1.1: Amino acids

There are twenty commonly occurring amino acids in mammalian proteins (nine essential and eleven nonessential). Each amino acid has a carboxyl group, a primary amino group, and a unique side chain (R-group) bonded to the \((\alpha)\)-carbon atom. At physiologic pH (approximately 7.4), amino acids are present as zwitter ions with the carboxyl group forming the negatively charged carboxylate ion \((\text{COO}^-)\), and the amino group is protonated \((\text{NH}_3^+)\) (figure 1.1).
Figure 1.1: Basic structure of amino acids and ionization.

Amino acids can be grouped largely by the functionality of their R-group (figure 1.2).
Nonpolar residues

Nonpolar amino acids can be further divided into: uncharged (aromatic and nonpolar aliphatic) and sulfur-containing groups. Nonpolar uncharged side chains do not gain or lose protons or participate in hydrogen or ionic bonding. These amino acids typically cluster in the internal regions of a protein, away from the aqueous interface. The exception to this is if these amino acids are present as part of a membrane-bound protein, and in this case, the amino acids may be exposed in the transmembrane region. Proline is also of note, as it forms an unconventional peptide bond and will add a

Figure 1.2: Chart of amino acids.

Although it is not essential to memorize the structures of the amino acids, a strong understanding of their general characteristics will be very helpful.

Amino acid functional groups

The primary sequence of a protein is determined by the amino acids in the chain and how these individual units function as a group. More generally, amino acids can be characterized as polar or nonpolar. These fundamental characteristics will determine where the residue resides within the protein (surface or core, within a transmembrane domain or part of the active site) and how the amino acid contributes to folding and catalysis.
kink in the primary structure of a protein. Sulfur-containing amino acids can participate in disulfide linkages, which are used to stabilize interactions between peptide chains or tertiary structures.

**Polar residues**

Amino acids with uncharged polar R-groups may participate in hydrogen bonding and undergo modifications such as phosphorylation. Tyrosine, serine, and threonine all have a hydroxyl group within the R-group, and they can also be readily modified by kinase-mediated phosphorylation.

Some amino acids are charged at a physiological pH and can be acidic or basic. These side chains may donate or accept protons, respectively, and the most notable charged amino acid is histidine, which can function as a buffer at a physiological pH.

**References and resources**

**Text**


**Figures**

Grey, Kindred, Figure 1.1 Basic structure of amino acids and ionization. 2021. Chemical structure by Henry Jakubowski. https://archive.org/details/1.1_20210924, CC BY 4.0.

Grey, Kindred, Figure 1.2 Chart of amino acids. 2021. Chemical structure by Henry Jakubowski. https://archive.org/details/1.2_20210924, CC BY 4.0.