Amino Acids Structure

General Structure

- Central α-carbon
- Amino group (-NH_2)
- Carboxyl group (-COOH)
- Variable R group (side chain)

Classification

- Nonpolar/hydrophobic
- Polar uncharged
- Positively charged (basic)
- Negatively charged (acidic)

Chirality

- All are L-amino acids in proteins
- D-amino acids rare in nature
- Asymmetric α-carbon
- Mirror image isomers

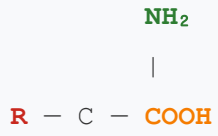
Ionization States

- pKa values determine charge
- Zwitterion at physiological pH
- Affects protein interactions
- Important for enzyme catalysis

Detailed Structure Examples

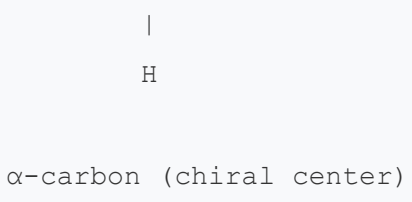
1. General Structure

Basic Amino Acid Structure



Key Features

The central α-carbon is bonded to four different groups, making it a chiral center (except glycine). This tetrahedral arrangement is fundamental to amino acid structure.



Components:
- Amino group
- Carboxyl group
- Variable R group
- Hydrogen atom

Tetrahedral geometry

Chiral center

Zwitterion Form

At physiological pH (~7.4), amino acids exist as zwitterions with NH_3^+ and COO^- groups, carrying both positive and negative charges.

pH dependent

Amphoteric

2. Classification by R Group Properties

Example R Groups

Nonpolar:

$-CH_3$ (Alanine)

$-CH(CH_3)_2$ (Valine)

Polar uncharged:

$-CH_2OH$ (Serine)

$-CH_2CONH_2$ (Asparagine)

Positive (+):

$-CH_2-CH_2-CH_2-CH_2-NH_3^+$

Nonpolar/Hydrophobic

Examples: Alanine, Valine, Leucine, Isoleucine, Methionine, Phenylalanine, Tryptophan, Proline

These amino acids have hydrocarbon R groups that avoid water. They're typically found in protein interiors and membrane proteins.

Hydrophobic effect

Protein core

Polar Uncharged

Examples: Serine, Threonine, Cysteine, Asparagine, Glutamine, Tyrosine

Contain polar groups (OH, SH, NH_2, C=O) that can form hydrogen bonds but don't ionize at physiological pH.

H-bonding

Surface residues

(Lysine)

Negative (-):

$-CH_2-COO^-$

(Aspartate)

Charged Amino Acids

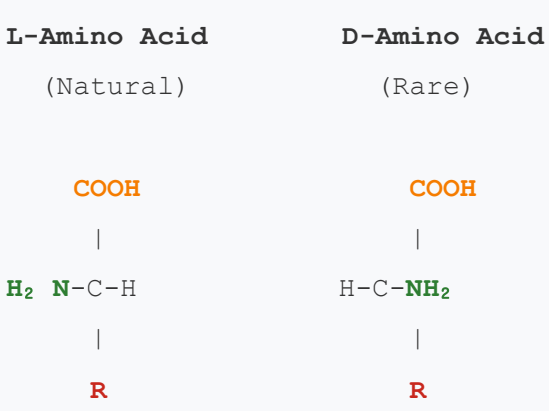
Basic (+): Lysine, Arginine, Histidine (pKa ~6-12.5)
Acidic (-): Aspartate, Glutamate (pKa ~3.5-4.5)

These residues are ionized at physiological pH and participate in salt bridges and electrostatic interactions.

Ionic interactions | Active sites

3. Chirality (Optical Isomerism)

L vs D Configuration



Fischer Projection
Vertical lines = away from viewer
Horizontal lines = toward viewer

L-Configuration Dominance

All amino acids in proteins are L-isomers. The L/D notation is based on the configuration relative to L-glyceraldehyde. In L-amino acids, the amino group is on the left in Fischer projection.

Biological selectivity | Homochirality

Glycine Exception

Glycine (R = H) is the only achiral amino acid because its α-carbon has two hydrogen atoms attached, making it superimposable on its mirror image.

Achiral | No optical activity

D-Amino Acids in Nature

D-amino acids are rare but found in bacterial cell walls, some antibiotics (e.g., gramicidin), and as neurotransmitters in mammals. They're not incorporated into proteins by ribosomes.

Bacterial walls | Specialized roles

4. Ionization States and pKa Values

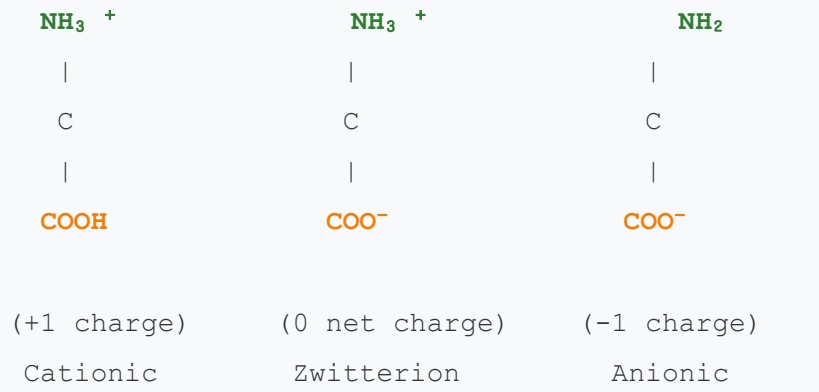
pH-Dependent Forms

Henderson-Hasselbalch Equation

$pH = pKa + \log([A^-]/[HA])$

This equation determines the ionization state of amino acids at different pH values. At pH = pKa, 50% of molecules are protonated.

Buffer capacity | pI calculation



Typical pKa Values:
α-COOH: ~2.2
α-NH_3^+: ~9.4
Side chains: 3.5-12.5

Isoelectric Point (pI)

The pH at which an amino acid has no net charge (zwitterion form predominates). For simple amino acids: pI = (pKa_1 + pKa_2)/2

Examples:
- Alanine: pI ≈ 6.0
- Lysine: pI ≈ 9.7 (basic)
- Aspartate: pI ≈ 2.8 (acidic)

Electrophoresis | Protein purification

Functional Significance

Ionization states control:
- Enzyme catalytic mechanisms (His, Asp, Glu in active sites)
- Protein-protein interactions via salt bridges
- Protein solubility and stability
- Signal transduction through protonation changes

Catalysis | Regulation | Binding