–Val–His–Leu–Thr–Pro–[Glu]–Glu–Lys–

Normal haemoglobin

–Val–His–Leu–Thr–Pro–[Val]–Glu–Lys–

Sickle cell haemoglobin

(ii) Secondary structure. *The conformation which the polypeptide chains assume as a result of hydrogen-bonding is called the secondary structure of the protein.* Depending upon the size of the R groups, the following two different secondary structures are possible.

(a) α-Helix structure. The α-helix model was postulated by Linus Pauling in 1951 purely on theoretical grounds and was later on verified experimentally. If the size of the R groups is quite large, the H-bonds (*intramolecular*) are formed between the C = O of one amino acid residue and the N -H of the fourth amino acid residue in the chain. This causes the polypeptide chain to coil up into a spiral structure called *right handed* α-helix structure (Figs. 3.6(a) and 3.6(b))

The α-helix is also known as **$3{\cdot}6_{13}$ helix** *since each turn of the helix has approximately 3·6 amino acids and a 13-membered ring is formed by H-bonding.* The pitch or the distance between two successive turns = 5·4 Å.

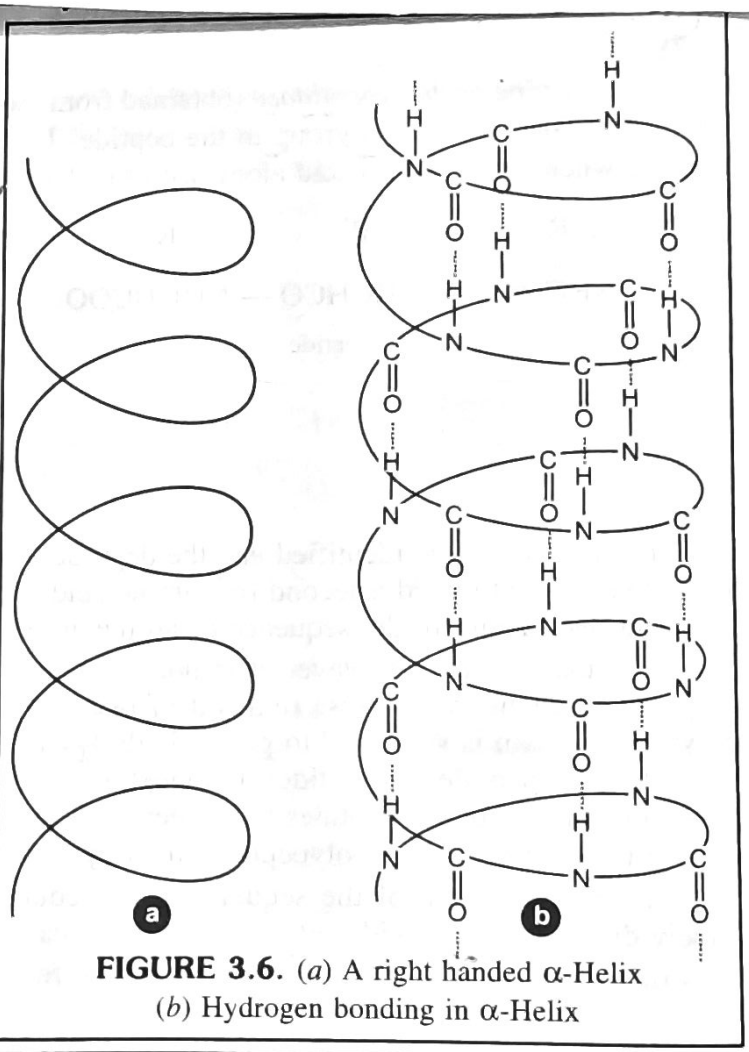


FIGURE 3.6. (*a*) A right handed α-Helix
(*b*) Hydrogen bonding in α-Helix

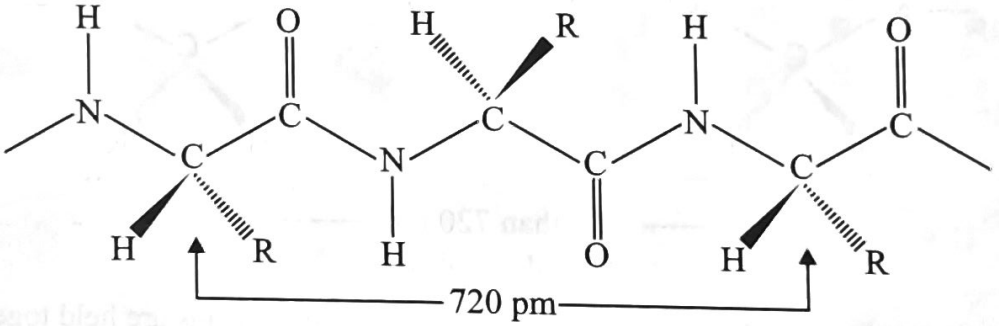
*Insulin is a peptide hormore and is produced in *pancreas*. It is essential for metabolism of carbohydrates in the body. It contains 51 amino acids arranged in two polypeptide chains containing 21 and 30 amino acid residues ss links.

The α-helix may be right-handed or left handed. All α-amino acids, except glycine, are optically active and all have the L-configuration. Moffitt (1956) deduced theoretically that for L-amino acids, right-handed helix is more stable than the left-handed helix. Thus, the helical structure of proteins is always right handed, *i.e.*, the polypeptide chain turns in the clockwise direction (Fig. 3.6*a*) along the helical axis just as the threads of a screw or bolt are right handed. Therefore, a stable helix results only if it is right-handed.

Many fibrous proteins such as α-*keratin* in hair, nail, wool, skin, beaks, claws and *myosin* in muscles have α-helix structure though globular proteins also contain segments of α-helix. Because of the helical structure, human hair fibres are stretchable and elastic to a small extent. When the human hair fibre is stretched, the hydrogen bonds are either stretched or broken but when the stretching force is removed, the hydrogen bonds are formed. This makes the hair fibres elastic.

(*b*) **β-Pleated sheet structure.** This structure was also proposed by Linus Pauling in 1951.

The simplest possible arrangement of the peptide chains is the one in which the peptide chains are fully extended to form flat zig-zag structure



Extended peptide chain

These chains lie side by side to form **flat sheet.** Each chain is held by hydrogen bonds to the two neighbouring chains Fig. 3.7.

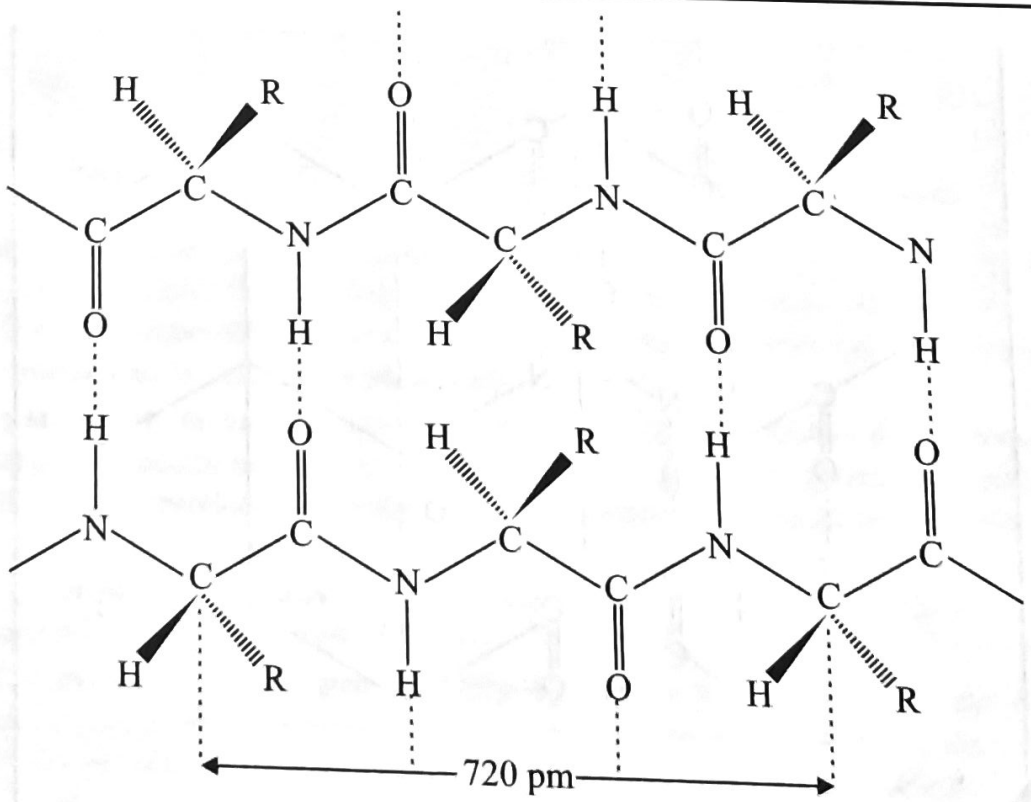
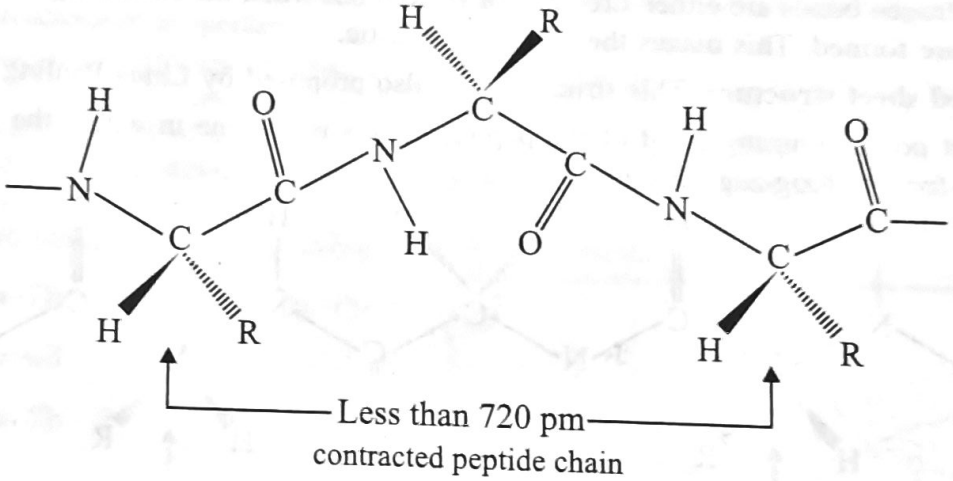


FIGURE 3.7. Hypothetical flat sheet structure of a protein.
The chains are fully extended and adjacent chains head in opposite directions.

In this flat sheet structure, repeat distance (distance between alternate amino acid residues side c which lie on the same side of the sheet) is 720 pm or 7·2 Å and the heads of the adjacent chains are i opposite directions. Because of the crowding between the side chain R groups, no natural protein is l to have this structure. Therefore, it is an ideal structure. At the best, it may be possible for synt polyglycine in which there are no side chains, *i.e.*, the groups R are the H-atoms.

However, if the size of the group R is small to medium, the polypeptide chains contract a little in to make room for them.



contracted peptide chain

This contraction results in *pleated sheet* in which the polypeptide chains are held together by H- with somewhat shorter distance between alternate amino acid residues. This is called β-pleated sheet str (Fig. 3.8).

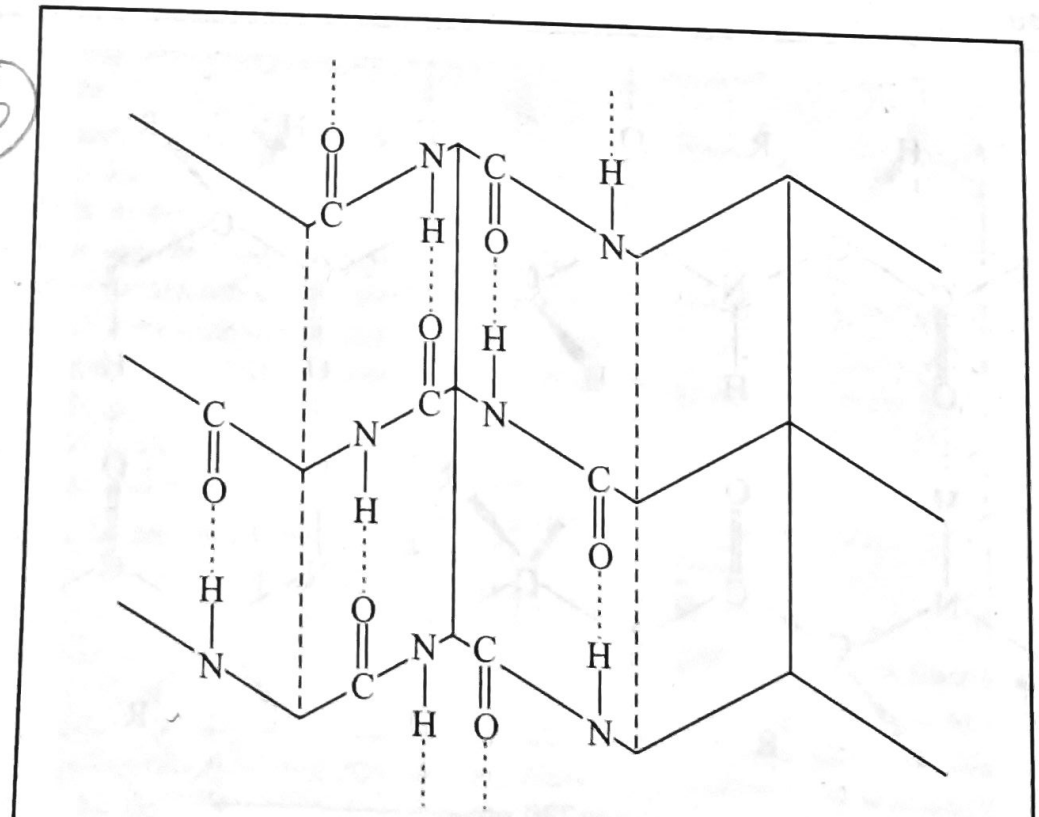


FIGURE 3.8. β-Pleated sheet structure of proteins.

The silk protein **fibroin** has β-pleated sheet structure with a repeat distance of 700 pm or 7·0 Å which is close to fully extended flat sheet structure. It may be noted that although fibroin contains 15 kinds of amino acid residues, 46% of these is glycine which has no side chain and another 38% are alanine and serine with the small chains $-CH_3$ and $-CH_2OH$. Because of the β-pleated structure, silk fibres are not stretchable or elastic. Thus, when a silk fibre is pulled, it would break some covalent bonds or many hydrogen bonds holding the individual protein molecules in the sheet. However, silk fibres can be easily bent just like the stack of pages of this book.

The β-pleated sheet structure may be either **parallel** or **antiparallel**. In the parallel conformation (Fig. 3.9 *a*), all the peptide chains run in the same direction. In other words, N-termini are aligned head to head, *i.e.*, on the same side. In the anti-parallel conformation (Fig. 3.9 b), the polypeptide chains run alternately in the opposite directions, *i.e.*, N-termini are aligned head to tail or N-terminus of one chain and C-terminus of another chain are on the same side. *Keratin* the protein present in hair has parallel β-pleated sheet structure while the silk protein *fibroin* has antiparallel β-pleated sheet structure.

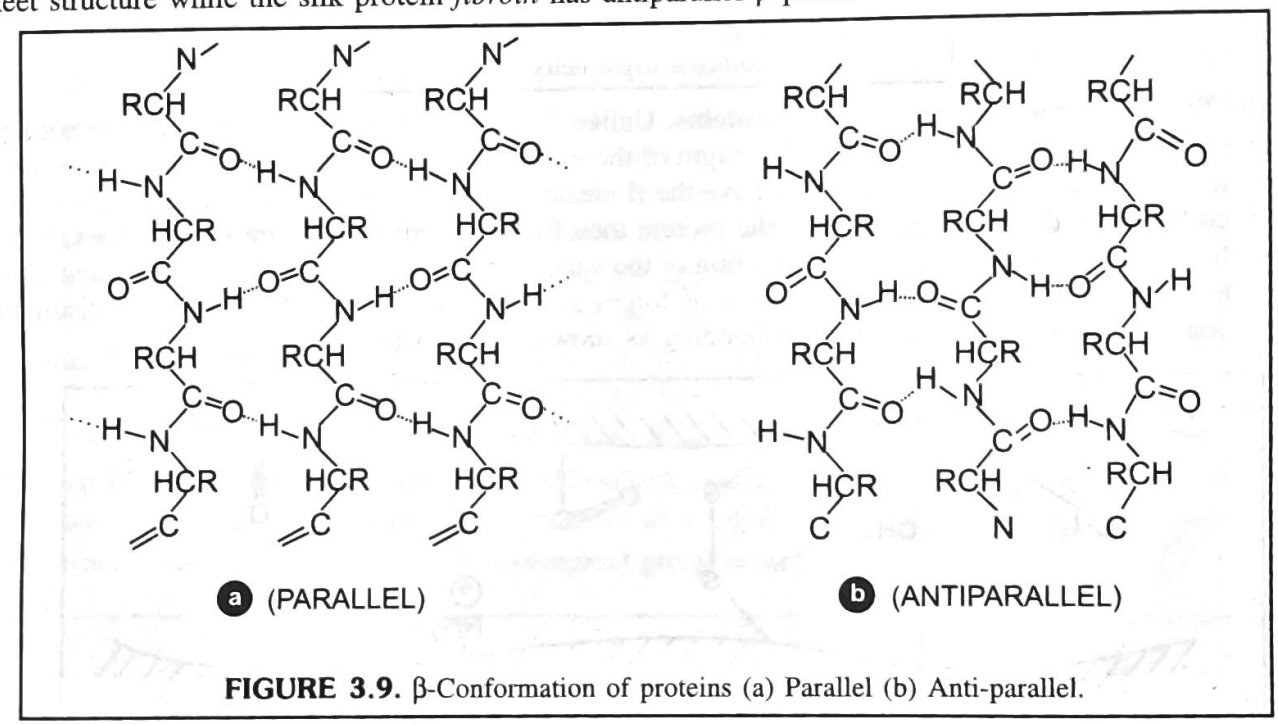


FIGURE 3.9. β-Conformation of proteins (a) Parallel (b) Anti-parallel.

It is important to remember that a protein may or may not have the same secondary structure throughout its length (*i.e.*, *secondary structure is a local structure*). Some parts may have α-helix structure, while others may have β-pleated sheet structure. Some parts of the chain may even have no secondary structure at all. Such a structureless part is called a **random coil**.

(iii) Tertiary structure. *Tertiary structure of a protein refers to its complete three-dimensional structure.* In other words, tertiary structure refers to the manner in which the entire protein molecule folds up in the three-dimensional space to produce a specific shape (or compact form). At normal pH and temperature, each protein will take up a shape (tertiary structure) that is energetically most stable. This shape is specific to a given amino acid sequence and is called the *native shape* of the protein. In other words, *primary structure of a protein dictates its tertiary structure.*

(a) Tertiary structure of fibrous proteins. Fibrous proteins have almost the same secondary (α-helix or β-pleated) structure throughout the length of the protein. For example, the α-keratins, the major proteins of hair and wool have the α-helix structure. In these proteins, several α-helices are coiled about each other to form molecular ropes or rods. *Thus, the tertiary structure of fibrous proteins is rope-like or rod-like*. The structure of collagen triple helix is shown in Fig. 3.10.