

AMINO ACIDS AND PROTEIN

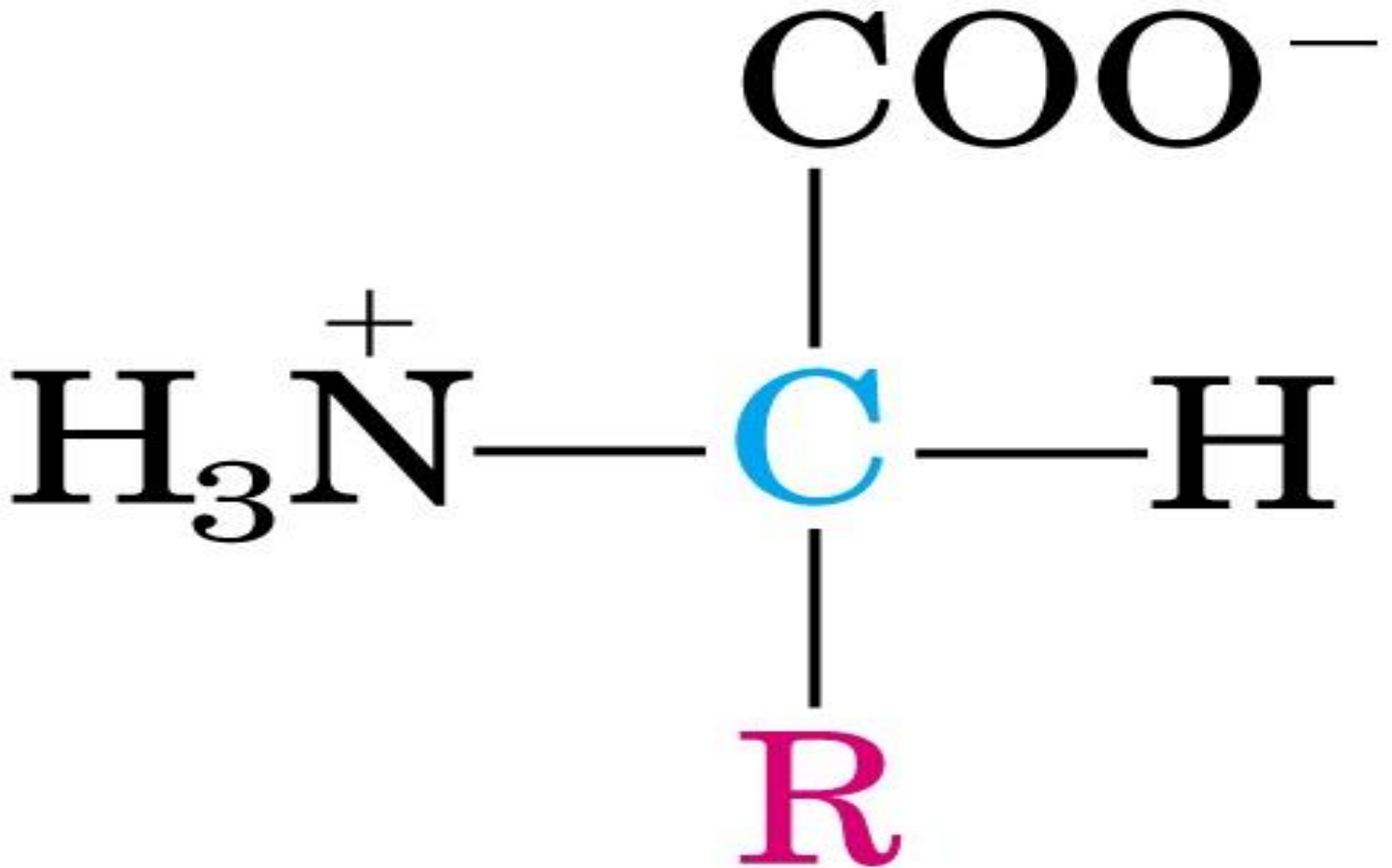
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UNIT-1

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Introduction

- **Proteins are key players in our living systems.**
- **Proteins are polymers consisting of 20 kinds of amino acids.**
- **Each protein folds into a unique three-dimensional structure defined by its amino acid sequence.**
- **Protein structure has a hierarchical nature.**
- **Protein structure is closely related to its function.**

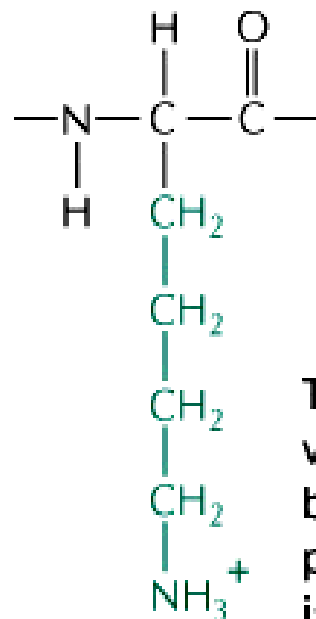
Amino acids



BASIC SIDE CHAINS

lysine

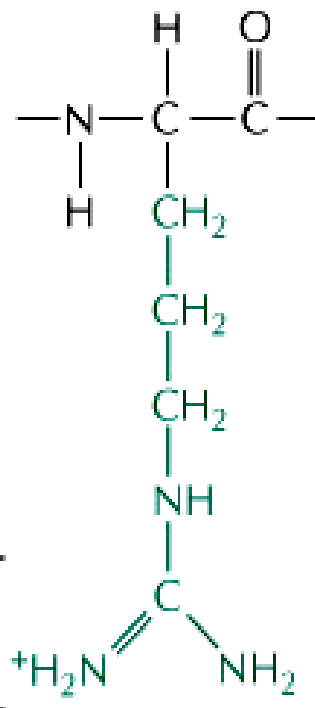
(Lys, or K)



This group is very basic because its positive charge is stabilized by resonance.

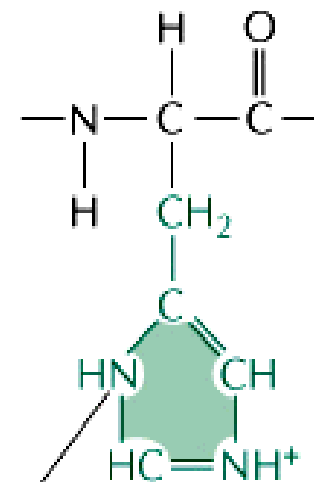
arginine

(Arg, or R)



histidine

(His, or H)

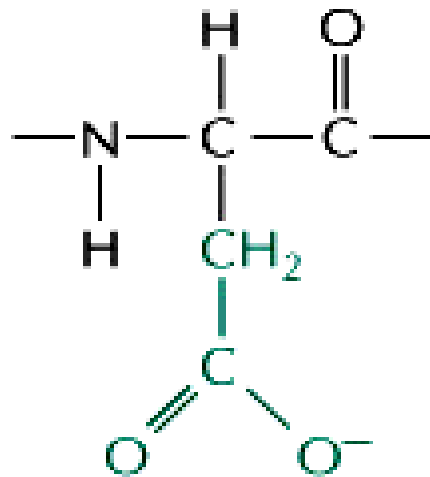


These nitrogens have a relatively weak affinity for an H^+ and are only partly positive at neutral pH.

ACIDIC SIDE CHAINS

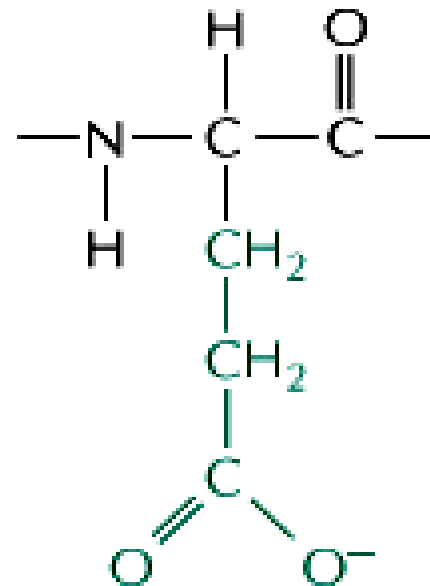
aspartic acid

(Asp, or D)



glutamic acid

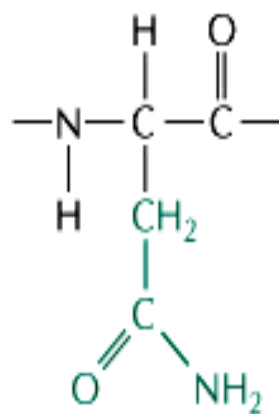
(Glu, or E)



UNCHARGED POLAR SIDE CHAINS

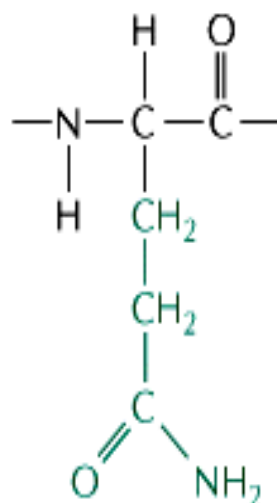
asparagine

(Asn, or N)



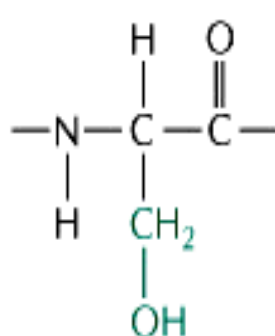
glutamine

(Gln, or Q)



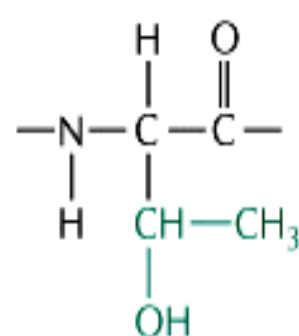
serine

(Ser, or S)



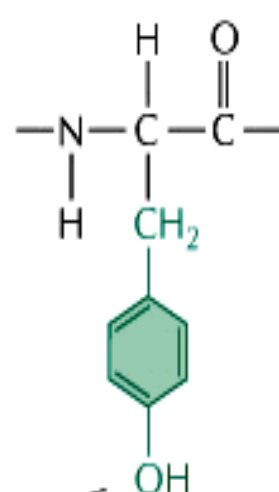
threonine

(Thr, or T)



tyrosine

(Tyr, or Y)



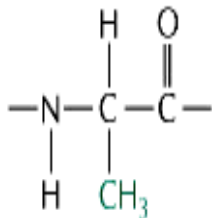
The -OH group is polar.

Although the amide N is not charged at neutral pH, it is polar.

NONPOLAR SIDE CHAINS

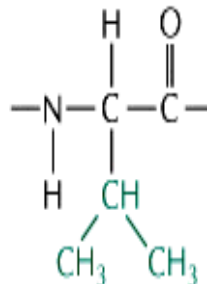
alanine

(Ala, or A)



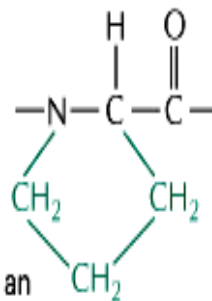
valine

(Val, or V)



proline

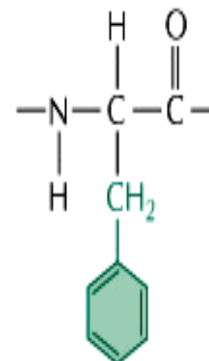
(Pro, or P)



(actually an imino acid)

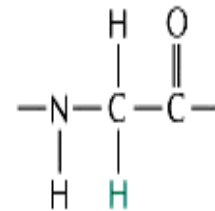
phenylalanine

(Phe, or F)



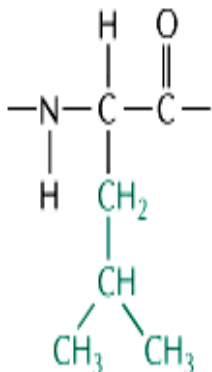
glycine

(Gly, or G)



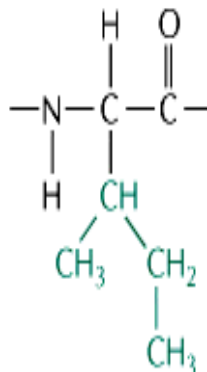
leucine

(Leu, or L)



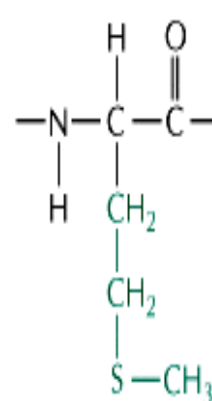
isoleucine

(Ile, or I)



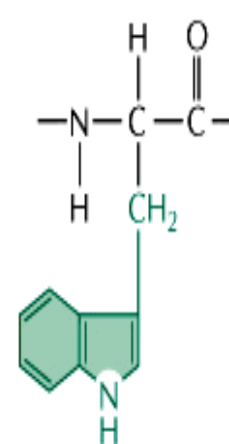
methionine

(Met, or M)



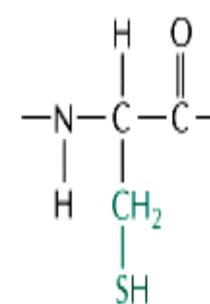
tryptophan

(Trp, or W)



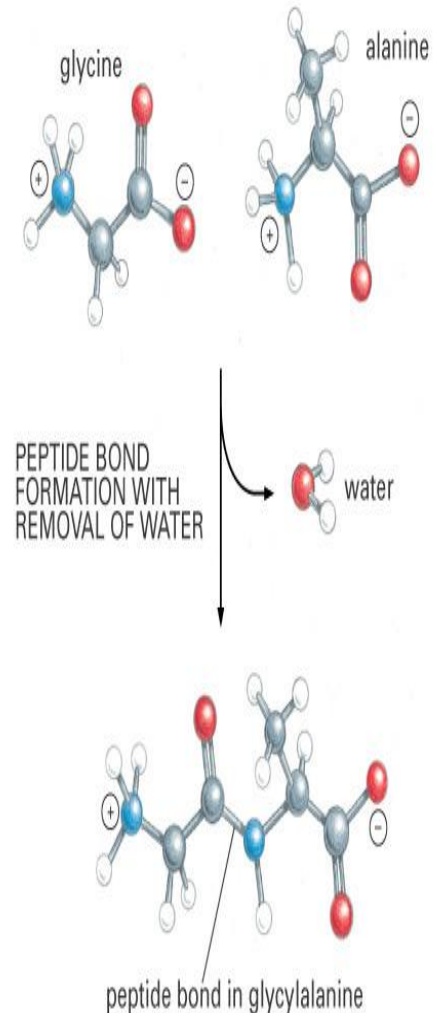
cysteine

(Cys, or C)

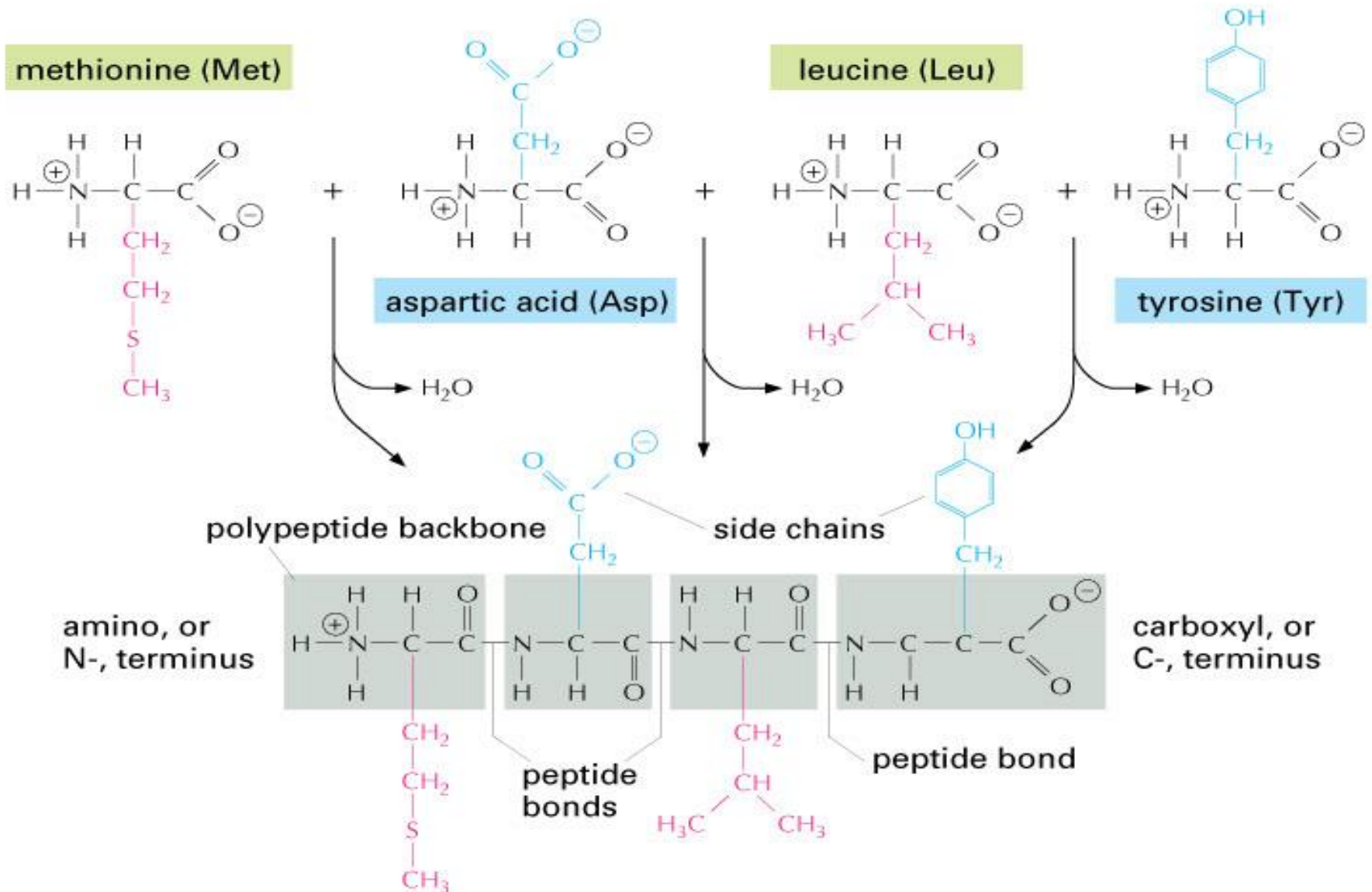


Peptide Bond

- Proteins are linear sequences of amino acids linked together by **peptide bonds**.
- The peptide bond is a chemical, covalent bond formed between the α -amino group of one amino acid and the α -carboxyl group of another.
- Once two amino acids are joined together via a peptide bond to form a dipeptide.
- There is still a free amino group at one end and a free carboxyl group at the other, each of which can in turn be linked to further amino acids.



Peptide bonds in peptide chains



Hierarchical nature of protein structure

Primary structure (Amino acid sequence)



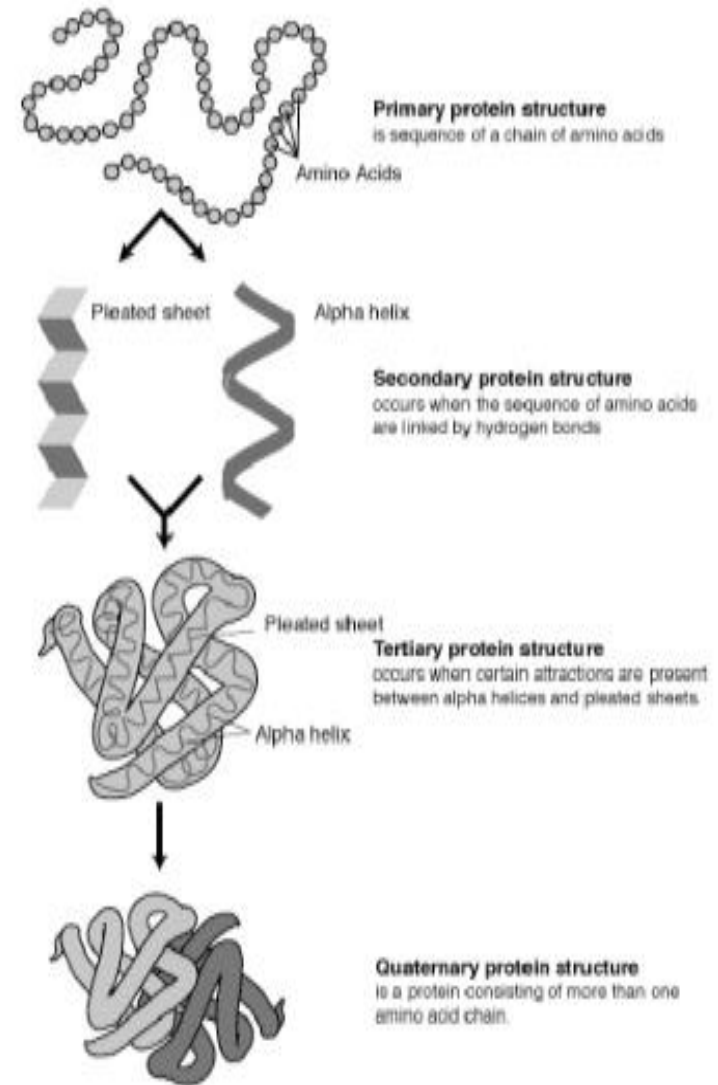
Secondary structure (α -helix, β -sheet)



Tertiary structure (Three-dimensional structure formed by assembly of secondary structures)

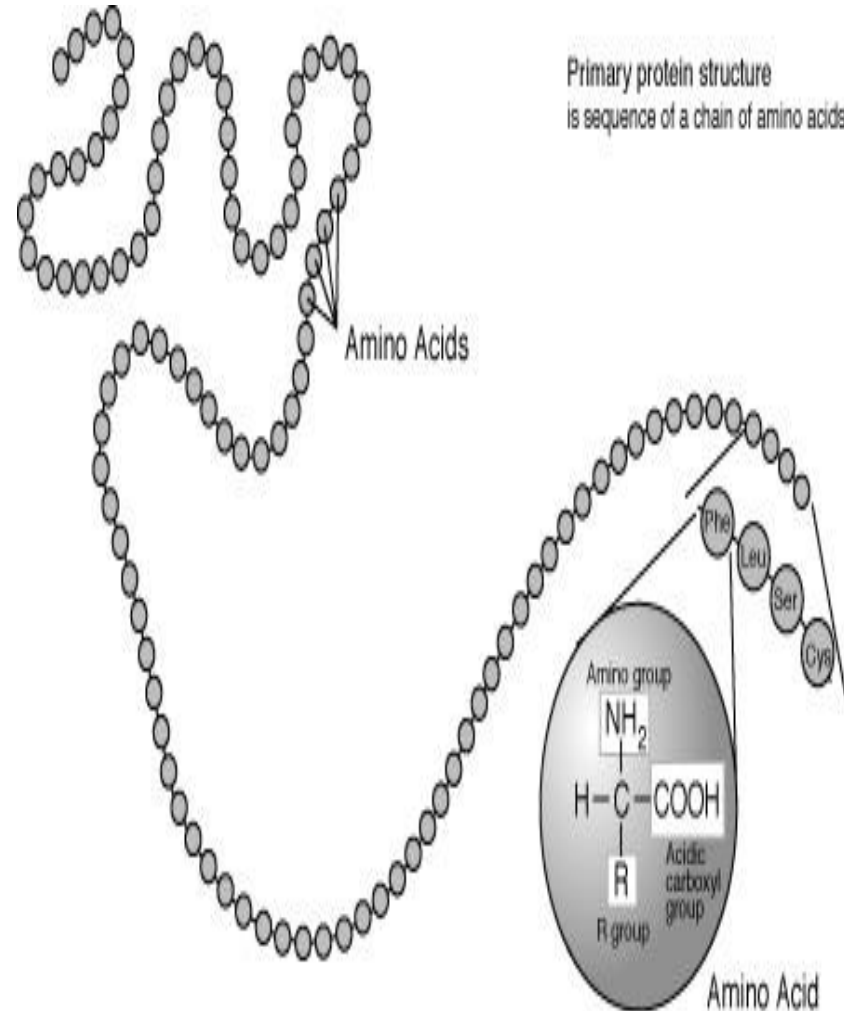


Quaternary structure (Structure formed by more than one polypeptide chains)



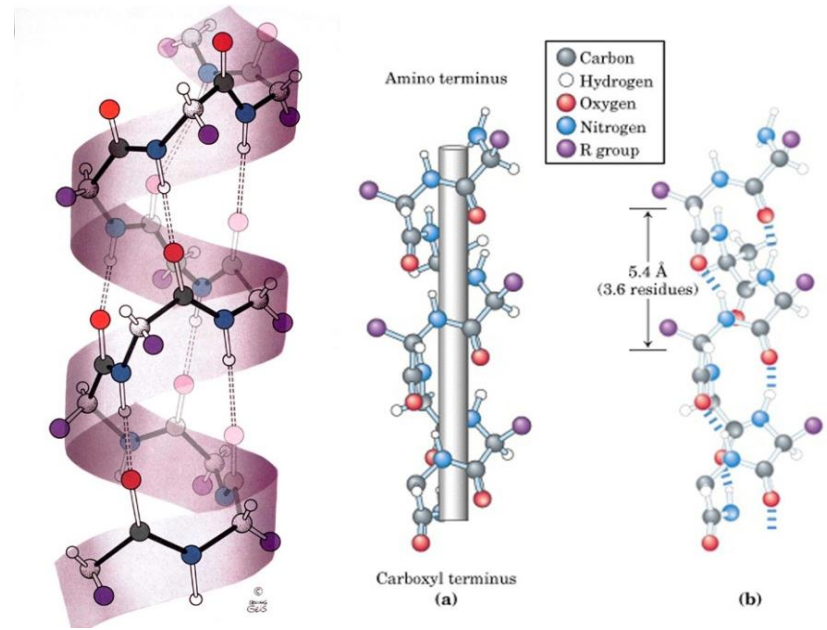
Primary Structure

- linear
- ordered
- 1 dimensional
- The primary level of structure in a protein is the linear sequence of amino acids as joined together by peptide bonds.
- This sequence is determined by the sequence of nucleotide bases in the gene encoding the protein .
- Also included under primary structure is the location of any other covalent bonds. These are primarily disulfide bonds between cysteine residues that are adjacent in space but not in the linear amino acid sequence.



Secondary Structure

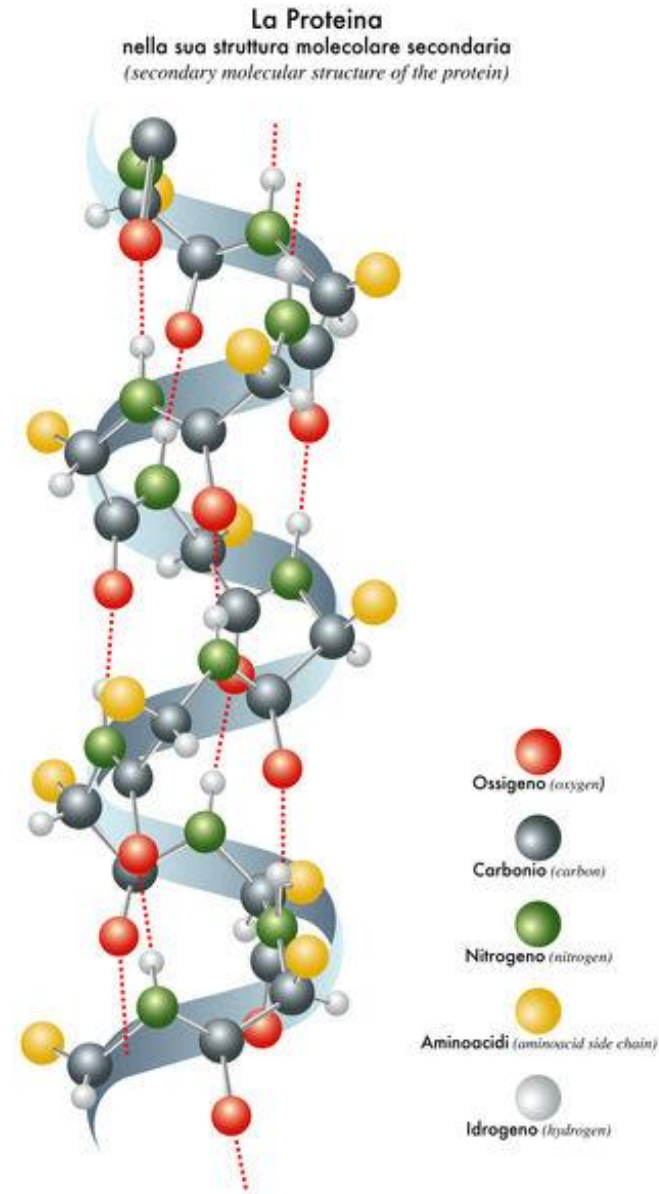
- Non-linear
- 3-dimensional
- Localized to regions of an amino acid chain
- Formed and stabilized by hydrogen bonding, electrostatic and van der Waals interactions.
- The secondary level of structure in a protein is the regular folding of regions of the polypeptide chain.
- The two most common types of protein fold are the α -helix and the β -pleated sheet.



Alpha-helix Structure

In the rod-like α -helix, the amino acids arrange themselves in a regular **helical conformation**.

The carbonyl oxygen of each peptide bond is hydrogen bonded to the hydrogen on the amino group of the **fourth amino acid away**, with the hydrogen bonds running nearly parallel to the axis of the helix.



In an α -helix there are **3.6 amino acids** per turn of the helix covering a distance of **0.54 nm**.

Each amino acid residue represents an advance of **0.15 nm** along the axis of the helix.

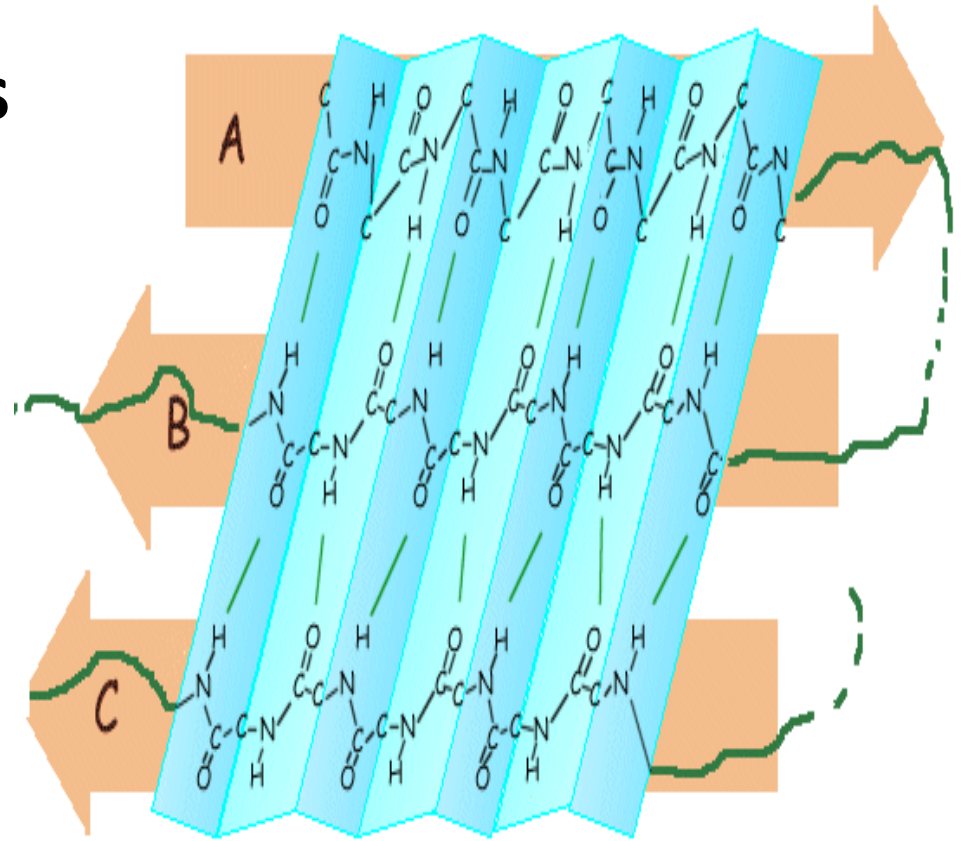
The side-chains of the amino acids are all positioned along the outside of the cylindrical helix .



secondary structure
(α -helix)

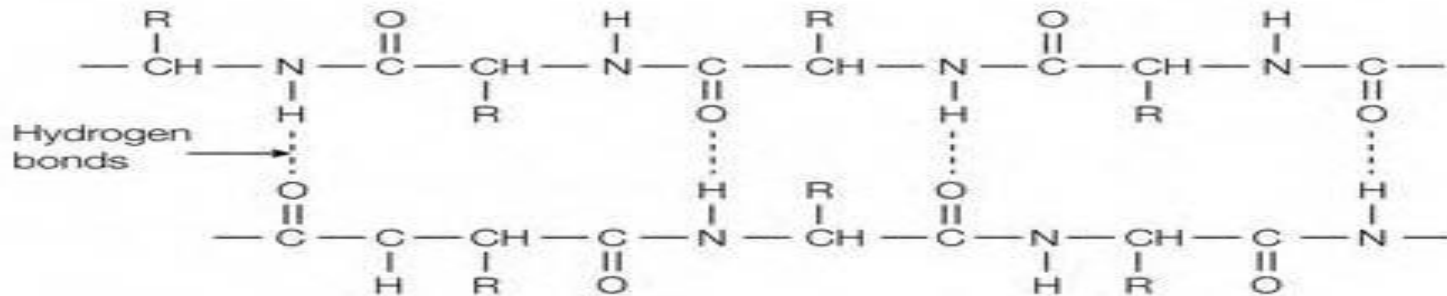
β -Sheets

- Sheets can be made up of any number of strands
- Orientation and hydrogen bonding pattern of strands gives rise to flat or twisted sheets
- Parallel sheets buried inside, while Antiparallel sheets occurs on the surface

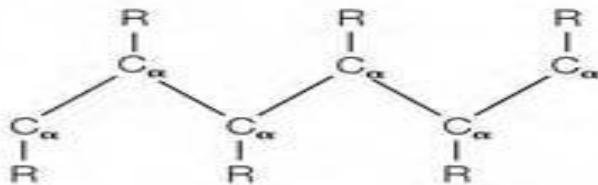


- In the β -pleated sheet, hydrogen bonds form between the peptide bonds either in different polypeptide chains or in different sections of the same polypeptide chain (Fig.a).
- The planarity of the peptide bond forces the polypeptide to be pleated with the side-chains of the amino acids protruding above and below the sheet (Fig.b).
- Adjacent polypeptide chains in β pleated sheets can be either parallel or anti-parallel depending on whether they run in the same direction or in opposite directions, respectively (Fig.c).

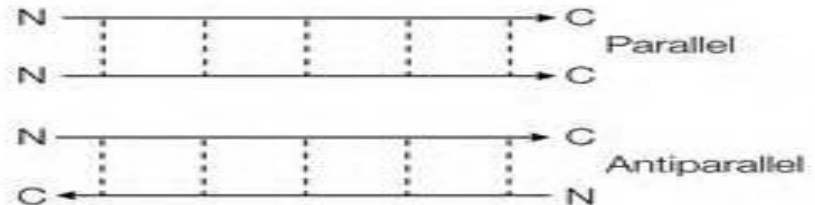
(a)



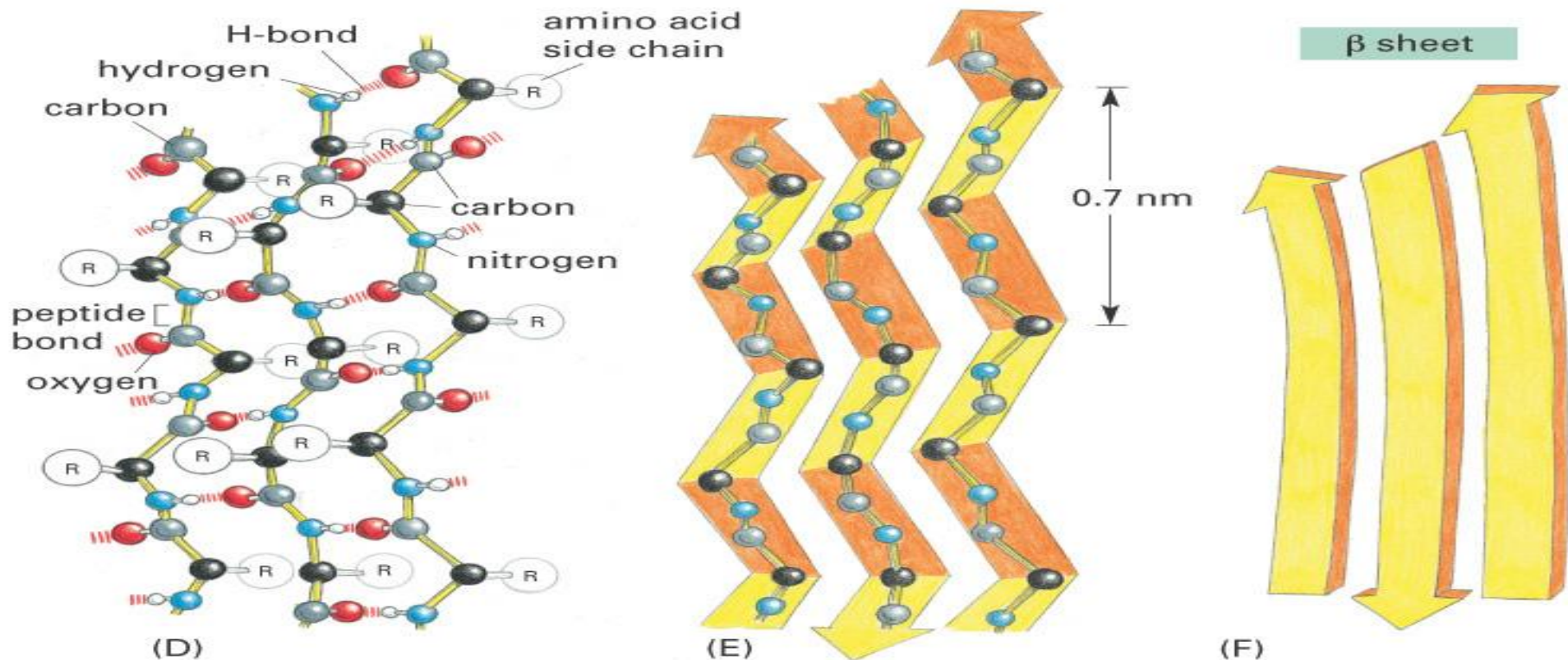
(b)



(c)



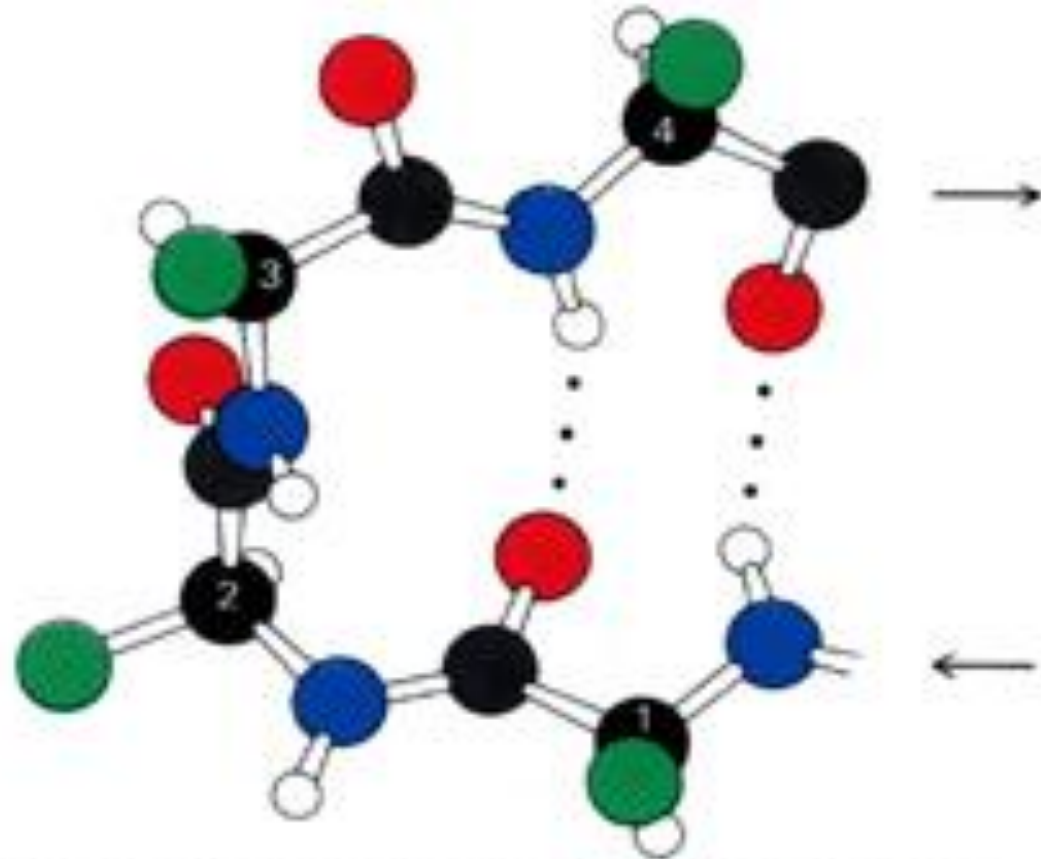
- The polypeptide chain within a β -pleated sheet is fully extended, such that there is a distance of 0.35 nm from one C- α atom to the next.
- β -Pleated sheets are always slightly curved and, if several polypeptides are involved, the sheet can close up to form a β -barrel.
- Multiple β -pleated sheets provide strength and rigidity in many structural proteins, such as silk fibroin, which consists almost entirely of stacks of anti-parallel β -pleated sheets.



B-turns

• In order to fold tightly into the compact shape of a globular protein, the polypeptide chain often reverses direction, making a **hairpin** or β -turn.

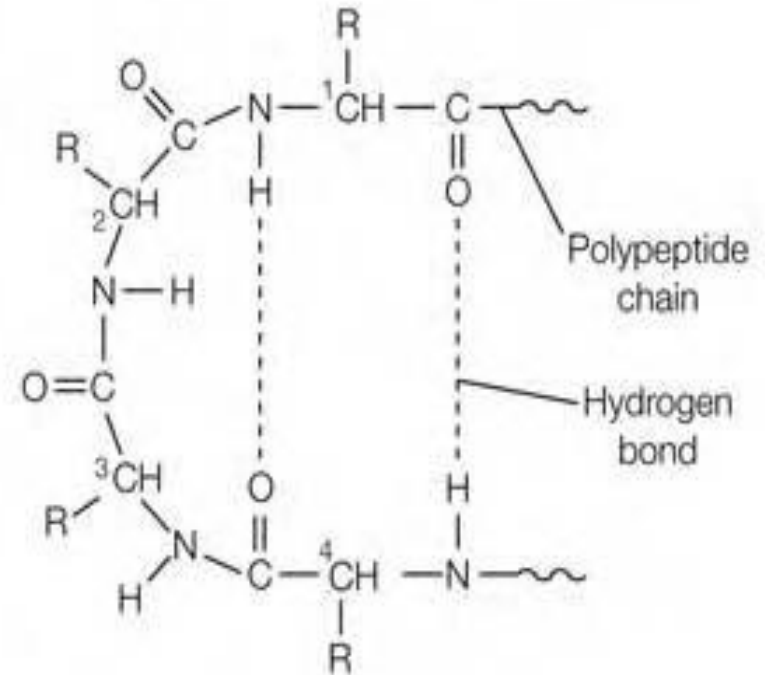
• In these β -turns the carbonyl oxygen of one amino acid is **hydrogen bonded to the hydrogen on the amino group of the fourth amino acid** along .



Structure of a β turn. The NH and CO groups of residue 1 of the tetrapeptide shown here are hydrogen bonded, respectively, to the CO and NH groups of residue 4, which results in a hairpin turn.

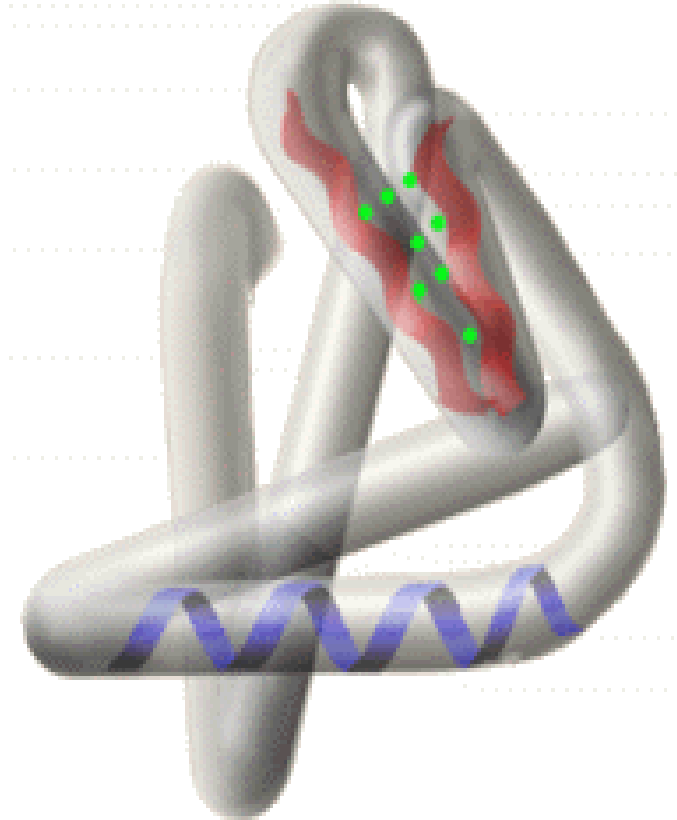
B-turns

- β -Turns are often found connecting the ends of anti-parallel β -pleated sheets.
- Regions of the polypeptide chain that are not in a regular secondary structure are said to have a coil or loop conformation.
- About half the polypeptide chain of a typical globular protein will be in such a conformation.



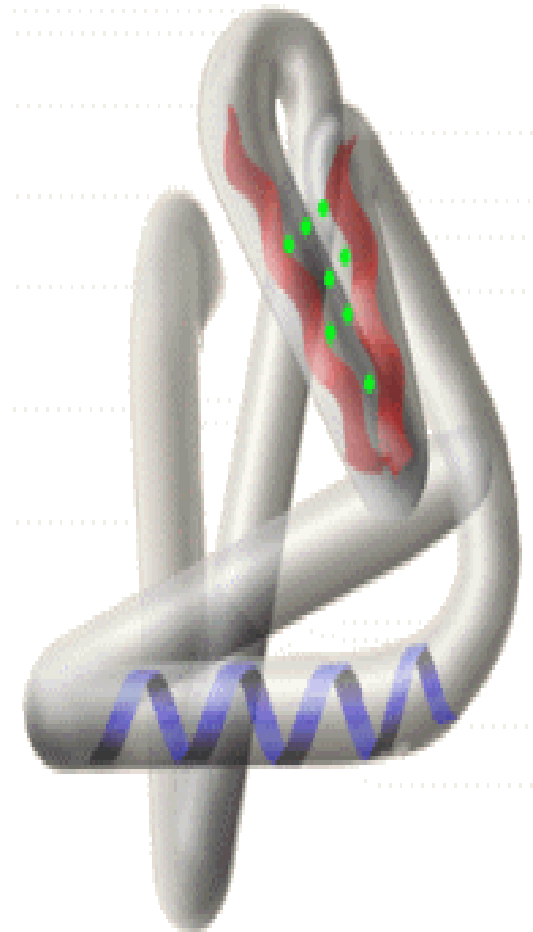
Tertiary Structure

- Non-linear
- 3 dimensional
- Formed and stabilized by hydrogen bonding, covalent (e.g. disulfide) bonding, hydrophobic packing toward core and hydrophilic exposure to solvent
- Defines the three dimensional conformation of an entire peptide chain in space
- Determined by the primary structure



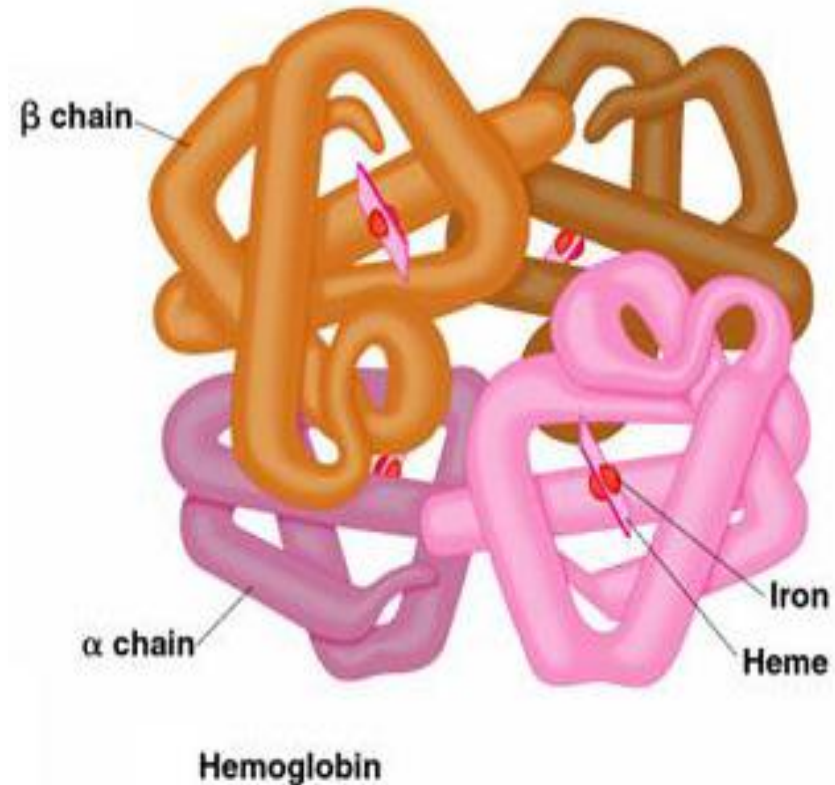
Aspects which determine tertiary structure

- Covalent disulfide bonds from between closely aligned cysteine residues form the unique Amino Acid cystine.
- Nearly all of the polar, hydrophilic R groups are located in the surface, where they may interact with water
- The nonpolar, hydrophobic R groups are usually located inside the molecule



Quaternary Structure

- non-linear
- 3 dimensional
- Exhibit a fourth level of protein structure called quaternary structure
- This level of structure refers to the spatial arrangement of the polypeptide subunits and the nature of the interactions between them.
- These interactions may be covalent links (e.g. disulfide bonds) or non-covalent interactions (electrostatic forces, hydrogen bonding, hydrophobic interactions).



Properties of proteins

- 1. U.V absorption:** Proteins absorb U.V radiation at 280 nm because of the presence of aromatic amino acids like tryptophan and tyrosine. This property is used in estimation of proteins.
- 2. Isoelectric point:** Isoelectric point is also called as isoelectric pH. This is the pH at which the number of positive and negative charges is equal in the protein and they are electrically neutral.
- 3. Zwitterions:** Proteins contain both positive and negative charges and hence they are called as zwitterions. Amino acids will act as zwitterions as they can donate a proton and forms cation.

Properties of proteins

5. Denaturation: Due to denaturation, there is a decrease in solubility and loss of biological activity of proteins.

Denaturation occurs at extreme temperatures and pH and also by many chemicals like organic solvents, urea, ionic detergents etc. On denaturation, non covalent bonds in the protein are broken and its primary structure remains intact.

6. Protein folding: Many proteins fold to their native conformation on their own by self assembly. However several other accessory proteins help in this process. They include-

a) Enzymes: Eg: Peptidyl prolyl cis-trans isomerase introduces reverse bends.

b) Molecular chaperons: They are a special class of proteins which will help in the folding of other proteins.

7. Solubility: Protein solubility is influenced by pH, heavy metals, salts and organic solvents.

Biological roles of Proteins in Plants

- 1. They are important macro-molecules that participate in every aspect of plant growth and development.**
- 2. Proteins are involved in processes such as**
 - a. catalyzing chemical reactions (enzymes),**
 - b. facilitating membrane transport,**
 - c. intracellular structure,**
 - d. energy generating reactions involving electron transport and**
 - e. Storage function-in germinating seed.**