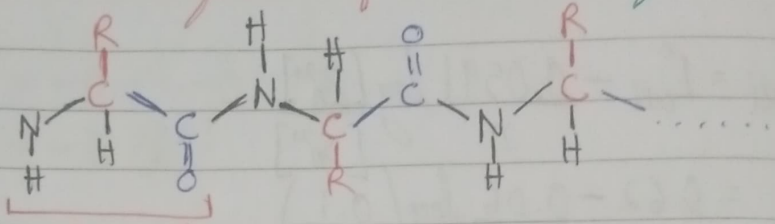
Protein Structure :-

1. Primary Structure :-

It consists of amino acid sequence linked together by peptide bonds along the polypeptide chain.
It is the structure formed after translation of mRNA



Amino acid (Amino group + R group + Carboxyl group)

2. Secondary Structure :-

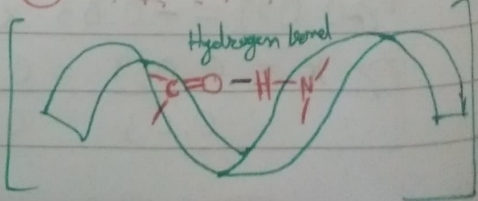
It refers to localized folding of the polypeptide chain into specific structures due to hydrogen bonding between backbone atoms. It contributes to the proteins' overall shape and function

(i) Alpha helix (α-helix) :-

- It is a right-handed coiled/spiral shaped strand
- Hydrogen bond forms between oxygen of carboxyl group of one amino acid and hydrogen of amino group of another amino acid which is 4 residues away.
- The backbone of polypeptide chain twists around itself to form a spiral staircase/helical structure.

Eg :- aa1 — aa2 — aa3 — aa4 ...

aa1 bonds with aa4
aa2 bonds with aa5
: so on



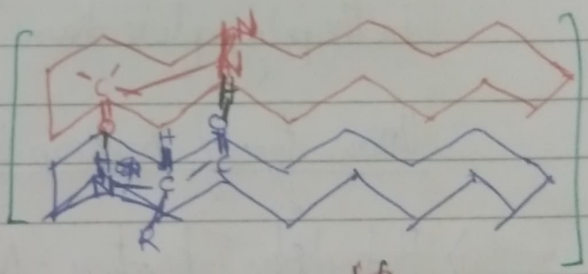
(ii) Beta sheet (β-sheet) :-

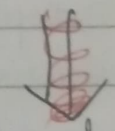
- It consists of extended polypeptide strands that align side by side.
- Hydrogen bond forms between oxygen of carboxyl group of one amino acid and hydrogen of amino group of another amino acid in adjacent strand.
- Rather than coiling, the chain extends and are oriented two ways:

1) Parallel β sheet :- The strands run in same direction
2) Anti-parallel β sheet :- The strands run in opposite direction

Eg:- aa1 — aa2 — aa3 — aa4 .....
aa1 — aa2 — aa3 — aa4 ..... } Two different strands

aa1 bonds with aa1
aa2 " " aa2
; so on

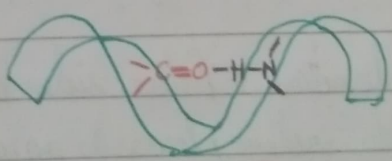




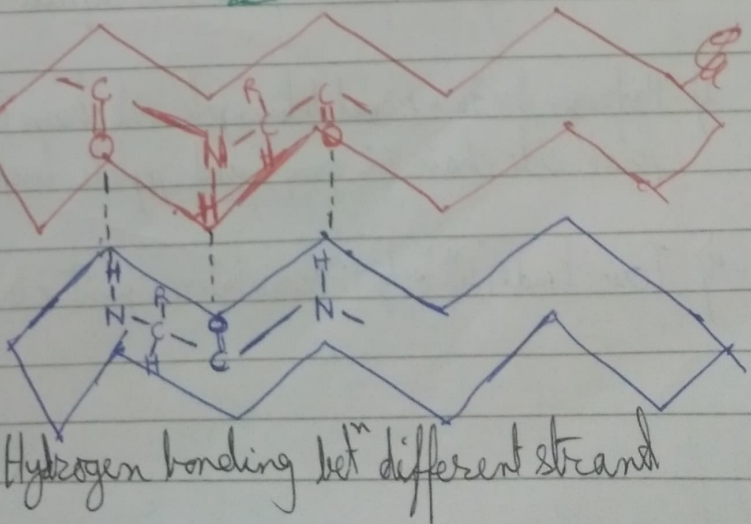
Hydrogen bonding in same strand itself

Structure of :-

i) Alpha helix



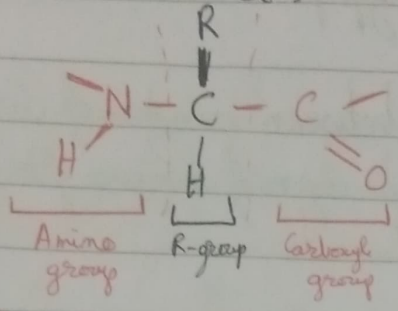
ii) Beta sheet



Hydrogen bonding bet" different strand

3. Tertiary Structure:-

In amino acid structure :-



Amino group ($-NH_2$) & Carboxyl group ($-COOH$) are considered the backbone atoms involved in peptide bond formation

R-group (side-chain) is considered the variable group that is attached to the α-carbon of the amino acid.

∴ Tertiary Structure of protein is determined by the interactions between various R groups (side chains) of the amino acids in the polypeptide chain.

Various types of R-group Interactions :-

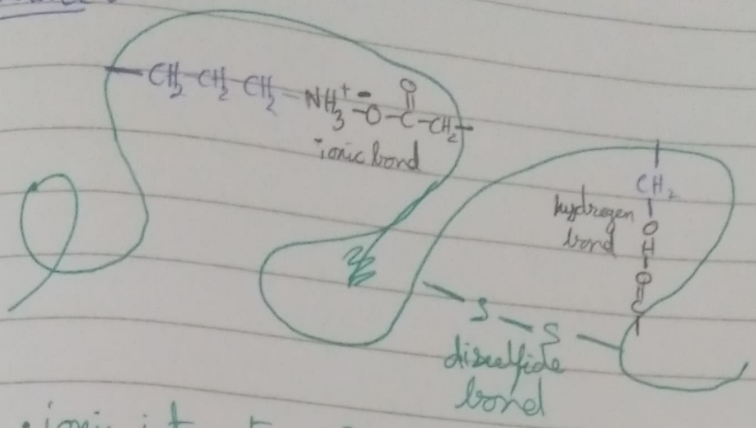
1) Hydrophobic Interactions :- Non-polar side chains cluster in the interior of the protein, away from aqueous environment.

2) Hydrophilic Interactions :- Polar side chains cluster in the exterior of the protein, towards aqueous environment.

3) Hydrogen bonds :- Formed between polar side chains (R-R interaction) or between polar side chain (R-group) and peptide back

4) Ionic bonds (salt bridge) :- Occurs between positive & negative charged side chains

Structure :-



Here, • ionic interaction
• hydrogen bond
• disulfide bond
} bet" amino acid residues (3D shape of a protein)

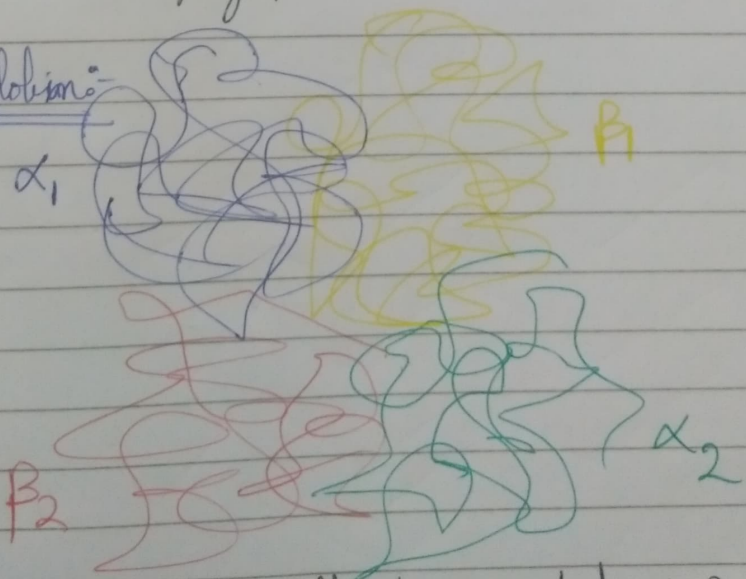
This structure has single polypeptide chain "backbone" with one or more protein secondary structures.

4. Quaternary Structure :-

Unlike Tertiary structure, which has 1 polypeptide chain
Quaternary structure has more than 1 polypeptide chain (subunits)

- It is the interactions of one or more subunits → functional protein
- It is the spacial arrangement of subunits Hence, it consists of more than one polypeptide chain.

Eg: Haemoglobin :-



Haemoglobin consists of 2 α-helix + 2 β-sheets