2. *Secondary structure*: This is the way the polypeptide chain is extended and is a result of hydrogen bonding between residues not widely separated. Two major types of secondary structure are (a) helixes and (b) sheets. Helical structure can be either α-helical or triple helix. In an α-helical structure, hydrogen bonding can occur between the α-carboxyl group of one residue and the —NH group of its neighbor four units down the chain, as shown in Fig. 2.10. The triple-helix structure present in collagen consists of three α-helixes intertwined in a superhelix. Triple-helix structure is rigid and stretch resistant. The α-helical structure can be easily disturbed, since H bonds are not highly stable. However, the sheet structure (β-pleated sheet) is more stable. The hydrogen bonds between parallel chains stabilize the sheet structure and provide resistance to stretching (Fig. 2.11).

3. *Tertiary structure:* This is a result of interactions between R groups widely separated along the chain. The folding or bending of an amino acid chain induced by interaction between R groups determines the tertiary structure of proteins. R groups may interact by covalent, disulfide, or hydrogen bonds. Hydrophobic and hydrophilic interactions may also be present among R groups. The disulfide bond can cross-link two polypeptide chains (for example, insulin). Disulfide bonds are also critical in proper chain folding, as shown in Fig. 2.12. The tertiary structure of a protein has a profound effect on its function.

4. *Quaternary structure:* Only proteins with more than one polypeptide chain have quaternary structure. Interactions among polypeptide chains determine the quaternary structure (Fig. 2.9). Hemoglobin has four subunits (oligomeric), and interaction among

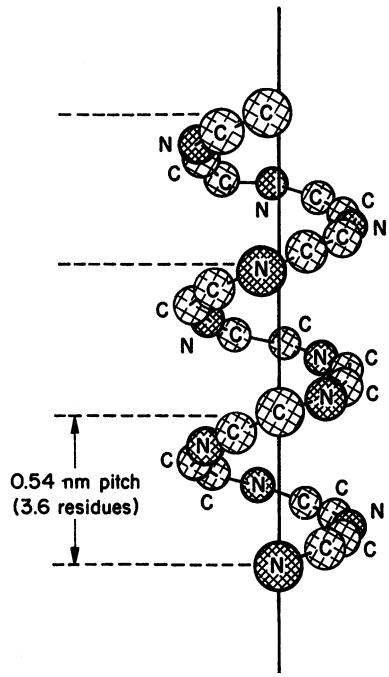

Figure 2.10. The α-helical structure of fibrous proteins.