Proteins

Proteins are organic nitrogenous compounds in which a large number of amino acids are joined together by peptide linkages to form long polypeptide chains.

Structure of Proteins

Primary Structure: It is the basic structure of a protein in which a number of polypeptides are involved having a sequence of amino acids. The first amino acid of the sequence is called N-terminal amino acid and the last amino acid of the peptide chain is called the C-terminal amino acid.

Secondary Structure: Secondary structure protein threads form a helix. There are three types of secondary structure- α helix, β pleated and collagen. In α helix, the polypeptide chain is coiled spirally in a right-handed manner. In β pleated secondary proteins, two or more polypeptide chains are interconnected by hydrogen bonds. In collagen, there are three strands or polypeptides coiled around one another by hydrogen bonds.

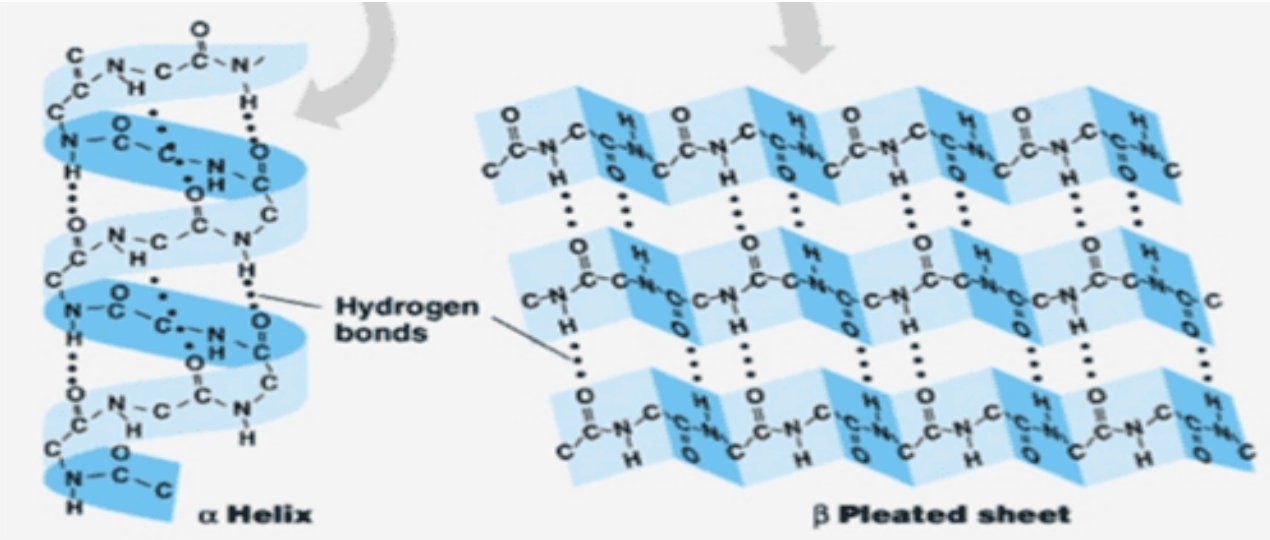
There are three types of secondary structures a-helix, B-pleated sheet and collagen helix. The turns of helices and sheets are attached by hydrogen bonds.

α-helix

- The -helix is a rigid, rod like structure that forms when a polypeptide chain twists into a helical conformation.
- The screw sense of helix can be right-handed (clockwise) or left-handed (counter clockwise).
- Right-handed helices are energetically more favourable.
- There are **6 amino acid residues per turn of the helix**
- The **pitch** (the distance between corresponding points per turn) **is 0.54 nm**.
- Each residue is related to the next one by a **rise of 1.5 Å (0.15 nm**) along the helix axis.
- **A single turn of -helix involves 13 atoms** from O to the H of the H bond.

For this reason, the -helix is referred to as the 3.6_{13} helix.

- Length of -helix is usually 10-15 amino acid residues.
- Hydrogen bonds form between the N-H group of each amino acids and the carbonyl group of the amino acid four residues away.



β-pleated sheets

- -pleated sheets form when two or more polypeptide chain segment line up side by side.
- Each individual segment is referred to as a -strand.
- Each -strand is fully extended.
- The distance between adjacent amino acids along a strand is approximately 3.5 .
- -pleated sheets are stabilized by hydrogen bonds that form between the polypeptide backbone N-H and carbonyl groups of adjacent strand.
- Adjacent strand can be either parallel or antiparallel.

Turns

- Most proteins have compact, globular shapes, requiring reversals in the direction of their polypeptide chains. Many of these reversals are accomplished by a common structural element called the turn.
- Turns, composed **of three or four residues**
- Tur are classified as a **third type of secondary structure**.
- They are **U-shaped** secondary structures are stabilized by a hydrogen bond between their end residues.
- **Glycine and proline** are commonly present in tuns.
- The lack of a large side chain in glycine and the presence of a built-in bend in proline allow the polypeptide backbone to fold into a tight U shape. Turns allow large proteins to fold into highly compact structure.

Conditions allowing denaturation of Proteins:

Strong acids or bases

- Changes in pH result in protonation or deprotonation of side group of amino acids of protein
- It alters hydrogen bonding and salt bridge patterns.

Organic solvents

- Water-soluble organic solvents such as ethanol interfere with hydrophobic interactions because they interact with nonpolar R groups and form hydrogen bonds with water and polar protein groups.

- Nonpolar solvents also disrupt hydrophobic interactions.

Detergents

- These amphipathic molecules disrupt hydrophobic interactions, causing proteins to unfold into extended polypeptide chains

Reducing agents

- In the presence of reagents such as urea, reducing agents such as -mercaptoethanol convert disulfide bridges to sulfhydryl groups.

Heavy metal ions

- They disrupt salt bridges by forming ionic bonds with negatively charged. groups. Heavy metals also bond with sulfhydryl groups.

Temperature change

- As the temperature increases, the rate of molecular vibration increases. Eventually, weak interactions such as hydrogen bonds, van der Waal interaction are disrupted and the protein unfolds.

SOLUBILITIES OF PROTEINS

Effect of pH:

- At pl, the protein molecules carry no net charge. At pl, protein has minimum solubility. Hence when the pH of a protein mixture is adjusted

to the pl of the protein to be isolated, its precipitation occurs due to decrease in solubility.

Effect of ionic strength:

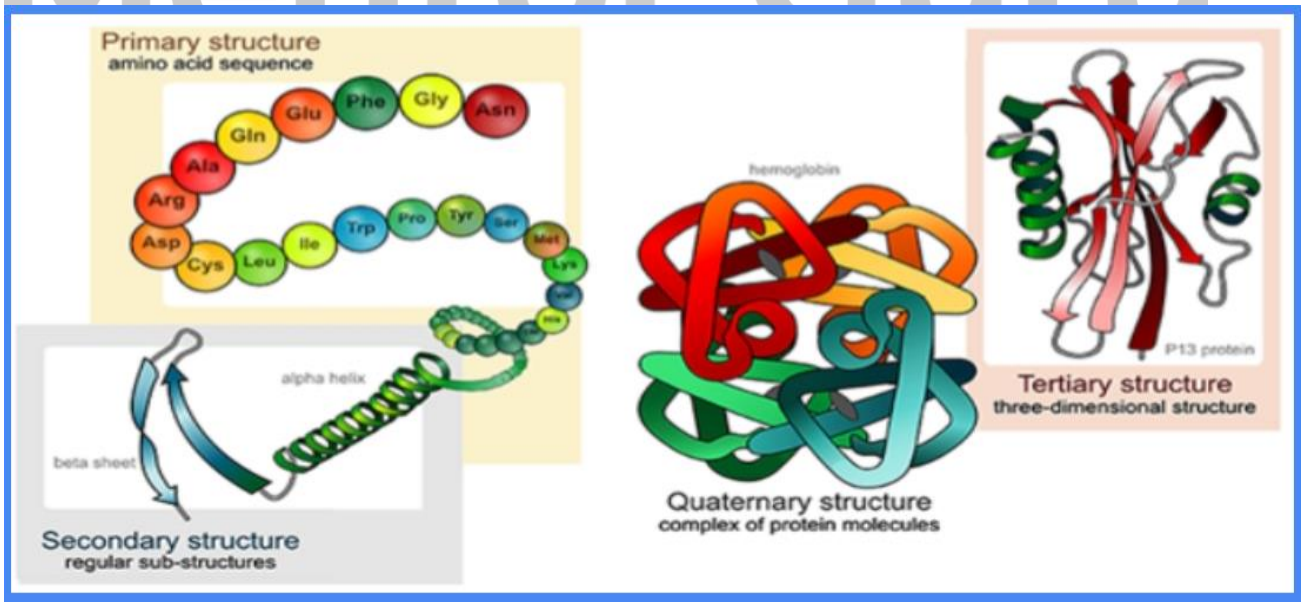
- The solubility of a protein at low ionic strength generally increases with salt concentration. This process is known as **salting in**.
- The binding of salt ions to the protein's ionizable groups decreases interaction between oppositely charged groups on the protein molecules. Water molecules then can form solvation spheres around these groups. However, when large amounts of salt are added to a protein in solution, a precipitate form. This process is referred to as **salting out**.

Effect of solvent:

- Organic solvents such as acetone, ethanol, due to their low dielectric constants lower the solvating power of their aqueous solutions for proteins.

<u>Tertiary structure:</u> The long protein chain is folded upon itself like a hollow woollen ball to give a three-dimensional view of protein.

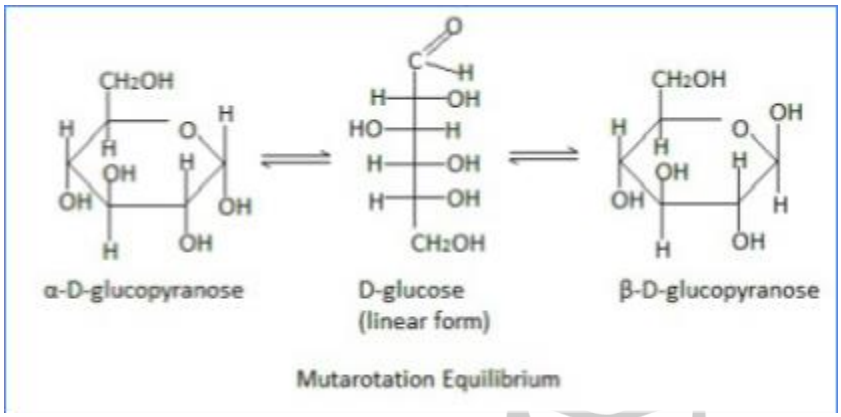
<u>Quaternary structure:</u> Each polypeptide develops its own tertiary structure and functions as a subunit of protein. E.g. Haemoglobin. In the adult, 4 human subunits of haemoglobin are involved. The two subunits are of α type and two subunits of β types.



Mutarotation:

Mutarotation was discovered by Dubrunfaut in 1844. He noticed that there was a change in the specific rotation of sugar, in an aqueous solution, with respect to time.

It is a deviation from the specific rotation, due to the change in the equilibrium between α anomeric and β anomeric form, in the aqueous solution. For Example: Mutarotation present in the glucose molecule



Points to Remember

- Glycosidic bonds are covalent chemical bonds that hold together a glycoside. A glycoside is simply a ring-shaped sugar molecule that is attached to another molecule.
- A glycosidic bond forms by a condensation reaction, which means that one water molecule is produced during the formation of a glycoside.