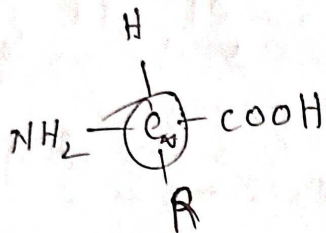


Proteins

Basic structure of amino acid :-



- Amino acid is ^{the} building blocks of protein. Amino acids are colourless, crystalline solids.
- They are water-soluble, high-melting solids and behave like salt. The general structure of an amino acid is represented above.
- It has a central carbon which is called α -carbon. The α -carbon is linked to the following four groups:
 1. Amino group (-NH₂)
 2. Carboxyl group (-COOH)
 3. Hydrogen atom (-H)
 4. Variable group (-R) which is specific for each amino acid.

There are twenty possible variable groups giving rise to twenty amino acids. These twenty amino acids are given below -

P.T.O >

Zwitter ions:-

molecule which are electrically neutral with no net charge are called Zwitter ions.

(GABA is a neurotransmitter which is non-protein amino acid) (Gamma Amino Butyric Acid)

- The bond between two amino acid is called peptide bond. It is formed by the removal of one H_2O molecule from amine group of one amino acid and carboxyl group of adjacent amino acid.

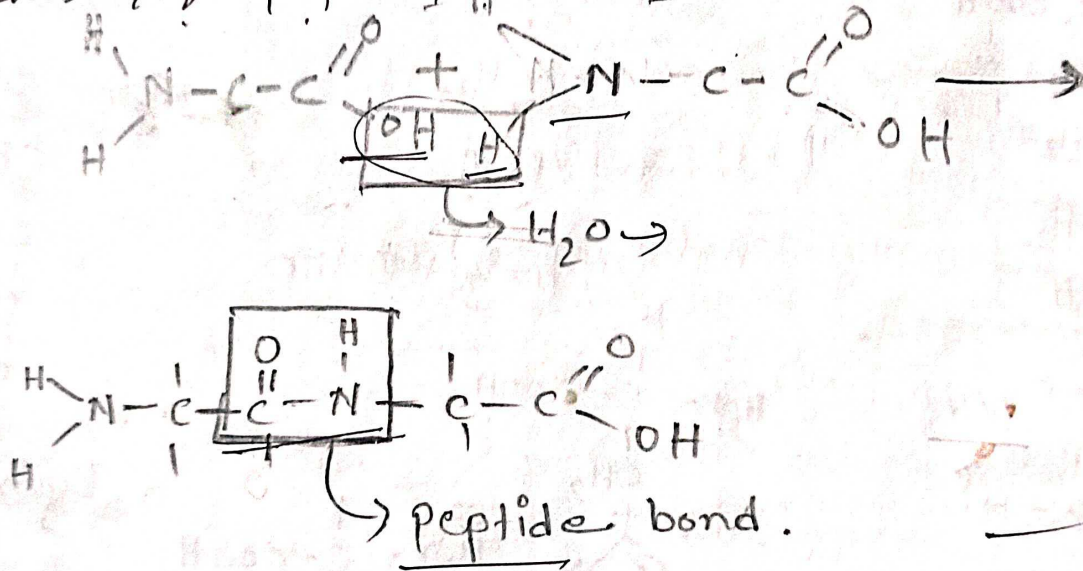


Fig: Formation of peptide bond

On the basis of reaction in ~~soluble~~ solution

Depending upon the reaction of amino acids, are grouped into three grouped categories.

① Acidic amino acid:-

This type of amino acid have two $COOH$ groups and one NH_2 group in each molecule. They

are called Monoaminodicarboxylic amino acid.

Example:- Aspartic acid (ASP), Glutamic acid (GLU).

② Basic amino acid:

This type of amino acid have two amino group and one carboxylic group. They are called -

Diamino monocarboxylic acid. Example:- Lysin (Lys),
Arginine (Arg)

③ Neutral amino acid:

They have one amino and one carboxyl group. Hence it is called Monoamino monocarboxylic amino acid.

Example:- Alanine (Ala), Glycine (Gly), Serine (Ser)
Aspartic acid, Glutamic acid, Lysin and Arginine all are neutral amino acid.

On the basis of charges:-

① Non-polar amino acid:

This type of amino acid having no charges. For example - Glycine, Serine and Threonine (Thr),
Cysteine (Cys), Asparagine (Asn), Glutamine (Gln),
Tyrosine (Tyr).

② polar uncharged amino acid:-

This type of amino acids have balanced charge making the molecule uncharged.

Example: - Alanine (Ala), Valine (Val), Leucine (Leu), Isoleucine (Ile), Phenylalanine (Phe), Tryptophan (Trp), Methionine (Met), proline (Pro)

③ polar-charged amino acid:-

This type of amino acids are either positive (basic) or negative (acidic) charged.

For example - Aspartic acid (Asp), Glutamic acid (Glu), Lysine (Lys), Arginine (Arg), Histidine (His)

④ On the basis of special structure:-

(a) Sulphur containing amino acid - Cysteine, Methionine

(b) Alcoholic amino acid - In this type of amino acid containing $(-OH)$ hydroxyl group. Serine and Threonine (Thr)

(c) Heterocyclic amino acid - They contain nitrogen ring. Example - Histidine (His) and proline (Pro)

Functions of amino acid -

① Formation of protein: The amino acids are the building blocks of protein. They form protein by polymerization through peptide bonds.

② Formation of non-protein compounds: Some amino acids are involved in the formation of various important compounds.

For example -

① The amino acid tyrosine produces the ^{associated with the production} of thyroxine hormone, epinephrine and Melanin.

② The amino acid Glycine forms Heme.

③ Tryptophan produces Nicotinamide (vit B-3).

④ Indole-3-Acetic acid (IAA)

⑤ The co-enzyme-A (CoA) and pantothenic acid (vit B-5) are derived from Alanine.

⑥ The co-enzyme Glutathione also derived from amino acid.

⑦ Formation of Glucose:

Many amino acids are converted into glucose by removing amino groups through the process gluconeogenesis.

④ Formation of amines:-

Amino acids are associated with the formation of amines by losing $-COOH$ group. For example Histamine are the derivatives of the amino acid Histidine. Histamine is a powerful stimulant of gastric secretion, constrictor of bronchial smooth muscles and vasodilator that causes lower the blood pressure.

⑤ Storage of Nitrogen:-

Amino acid derivatives Amide serve as a storage of Nitrogen.

⑥ Biosynthetic pathways:-

Amino acids are amphoteric (acts as a both acid and base) so that acts as a buffer.

Some non-protein amino acids participate in some important biosynthetic pathways. For example - Ornithine and Citrulline play crucial role in urea cycle.

⑦ Amino acids as a biological buffers:-

Amino acids are the amphoteric in nature and acts as a buffer in solution. This property of amino acids provided resistance

against changes in pH by donating hydrogen ions (H^+) as pH increases and accepting H^+ as pH decreases

⑧ As antibiotics:-

The non-protein amino acids are components of antibiotics

⑨ Formation of prokaryotic cell wall:-

Some small peptides are components of peptidoglycans which formed prokaryotic cell wall.

⑩ Formation of Enkephalins:-

Enkephalins are pentapeptides formed in certain part of brain. These are associated with perception of pain and pleasure.

Bonds that stabilizing the protein structure:-

Proteins are made up of amino acid chains called polypeptide formed by interaction between amino and carboxylic group of adjacent amino acid. This polypeptide chains are formed either helix or sheets (α -helix and β -pleated sheet) which give 3D structure to proteins. The 3D structure of protein is called tertiary structure. The process of folding protein into their tertiary structure is spontaneous involved

bonds and inter-molecular forces which makes the protein stable in structure. The bonds and intermolecular forces which give stability to protein are categorized into two classes -

- ① Covalent interactions.
- ② Noncovalent interactions.

Covalent interactions:-

- The covalent bonds are the strongest chemical bonds that contributing to protein structure. In addition to the covalent bonds that connect the atoms of single amino acids and covalent peptide bond that links amino acid in a protein chain.

- The covalent bonds between cysteine side chains are important determinants of protein structure. Cysteine is the only amino acid whose side chains can form covalent bond called disulphide bridges.

- Disulphide bridges - Disulphide bonds are formed between two sulphur atoms which are found in the side chains of cysteine (R) when two cysteines are close in close proximity in the tertiary structure, covalent disulphide bond can be formed as a result of oxidation.

Non-covalant interaction:-

The 3D structure of proteins results from various types of non-covalant interaction between the amino acids present in the polypeptide chain and the surrounding environment.

Although non-covalant interactions are typically weaker magnitude than covalant bonds, but they play important role in the formation and maintainance of 3-D structural integrity of protein.

Some of the common non-covalant interactions found in the proteins are -

① Hydrophobic bond or interaction.

② Van der waals force

③ Electrostatic or ionic force.

④ Hydrogen bond.

Hydrophobic bond:-

The hydrophobic bonds are the major driving force of protein folding. Some amino acids have side chains which repel water, so called hydrophobic. The hydrophobic nature of amino acids enables them to interact with one another. The hydrophobic interaction forms an interior hydrophobic protein core, where most of the hydrophobic side chain can easily associated and protected from

Interactions with solvent H₂O

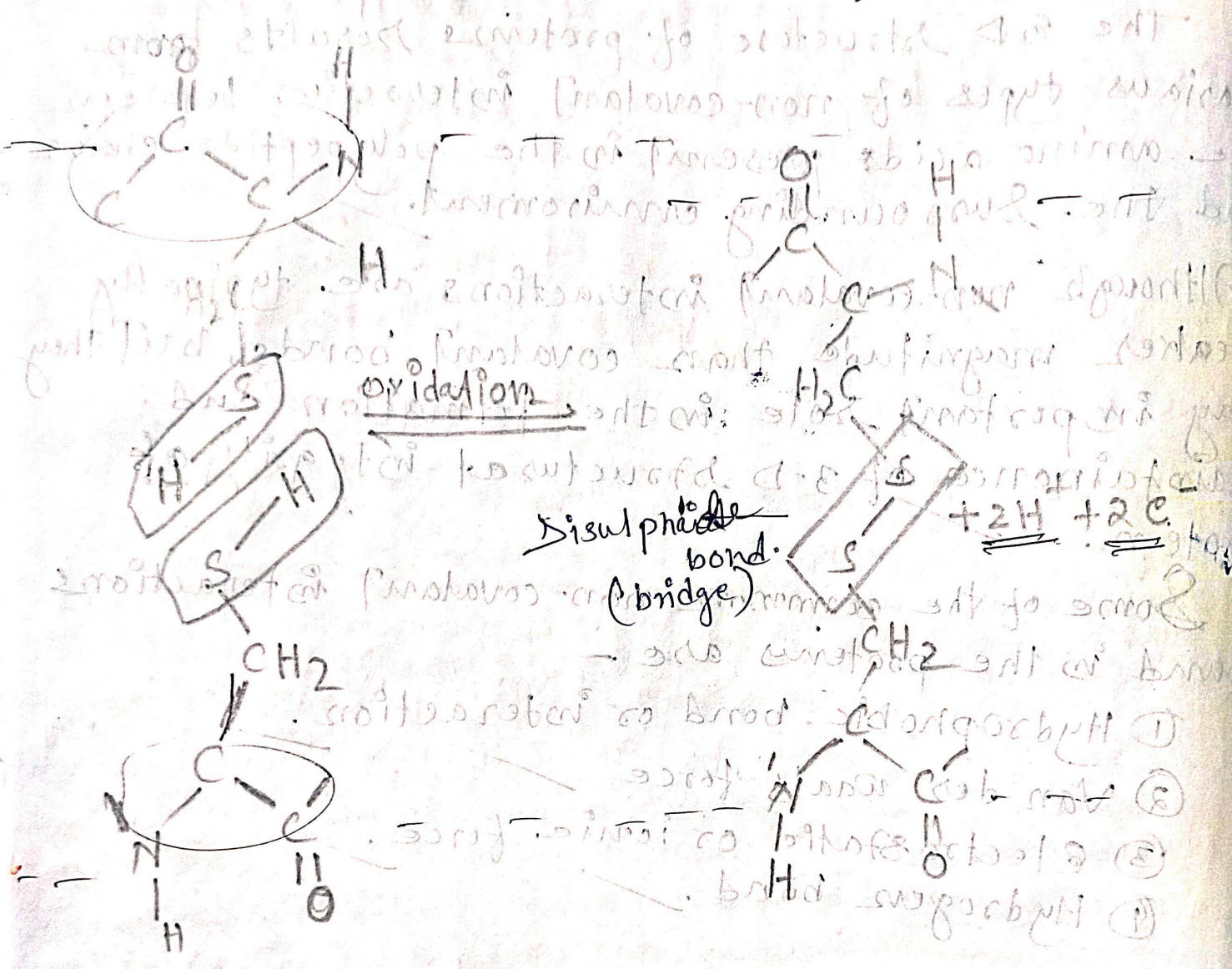


Fig: - Formation of disulphide bond.

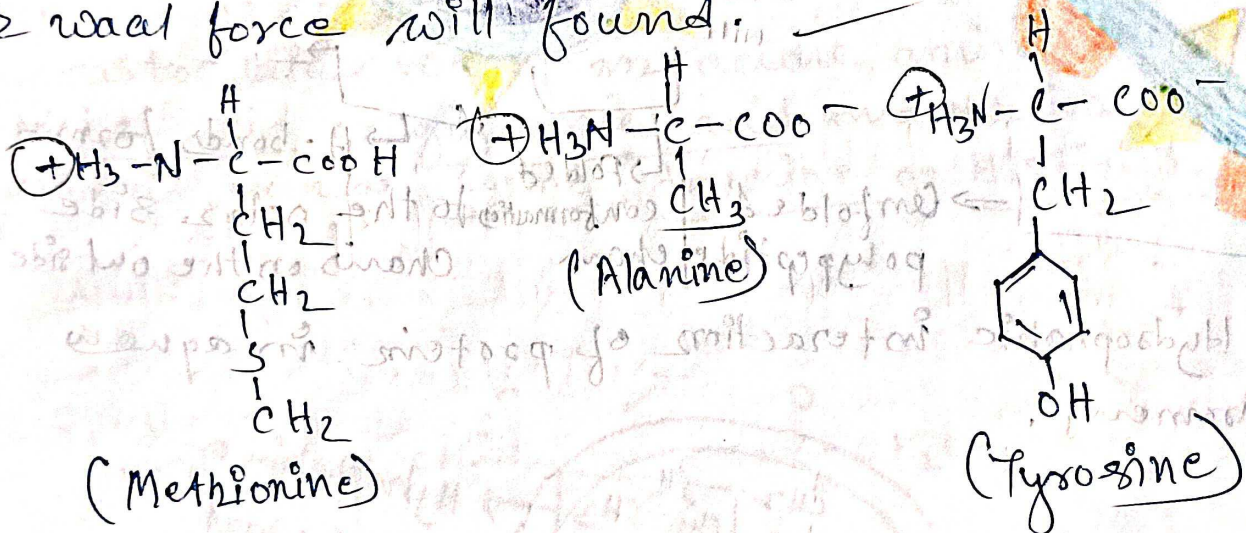
Van Der Waals force:-

Van Der Waals force is a transient weak electrical attraction of one atom to another. This force exist because every atom has an electron cloud that can fluctuate which yields a temporary

electric dipole.

The transient dipole is one atom can induce a complimentary dipole in another atom. This short lived complimentary dipoles provide a weak electrostatic attraction known as Van-der waal force.

In 3-D structure of protein that formation of Van-der waal force depends on the shape or structure of the side chain. If the atoms within the side chain of neighboring amino acid fits well the Van der waal force will found.



Fig^o - Hydrophobic amino acid.

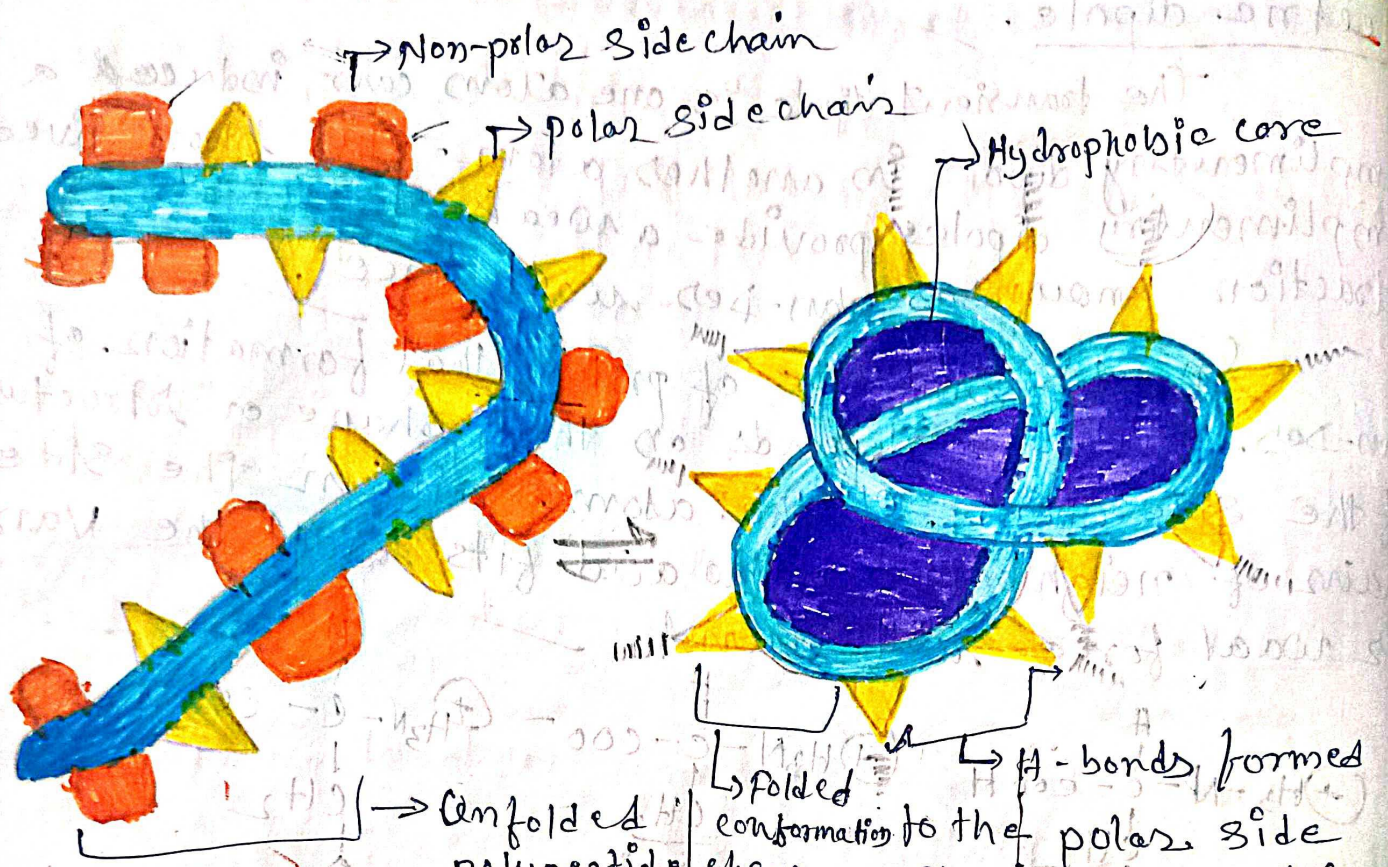


Fig: Hydrophobic interaction of protein in aqueous environment.

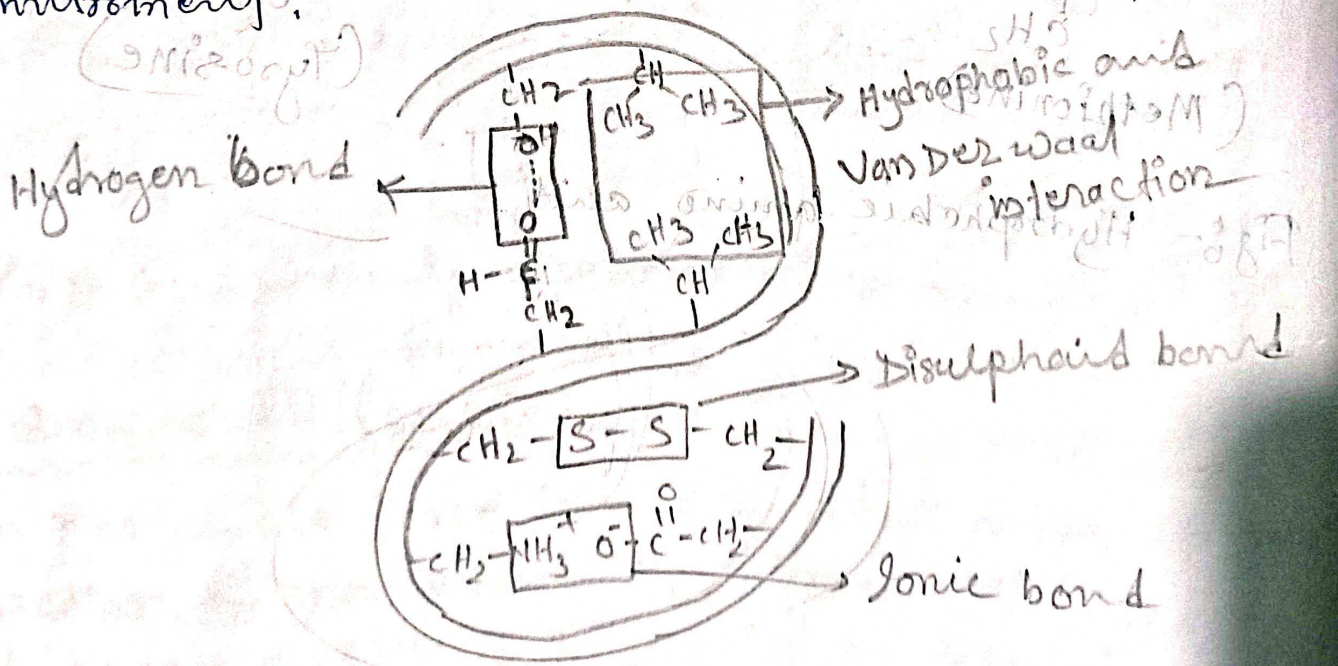


Fig: Bond formation that stabilizes protein structure.

Ionic bond (Salt bridge):

- Salt bridges in proteins are ~~new~~ the bond between oppositely charged residue that are close to each other which formed electrostatic attraction. Ionic bonds are formed as amino acids bearing opposite electrical charges are ~~justaposed~~ ^{juxtaposed} in the hydrophobic core of protein.
- Ionic bonds can be important to protein structure because they have potent electrostatic attraction.
- Ionic bond or salt bridge can be formed between the carboxylate ion of an acidic amino acid such as aspartic acid or glutamic acid and NH_2 ion of the basic amino acid such as lysine, Arginine or Histidine.

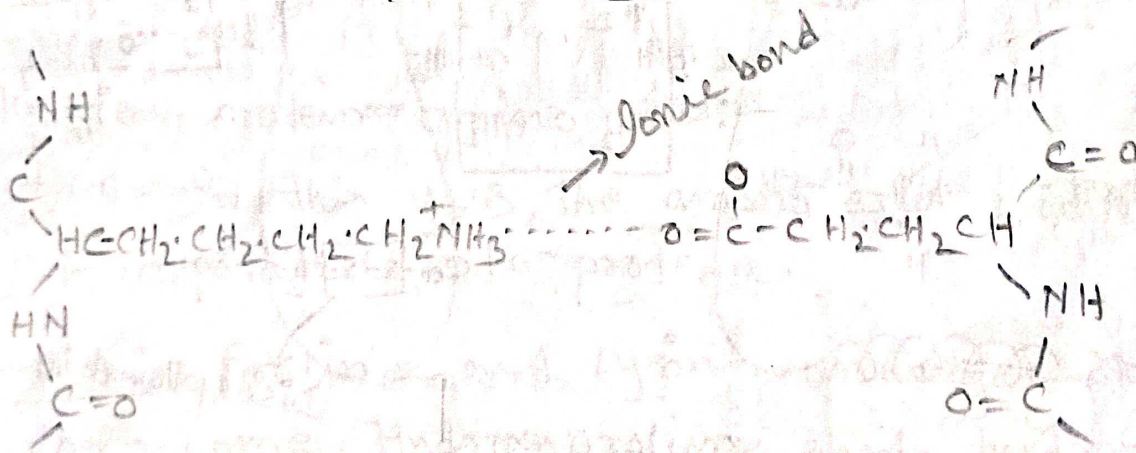


Fig: Ionic bond between side chain of amino acid.

Hydrogen bond:-

When two atoms bearing partial negative charges share a partially positively charged hydrogen atoms bearing hydrogen bond.

- H-bond is a form of weak attractive bond force between molecules that contain an electric charge.
- This is caused by electrostatic attraction and can occur the chemical properties of the molecule.

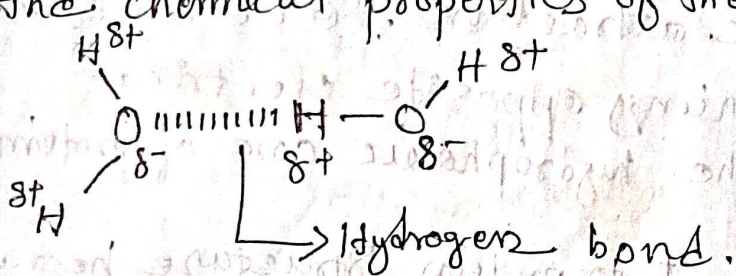


Fig:- Formation of hydrogen bond.

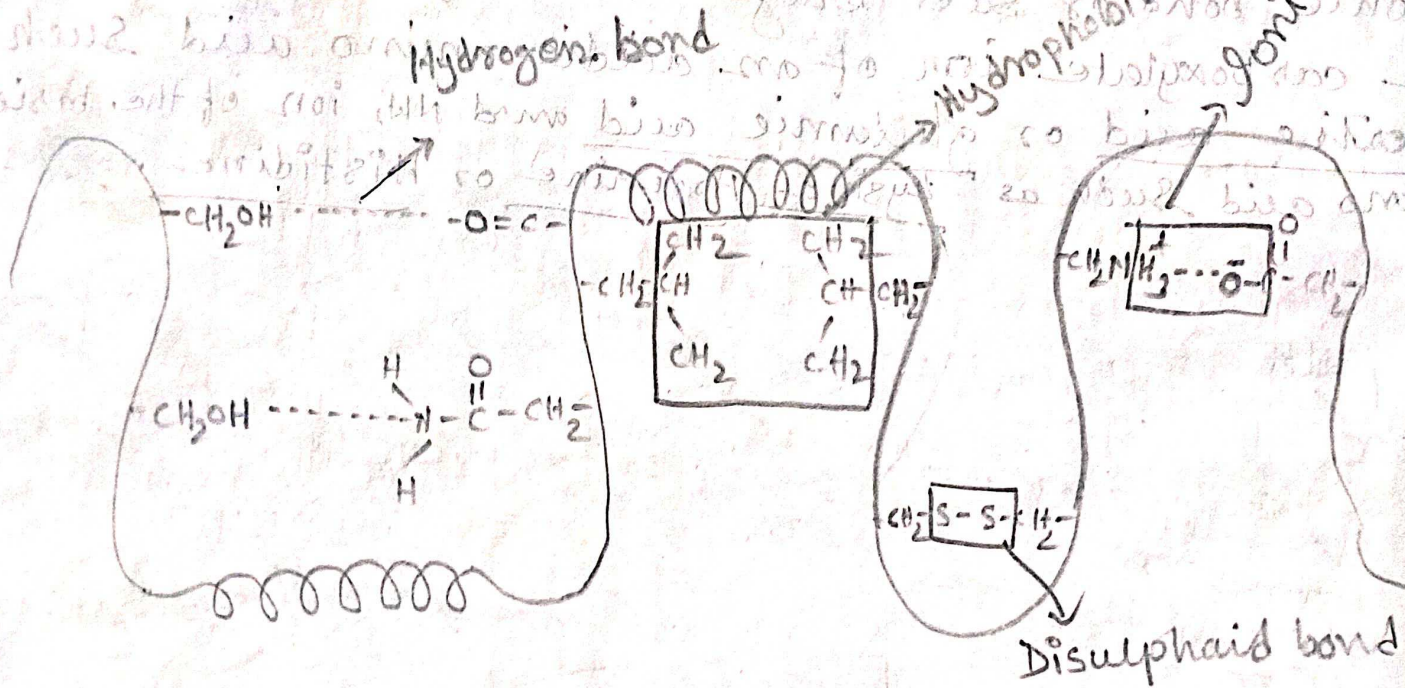


Fig: Various type of bond stabilizing protein

Structure of protein is maintained by various bonds. When a partially positive hydrogen atom is attracted to a partially negative hydrogen atom, a hydrogen bond is formed.

Classification of amino acid:-

① Non-protein amino acid:-

This type of AA are not naturally encoded by Genetic code but found ~~is a stage~~ as intermediates of metabolic pathway for ~~standard~~ amino acids.

Example:- Ornithine is intermediate in urea biosynthesis

② Non α amino acid:-

In this class of amino acids, the amino group is not attached to α carbon atom but some other carbon.

Example:- ~~Gamma~~ γ -Amino butyric acid (GABA)

③ Modified protein amino acid:-

In this class, the amino acid modified after the incorporated into protein.

Example:- Proline and Lysine undergoes hydroxylation to become Hydroxyproline and hydroxylysine.

Organisation of protein:-

① Primary Structure:-

Amino acids are polymerized in linear chains by covalent peptide bonds that link the amino group ($-NH_2$) of one amino acid to the carboxyl group ($-COOH$) of another amino acid.

At one end of the polymer, called the c-terminal the amino acids has an unbound carboxyl group.

At the other end, the n-terminal the amino acid has an unbound amino group.

The linear sequence of amino acids is a protein's called (polypeptide chain) primary structure of protein.

Once the primary structure is established, proteins are organised into more complex 3-D conformations.

② Secondary Structure :-

After forming the linear structure, proteins are folds on to itself to assume its secondary structure. The information for proper folding is contained directly in the primary structure.

The size, charge and polarity of the side chain (R) influence the interactions between amino acid in the chain.

Secondary structure of proteins arise when side chain of amino acids interact to form a structure that is more stable than primary structure.

The two most common protein structural motifs are α -helix and β -sheet.

In α -helix, the protein is twisted into spiral with 3.6 amino acids per turn and side chain extending outwards.

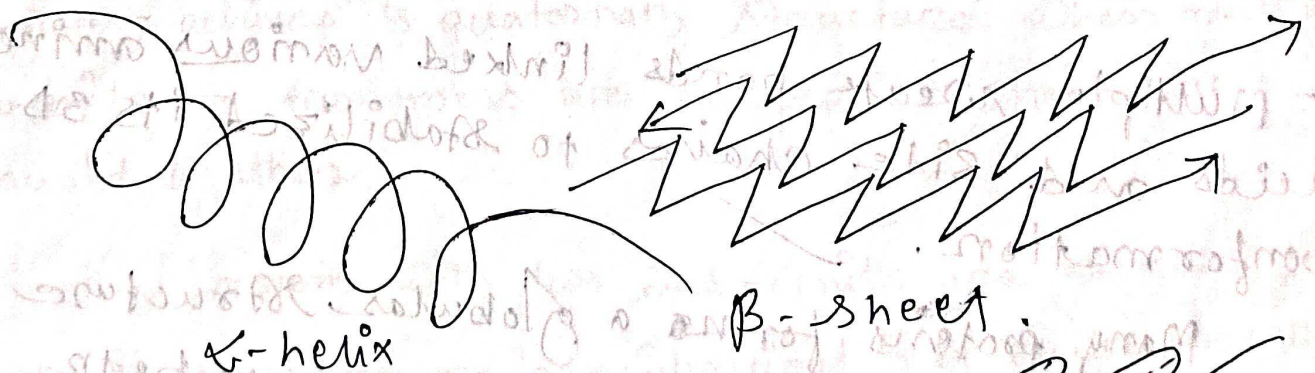
- This α -helix structure is stabilized in two ways -

(1) Hydrogen bond forms betⁿ the C=O of one amino acid and the N-H of the amino acid four positions along the chain.

(2) The α -helix structure is stabilized when opposing side chains can interact.

- The β -sheet forms when linear regions of a protein align side by side and form hydrogen bond.

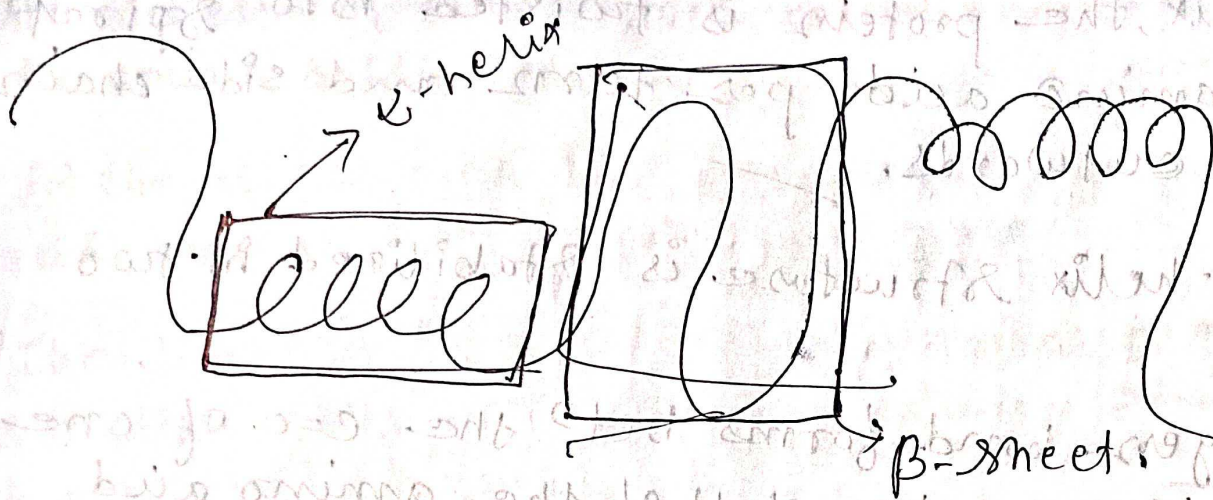
- In this conformation, the side chain extends above and below the face of the sheet.



α -helix

β -sheet

Fig. α helix & β -sheet in Secondary structure of proteins.



③ Tertiary Structure:-

Once a protein forms its secondary structure, the different regions of the protein fold together and create its tertiary structure.

If the proteins fold in a way that allows two adjacent cysteine residues to come into close proximity, they form a covalent bond called disulphide bond or bridge.

- multiple weak bonds linked various amino acids and side chains to stabilize its 3D conformation.

Many proteins form a globular structure when hydrophobic interactions form between the regions scattered throughout the protein.

By pulling together hydrophobic regions a hydrophobic core is formed which stabilizes the structure of protein.

21, 26, 28, 2

④ Quaternary Structure:-

A protein achieves its quaternary structure when multiple sub-units or monomers or ~~poly~~ polypeptide chains are brought together.

Protein with two sub-units are called dimers. If the monomers are identical, it is called homodimer. If the monomers are not identical it is called heterodimer.

Proteins can be composed of even larger numbers of sub-units such as trimers (3-sub-units) and tetrameres (4-sub-units).

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