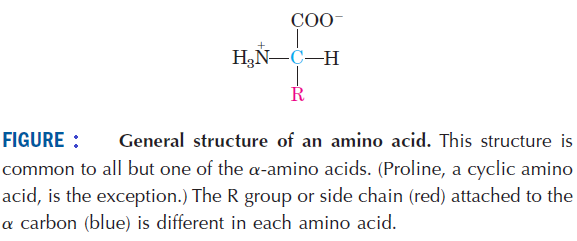
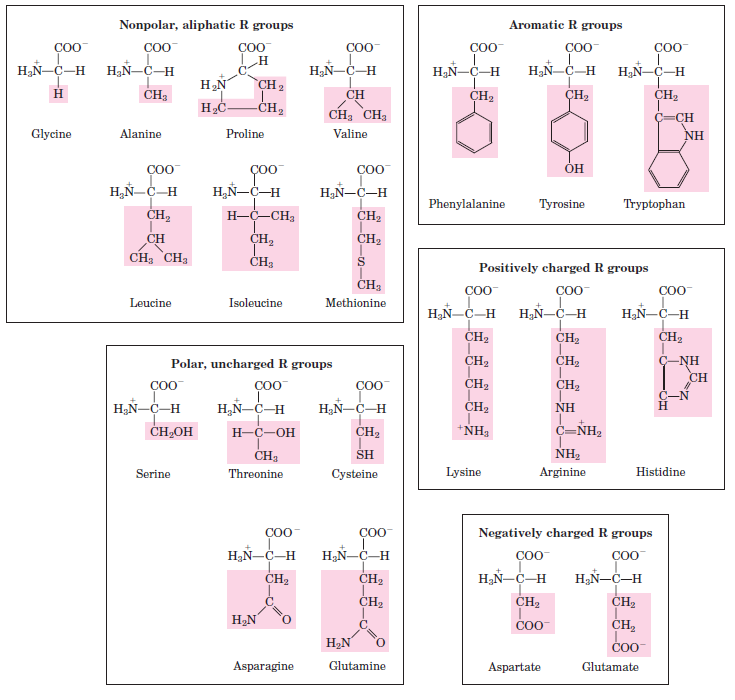
**Introduction to protein structure**

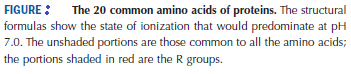
* Proteins are polymers of amino acids. Protein structure depends on its amino acid sequence and local, low-energy chemical bonds between atoms in both the polypeptide backbone and in amino acid side chains.
* Protein structure plays a key role in its function; if a protein loses its shape at any structural level, it may no longer be functional.
* Structure of protein is divided into 4 levels of organization: primary secondary, tertiary and quaternary structure.

**Primary Structure**

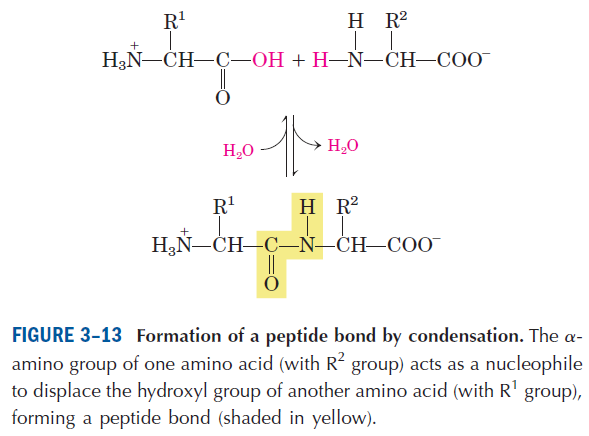
* A protein’s primary structure is the unique sequence of amino acids in each polypeptide chain that makes up the protein.
* The common amino acids are *α-*amino acids. They have a carboxyl group and an amino group bonded to the same carbon atom (the *α-*carbon). They differ from each other in their side chains, or **R groups,** which vary in structure, size, and electric charge, and which influence the solubility of the amino acids in water.







* Two amino acid molecules can be covalently joined through a substituted amide linkage, termed a **peptide bond,** to yield a dipeptide. Such a linkage is formed by removal of the elements of water (dehydration) from the *α-*carboxyl group of one amino acid and the *α-*amino group of another.



* The peptide bond is rigid and planar. The six atoms of the **peptide group** lie in a single plane, with the oxygen atom of the carbonyl group and the hydrogen atom of the amide nitrogen trans to each other. The peptide C-N bonds are unable to rotate freely because of their partial double-bond character. Rotation is permitted about the N-C*α* and the C*α* -C bonds. The backbone of a polypeptide chain can thus be pictured as a series of rigid planes with consecutive planes sharing a common point of rotation at C*α*.

By convention, the bond angles resulting from rotations at C*α* are labeled Φ(phi) for the N-C*α* bond and ψ(psi) for the C*α* -C bond. Again, by convention, both Φand ψare defined as 180˚ when the polypeptide is in its fully extended conformation and all peptide groups are in the same plane.

In principle, Φand ψ can have any value between -180˚ and 180˚, but many values are prohibited by steric interference between atoms in the polypeptide backbone and amino acid side chains. The conformation in which both Φand ψare 0˚ is prohibited for this reason; this conformation is used merely as a reference point for describing the angles of rotation. Allowed values for Φand ψare graphically revealed when ψis plotted versus Φ *in* a **Ramachandran plot**, introduced by G. N. Ramachandran.

