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Biochemistry

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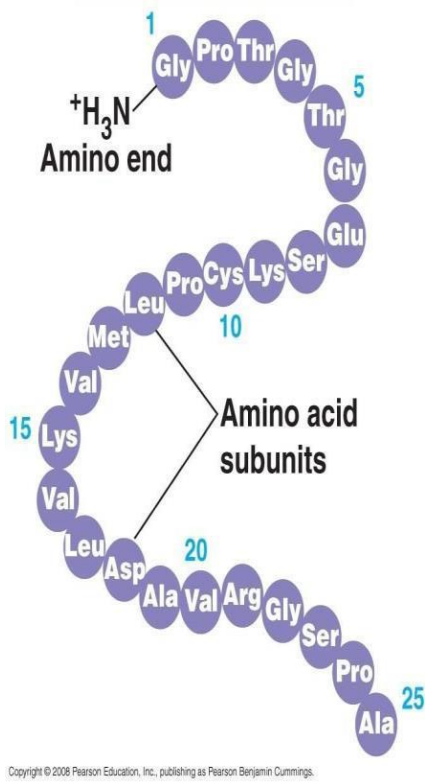
lec4

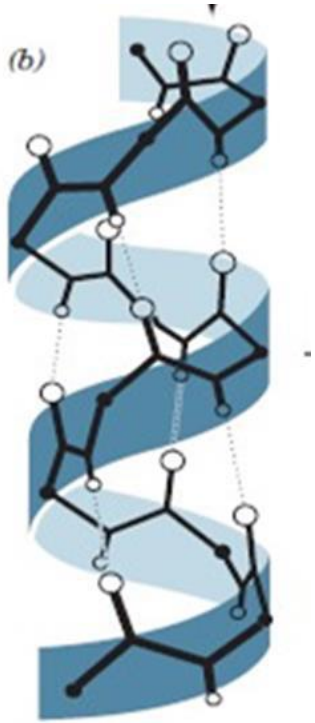
Structure of Protein

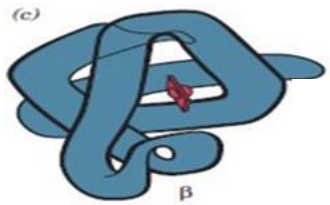
Overview

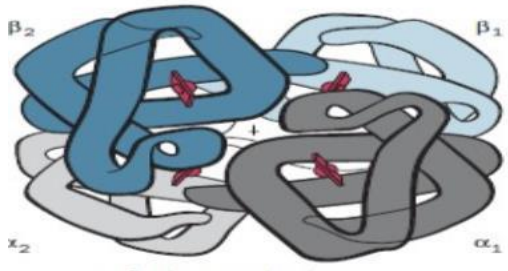
- The 20 amino acids commonly found in proteins are joined together by peptide bonds.
- The linear sequence of the linked amino acids contains the information necessary to generate a protein molecule with a unique three-dimensional shape..
- The complexity of protein structure is best analyzed by considering the molecule in terms of four organizational levels, namely: Primary, Secondary, Tertiary & Quaternary.

A.Primary **B. Secondary** **C. Tertiary** **D. Quaternary**









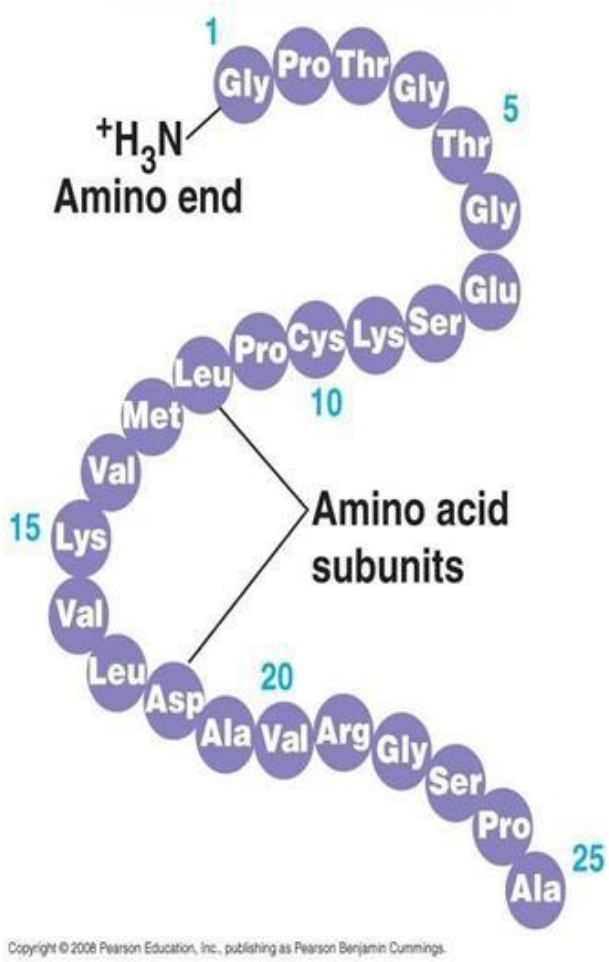
Levels of Protein Structure

1. Primary Structure of Protein:

A. It's a linear sequence of amino acids. This linear sequence is referred to as a **polypeptide chain**.

B. The amino acids in the primary structure are held together by **covalent bonds**

The primary structure of the protein starts from the **Amino terminal(N) end** and ends in the **carboxyl terminal (C) end**.

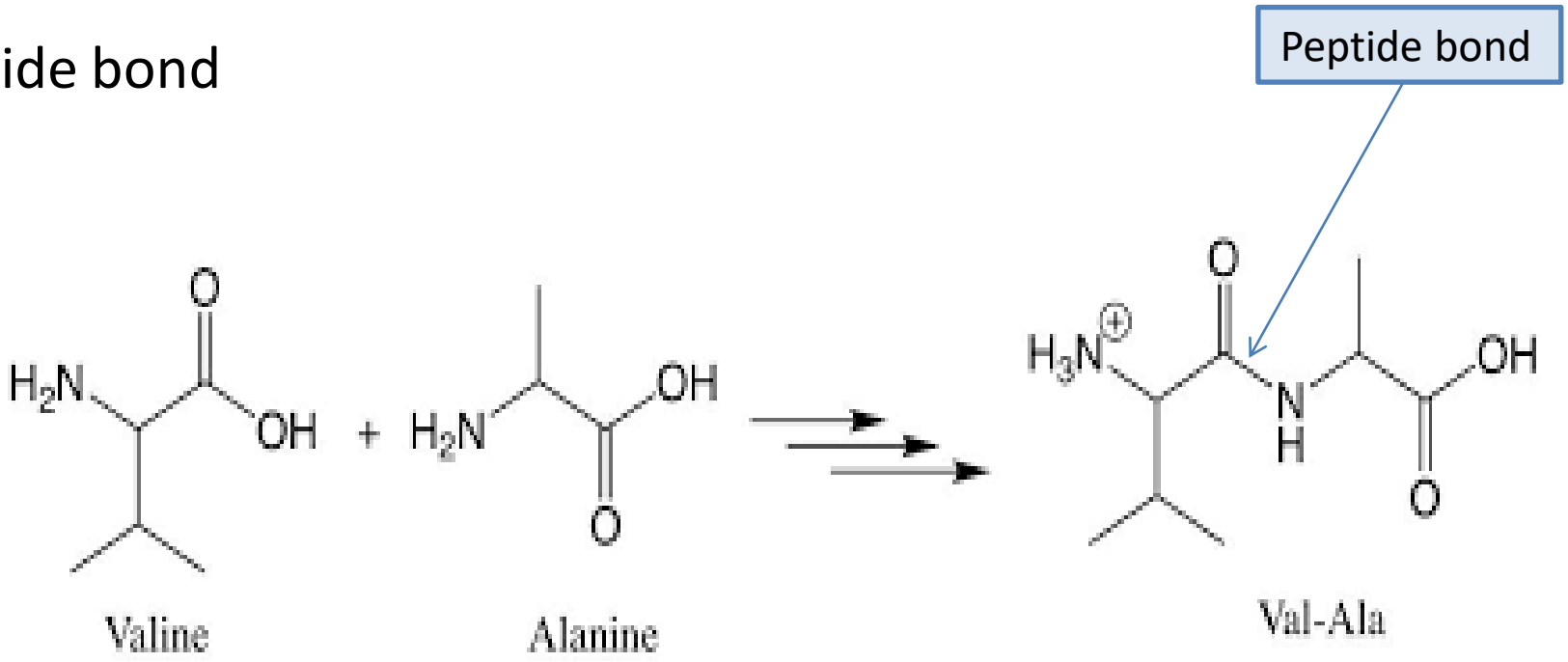


- The sequence of an amino acids is unique, and defines the structure and function of the protein.
- The importance of the primary structure of proteins **is to understanding the genetic diseases that results due to proteins with abnormal amino acid sequences.**

A. Peptide bond

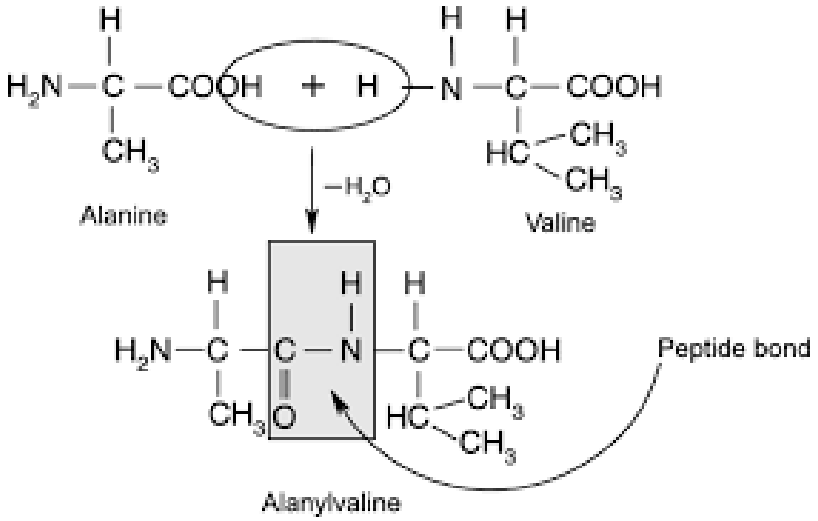
In proteins, amino acids are joined covalently by peptide bonds.

Peptide bond are amide linkages between the α-carboxyl group of one amino acid and the α-amino group of another. For example, valine and alanine can form the dipeptide valylalanine through the formation of a peptide bond



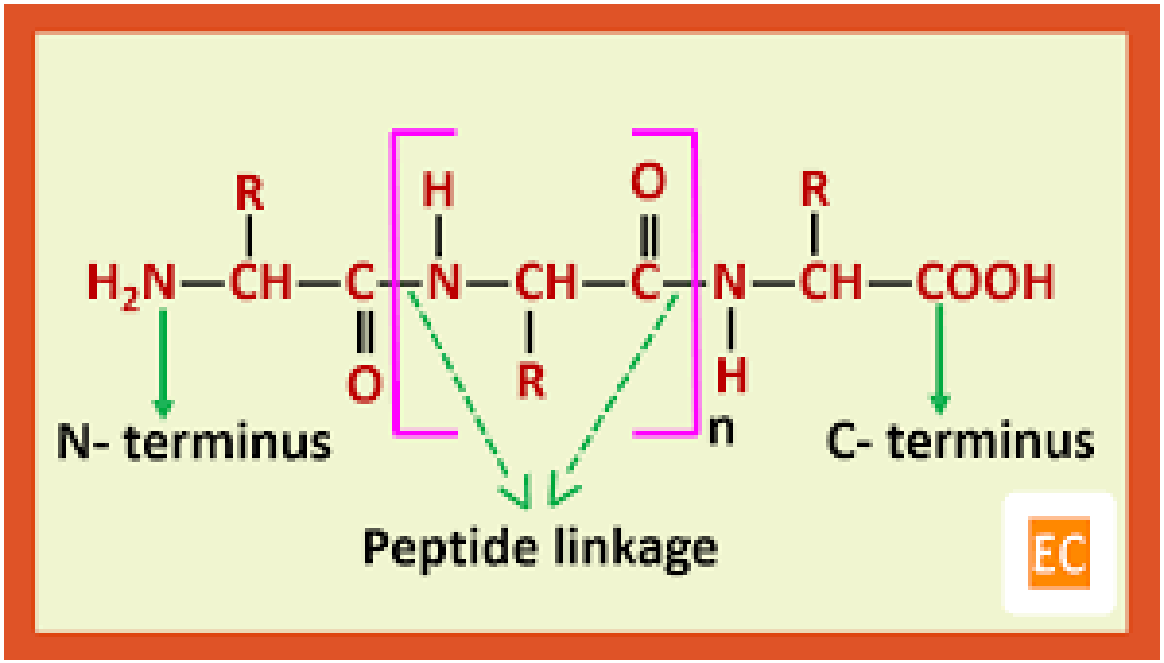
B. Characteristics of the peptide bond:

- The peptide bond has a partial double-bond character, that is, it is shorter than a single bond, and is rigid and planar.
- The peptide bond is generally a trans bond (instead of cis) in large part because of steric interference of the R-groups when in the cis position.
- Peptide bonds are **not broken** by conditions that denature proteins, such as heating & high concentrations of urea.
- Prolonged exposure to a strong acid or base at elevated temperatures is required to hydrolyze these bonds non enzymically

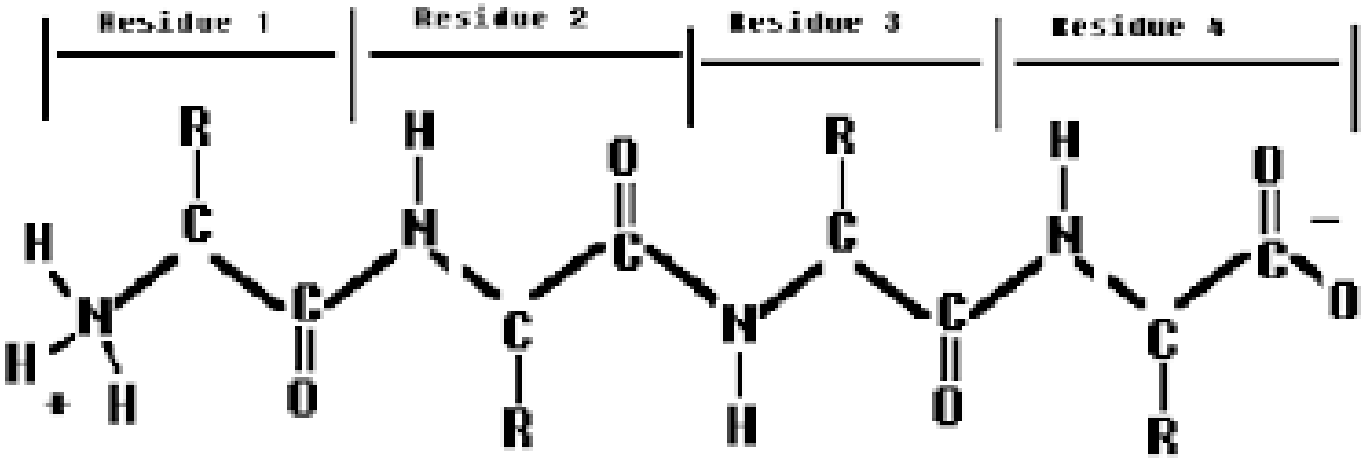


C. Naming the peptide:

- By convention, the free amino end (N-terminal) of the peptide chain is written to the **left** and the free carboxyl end (C-terminal) to the **right**. Therefore, all amino acid sequences are read from the N- to the C-terminal end of the peptide. Linkage of many amino acids through peptide bonds results in an <u>unbranched chain</u> called a polypeptide.

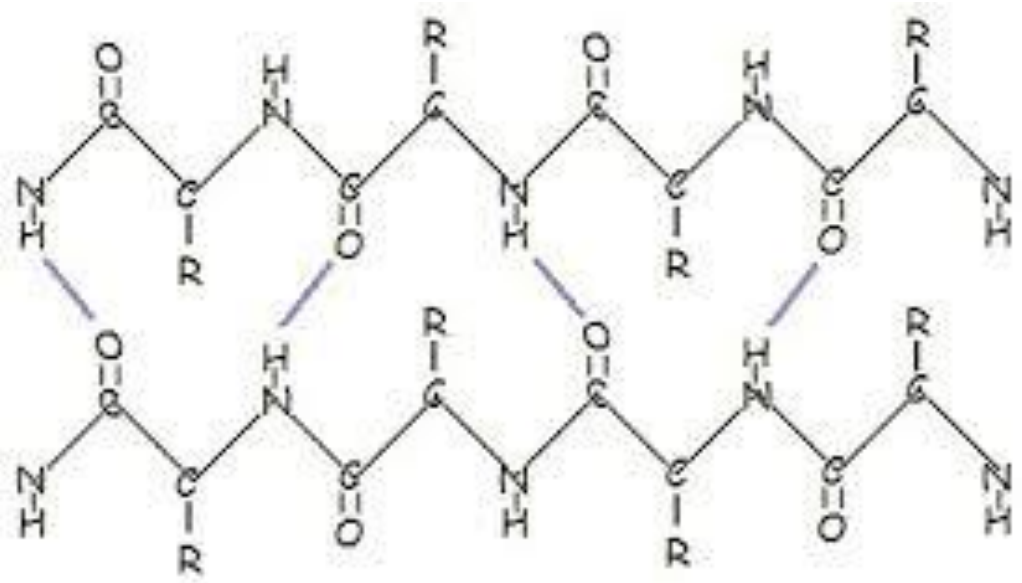


- Each component amino acid in a polypeptide is called a "**residue**" because it is the portion of the amino acid remaining after the atoms of water are lost in the formation of the peptide bond.
- When a polypeptide is named, all amino acid residues have their suffixes (-ine, -an, -ic, or -ate) changed to -yl, with the exception of the C-terminal amino acid. For example, a tripeptide composed of an N-terminal valine, a glycine, and a C-terminal leucine is called valyl glycyl leucine.



2. Secondary Structure of Proteins:

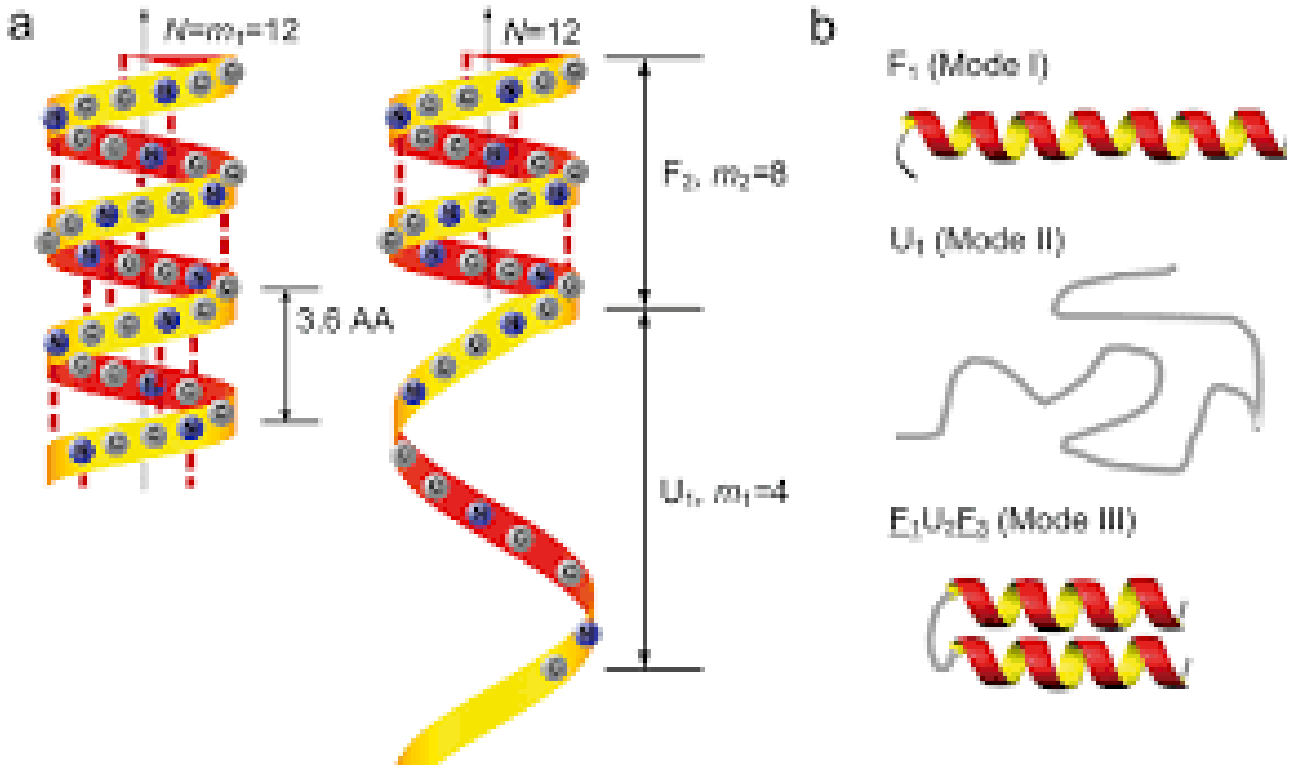
- The secondary structure of the polypeptide is a three-dimensional structure.
- It results from hydrogen bond formation between hydrogen of –NH group of peptide bond and the carbonyl oxygen –C=O of another peptide bond.
- According to H-bonding there are two main forms of secondary structure:



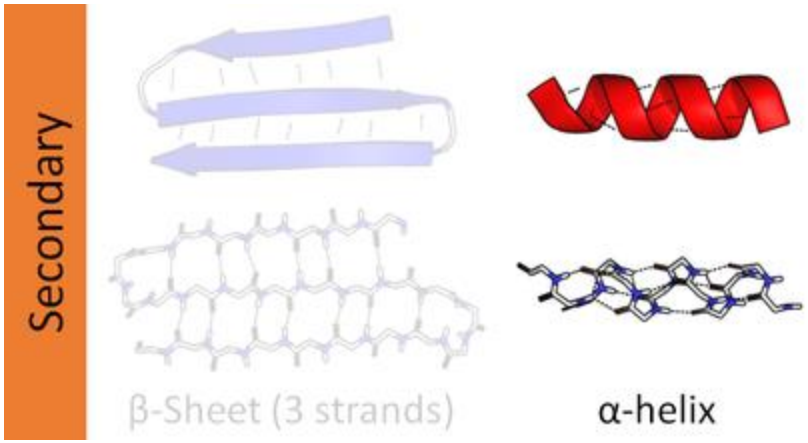
Parallel

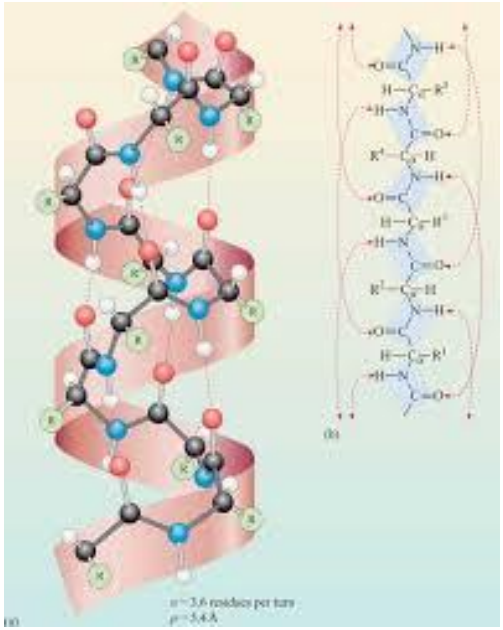
1. α-helix:

α-helix is a spiral structure, consisting of a tightly packed, coiled polypeptide backbone core, with the side chains of the component amino acids extending outward from the central axis to avoid interfering sterically with each other.



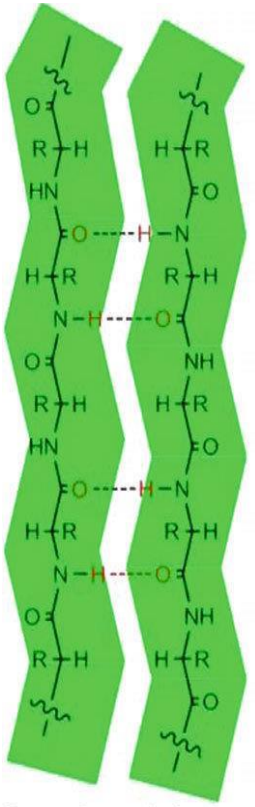
- Formed by a H-bond between every 4th peptide bond –C=O to N-H
- Usually found in proteins that span a membrane
- The α- helix can either coil to the right or the left.
- Each turn of an α-helix contains 3.6 amino acids.
- Proline disrupts an α-helix because its secondary amino group is not geometrically compatible with the right-handed spiral of the α-helix.
- Example of proteins contains α-helices **keratins** are a fibrous protein. They are a major component of tissues such as **hair and skin**





2. β-sheets:

- ❖ It is another form of secondary structure in which two or more polypeptides (or segments of the same peptide chain) are linked together by hydrogen bond between H-of NH-of one chain and carbonyl oxygen of adjacent chain (or segment).
- ❖ In β-sheet all of the peptide bond components are involved in hydrogen bonding.
- ❖ Unlike the α-helix, β-sheets are composed of two or more peptide chains (β-strands), or segments of polypeptide chains,which are almost fully extended.
- ❖ The surfaces of β-sheets appear “pleated,” and these structures are, therefore, often called “β-pleated sheets.”



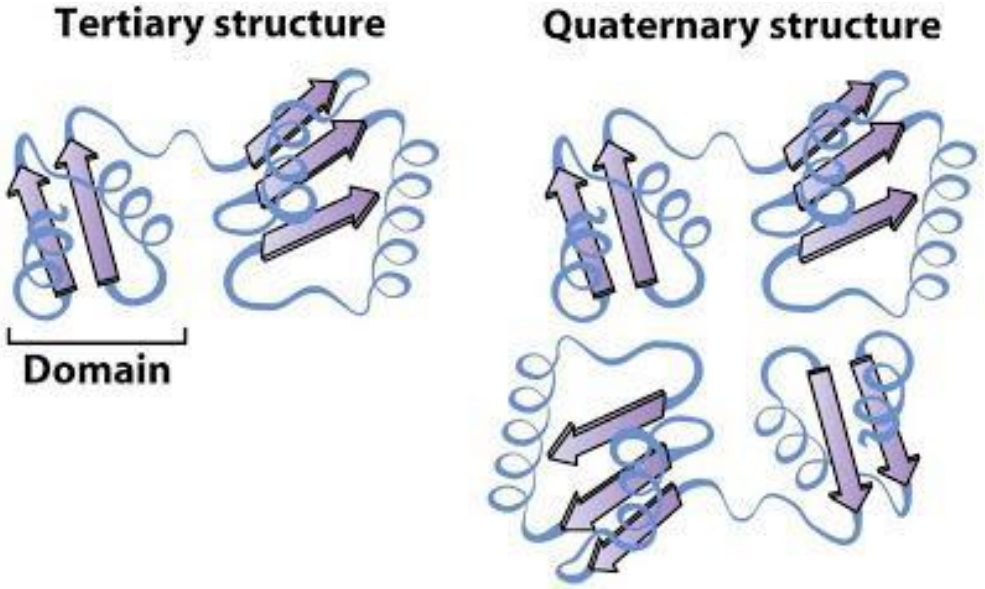
Beta pleated sheets

3. Tertiary structure of proteins

- Folding up of the secondary structures, so that amino acids far apart in the primary sequence may interact, and a **3-dimensional structure** is formed.

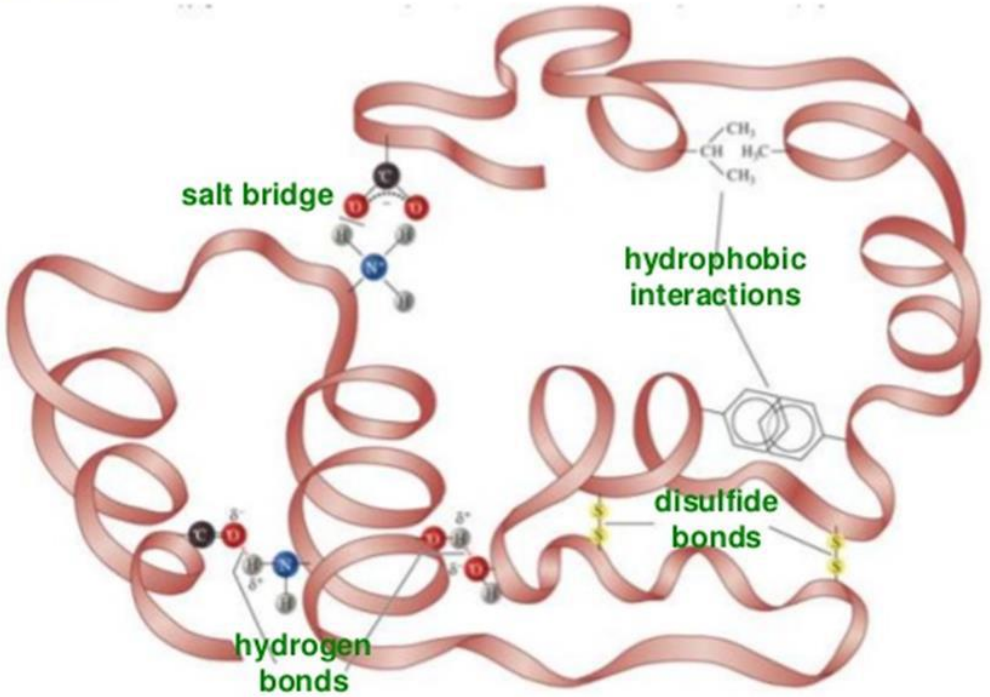
- Poly peptide chains that are

Greater than**~200** amino acids in length generally consist of two or more **domains**.



Domains: are regions of the polypeptide that have distinct structures and serve particular roles (e.g. ligand binding, interaction with other proteins etc.)

- Tertiary structure is a result of side chains interactions

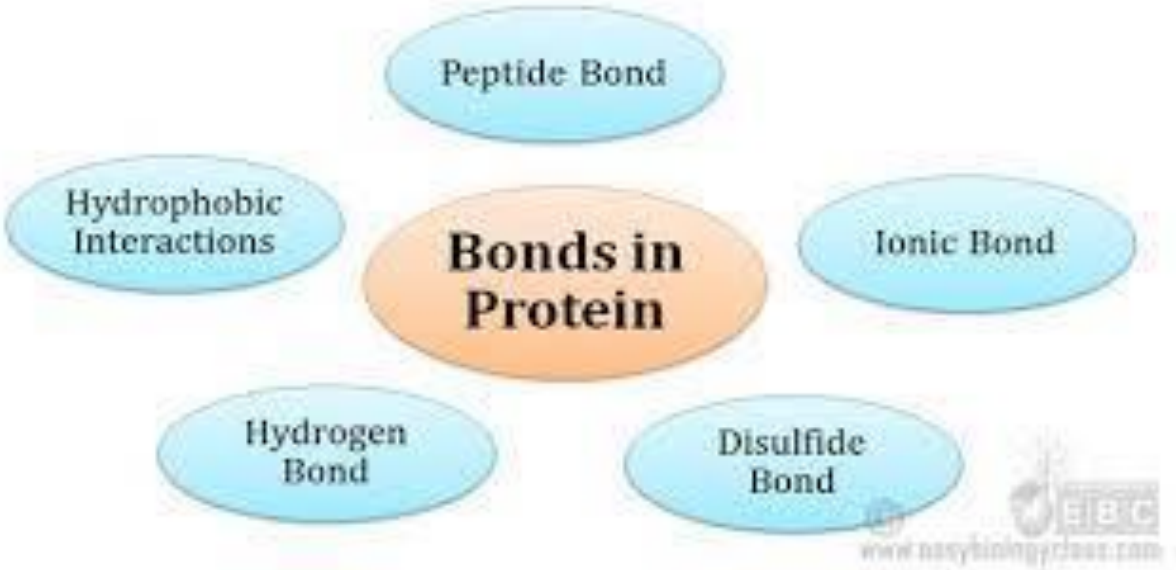


Tertiary structure of protein is stabilized by different types of bonds and interactions between amino acids R groups.

These includes:

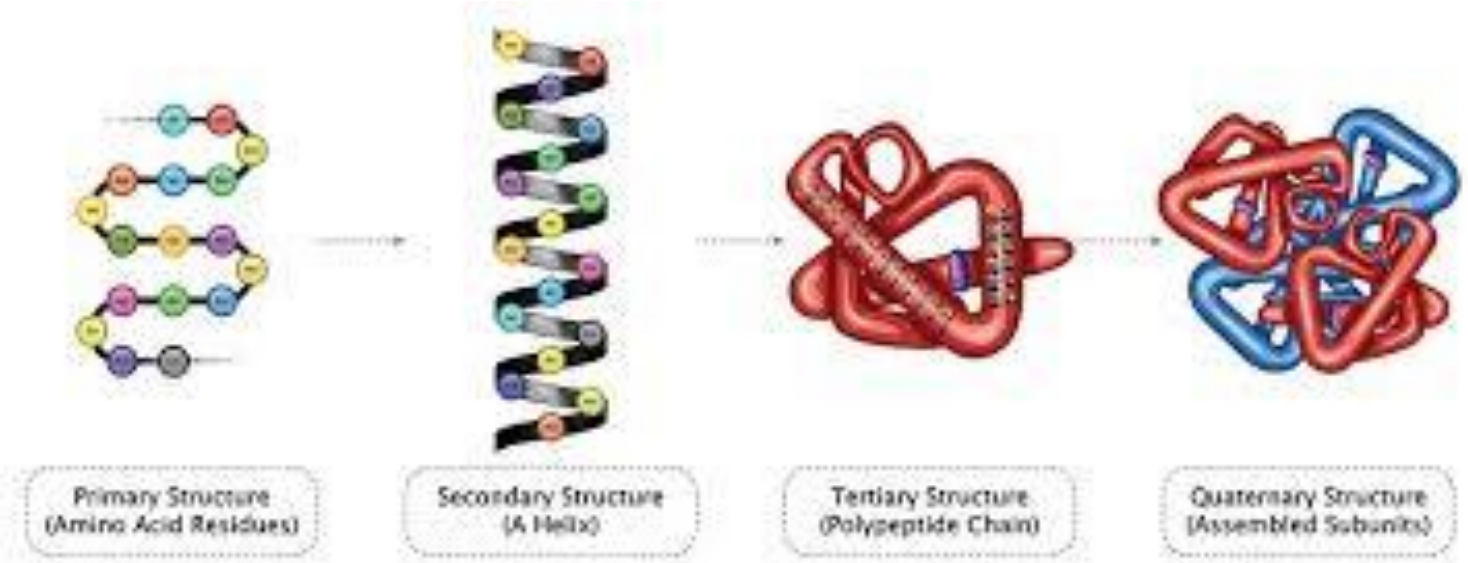
A. Hydrogen bonds. .
B. Covalent(disulphide) bond
C. Hydrophobic interactions
D. Ionic interactions &VanderWaals interaction

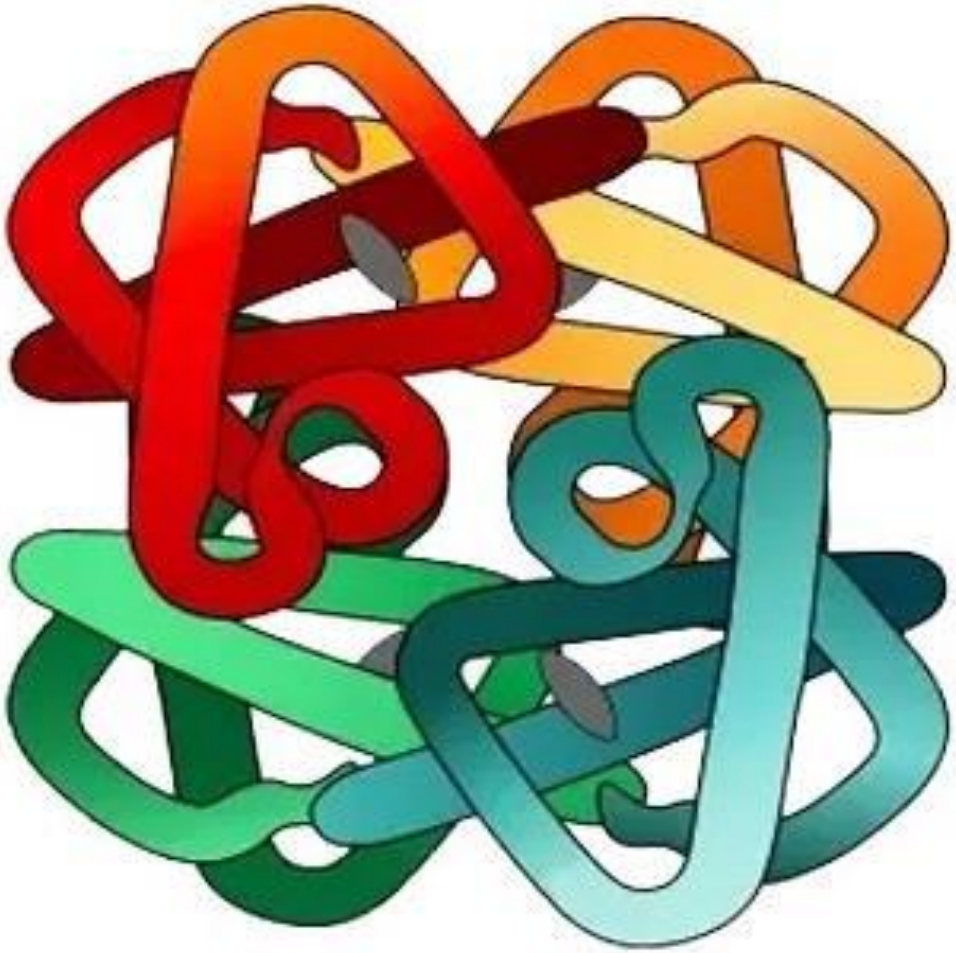
e. g: **myoglobin**(1 polypeptide chain **monomeric**proteins)



4. Quaternary Structure of Proteins

- Many proteins consist of a single polypeptide chain, and are defined as monomeric proteins. However, others may consist of two or more polypeptide chains that may be structurally identical or totally unrelated.
- The arrangement of these polypeptide subunits is called the quaternary structure of the protein. Subunits are held together by noncovalent interactions (for example, hydrogen bonds, ionic bonds, and hydrophobic interactions).





Quaternary Structure

Complex of protein molecules

Protein Classification

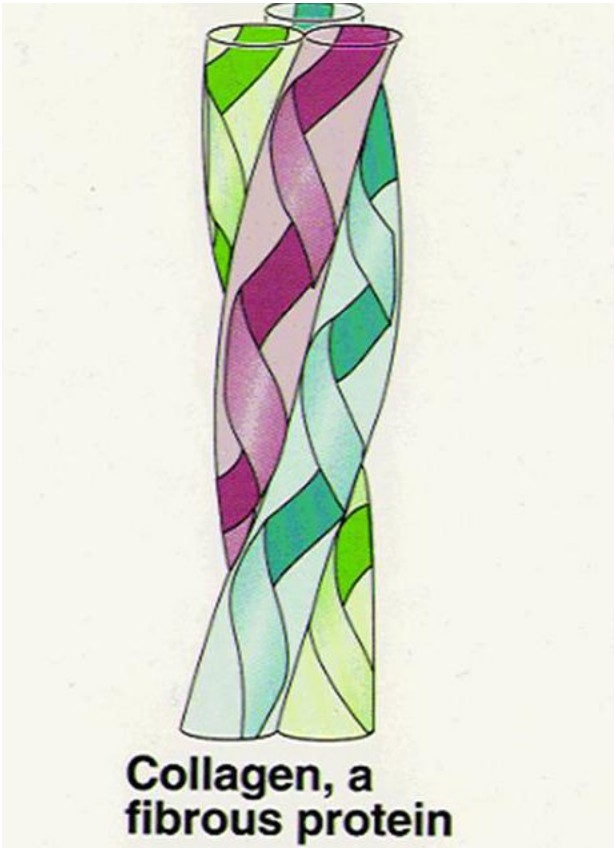
There are two general classes of protein molecules:

a) globular proteins

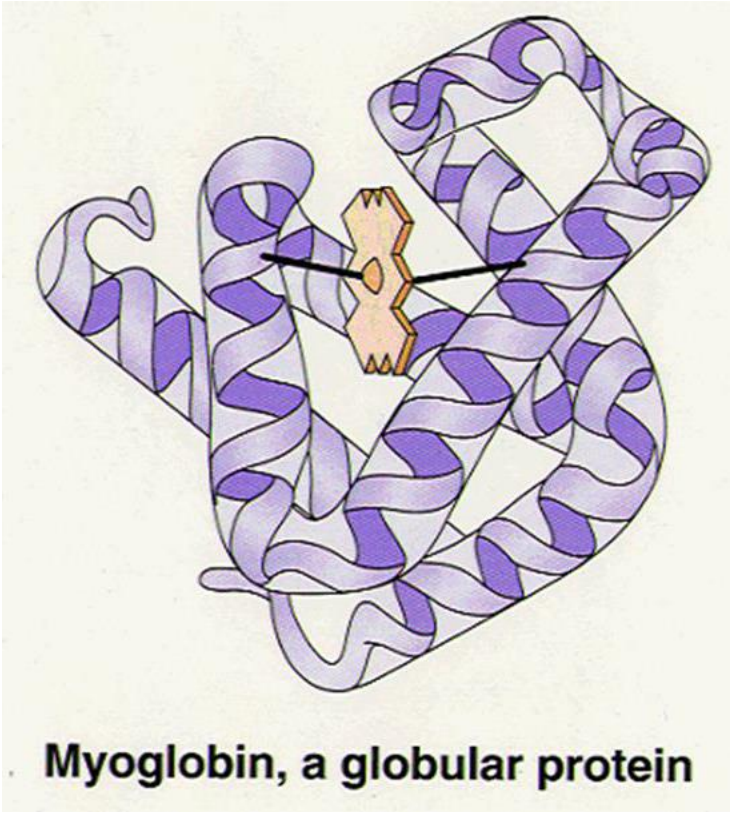
1-Compact. 2-Soluble. 3- spherical in shape.

b) **fibrous proteins**

1-Elongated. 2- insoluble

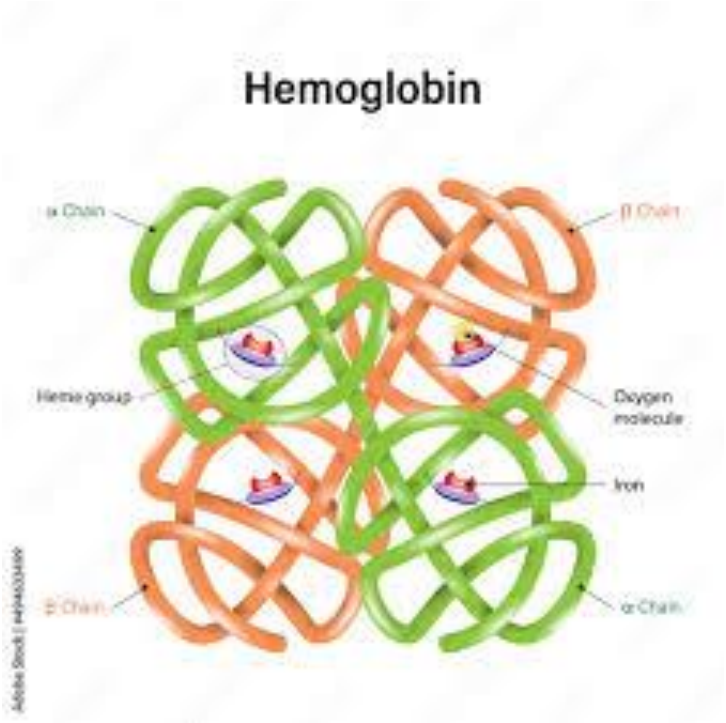


Collagen, a fibrous protein



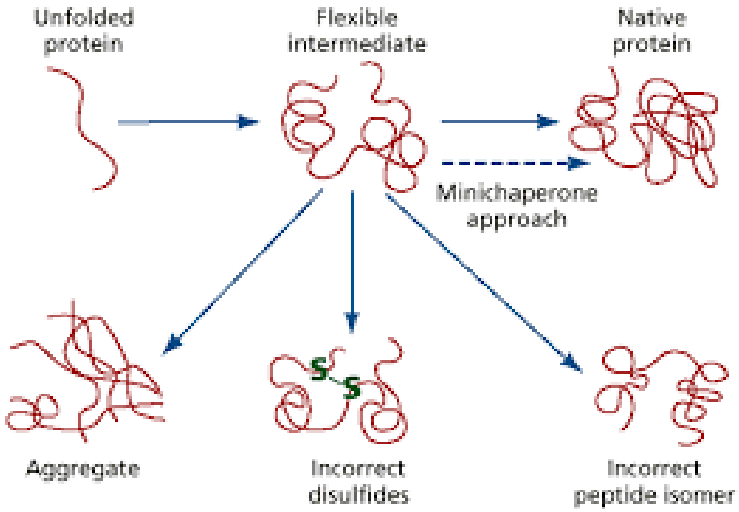
Myoglobin, a globular protein

- **Collagen** is a fibrous protein of three polypeptides that are supercoiled like a rope.
- **Hemoglobin** is a globular protein with two copies of two kinds of polypeptides.
- Subunits may either function independently of each other, or may work cooperatively, as in hemoglobin, in which the binding of oxygen to one subunit of the tetramer increases the affinity of the other subunits for oxygen

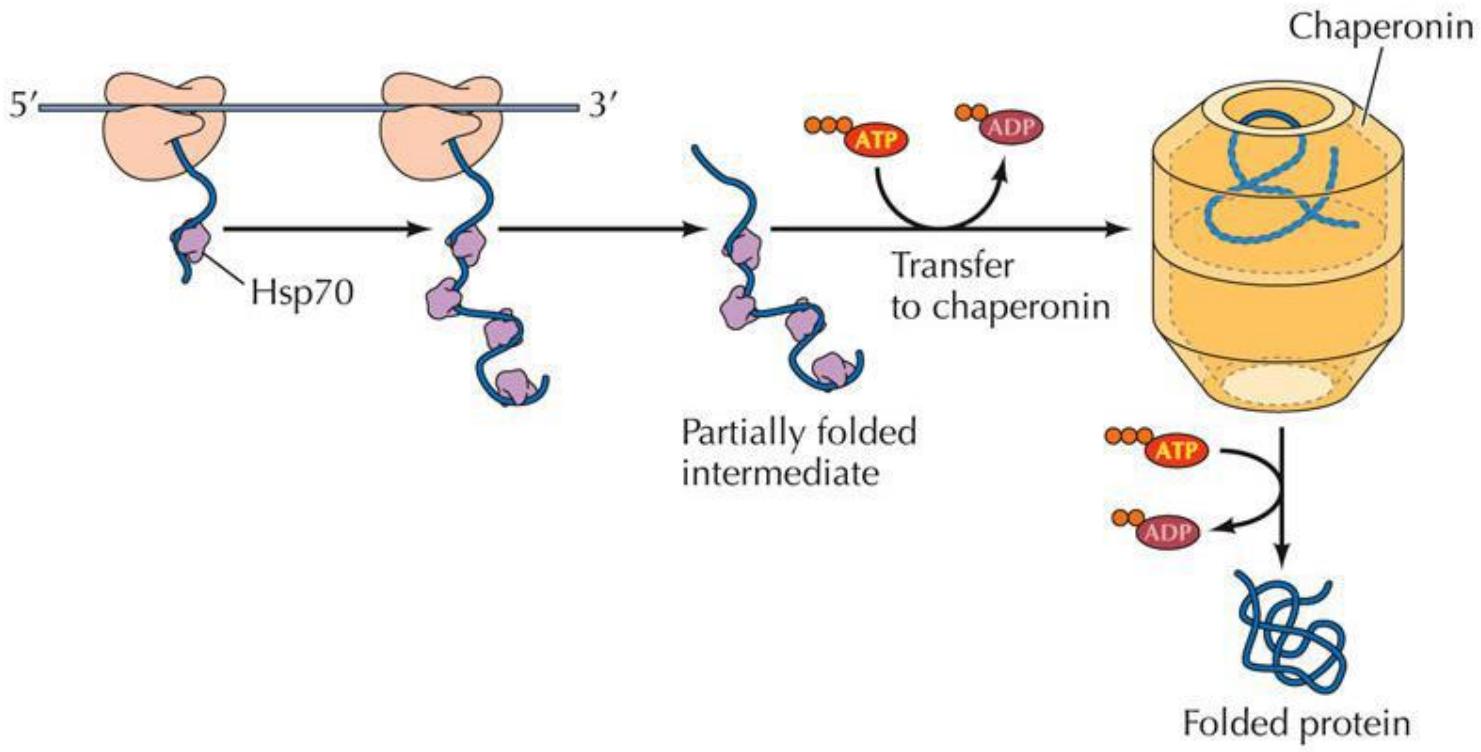


Protein folding

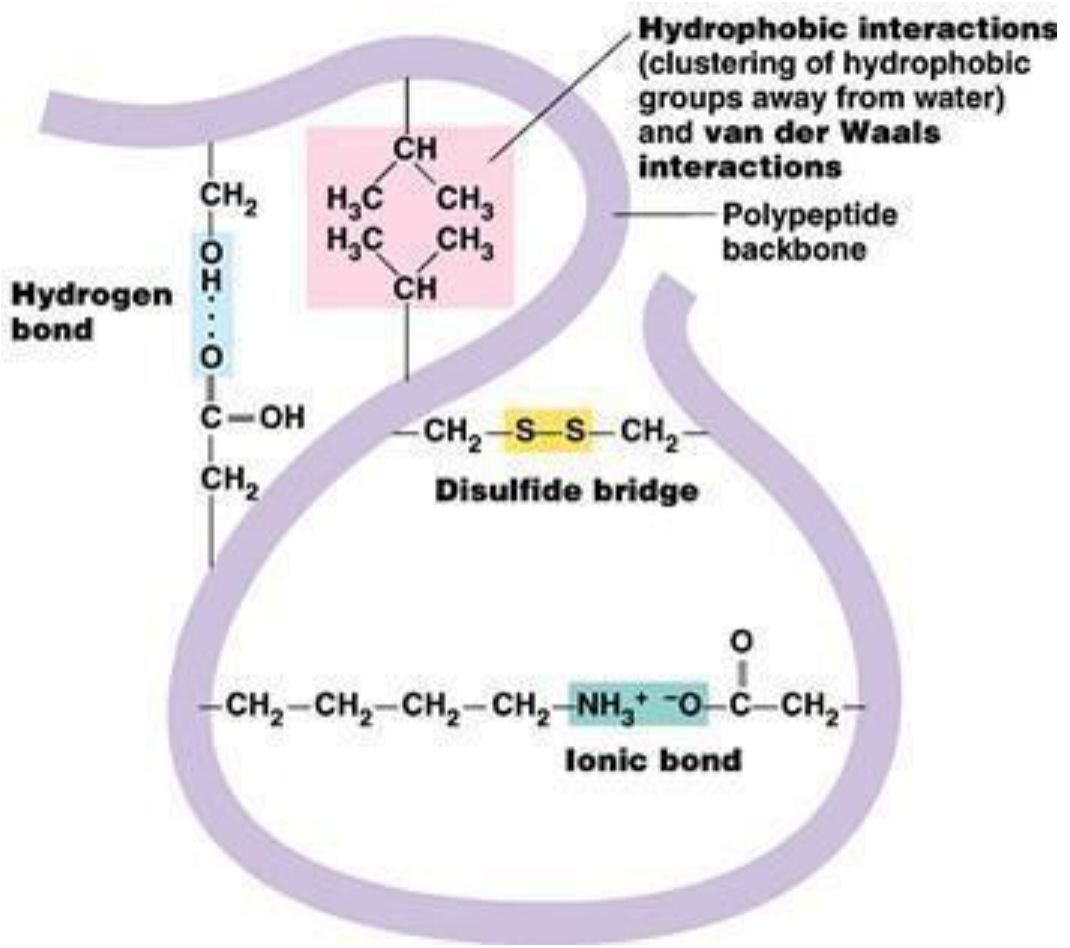
- Protein folding is the process by which a protein structure assumes its functional shape or conformation.
- By coiling and folding into a specific three-dimensional shape they are able to perform their biological function.
- Unfolded or misfolded **proteins** contribute to the pathology of many diseases.
- Protein folding occurs in a cellular compartment called the **endoplasmic reticulum**.



Chaperones are proteins that facilitate the folding of other proteins. The classic principle of protein folding is that all the information required for a protein to adopt the correct three-dimensional conformation is provided by its amino acid sequence

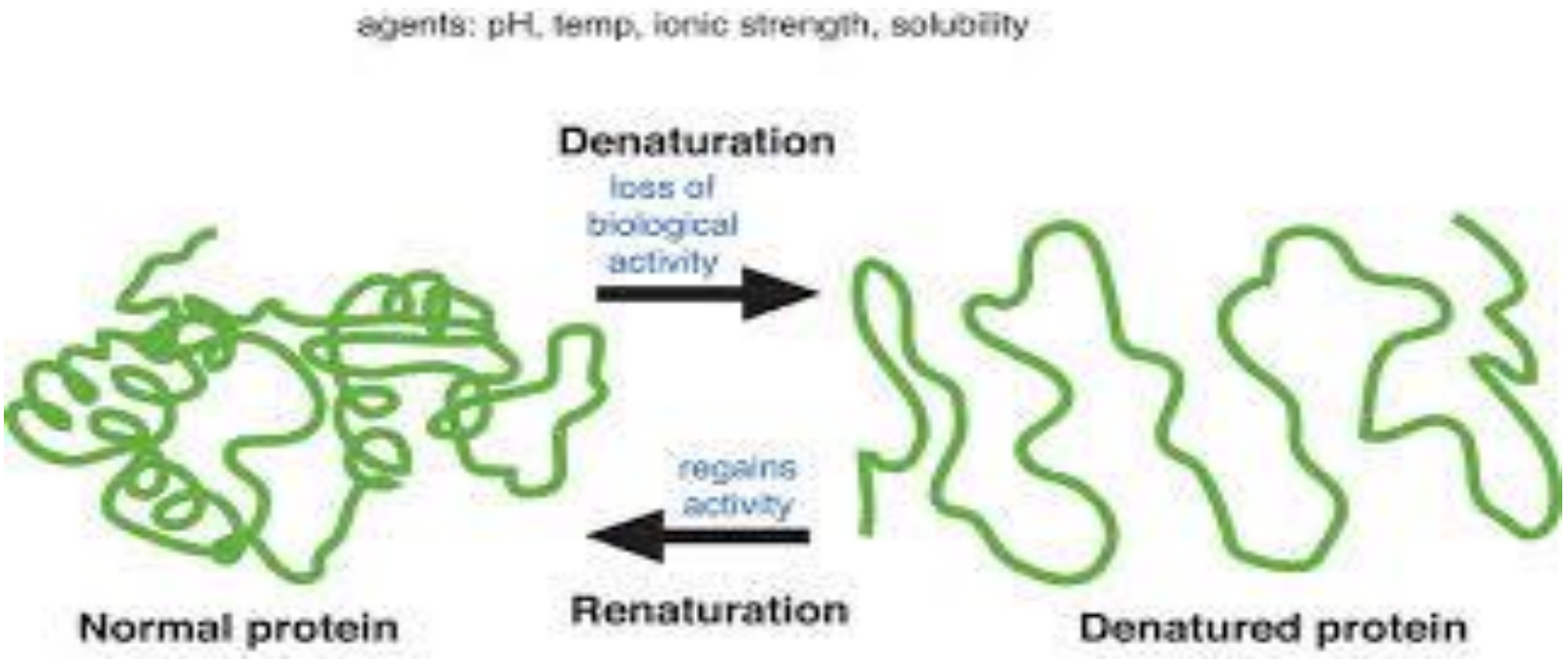


The side chains of highly **polar** amino acids tend to reside on the **exterior** of proteins, where they can form hydrogen bonds with water.
The side chains of **Nonpolar** amino acids are normally clustered
In the **interior** of proteins to shield them from water.



Protein Denaturation:

- The loss of protein structure sufficient to cause the loss of function is known as **denaturation**.
- Denaturation is brought about by breaking the bonds that hold and maintain the protein's tertiary and secondary structure.



Denaturing agents include heat, organic solvents ,mechanical mixing ,strong acids or bases, detergents, and ions of heavy metals such as lead and mercury.

- As the disulfides are reduced by **B-mercaptoethanol,**

the latter is oxidized and forms dimers.

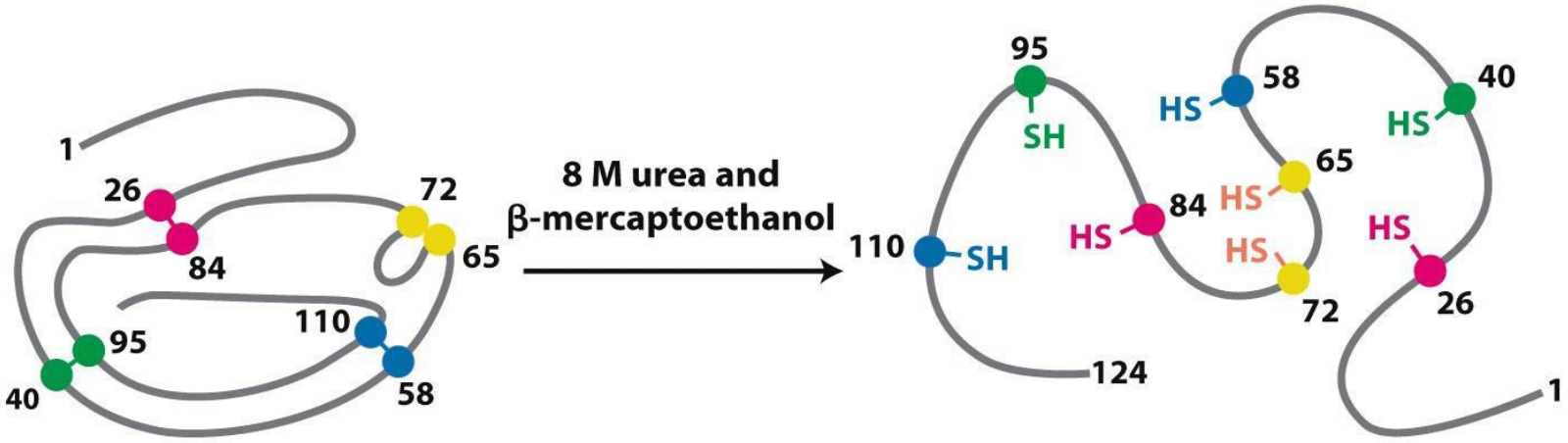


Figure 2.53
***Biochemistry*, Seventh Edition**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