycoproteins simple proteins are covalently linked with carbohydrate group. The percent of carbohydrate group in different glycoproteins may vary from less than1% in egg albumin to as high as 80% in mucoproteins. Glycoproteins which have very high carbohydrate content are called proteoglycans. Examples of glycoproteins are mucin (saliva), heparin (bile juice), and immunoglobulins (plasma).

Nucleoproteins: In nucleoproteins protein molecules are combined with nucleic acid. The chromatin material of the nuclei of cells is composed of nucleoproteins e.g. nucleohistones.

Lipoproteins: Lipoproteins are the proteins in combination with lipids. These are present in the brain, egg, milk and plasma.

Phosphoproteins: Phosphoproteins are formed by the combination of simple proteins with phosphoric acid. Examples of phosphoproteins are vitelline (egg) and casein (milk).

Metalloproteins: These are proteins linked to some metallic prosthetic group, which also gives colour to the proteins. They are also known as chromoproteins e.g. haemoglobin, hemocynin, cytochromes and flavoproteins.

3. Derived Proteins: These proteins are derived from some previously existing proteins either by its hydrolysis or by its coagulation. Derived proteins can be divided into two major subclasses-

Primary derived proteins:- These are denaturated or coagulated proteins. The denaturation is caused by heat, acid or alkali treatment. Their molecular weight is same as the native protein but they differ in solubility, precipitation and crystallization. Examples are proteans, metaproteins and coagulated proteins.

Secondary derived proteins:- These are formed by the hydrolysis of complex protein of their peptide linkage. The hydrolysis is caused by the action of digestive enzymes, acids or alkalis. Their molecular weight is different from the native proteins. Examples are proteoses, peptones and peptides. On the basis of their biological functions they are classified into seven major classes:

i. Structural Proteins: Their function is strengthening or protecting biological structures e.g. keratin, fibroin, collagen, elastin etc.
ii. Storage and Nutrient Proteins: Their function is to provide nourishment to growing e.g. ovalbumin, giadin, ferritin etc.
iii. Enzymatic Proteins: Their function is to transport molecules in body e.g. haemoglobin, serum albumin, myoglobin etc.
iv. Transport Proteins: Their function is to transport molecules or ions in body e.g. haemoglobin, myoglobin and serum albumin.
v. Regulatory Proteins: Their function is to regulate cellular or metabolic activities e.g. hormones, repressors etc.
vi. Contractile Proteins: Their function is in contractile system e.g. actin, myosin, tubulin etc.
vii. Defense Proteins: Their function is to provide defense against another organisms e.g. antibodies, ricin etc.

12.4 Structural Organization of Proteins

Proteins are long polypeptide chains formed by the linkages of several thousand molecules of amino acid with a peptide bond. Proteins can be very long polypeptide chains of 100 to several thousand amino acid residues. There are four different structural level of organization are present in proteins, they are:

1. Primary structure
2. Secondary structure
3. Tertiary structure
4. Quartiary structure

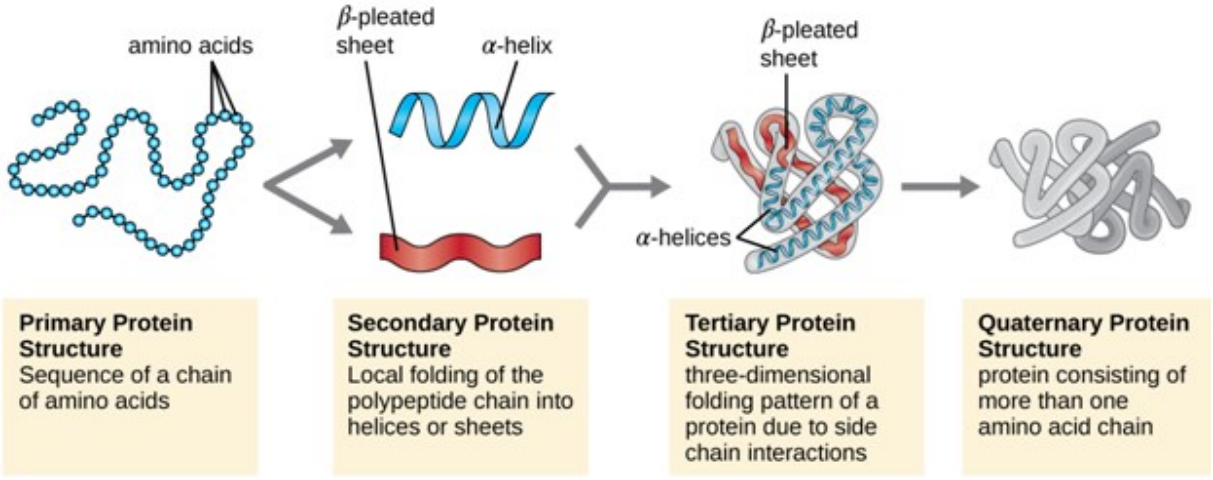


Fig.12.2. Structural organization of proteins

12.4.1 PRIMARY STRUCTURE

The sequence of amino acids in a protein and a description of all covalent bonds joining amino acid residues in the protein are called its primary structure. The linear sequence of amino acids in a protein is its characteristics feature. It determines the three dimensional structures of protein and also essential to elucidating mechanism of action of that protein. Fredrick Sanger (1953) for the first time presented the primary structure of protein insulin. Each polypeptide chain has at one end N-terminal amino acid containing a free amino group and at the other ends a C-terminal amino acid containing free carboxyl group. Any single alteration in amino acid sequence can produce a defective protein e.g. sickle cell anemia disease can result from a change in a single amino acid of haemoglobin polypeptide chain.

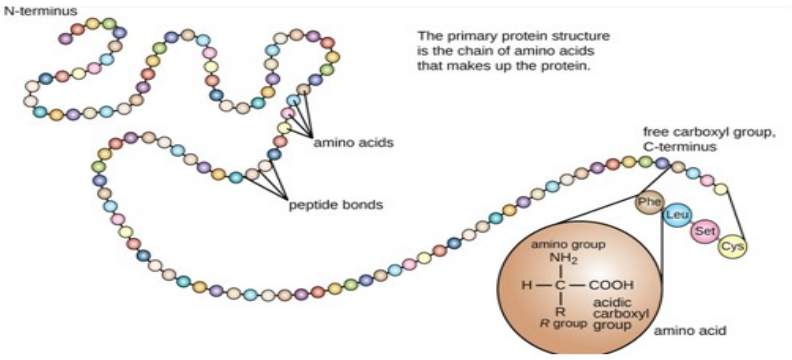


Fig.12.3. Primary structure: Amino acid sequence of proteins

12.4.2 SECONDARY STRUCTURE

Secondary structure refers to regular folding patterns of amino acid residues in a segment of a polypeptide chain. Folding of the polypeptide chain is the result of formation of hydrogen bond interaction between amino acid residues which are close to one another. The most prominent secondary structure which occurs widely in proteins is α-helix and β pleated sheets. In 1951 Robert Corey and Linus Pauling determine these confirmations of protein molecules.

α-helix: The most simple and common type of secondary structure is α-helix. It is a rod like structure in which the polypeptide backbone is tightly wound around an imaginary axis. Longitudinally and the side chains extend outwards a helical backbone. The helical structure of protein is formed by the hydrogen bond between peptide groups within the same polypeptide chains. In the α-helix each amino acid residue is away from the other at a distance of 1.5 Å and there are 3.6 amino acid residues per turn of helix. Almost all naturally occurring proteins have right handed α-helix. Examples of α-helices are α-keratin in hair and nails, fibrin in blood clots, myosin and tropomyosin in muscles etc.

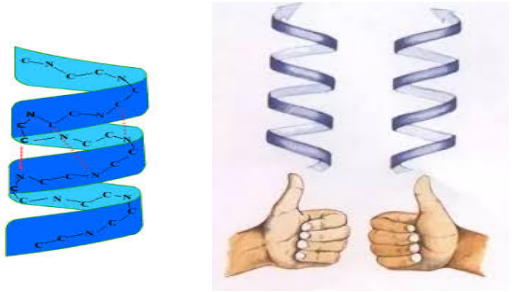


Fig.12.4. α-helix structure of protein (Left and Right handed helix)

β-Pleated Sheets: In this type of confirmation the backbone of polypeptide chain is extended into a zigzag rather than helical structure. The zigzag polypeptides are arranged side by side to form pleats like structure, thus called β-pleated sheets. In this type of structure hydrogen bonds are formed between two adjacent polypeptide chains rather than within the same polypeptide chain as in α-helix. There are two types of β-pleated sheets parallel and anti parallel.

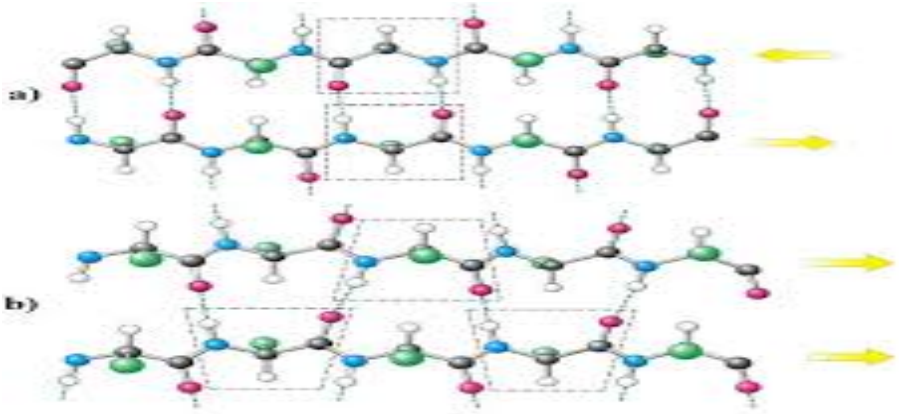


Fig.12.5. β-pleated structure of protein (a) Anti parallel β-pleated sheet (b) Parallel β-pleated sheet

In parallel β-pleated sheets, the adjacent hydrogen bonded polypeptide chains run in the same direction i.e. the N-terminal end of the polypeptide chains point in the same direction while in the antiparallel β-pleated sheets the adjacent hydrogen bonded polypeptide chains run in the opposite directions. Example of parallel β-pleated sheet is β-keratin and antiparallel β-pleated sheet is silk fibroin.

12.4.3 TERTIARY STRUCTURE

Tertiary structure refers to the final 3-dimentional structure that protein molecule assumes under the normal conditions by coiling and folding of the long polypeptide chain with or without a helix. This type of structure is more stable and complex than the secondary structure and is found in globular proteins. Tertiary structure is stabilized by several non covalent interactions such as hydrogen bonds, ionic bonds and hydrophobic interactions. The only covalent linkage involved in tertiary structure is disulphide bond formed between two cystein residues. Myoglobin, cytochrome C and ribonuclease exist in tertiary structure.

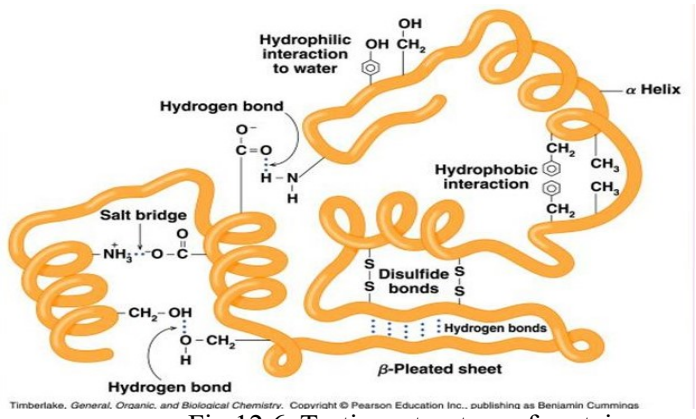


Fig.12.6. Tertiary structure of protein

Myoglobin is a primary oxygen carrying pigment of muscle tissues. In 1957, Jhon Kendrew and associates successfully determined the structure of myoglobin by high resolution X-ray crystallography. Myoglobin is a single polypeptide chain of 153 amino acid residues containing a heme group in the center. The molecular weight of myoglobin is 16700, Daltons. It is an extremely compact molecule with overall dimensions with 45×35×25 Å. A myoglobin polypeptide is made up of eight separate right handed α-helices interrupted by short non helical regions. Each myoglobin molecule contains one heme prosthetic group inserted into a hydrophobic cervice or pocket in the protein. Each heme residue contains one central coordinately bound iron atom that is normally in the ferrous (Fe^{2+}) form. When exposed to oxygen the Fe^{2+} atom of the isolated heme is irreversibly oxidized to the ferric (Fe^{3+}) form. Myoglobin is the oxygen carrier in the muscles and the oxygen carrying (binding) capacity depends on the presence of heme. The protein portion of myoglobin prevents this oxidation and makes it possible for O_2 to bind reversibly to the heme group.

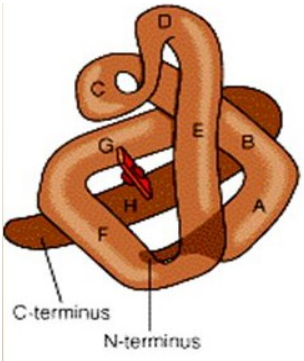


Fig.12.7. Structure of myoglobin

12.4.4 QUATERNARY STRUCTURE

Quaternary structure of proteins concerns the non covalent association of two or more polypeptide chains to form an ordered biologically active protein. The individual polypeptides are called subunits or protomers and ordered total proteins is called oligomer. The forces involved in binding the subunits are same as those in tertiary structure e.g. hydrophobic interaction, hydrogen bonding and ionic bonding are quite common in oligomeric proteins. If the subunits in an oligomer are identical the protein is said to be homogenous e.g. enzyme phosphorylase a, contains two subunits which are identical to each other. However, if the subunits are different, the protein is heterogeneous e.g. human haemoglobin consists of four subunits two subunits of one type α and two subunits of another type β.

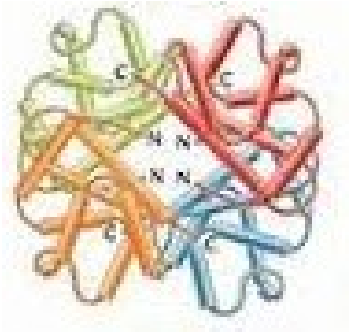


Fig.12.8. Quarternary structure of protein

Hemoglobin is a respiratory pigment present in the red blood corpuscles (RBCs in the blood) of most of the animals. The structure of hemoglobin was determined by Max Perutz and associates by X-ray analysis. They revealed that the hemoglobin molecule is roughly spherical with a diameter of about 5.5 nm. Mammalian hemoglobin is a tetrameric protein consists of two α and two β chains which held together by non-covalent factors. The molecular weight of the molecule is 68000 Daltons and has overall dimensions 64×55×50 Å. Haemoglobin contain four iron containing heme prosthetic groups, each with one subunit. In haemoglobin iron remain in ferrous (Fe^{2+}) form. The protein part of hemoglobin helps heme to keep the iron in Fe^{2+} form and to combine loosely and reversibly with oxygen.

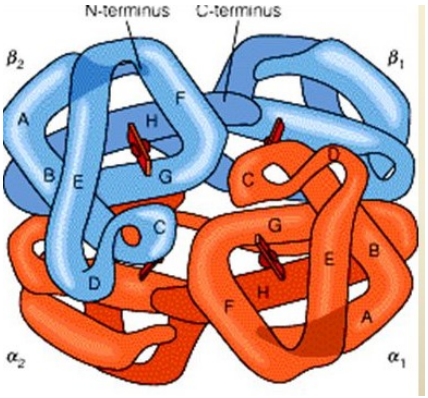


Fig12..9. Structure of haemoglobin

12.5 GENERAL PROPERTIES OF PROTEINS

12.5.1 SOLUBILITY

The solubility of protein varies to the native because proteins are colloids of large-sized molecules these form turbine solution in water. These are also soluble in acid and salt solution while insoluble in alcohol.

12.5.2 AMPHOTERIC NATURE

Like a-acid proteins are amphoteric in nature. They behave as acid alkaline solution and alkaline to acidic solution due to presence of several free- NH_2 and COOH groups.

12.5.3 ZWITTERION FORMATION

The protein is either positively or negatively charged molecule and in an electric field migrate either towards cathode or towards anode. They are electrically neutral and do not move towards any pole.

12.5.4 HYDROLYSIS

The protein undergoes hydrolysis by acid, alkali or hydrolytic enzymes which lead the protein to amino acids. Complete hydrolysis with HCl or H_2SO_4 and yields free a-acid thin breakdown products.

12.5.5 DENATURATION

Under certain conditions there is a disruption of secondary tertiary and quaternary structures of functional protein molecule resulting in the changes of its physical, chemical and biological characteristics. These changes occurring in proteins are collectively called denaturation. During denaturation only primary structure of protein is retained. Various physical and chemical elements such as heat, UV-rays, X-rays, ultrasonic waves, high pressure, acids, alkalis, detergents or certain organic solvents can cause denaturation of proteins. Physical and chemical properties of denatured proteins are different then the native proteins and they lose most of their biological activities, in denatured proteins the solubility is decreased or lost. During denaturation the soluble globular proteins are changed into insoluble fibrous proteins. The process of denaturation also destroys enzyme and hormonal activity and the proteins become biologically inactive. The process of denaturation in some proteins is returned to its native stable confirmation and regains their native structure and biological activity, this process is called renaturation.

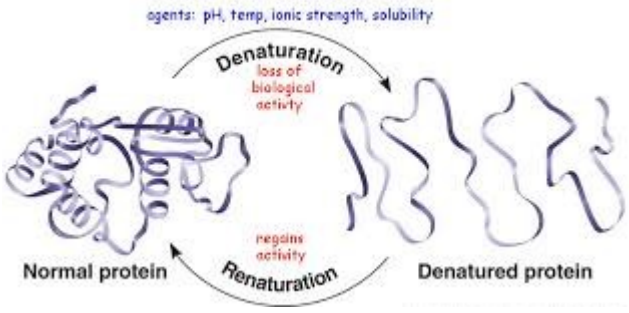


Fig.12.10. Denaturation of protein

12.6 METABOLISM OF PROTEINS

Amino acids are the building blocks of proteins and proteins are the building material in the body. Metabolism of proteins involves both biosynthesis of amino acids as well as breakdown of amino acids.

12.6.1 BIOSYNTHESIS OF AMINO ACID

There are 20 standard amino acids known and these can be classified into the group on the basis of their synthesis in human and animals are called the non essential amino acid whereas the amino acid which cannot be synthesized by the organisms and they must be obtained through diet are called the essential amino acids. The pathways for the synthesis of these two types of amino acids are quite different. Non essential amino acids can be synthesized by quite simple reaction while synthesis of essential amino acids is quite complex.

Biosynthesis of non-essential amino acids:-

Biosynthesis of essential amino acids:-

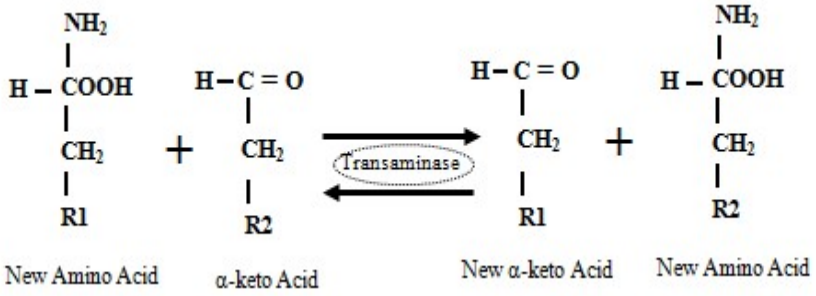
12.6.2 CATABOLISM OF AMINO ACIDS

Amino acids are not only served as the building blocks of proteins but also serve as source of carbon and nitrogen, when required. The very first step in their catabolism is removal of $–NH^2$ group and formation of corresponding keto-acid. The ammonia which is librated, quickly converted to urea and it is incorporated in some other a-acid. Catabolism of a-acid involves the following process:

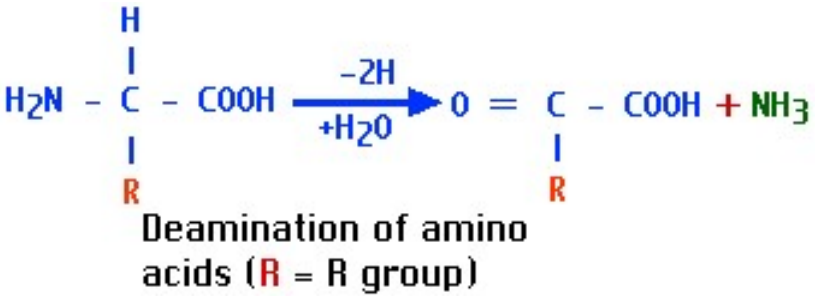
1. Transamination
2. Deamination
3. Urea formation
4. Decarboxylation

Transamination: Russian workers Braunstein and Bychkou had shown the importance of transamination for the first time in 1939. It is the most important process of conversion of amino acid into keto acid. In this process amino group of one amino acid (donor) is transferred to an α-keto acid (recipient) resulting in the formation of a new amino acid and a new keto acid.The donor amino acid is converted into a new keto acid and the recipient keto acid is converted into a new amino acid. Transamination is a reversible process and is catalyzed by the enzyme transaminase or amino transferase. Co-enzyme for the reaction is pyridoxal-5'-phosphate, a

derivative of vitamin B_6 (Pyridoxine). Transamination takes place principally in liver, kidney, heart and brain.



Deamination: Deamination is a process in which amino group ($-NH_2$) is removed from the amino acid, which then changes to a α-keto acid. In this process amino group is removed as ammonia.



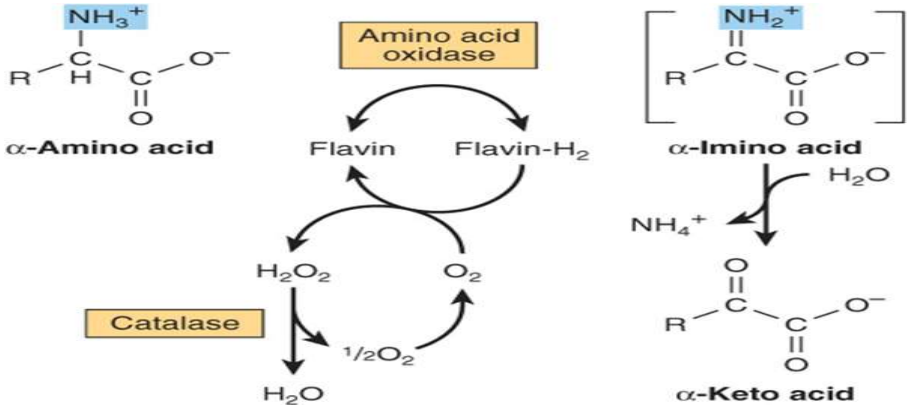
Deamination usually takes place in liver and kidney cells to catabolize excess of amino acids. There are two types of deamination:

i. Oxidative deamination

ii. Non oxidative deamination

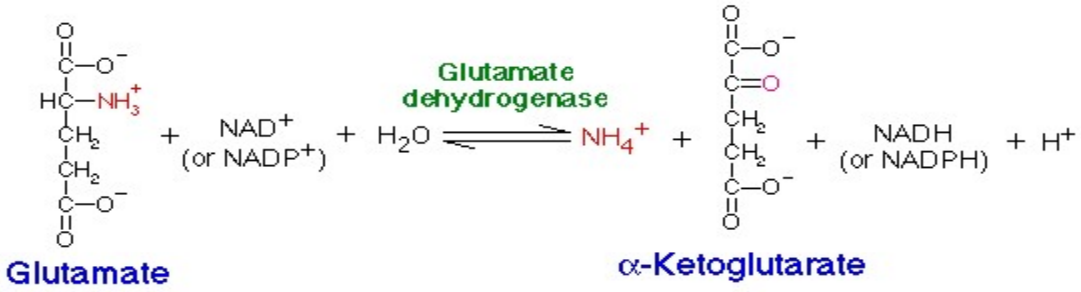
Oxidative Deamination: When deamination process is accompanied by an oxidative reaction, it is known as oxidative deamination. This process is catalyzed by a group of flavin containing enzymes known as amino acid oxidases. This is the two step reaction, in the first step the amino acid is dehydrogenated by the flavoprotein of the enzyme L-amino oxidase to form α-imino acid.

In the next step with addition of H_2O molecule, α-imino nitrogen is released as NH_3 and α- keto acid is formed.



The enzyme amino acid oxidase is auto oxidizable flavoprotein. Reduced flavoprotein is oxidized to form hydrogen peroxide, which then broken up into H_2O and O_2 by the enzyme catalase.

Non oxidative Deamination: There are certain amino acids which can be deaminated non oxidatively. Non oxidative deamination is catalyzed by specific enzymes and NH_3 is liberated in this process. One example of non oxidative deamination is deamination of glutamate by the enzyme glutamate dehydrogenase.



This reaction is reversible in which NAD act as coenzyme.

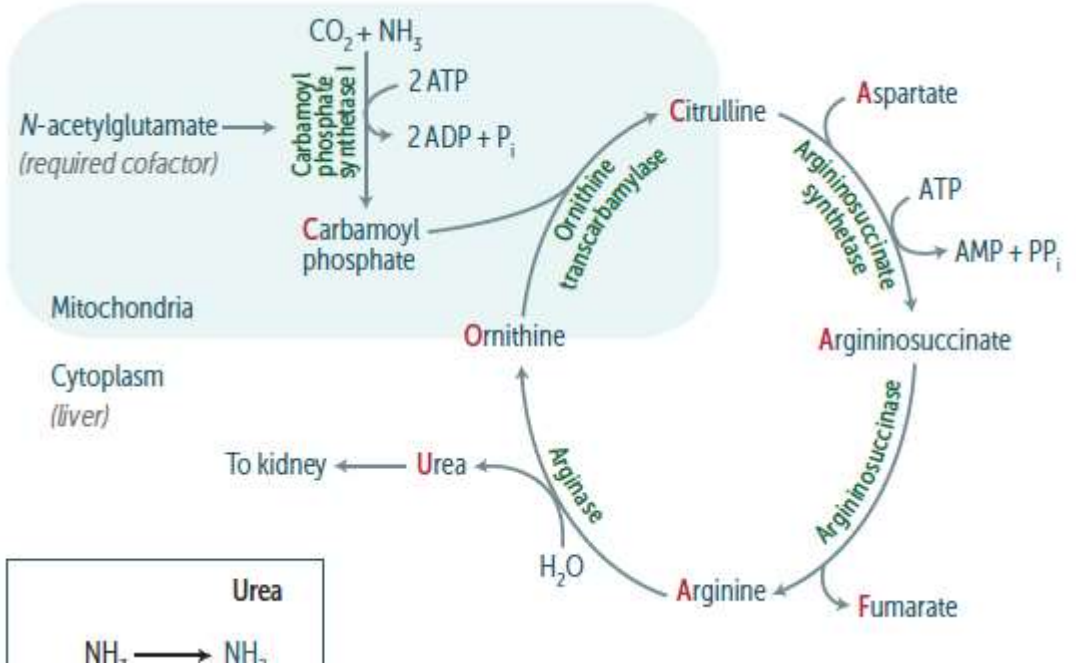
Fate of Deaminated Amino Acids: Acids produced from transamination and deaminations of amino acids are channeled to several metabolic routes. Some amino acids are deaminated to produce keto acids which are eventually oxidyzed to CO_2 and H_2O through acetoacetate and acety-co-A. ***Acetoacetone*** is one of the chemical constituent of 'ketone bodies' formed in the pathological conditions of urine. Thus the amino acid which leads to the formation of acetoacetate during their metabolism are called ketogenic e.g. leucine & lycine. Some amino acids are deaminated to produce keto acids which are broken down to pyruvate, α-keto glutarate,

succinyle co-A, fumerate or oxaloacetate which can be utilized for the synthesis of glucose or glycogen. This amino acid is called glycogenic or antiketogenic amino acid example of glucogenic amino acids are called glucogenic or antiketogenic amino acids. Examples of glucogenic amino acids are alanine, glycine, serine, aspertate, glutamate, valine, histidine argine, proline, metheonine, cystine and arginine. Some amino acids are precursors of both glucose and ketone bodies are known as glucogenic and ketogenic amino acids. Examples are phenylalanine, tyrosine, isoleucine, threonine and tryptophan.

Fate of Ammonia: Ammonia released during deamination is either converted into ammonium salt or into urea.

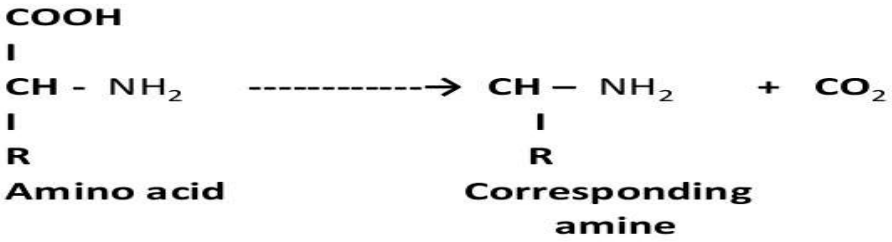
Formation of ammonium salts: - Ammonium ions ($NH_{4+)}$ are formed from some of the ammonia released by deamination of amino acids. These ammonium ions are excreted out from the body in the form of ammonium salts.

Formation of Urea (Urea cycle): When production of ammonia exceeds beyond a certain level it become toxic. Excess of ammonia produced during the deamination of amino acids is converted to less toxic substance, urea, before been excreted in the urine. Formation of urea is a cyclic process and the cycle is known as urea cycle. This cycle was first outlined by Hans Krebs and Kurt Henseleit in 1932; hence it is also known as Kreb's Hanseleit cycle. The chief site for urine formation is liver and after its formation urea passes into the blood stream and from blood to kidneys and finally excreted into the urine. Urea synthesis takes place in five steps. Each step is catalyzed by a specific enzyme. Out of these five enzymatic reactions, two take place in the mitochondria and three take place in the cytoplasm. This cycle is also known as ornithin cycle as it involves conversion of amino acid ornithin to citrulline though glutamic acid which is derived from aspartic acid by transamination and/or form α-ketoglutaric acid and ammonia.



Decarboxylation: Decorboxylation is the process in which CO_2 is removed from the carboxyl group of an amino acid resulting the formation of an amine. Enzyme aminoacid decarboxylases catalyse these reactions which require pyridoxal phosphate as coenzyme.

Decarboxylation reaction



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For example histdine is decarboxylated to histamine by histidine decarboxylase and 3,4-dihydroxyphenylalanine is decarboxylated to dopamine. These types of amines are called biogenic amines. Many of these amines have strong pharmacological effects and others are important as precursors of hormones or as co-enzymes.

12.7 SOURCES OF PROTEINS

Proteins are widely distributed in plants and animals. Common sources of proteins are milk, yogurt, cheese, fishes, beans, nuts, green peas, meat, eggs, lentils, soy products, quinoa and sea foods.

12.8 BIOLOGICAL SIGNIFICANCE OF PROTEINS

Proteins are the most significant macromolecules in living beings because of the following physiological roles performed by them in all biological processes:

1. Proteins which are involved in the formation and maintenance of various cellular structures are called structural proteins. These proteins form an important part of all membranes and membrane bound organelles of the cell. The cell wall and primary fibrous of the cell have structural proteins e.g. Collagen is the most abundant fibrous protein found in animals forming a major part of the skin, cartilage, ligament, tendons and bones. Keratin is another animal protein involved in the formation of scales, hair, feather, horns, hoofs, fur wool, nails and claws.
2. Capacity of motion and flexibility in the organisms is due to the presence of certain proteins called contractile proteins e.g. Muscle proteins- actin and myosin.
3. Proteins acts as enzymes or biocatalysts and catalyzes a variety of chemical reactions in the living organisms. Almost all the enzymes are protein in nature.
4. Some proteins bind and transport specific types of molecules via blood e.g. haemoglobin is important protein, transports oxygen from lungs to cell tissues. Myoglobion binds and transports oxygen in the muscles. Certain membrane proteins transport ions and small molecules across the cell membrane.
5. Some proteins are stored as reserve food such as albumin in egg and gluttelin in rice. In the liver ferritin stores iron.
6. A few proteins functions as hormone e.g. insulin.
7. Proteins also play important role in the immune system of vertebrates. Antibodies are immunoglobulins which combine and neutralize the antigen entering the body.
8. Proteins also take part in blood coagulation e.g. thrombin and fibrinogen.

12.9 DEFICIENCY DISEASES OF PROTEINS

Protein deficiency can lead to weak muscle tone, thin and brittle hair, edema or swelling, skin lesions, fatigue, stunted growth and cognitive development as well as mental health in children. Following diseases can occur due to protein deficiency:

Marasmus: It affects infants and very young children, often resulting in weight loss and dehydration. People with marasmus appear bony with little muscle tissue.
Kwashiorkor: It usually affects older children. People with Kwashiorkor appear swollen stomach due to fluid retention.
Cachexia: It is a condition that involves protein deficiency, depletion of skeletal muscle and an increased rate of protein degradation. It causes weight loss and mortality and is associated with cancer, AIDS, heart disease and chronic kidney failure.

12.10 SUMMARY

- Proteins are polymers of amino acids in which amino acids are joined together by peptide bonds.
- Proteins are the most abundant and significant compounds in the living body.
- Proteins are involved in wide variety of functions in living beings. They function as catalyst; take part in structural organization and transportation; control growth and differentiation; provide support and immune protection.
- Proteins can be classified on the basis of their functions, shape, structure and complexity.
- Protein structure can be described by its four levels of organization. Primary structure refers to the amino acid sequence. Secondary structure describes the regular polypeptide folding pattern such as α-helices and β-sheets. Tertiary structure refers to the folding secondary structural elements of the protein. Proteins with more than one polypeptide chains exhibit quaternary structure which describes the spatial rearrangement and noncovalent association of the subunits in a protein.
- Proteins are soluble in acids and salt solutions, amphoteric in nature and denatured by heat, acids, detergents and certain radiations.

- Amino acids are the building blocks of protein thus metabolism of protein refers to the synthesis of amino acids (anabolism) and breakdown of amino acids (catabolism).
- Biosynthetic pathways for essential and non essential amino acids are quite different.
- Non essential amino acids are synthesized in simple pathways from pyruvate, oxaloacetate, α-ketoglutarate or 3-phosphoglycerate whereas the pathways for the synthesis of essential amino acids are much more complicated as compared to the synthesis pathways of non essential amino acids.
- Degradation of amino acids involves transamination, deamination and decarboxylation.
- Urea synthesis takes place in five different steps, each step is catalyzed by a specific enzyme.