## Secondary Structure of proteins {essay}

- Configurational relationship between residues, which are about 3-4 Å's apart in linear sequence.

- Secondary structure

### Forces stabilising protein structure

# protein structure is stabilized by 2 types of forces.

1. Covalent Bonds.
- Includes peptide & disulphide bonds

2. Non-covalent Bonds.

Individually weak, but numerous in number.
Hence contribute cedensively to structural stability of proteins

## Non - covalent Bonds.

- Secondary and tertiary structures are preserved by non - covalent forces like;
- Hydrogen Bond
- Electrostatic bond (Ionic bond)
- Hydrophobic bonds
- Vanderwaals forces

## Hydrogen Bond.

- weak electrostatic attraction formed between H atom attached to peptide N, & O atom attached to peptide C.

$$-N-H \cdots O=C \cdots$$

Hydrogen Bonds are donated by.

- -NH of heterocyclic amino acids His, Trp and peptide.
- -OH of hydroxy aminoacids like Ser, Thr.
- $-NH_2$ of Basic acids like Arg, Lys.

Hydrogen Bonds are accepted by.

- $-COO^-$ of acidic aminoacids like Asp, Glu.
- -S-S of disulphide.
- -C=O of peptide.

2. Electrostatic bonds (ionic bonds)

- positive charge are donated by basic AA
  - Amino grp of lys
  - Guanidium gp of Arg.
  - imidazole gp of His.
- Negative charges are donated by acidic AA
  - Beta & gamma $-COOH$ gp of Asp & Glu

$---NH_3^+ ----- COO^- ------$

3. Hydrophobic Bonds.

- Interaction between non-polar hydrophobic side chains by eliminating water molecules.
- Helps to hold lipophilic side chains together.

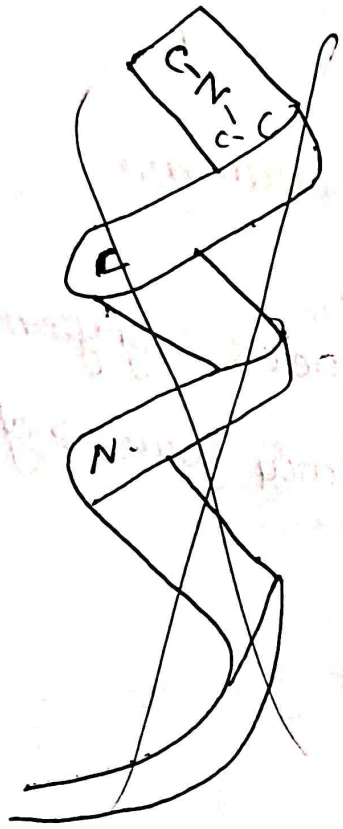
4. Van der waal's force.

- weakes of all non-covalent forces.
- But collectively contribute maximum towards the stability of protein structure.

protein conformation in secondary structure

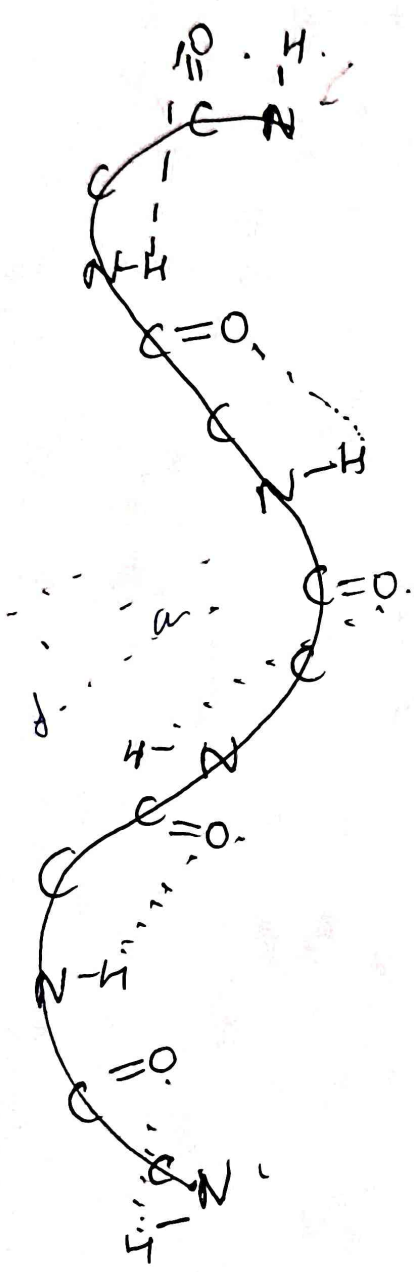
- Linus pauling and Robert Corey made significant contributions in describing secondary structure of proteins
  - $\alpha$ Helix
  - $\beta$-pleated sheet
  - collagen helix.

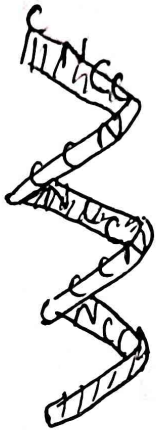
# Alpha Helix.




Must draw str (2 marks).

- Most common & stable conformation of a for a polypeptide chain.
- It is a spiral str. polypeptide bonds form the back bone & side chains of aminoacids extend outward.
- stabilized by hydrogen bonds between NH & C=O gap of main chain
- Each turn is formed by 3.6 residues. distance btw each AA residue is 1.5 Å.
- Generally right handed.





3.6 A°
1.5 A°.

α Helix mostly in.

- Hb & myoglobin.

absent:

hydroxy proline / proline. not in α helix

- proline & hydroxy proline will not allow formation of α-helix.

- α helix is seen in Hb & myoglobin.

- α helix absent in chymotrypsin.

β pleated sheet.

- polypeptide chains in beta pleated sheet is almost fully extended.
- Distance btwn adjacent A.A is 3.54°
- stabilised by hydrogen bonds btw. -NH & -C=O gps of neighbouring polypeptide segments.

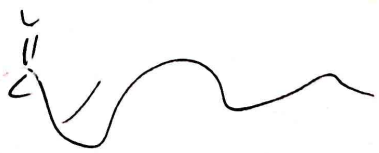
- parallel & antiparallel beta sheets

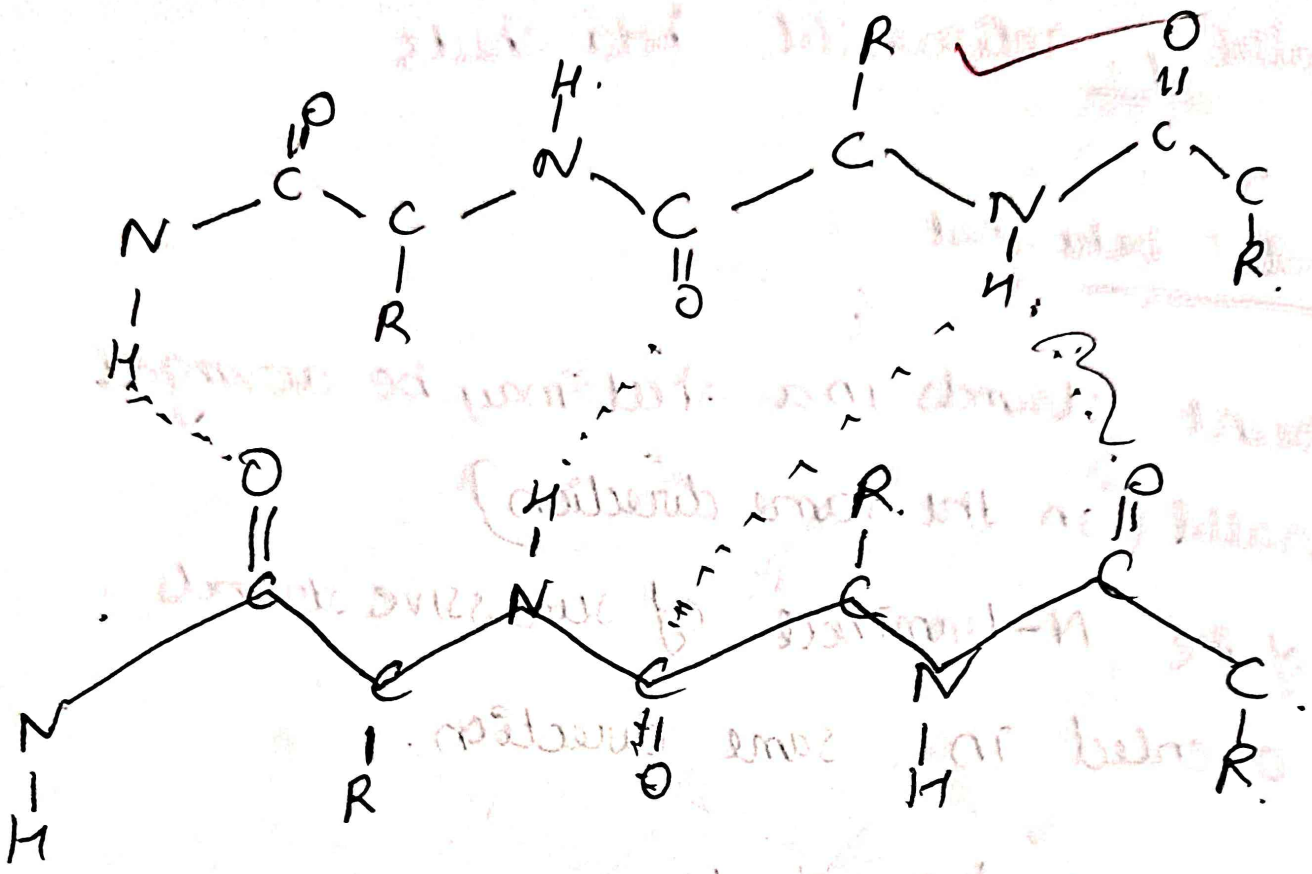
- parallel beta sheet.

- adjacent strands in a sheet may be arranged in parallel (in the same direction)
- All of the N-terminal of successive strands are oriented in same direction.

- Anti-parallel beta sheet.

- adjacent strands in a beta sheet may be arranged in the opposite direction.
- The N-terminus of one strand is adjacent to the C-terminus of the next.

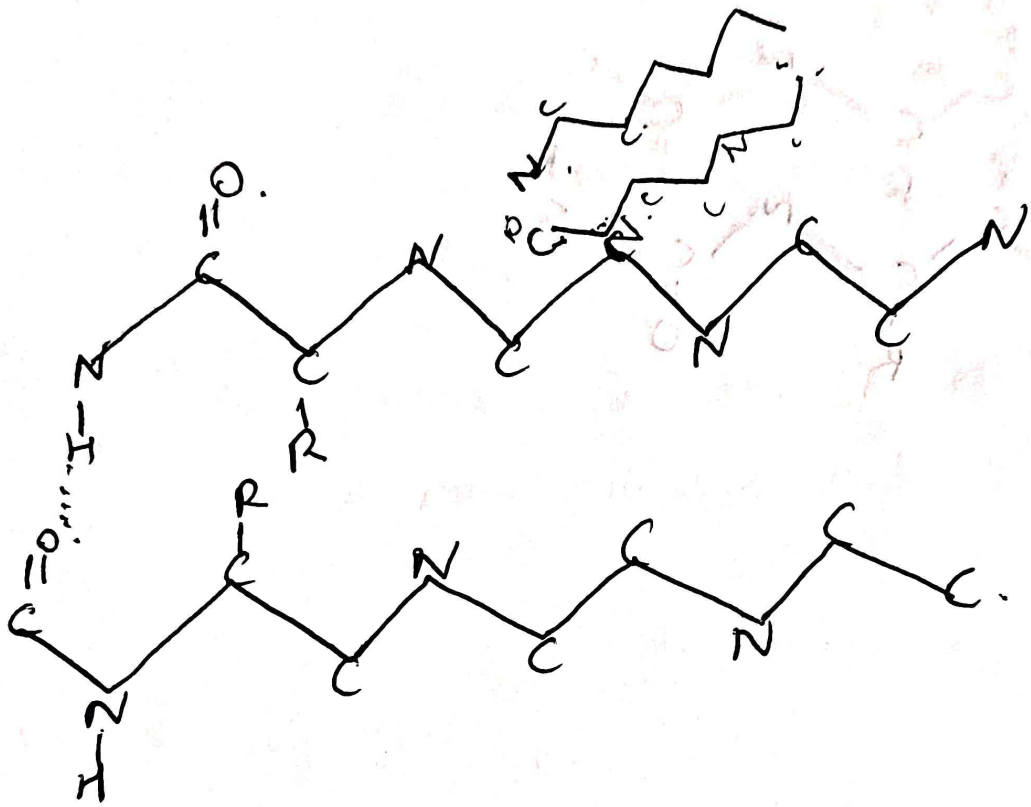




parallel.

Antiparallel

Sto must



Examples.

- Antiparallel β pleated sheet : in proteins like, silk fibroin.
- parallel β pleated sheet : Flavodoxin.
- Both types found in : Carbonic anhydrase.

loops and turns in secondary structures.

- some times loop-like structure or U-turns may act as a linking material btw regular α-helix & β-pleated sheets.

- In some, reverse turns are seen in polypeptide chain as many proteins are globular in shape.

- peptide chains in anti-parallel direction, connected by small reverse-turn loops.

- parallel beta sheets require long loop-like structure for cross connection.

## Secondary Structure - Triple Helix

- 3 polypeptide chains woven together.
- H bonding between -OH groups gives a strong structure
- major fibrous elements of tissues like bones, teeth, tendons, cartilage and blood vessels.

# Collagen - helix.

- collagen is a rod-like structure.
- The super helix is formed by winding 3 polypeptide chain.
- One turn has 3.3 aminoacid residues
- Each turn is also seperated by 2.9 Å.
- collagen fibres are strengthened by cross linking between lysine and hydroxy-lysine residues.
- cross links are formed by LYSYL OXIDASE, a Cu containing enzyme, which converts these aminoacids into aldehydes.

X——X

end of secondary structure of proteins.