Shape and Structure of Protein Molecules

The interaction of amino acid side chains determines the shape and structure of proteins, which in turn are important to the proteins' biological functions. In a polypeptide chain or protein, the sequence of the amino acids is called the *primary* (1°) *structure*. The *secondary* (2°) *structure* describes how the chain is coiled or otherwise arranged in space. For example, the alpha (α) helix is a secondary structure that resembles a coiled spring. Another type of secondary structure is the beta (β) pleated sheet, which has accordion-like folds. Both of these secondary structures form because hydrogen bonding occurs between a hydrogen atom attached to the nitrogen atom in one peptide bond and the oxygen atom of another peptide bond farther down the backbone of the protein.

In a protein, the amino acid side chains project out in such a way that they often interact with other side chains located at various positions along the protein backbone. These interactions give the protein its characteristic three-dimensional shape, which is called its *tertiary* (3°) *structure*. The side-chain interactions can include hydrogen bonding, salt bridges, and cysteine-cysteine disulfide bonds. Hydrophobic interactions that occur between nonpolar side chains also contribute to a protein's tertiary structure. Because nonpolar side groups are repulsed by the water found in cells and body fluids, these groups tend to be found in the interior of the protein, where contact with water is minimal. Polar and ionic side chains tend to be on the protein surface, where they are in contact with water. In some proteins, different polypeptides, each of which has its own 3° structure, come together. In the case of hemoglobin, four different polypeptides make up the *quaternary* (4°) *structure*. The four structural levels of proteins are shown in **Figure 10.**

FIGURE 10