Macromolecule : PROTEIN (Part 1 of 2)

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Overview

- 1. Amino acid
- 2. Peptide bond
- 3. Protein structure (Part 2)
- 4. Protein functions (Part 2)



FIGURE 1–11 Structural hierarchy in the molecular organization of cells. In this plant cell, the nucleus is an organelle containing several types of supramolecular complexes, including chromosomes. Chro-

mosomes consist of macromolecules of DNA and many different proteins. Each type of macromolecule is made up of simple subunits— DNA of nucleotides (deoxyribonucleotides), for example.



Food \rightarrow source of proteins, lipids and polysaccharides \rightarrow enzymatic digestion \rightarrow from large polymeric molecules into monomeric subunits - proteins into amino acids, polysaccharides into sugars, fats into fatty acids and glycerol \rightarrow enter cytosol of cells \rightarrow source of energy or as building blocks for other molecules.

THE ESSENTIAL AMINO ACIDS



Figure 2–87 The nine essential amino acids. These cannot be synthesized by human cells and so must be supplied in the diet.

Functions of PROTEIN

- Catalysis → enzymes
- Immunity \rightarrow antibodies
- Growth & development → DNA binding proteins
- Transport of metabolites \rightarrow carrier proteins
- Relaying biological signals hormones
- Biological structures \rightarrow fibrous proteins
- etc

Amino acid

- Proteins are polymers of amino acids
- 20 different amino acids are commonly found in proteins $\rightarrow \alpha$ -amino acids, except proline.
- a carboxyl group and an amino group bonded to the same carbon atom (the α carbon)
- Proteins 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 wa- ter.







Only L-Amino Acids Are Found in Proteins

- The α -carbon atom is a **chiral center** \rightarrow the tetrahedral arrangement of the bonding orbitals around the α -carbon atom has the four different groups.
- Amino acids have two possible stereoisomers→ enantiomer→ nonsuperimposable mirror images of each other
- By Fischer's convention (Emil Fischer in 1891), L and D refer only to the absolute configuration of the four substituents around the chiral carbon, not to optical properties of the molecule.
- 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.





The Amino Acid Residues in Proteins Are L Stereoisomers

Cells are able to specifically synthesize the L isomers of amino acids because the active sites of enzymes are asymmetric, causing the reactions they catalyze to be stereospeçific

Amino Acids Can Be Classified by R Group

1. Nonpolar, Aliphatic R Groups



- nonpolar and hydrophobic
- Glycine has the simplest structure → nonpolar but no real contribution to hydrophobic interactions.
- Methionine → sulfurcontaining amino acids, has a non-polar thioether group
- **Proline** has an aliphatic side chain with a cyclic structure.

2. Aromatic R Groups



- aromatic side chains → relatively nonpolar (hydrophobic)
- The hydroxyl group of tyrosine can form hydrogen bonds → an important functional group in some enzymes
- Tryptophan and tyrosine, absorb ultraviolet light → the characteristic strong absorbance of light by most proteins at a wavelength of 280 nm



FIGURE 3-6 Absorption of ultraviolet light by aromatic amino acids.

3. Polar, Uncharged R Groups



- more soluble in water (hydrophilic) because they contain functional groups that form hydrogen bonds with water.
- The polarity of serine and threonine is contributed by hydroxyl groups; cysteine by its sulfhydryl group; asparagine and glutamine by their amide groups.
- Cysteine is oxidized to form a covalently linked dimeric amino acid → cystine → two cysteine residues are joined by a disulfide bond → stabilize proteins structure



4. Positively Charged (Basic) R Groups



positively charged :

Lysine, has a second primary amino group Arginine, has a guanidino group; Histidine, has an imidazole group.

5. Negatively Charged (Acidic) R Groups



each of which has a second carboxyl group → negatively charge

				pK _a values				
Amino acid	Abbreviation/ symbol	M _r	рК ₁ (—СООН)	рК ₂ (—NН ₃ +)	pK _R (R group)	pl	Hydropathy index*	Occurrence in proteins (%) [†]
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	lle 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	Gin Q	146	2.17	9.13		5.65	-3.5	4.2
Positively charged								
R groups								
Lysine	Lvs 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								
Aspartate	Asp D	133	1.88	9.60	3.65	2 77	-35	53
Glutamate	Glu E	1/17	2.10	9.67	4.25	2.17	-2.5	63
Glutaniate	GIU E	147	Eucia D	hiantika'Wi	tasari - 20	3.22	-3.5	0.5

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

The **peptides** and **proteins**, polymers of amino acids

- Two amino acid molecules can be covalently joined through a substituted amide linkage, termed a **peptide bond**, to yield a dipeptide.
- Oligopeptide → a few amino acids are joined
- **polypeptide** \rightarrow many amino acids are joined. MW < 10.000
- Proteins → have thousands of amino acid residues.
- In a peptide, the amino acid residue at the end with a free α -amino group is the **amino**terminal (or N-terminal) residue; the residue at the other end, which has a free carboxyl group, is the **carboxyl-terminal** (*C*-terminal) 28/residue. Lucia Dhiantika Witasari



FIGURE 3–13 Formation of a peptide bond by condensation. The α amino group of one amino acid (with R² group) acts as a nucleophile to displace the hydroxyl group of another amino acid (with R^1 group), forming a peptide bond (shaded in yellow). Amino groups are good nucleophiles, but the hydroxyl group is a poor leaving group and is not readily displaced. At physiological pH, the reaction shown does not occur to any appreciable extent.

By convention, the amino end is taken to be the beginning of a polypeptide chain



Pentapeptide (YGGFL)→ Leu-enkephalin → an opioid peptide that modulates the perception of pain.

the sequence of amino acids in a polypeptide chain is written starting with the aminoterminal residue.

	Molecular weight	Number of residues	Number of polypeptide chains
Cytochrome c (human)	13,000	104	1
Ribonuclease A (bovine pancreas)	13,700	124	1
Lysozyme (chicken egg white)	13,930	129	1
Myoglobin (equine heart)	16,890	153	1
Chymotrypsin (bovine pancreas)	21,600	241	3
Chymotrypsinogen (bovine)	22,000	245	1
Hemoglobin (human)	64,500	574	4
Serum albumin (human)	68,500	609	1
Hexokinase (yeast)	102,000	972	2
RNA polymerase (E. coli)	450,000	4,158	5
Apolipoprotein B (human)	513,000	4,536	1
Glutamine synthetase (E. coli)	619,000	5,628	12
Titin (human)	2,993,000	26,926	1

TABLE 3-2 Molecular Data on Some Proteins

- The mean molecular weight of an amino acid residue is about 110.
- The mass of a protein is expressed in units of daltons; one *dalton* is equal to one atomic mass unit
 →A unit of mass very nearly equal to that of a hydrogen atom John Dalton (1766-1844)
- A protein with a molecular weight of 50,000 has a mass of 50,000 daltons, or 50 kd (kilodaltons)

Recommended video for learning

- <u>https://www.youtube.com/watch?v=wvTv8TqWC48</u>
- <u>https://www.youtube.com/watch?v=qBRFIMcxZNM</u>
- https://www.youtube.com/watch?v=2BsnnhMC0Ms

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