Protein Structure

The linear sequence of amino acid residues in a polypeptide chain determines the three-dimensional configuration of a protein, and the structure of a protein determines its function. All proteins contain the elements carbon, hydrogen, oxygen, nitrogen and sulfur some of these may also contain phosphorus, iodine, and traces of metals like ion, copper, zinc and manganese.

A protein may contain 20 different kinds of amino acids. Each amino acid has an amine group at one end and an acid group at the other and a distinctive side chain. The backbone is the same for all amino acids while the side chain differs from one amino acid to the next.

The structure of proteins can be divided into four levels of organization:

**1. Primary Structure**

The primary structure of a protein consists of the amino acid sequence along the polypeptide chain. Amino acids are joined by peptide bonds. Because there are no dissociable protons in peptide bonds, the charges on a polypeptide chain are due only to the N-terminal amino group, the C-terminal carboxyl group, and the side chains on amino acid residues.

The primary structure determines the further levels of organization of protein molecules.

**2. Secondary Structure**

The secondary structure includes various types of local conformations in which the atoms of the side chains are not involved. Secondary structures are formed by a regular repeating pattern of hydrogen bond formation between backbone atoms. The secondary structure involves α-helices, β-sheets, and other types of folding patterns that occur due to a regular repeating pattern of hydrogen bond formation.

The secondary structure of protein could be :

Alpha-helix or Beta-helix

1. The α-helix is a right-handed coiled strand. The side-chain substituents of the amino acid groups in an α-helix extend to the outside.

2. Hydrogen bonds form between the oxygen of the C=O of each peptide bond in the strand and the hydrogen of the N-H group of the peptide bond four amino acids below it in the helix.

3. The side-chain substituents of the amino acids fit in beside the N-H groups.

4. The hydrogen bonding in a ß-sheet is between strands (inter-strand) rather than within strands (intra-strand).

5. The sheet conformation consists of pairs of strands lying side-by-side.

6. The carbonyl oxygens in one strand hydrogen bond with the amino hydrogens of the adjacent strand.

7. The two strands can be either parallel or anti-parallel depending on whether the strand directions (N-terminus to C-terminus) are the same or opposite.

8. The anti-parallel ß-sheet is more stable due to the more well-aligned hydrogen bonds.

**3. Tertiary Structure**

Tertiary structure of a protein refers to its overall three-dimensional conformation. The types of interactions between amino acid residues that produce the three-dimensional shape of a protein include hydrophobic interactions, electrostatic interactions, and hydrogen bonds, all of which are non-covalent. Covalent disulfide bonds also occur. It is produced by interactions between amino acid residues that may be located at a considerable distance from each other in the primary sequence of the polypeptide chain.

Hydrophobic amino acid residues tend to collect in the interior of globular proteins, where they exclude water, whereas hydrophilic residues are usually found on the surface, where they interact with water.

**4. Quaternary Structure**

Quaternary structure refers to the interaction of one or more subunits to form a functional protein, using the same forces that stabilize the tertiary structure.

It is the spatial arrangement of subunits in a protein that consists of more than one polypeptide chain.

