

β -Pleated Structure (Secondary structure of protein)

Beta-strands represent for an extended form in which the side chains alternate on either side of the extended chain. Beta pleated structures are so called because the pleated or folded appearance.

Important features :

In brief— (For 3 marks question)

1. The second (hence "beta") recognizable regular secondary structure in proteins is the β sheet. The amino acid residues of a β sheet, when viewed edge-on, form a zigzag or pleated pattern in which the R groups of adjacent residues point in opposite directions.
2. Unlike the compact backbone of the α helix, the peptide backbone of the β sheet is highly extended. But like the α helix, β sheets derive much of their stability from hydrogen bonds between the carbonyl oxygens and amide hydrogens of peptide bonds.
3. In contrast to the α helix, these bonds are formed with adjacent segments of β sheet (Figure).
4. Interacting β sheets can be arranged either to form a **Parallel β sheet**, in which the adjacent segments of the polypeptide chain proceed in the same direction amino to carboxyl, or an antiparallel sheet, in which they proceed in opposite directions (Figure).
5. Either configuration permits the maximum number of hydrogen bonds between segments, or strands, of the sheet. Most β sheets are not perfectly flat but tend to have a right-handed twist. Clusters of twisted strands of β sheet form the core of many globular proteins .
6. Schematic diagrams represent β sheets as arrows that point in the amino to carboxyl terminal direction.

(For 6 marks question)

1. **Pauling and Corey** postulated the β -sheet in 1951. Like the α helix the β sheet uses the full hydrogen-bonding capacity of the polypeptide backbone.
2. In β sheets hydrogen bonding occurs between neighboring polypeptide chains rather than within one as in an α helix.
3. Sheets come in two varieties:
 - a) **The antiparallel β sheet**, in which neighboring hydrogen-bonded polypeptide chains run in opposite directions .
 - b) **The parallel β sheet**, in which the hydrogen-bonded chains extend in the same direction .
4. The conformations in which these β structures are optimally hydrogen bonded vary somewhat from that of the fully extended polypeptide shown. They therefore have a rippled or pleated edge-on appearance and for that reason are sometimes called "pleated sheets."
5. Successive side chains of a polypeptide chain in a β sheet extend to opposite sides of the sheet with a two-residue repeat distance of 7.0 Å
6. Parallel β sheets containing fewer than five strands are rare. This observation suggests that parallel β sheets are less stable than antiparallel β sheets, possibly because the hydrogen bonds of parallel sheets are distorted compared to those of the antiparallel sheets.
7. β Sheets containing mixtures of parallel and antiparallel strands frequently occur.
8. β Sheets almost invariably exhibit a pronounced right-handed twist when viewed along their polypeptide strands).
9. Conformational energy calculations indicate that the twist is a consequence of interactions between chiral L-amino acid residues in the extended polypeptide chains. The twist actually distorts and weakens the β sheet's interchain hydrogen bonds.
10. The geometry of a particular β sheet is thus a compromise between optimizing the conformational energies of its polypeptide chains and preserving its hydrogen bonding.
11. The topology (connectivity) of the polypeptide strands in a β sheet can be quite complex. The connection between two antiparallel strands may be just a small loop, but the link between tandem parallel strands must be a crossover connection that is out of the plane of the β sheet. The connecting link in either case can be extensive, often containing helices.