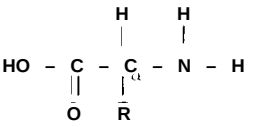
Structure of Proteins

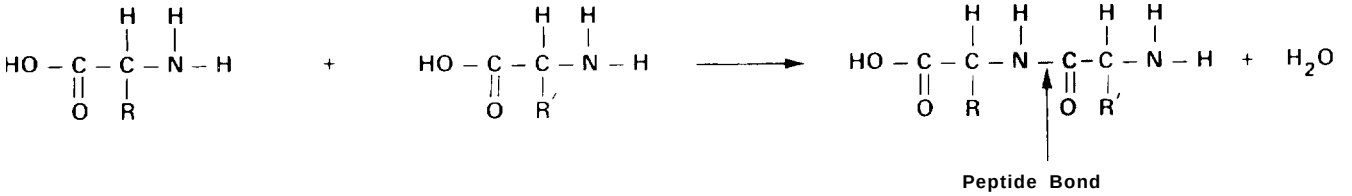
Proteins are constructed from individual building blocks called amino acids. In all about twenty different amino acids are commonly found in proteins, and about five others are found rarely. Each amino acid has an amino group (NH_2), a carboxyl group COOH), and a side group, or radical (R), attached to the alpha carbon atom. It is the radical that distinguishes one amino acid from another.

Amino Acid



R = Side Chain on Alpha Carbon

Amino acids polymerize to form long chains of residues that constitute a protein. When two amino acids join together, they liberate one molecule of water and form a peptide bond as shown below. Thus the protein is a long polypeptide chain.

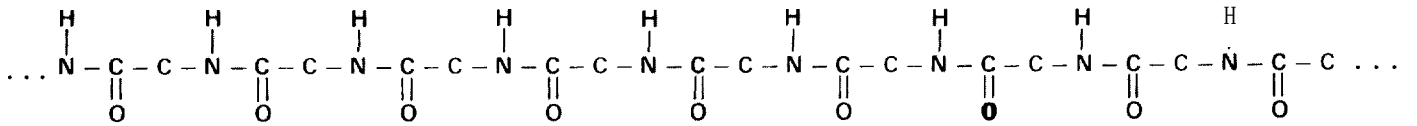


Once a protein chain forms, it can fold into a variety of complex three-dimensional conformations. Among the possible conformations usually only one exhibits biological activity. This "native" conformation generally minimizes the free energy of the protein and is therefore the most stable. Many factors contribute to this stability including hydrogen bonding, disulfide bonding, Van der Waals forces, and solvent interactions.

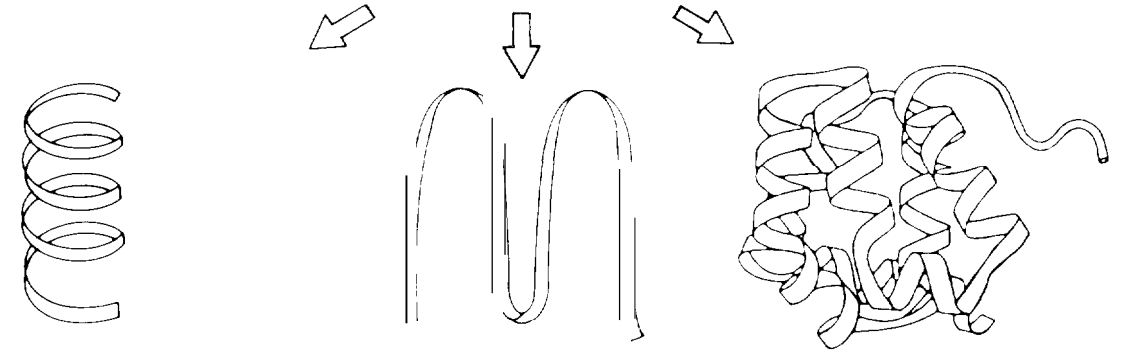
Three common structural motifs recur over and over again in proteins: the α helix, the β sheet, and the globular conformation. In the a helix the chain is tightly coiled about its longitudinal axis. In the zigzag β sheet the chain can be visualized as pleated strands of protein. In the globular conformation, which is the most complex, the chain is irregularly and tightly folded into a compact, nearly spherical shape. Short stretches of the chain are often constructed from a helices or β sheets.

Many large proteins consist of smaller protein subunits that interlock into one macromolecule, Such complex structures operate as coordinated factories in which each subunit contributes a specialized function to the macromolecular protein. ■

Protein Backbone



Energy Minimization



α Helix

β Sheet

Globular Conformation