

BASUDEV GODABARI DEGREE COLLEGE KESAIBAHAL



BLENDED LEARNING STUDY MATERIALS

UNIT-II

DEPARTMENT: ZOOLOGY

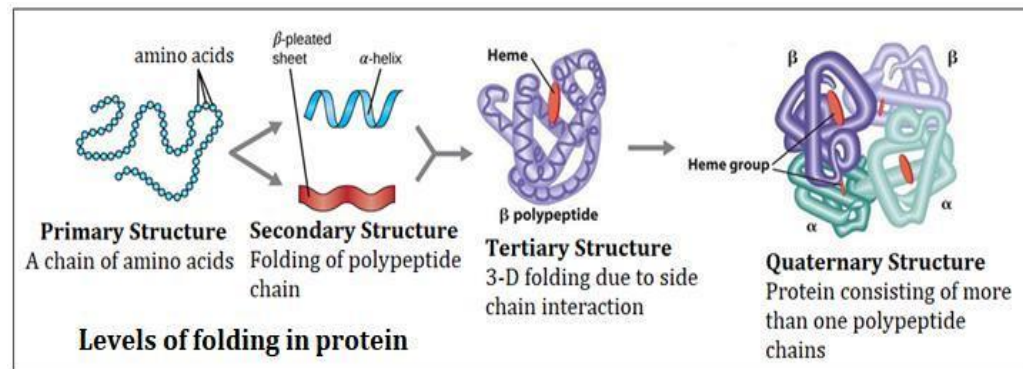
**SUBJECT : LEVELS OF ORGANIZATION IN
PROTEINS**

SEMESTER : III

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Lect in zoology**

Levels of organization in proteins

- ❖ Proteins are structurally organized into four levels; primary structure, secondary structure, tertiary structure and quaternary structure.



1. Primary structure of protein:

- ❖ Primary structure of protein refers to the sequence and arrangement of amino acids in polypeptide chain.
- ❖ α -COOH group (carboxyl group) of one amino acid is linked with α -NH₂ group (amino group) of other amino acid by peptide bond. The Peptide bond linked successive amino acids in polypeptide chain.
- ❖ In polypeptide chain α -COOH group and α -NH₂ group of most amino acids are involved in formation of peptide bond. However, two amino acids which are situated at either end of polypeptide chain have either -COOH group free or -NH₂ group free.
- ❖ The end at which -COOH group is free is called C-terminal and another end at which -NH₂ group is free is called N-terminal of polypeptide chain.

- ❖ Since, most of α -COOH and α -NH₂ group formed peptide bond, they are not available for other bonding except Hydrogen bonding.
- ❖ The peptide bond occurs in TRANS-configuration and have partial double bond character.
- ❖ Due to partial double bond character between –CO and –NH group, they do not rotate during formation of folded secondary and tertiary structure. However, bonds between –C α and –NH and –C α and –CO rotate freely during folded structure formation.

2. Secondary structure of protein:

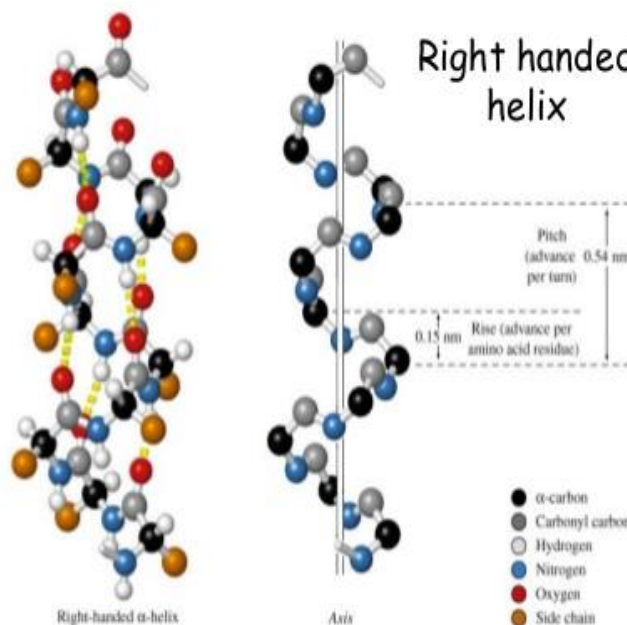
- ❖ Amino acids that are located near to each other interacts to form regular arrangement called secondary structure.
- ❖ Formation of secondary structure involve local folding of polypeptide chain.
- ❖ There are three commonly occurring secondary structure. They are;
 - α -Helix
 - β -sheet
 - β -bends or β -turn

i. α -helix structure:

- ❖ α -helix is a right-handed helical structure formed by twisting of polypeptide chain.
- ❖ It is a spiral structure.

- ❖ Each helix in α -helix structure contains 3.6 amino acids residues. Vertical length of each helix is known as pitch which is 5.4 Å. Therefore, the vertical distance between two nearest amino acids is 1.5Å which is called Identity period of α -helix.
- ❖ In α -helix, $-C=O$ group of each amino acid is hydrogen bonded with $-NH$ group of other amino acid which is situated four amino acid ahead. Therefore, $-C=O$ and $-NH$ group of all amino acids are hydrogen bonded in α -helical structure.
- ❖ R-group of amino acid in α -helix are projected outward to minimize steric hindrance.

Alpha-Helix



- Residues per turn: 3.6
- Rise per residue: 1.5 Angstroms
- Rise per turn (pitch): $3.6 \times 1.5\text{A} = 5.4\text{ Angstroms}$
- amino hydrogen H-bonds with carbonyl oxygen located 4 AA's away forms 13 atom loop

- ❖ Some amino acids disrupt α -helix. For examples, the amino acids with charged R-group disrupt α -helix by electrostatic repulsion or

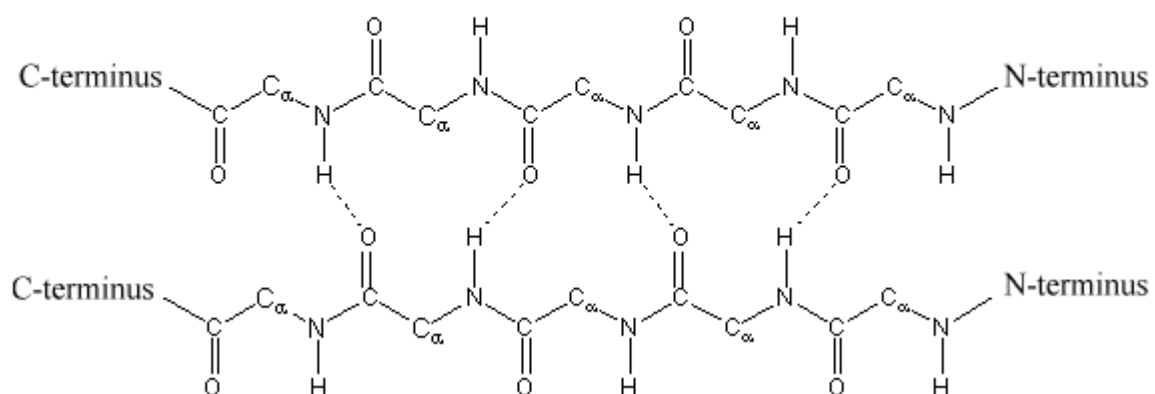
by formation of ionic bond. Similarly amino acids with bulky R-group disrupt α -helix by steric interference.

- ❖ Amino acids glycine and proline bring bend in polypeptide chain and disrupt α -helix.

ii. β -sheet structure:

- ❖ β -Sheet is the most stable form of secondary structure of protein.
- ❖ It is formed between two different polypeptide chains which are placed parallel or antiparallel to each other.
- ❖ It can also be formed by folding of same polypeptide chain.
- ❖ In β -sheet structure, two polypeptide backbones are linked with each other by H-bond which are formed between $-\text{CO}$ and $-\text{NH}$ group.
- ❖ R-group of amino acids are alternately projected above and below the plane of β -sheet.
- ❖ The surface of β -sheet is not straight but it is pleated. Therefore, it is also known as β -pleated sheet.

Parallel β Sheet

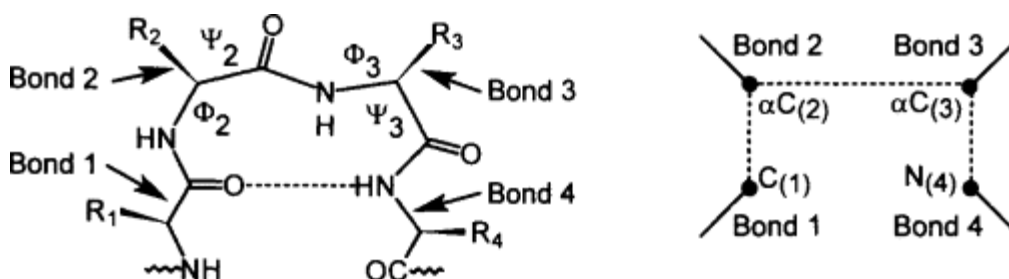


β -sheet differ from α -helix in many characteristics as given below;

- ❖ Polypeptide backbone in β -sheet is extended rather than being tightly coiled as in α -helix.
- ❖ The axial distance between two nearest amino acid is 3.5 Å in contrast with 1.5 Å in α -helix.
- ❖ In β -sheet hydrogen bond may be inter chain or intra chain but they are always inter chain in α -helix.

iii. β -bends or β -turn structure:

- ❖ β -bend reverse the direction of polypeptide chain and helps it to form globular (spherical) structure.
- ❖ β -bend structure consists of at least 4 amino acids in which n th amino acid is hydrogen bonded with $(n+3)$ the amino acids.
- ❖ Glycine and proline are always found in β -bend structure.
- ❖ Ring of Proline attached with α -carbon atom helps to bend the chain. Similarly, lack of R-group in glycine permits great degree of rotation around α -carbon atom and bring bend in the polypeptide chain.



3. Tertiary structure of protein:

- ❖ Tertiary structure refers to the overall folding of a polypeptide chain to form a final three-dimensional structure.
- ❖ For example, a globular protein which are larger than 200 amino acids units forms two or more domains by folding of polypeptide chain by either α -helix, or β -pleated sheet or β -bend. Finally, these domains associates with each other to form final 3D structure.
- ❖ Therefore, tertiary structure refers to the formation of these domains by overall folding of polypeptide chain and then final association of these domains to form globular 3D structure.
- ❖ Bonds like H-bond, hydrophobic interaction, ionic bond and disulphate bond help in folding of polypeptide chain during formation of tertiary structure.

4. Quaternary structure of protein:

- ❖ Some proteins are composed of more than one polypeptide chain. Each polypeptide chain in such protein are called sub-units.
- ❖ The quaternary structure refers to interaction between these sub-units to form large final 3D structure. Therefore, quaternary structure is interaction between different polypeptide chains of multi chain protein.
- ❖ Quaternary structure is found only in protein which are composed of more than one polypeptide chains such as haemoglobin
- ❖ Bonds like H-bond, ionic bond, hydrophobic interaction helps to from quaternary structure.

