



AMINO ACIDS, PEPTIDES, AND PROTEINS

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- Proteins are the most abundant biological macromolecules, occurring in all cells and all parts of cells.
- All proteins, whether from the most ancient lines of bacteria or from the most complex forms of life, are constructed from the same ubiquitous set of 20 amino acids, **covalently** linked in characteristic linear sequences.





Amino Acids

- Proteins are polymers of amino acids, with each amino acid residue joined to its neighbor by a specific type of covalent bond.
- All 20 of the common amino acids are α -amino acids.
- They have a carboxyl group and an amino group bonded to the same carbon atom (the *alpha-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.

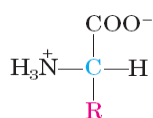
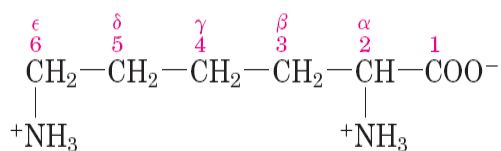


FIGURE 3-2 General structure of an amino acid. This structure is common to all but one of the α -amino acids. (Proline, a cyclic amino acid, is the exception.) The R group or side chain (red) attached to the α carbon (blue) is different in each amino acid.



Lysine



The Amino Acid Residues in Proteins Are L Stereoisomers

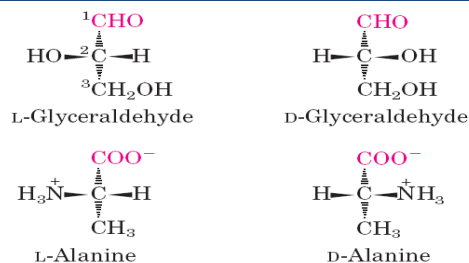


FIGURE 3-4 Steric relationship of the stereoisomers of alanine to the absolute configuration of L- and D-glyceraldehyde. In these perspective formulas, the carbons are lined up vertically, with the chiral atom in the center. The carbons in these molecules are numbered beginning with the terminal aldehyde or carboxyl carbon (red), 1 to 3 from top to bottom as shown. When presented in this way, the R group of the amino acid (in this case the methyl group of alanine) is always below the α carbon. L-Amino acids are those with the α -amino group on the left, and D-amino acids have the α -amino group on the right.

TABLE 3-1 Properties and Conventions Associated with the Common Amino Acids Found in Proteins

Amino acid	Abbreviation/ symbol	M_r	pK_a values			pI	Hydropathy index*	Occurrence in proteins (%) [†]
			pK_1 (-COOH)	pK_2 (-NH ₃ ⁺)	pK_R (R group)			
Nonpolar, aliphatic R groups								
Glycine	Gly G	75	2.34	9.60		5.97	-0.4	7.2
Alanine	Ala A	89	2.34	9.69		6.01	1.8	7.8
Proline	Pro P	115	1.99	10.96		6.48	1.6	5.2
Valine	Val V	117	2.32	9.62		5.97	4.2	6.6
Leucine	Leu L	131	2.36	9.60		5.98	3.8	9.1
Isoleucine	Ile I	131	2.36	9.68		6.02	4.5	5.3
Methionine	Met M	149	2.28	9.21		5.74	1.9	2.3
Aromatic R groups								
Phenylalanine	Phe F	165	1.83	9.13		5.48	2.8	3.9
Tyrosine	Tyr Y	181	2.20	9.11	10.07	5.66	-1.3	3.2
Tryptophan	Trp W	204	2.38	9.39		5.89	-0.9	1.4
Polar, uncharged R groups								
Serine	Ser S	105	2.21	9.15		5.68	-0.8	6.8
Threonine	Thr T	119	2.11	9.62		5.87	-0.7	5.9
Cysteine	Cys C	121	1.96	10.28	8.18	5.07	2.5	1.9
Asparagine	Asn N	132	2.02	8.80		5.41	-3.5	4.3
Glutamine	Gln Q	146	2.17	9.13		5.65	-3.5	4.2
Positively charged R groups								
Lysine	Lys K	146	2.18	8.95	10.53	9.74	-3.9	5.9
Histidine	His H	155	1.82	9.17	6.00	7.59	-3.2	2.3
Arginine	Arg R	174	2.17	9.04	12.48	10.76	-4.5	5.1
Negatively charged R groups								
Aspartate	Asp D	133	1.88	9.60	3.65	2.77	-3.5	5.3
Glutamate	Glu E	147	2.19	9.67	4.25	3.22	-3.5	6.3

*A scale combining hydrophobicity and hydrophilicity of R groups; it can be used to measure the tendency of an amino acid to seek an aqueous environment (- values) or a hydrophobic environment (+ values). See Chapter 11. From Kyte, J. & Doolittle, R.F. (1982) A simple method for displaying the hydrophobic character of a protein. *J. Mol. Biol.* **157**, 105-132.

[†]Average occurrence in more than 1,150 proteins. From Doolittle, R.F. (1989) Redundancies in protein sequences. In *Prediction of Protein Structure and the Principles of Protein Conformation* (Fasman, G.D., ed.), pp. 599-623. Plenum Press, New York.

