Topic: Primary, Secondary, Tertiary, Quaternary domains & Fold structures of Proteins

(Part I)

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Introduction :- Acid hydrolysis of Proteins by Emil Fisher in 1902 provided free amino acids, hence proteins are recognised basically as polymer of Amino Acids. Carboxyl group of an amino acid, after reacting with amino group of the next amino acid, forms an amide bond and releases a molecule of water. The term polypeptide is mostly used when the no. of amino acids exceeds 10. Likewise, the term 'protein' is used when molecular weight of polypeptide exceeds 5,000 - 8000 daltons. In Protein, polypeptide chains are rarely in simple straight chain form but are in different conformations arising out of straight chain forms. Accordingly, Proteins have been found to exhibit four different successive structural levels — (i) Primary Structure (ii) Secondary Structure (iii) Tertiary structure (iv) Quaternary structure;

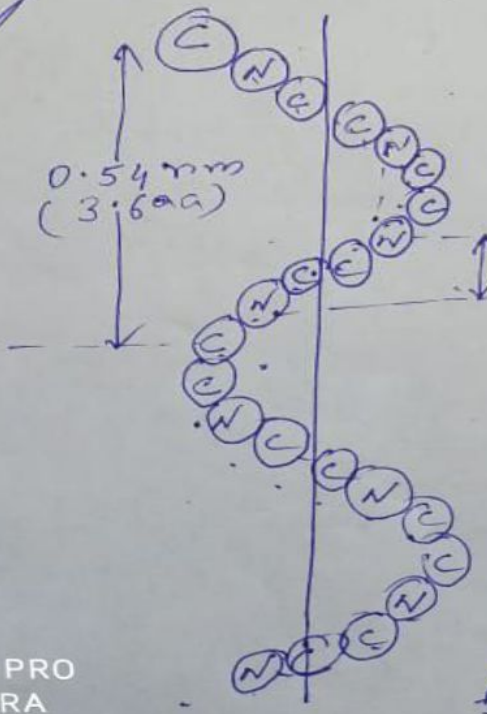
1. Primary Structure → This is the simplest of protein structure. Here, polypeptide chain is linearly elongated to different lengths. The sequence of arrangement of the amino acids is specific which places R-group at specific position in chain that determine the protein structure of the next order and ultimately functional groups of globular proteins enzymes. However, the primary structure of protein has only one conformation because the R-groups linked to the Carbon is the covalent backbone don't have full freedom of rotation.

2. Secondary structure :- This is a higher level of structural organisation next to primary structure. It is in the form of helix or pleated sheet. ~~α-Keto~~ α-Keratin, the most basic secondary protein structure was studied by Williams Astbury in early 1930s. He found that α-keratins produced characteristic diffraction pattern showing repeat unit of 0.50 - 0.55 nm along a long axes of molecules. Two Typycal examples of Secondary structures are a α-helix and b β-pleated sheet.

a α-helix → Each turn of α-helix comprises of 3.6 amino

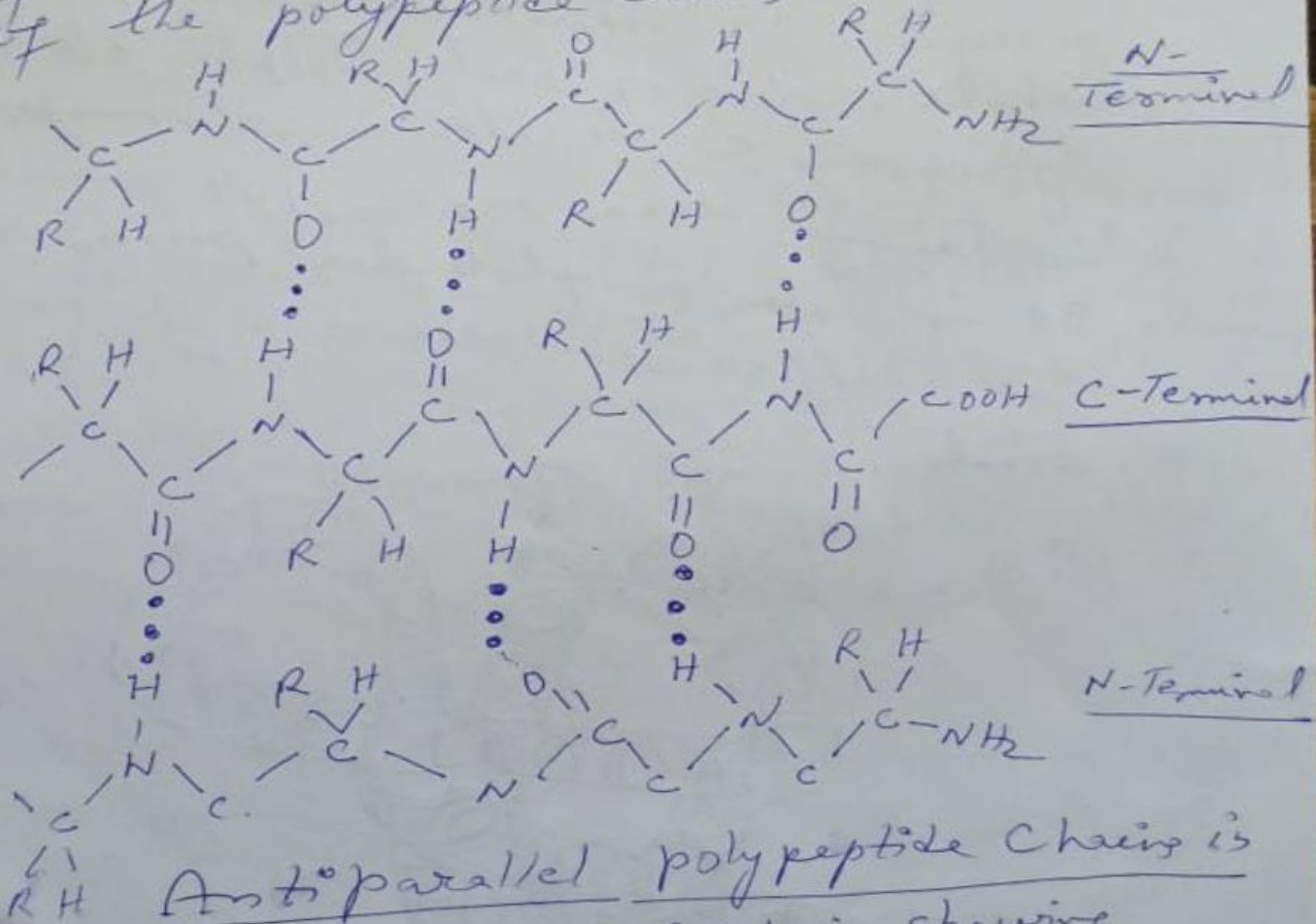
with an axial rise of 0.54 nm and rise per amino acid being 0.15 nm. Shown by x-ray diffraction data.

- α-helix permit the formation of intrachain hydrogen bond in between adjacent turns of the helix.
- All peptide bonds participate in hydrogen bonding imparting maximum possible stability.
- Electrical vectors of all hydrogen bonds are linear and are parallel to each other, thus reinforcing stability.
- All the R-groups of the helix are directed outward.
- However, the stability of conformation of α-helix is subject to change under the influence of R-groups present in close proximity in the adjacent turns.



Right handed α-helix

b. **β-pleated Sheet** → Pauling & Corey explained that a different conformation was presented by β-keratin wherein the polypeptide chain exhibit a zig-zag conformation, hence the periodicity of repeat unit increases from 0.5 nm to 0.70 nm. The polypeptide chains in pleated sheet runs antiparallel to each other and are held together by interchain hydrogen bond. (~~Fig IA 3.7~~). Prof. G.N. Ramachandran, an Indian biophysicist of Indian Institute of Science, Bangalore, studied the possibilities of rotation of adjacent planes of the peptide bonds around the α-carbons of the polypeptide chains.



Antiparallel polypeptide Chains in β-pleated sheet of Fibroin showing interchain H-bonds