Proteine

- Le macromolecole più abbondanti nella cellula
- Più di 20,000 diversi tipi nell'uomo
- Grande diversità di funzioni biologiche
- Polimeri lineari

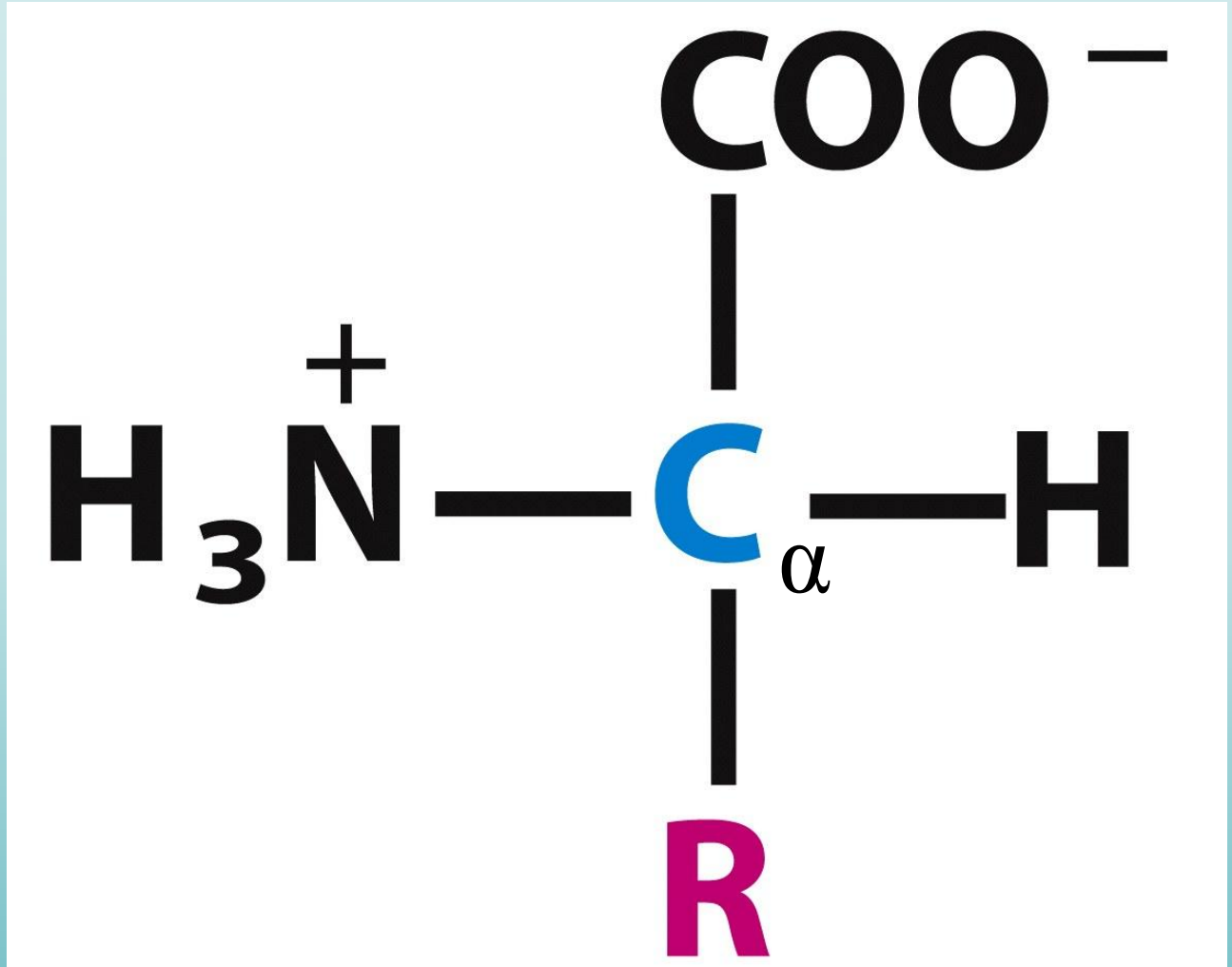

Figure 3-2
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TABLE 3–1 Properties and Conventions Associated with the Common Amino Acids Found in Proteins

Amino acid	Abbreviation/ symbol	M_r*	pK_a values: pK_1 (—COOH)	pK_2 ($—NH_3^+$)	pK_R (R group)	pI	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	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

*M_r values reflect the structures as shown in Figure 3–5. The elements of water (M_r 18) are deleted when the amino acid is incorporated into a polypeptide.

†A scale combining hydrophobicity and hydrophilicity of R groups. The values reflect the free energy (ΔG) of transfer of the amino acid side chain from a hydrophobic solvent to water. This transfer is favorable ($\Delta G < 0$; negative value in the index) for charged or polar amino acid side chains, and unfavorable ($\Delta G > 0$; positive value in the index) for amino acids with nonpolar or more hydrophobic side chains. See Chapter 11. From Kyte, J. & Doolittle, R.F. (1982) A simple method for displaying the hydropathic 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.

§Cysteine is generally classified as polar despite having a positive hydropathy index. This reflects the ability of the sulfhydryl group to act as a weak acid and to form a weak hydrogen bond with oxygen or nitrogen.

Table 3-1

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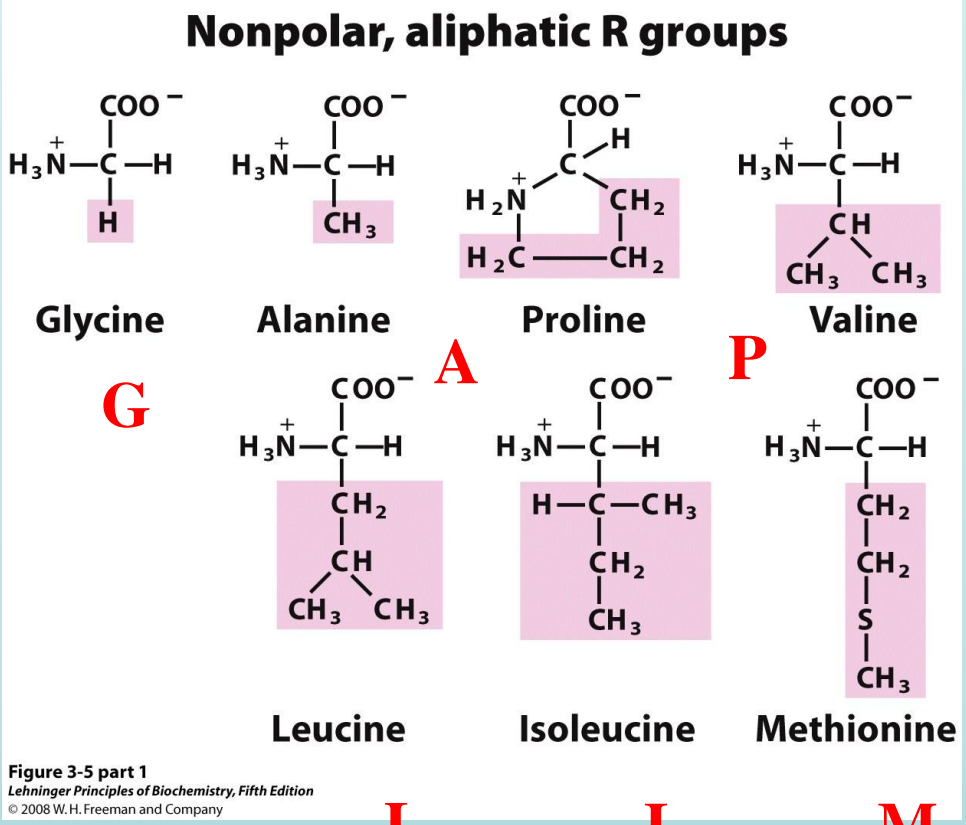

Figure 3-5 part 1
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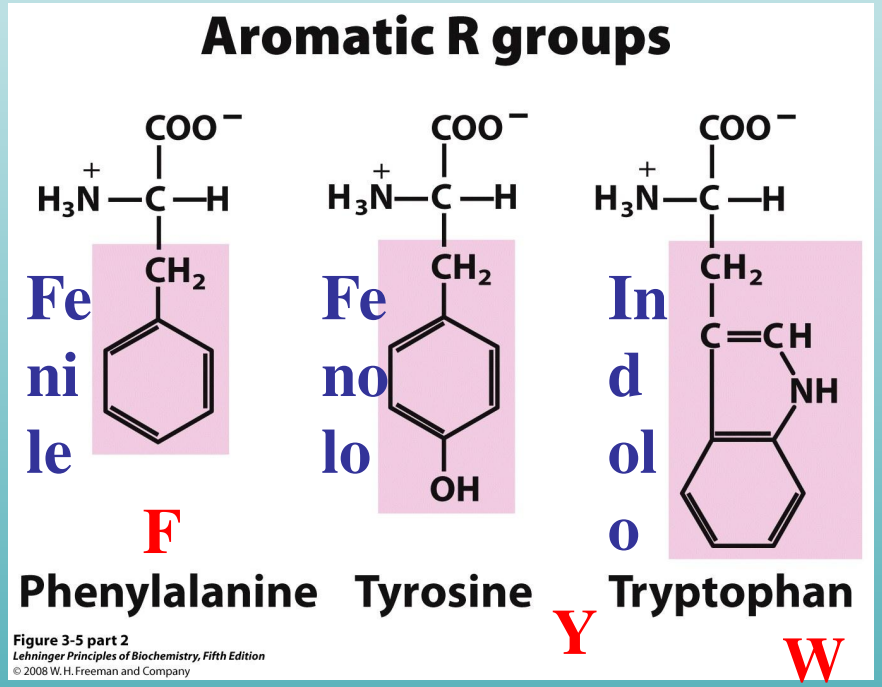

Figure 3-5 part 2
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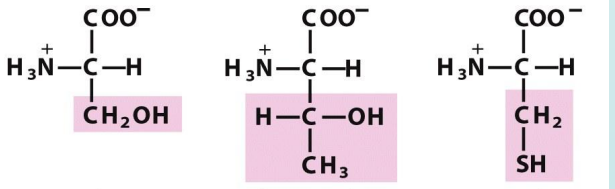
Polar, uncharged R groups

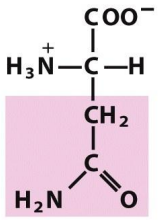


Serine

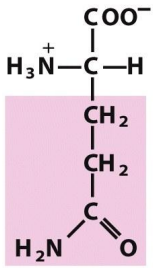
Threonine

Cysteine

S T C



Asparagine



Glutamine

N Q

Figure 3-5 part 3
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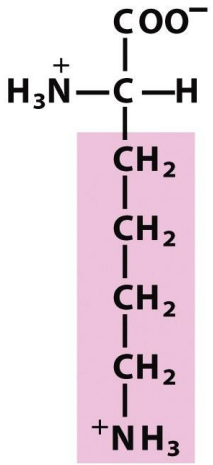
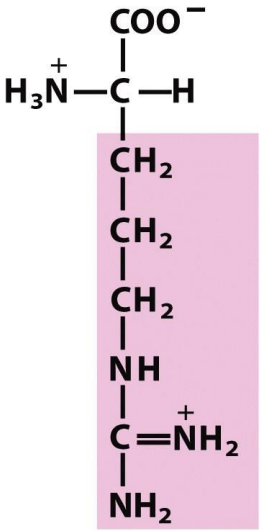
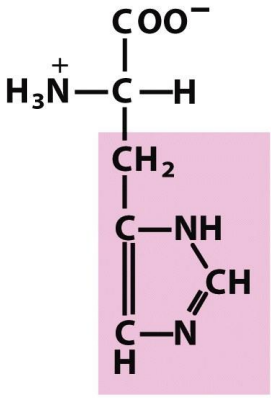
Positively charged R groups



Lysine



Arginine



Histidine

K R H

Figure 3-5 part 4
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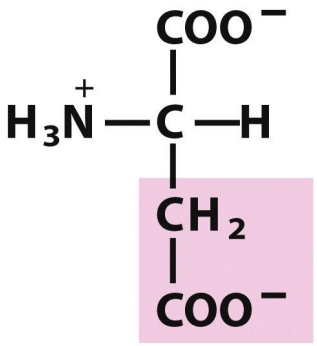
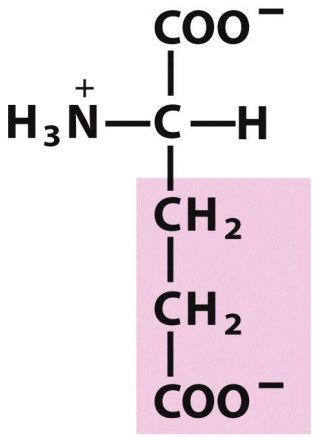
Negatively charged R groups



D Aspartate



Glutamate

E

Figure 3-5 part 5
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Guanidinio

Imidazolo

Formazione di ponti a disolfuro (ossidazione)

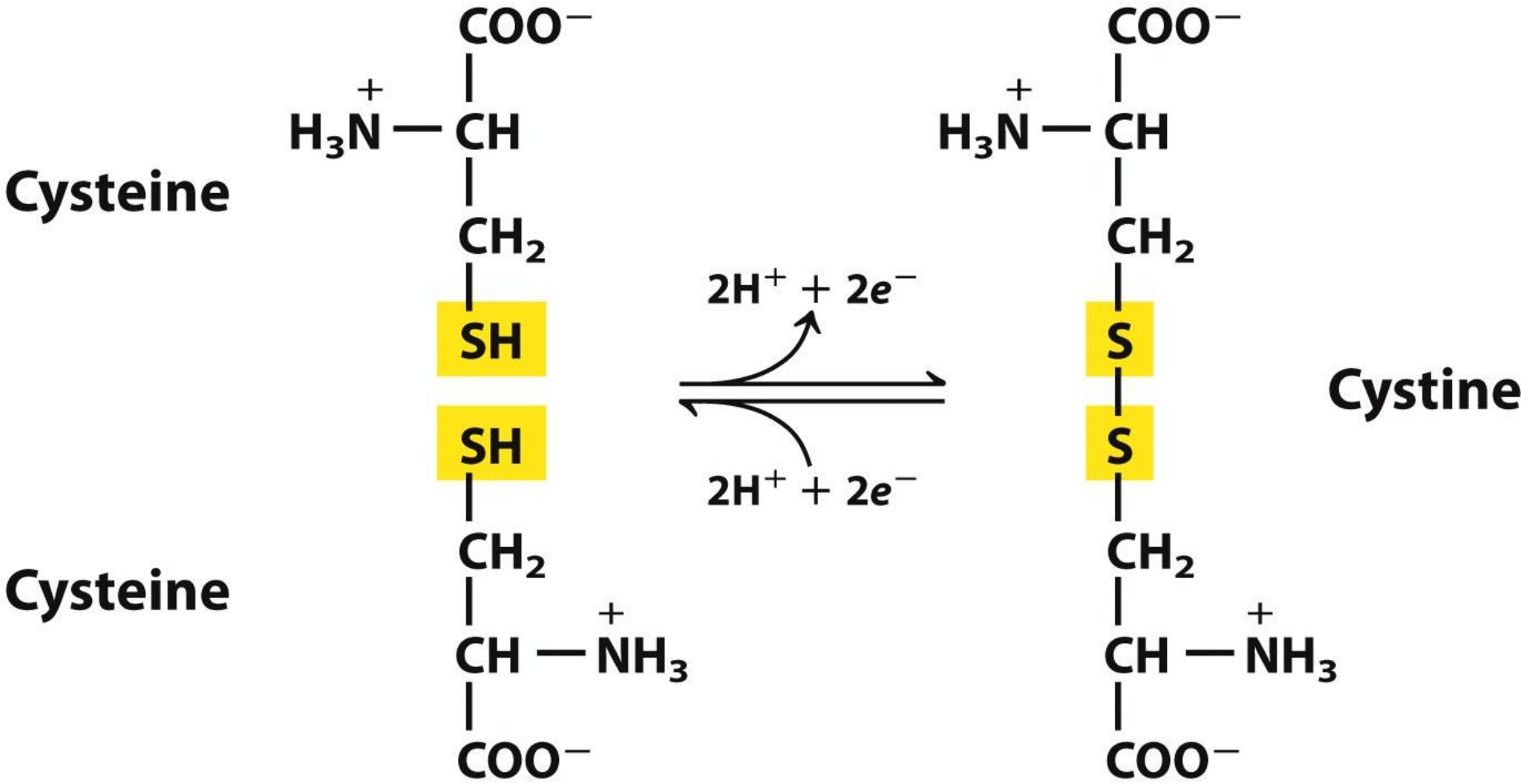

Figure 3-7
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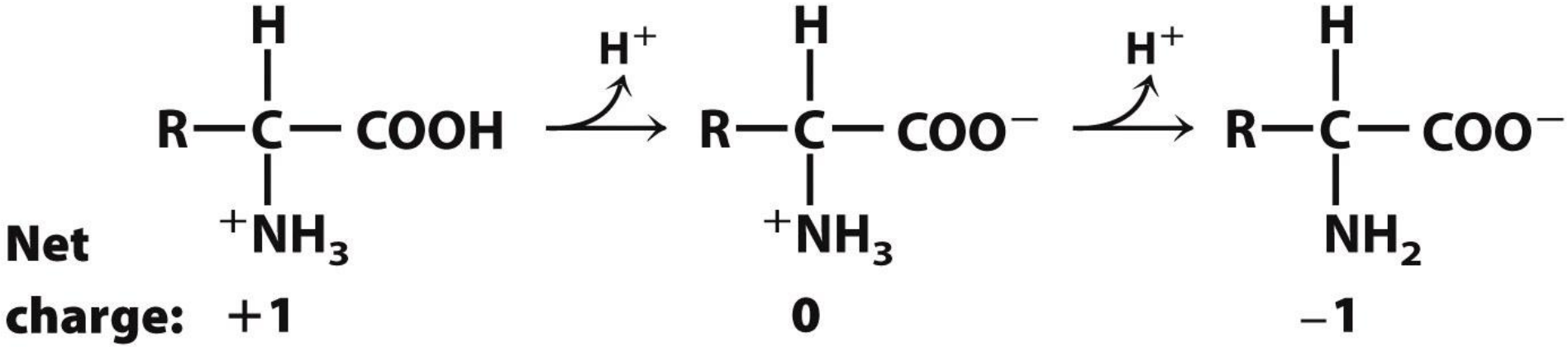
Equilibri acido-base



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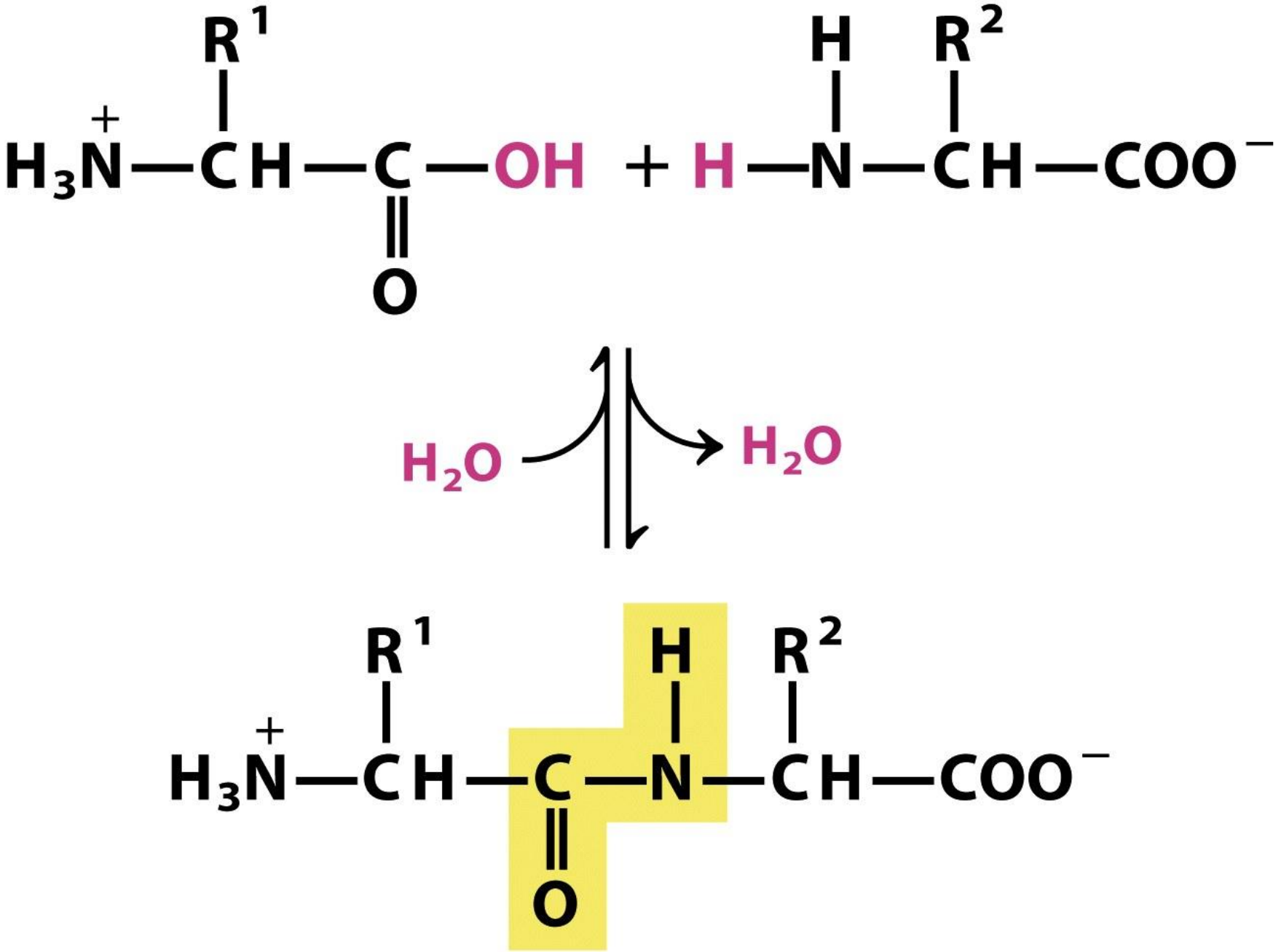

Figure 3-13
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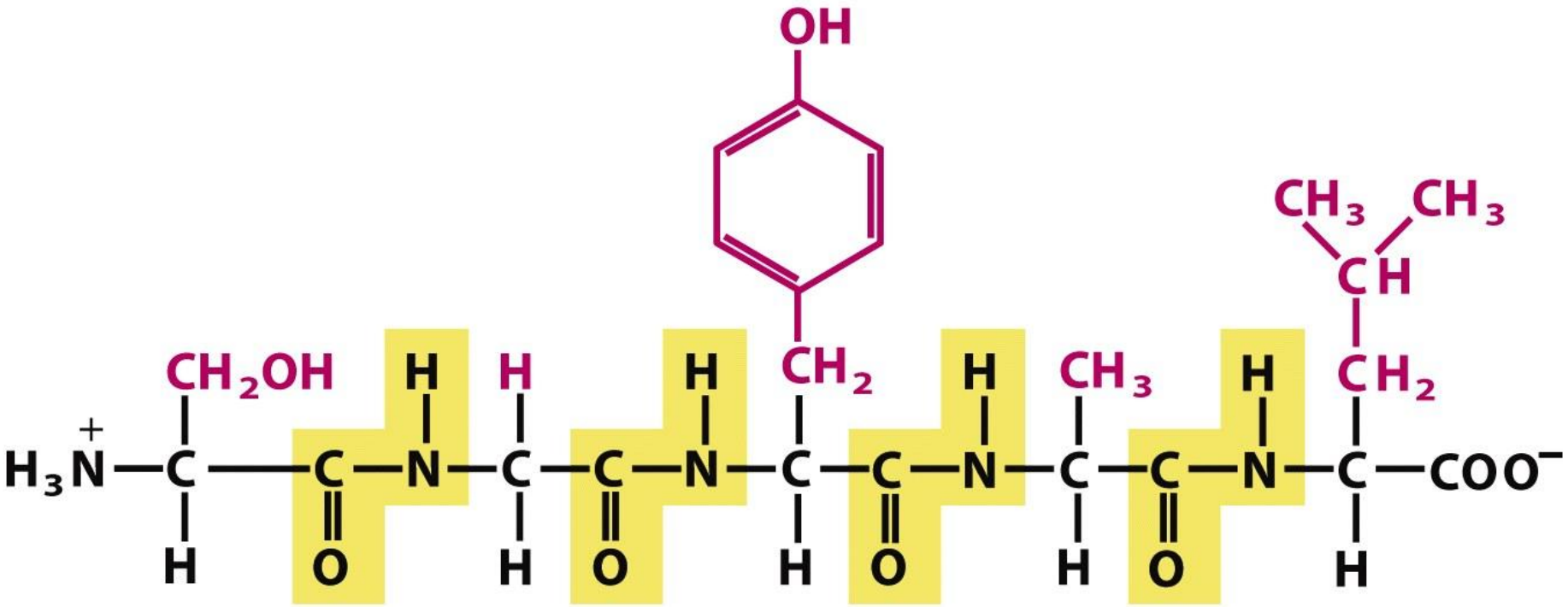

Figure 3-14
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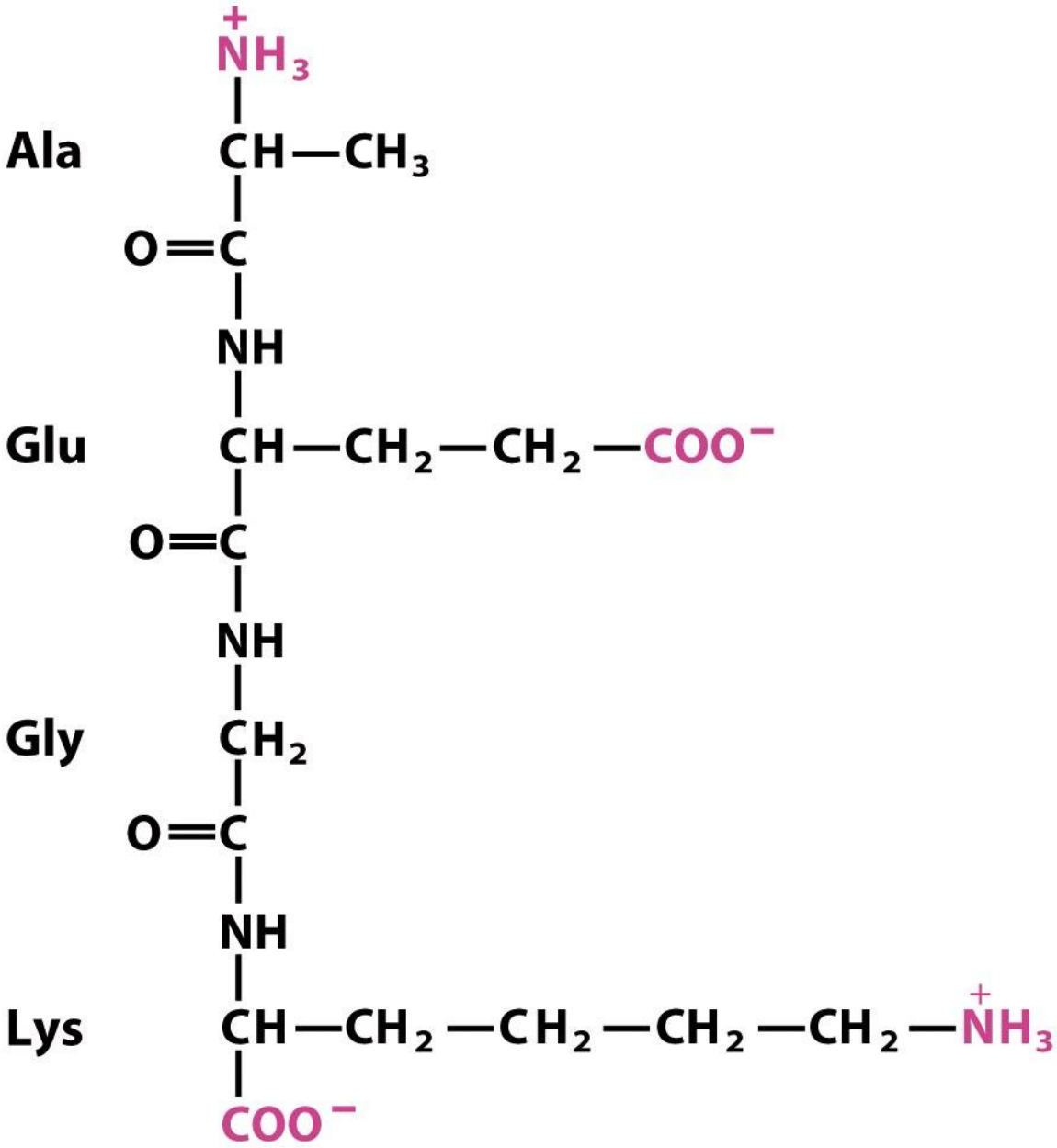

Figure 3-15
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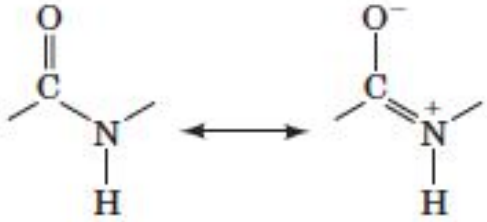
consequence of resonance interactions that give the peptide bond an ~40% double-bond character:



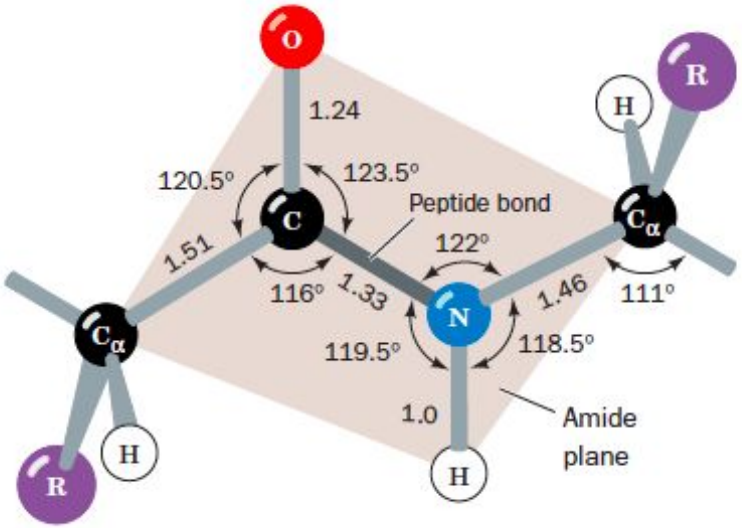


Figure 8-1 **The trans-peptide group.** The standard dimensions (in angstroms, Å, and degrees, °) of this planar group were derived by averaging the corresponding quantities in the X-ray crystal structures of amino acids and peptides. [After Marsh, R.E. and Donohue, J., *Adv. Protein Chem.* **22,** 249 (1967).]

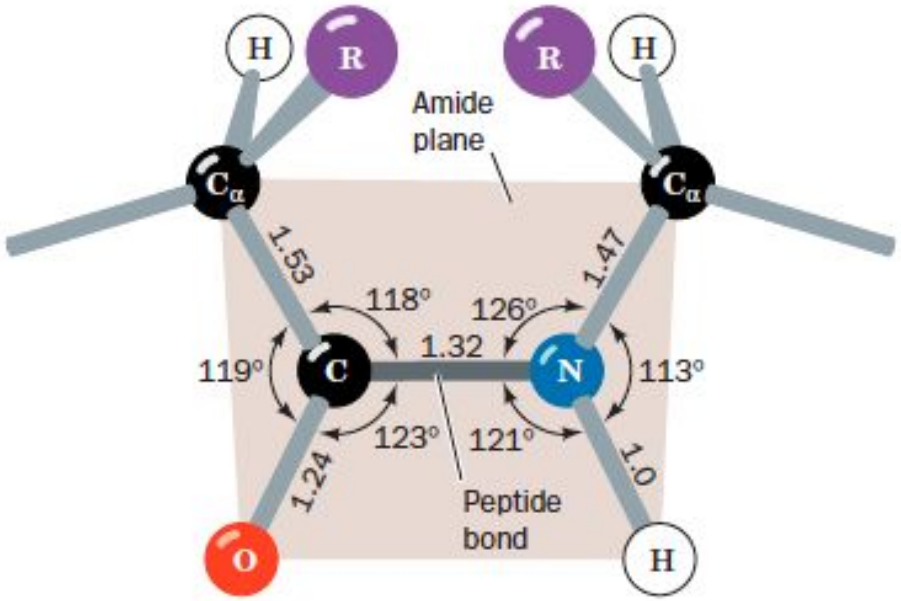


Figure 8-2 **The cis-peptide group.** **See Kinemage Exercise 3-1**

A polypeptide chain in a fully extended conformation

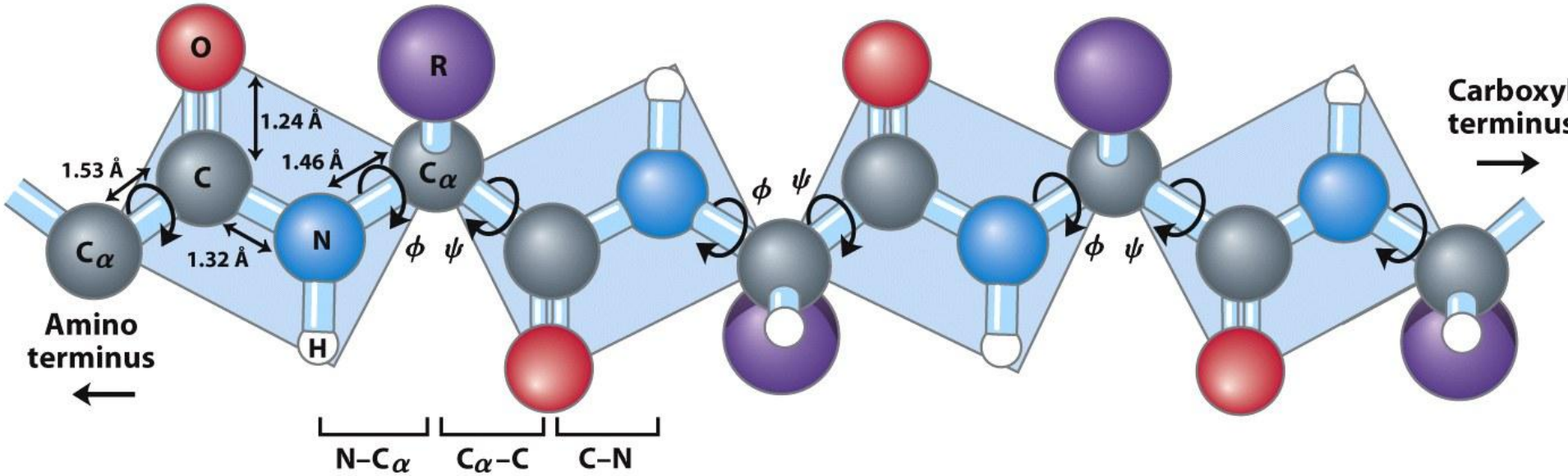


Figure 4-2b
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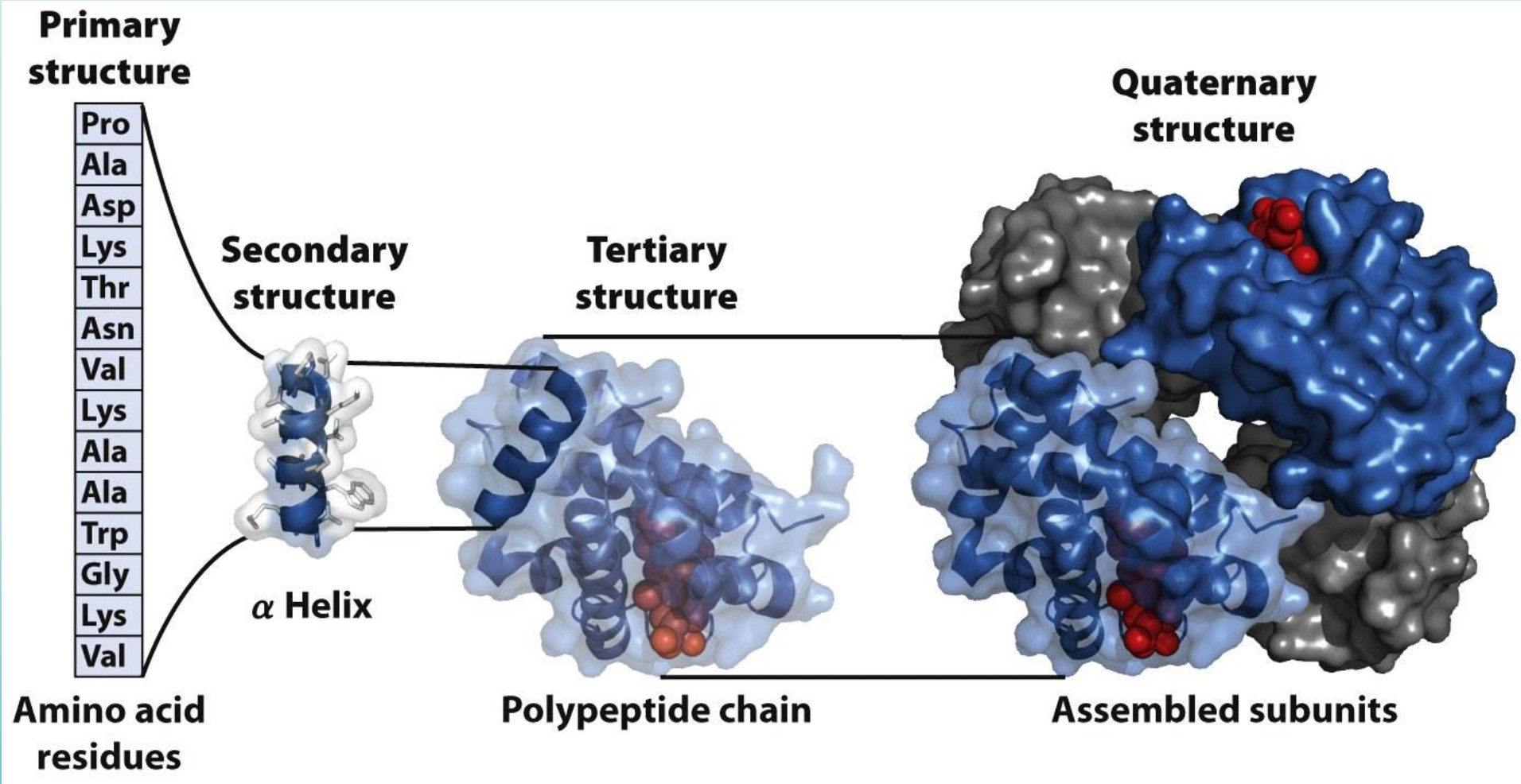

Figure 3-23
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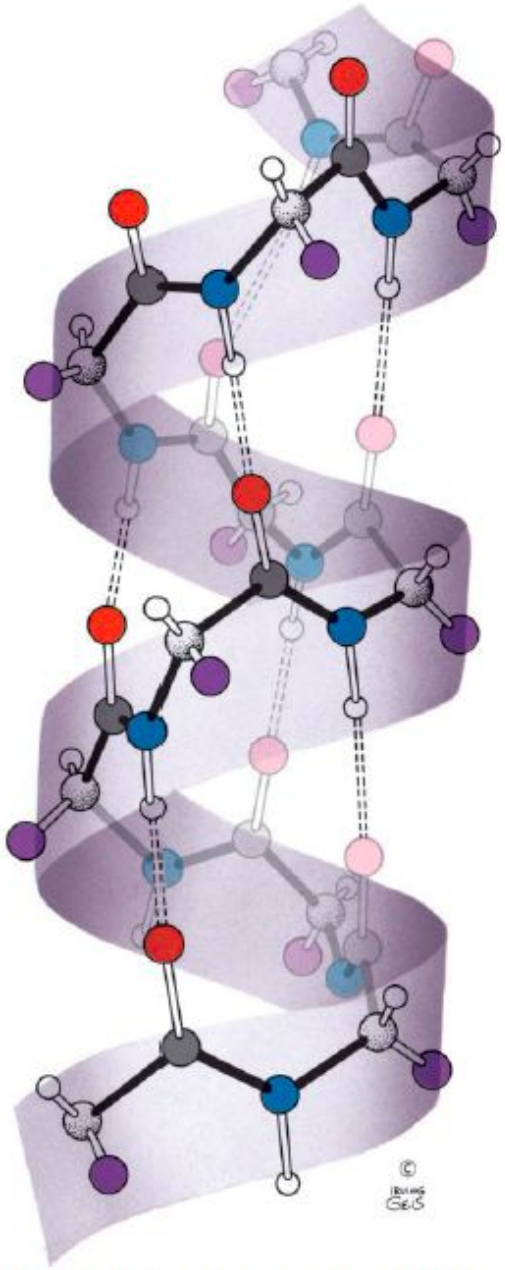
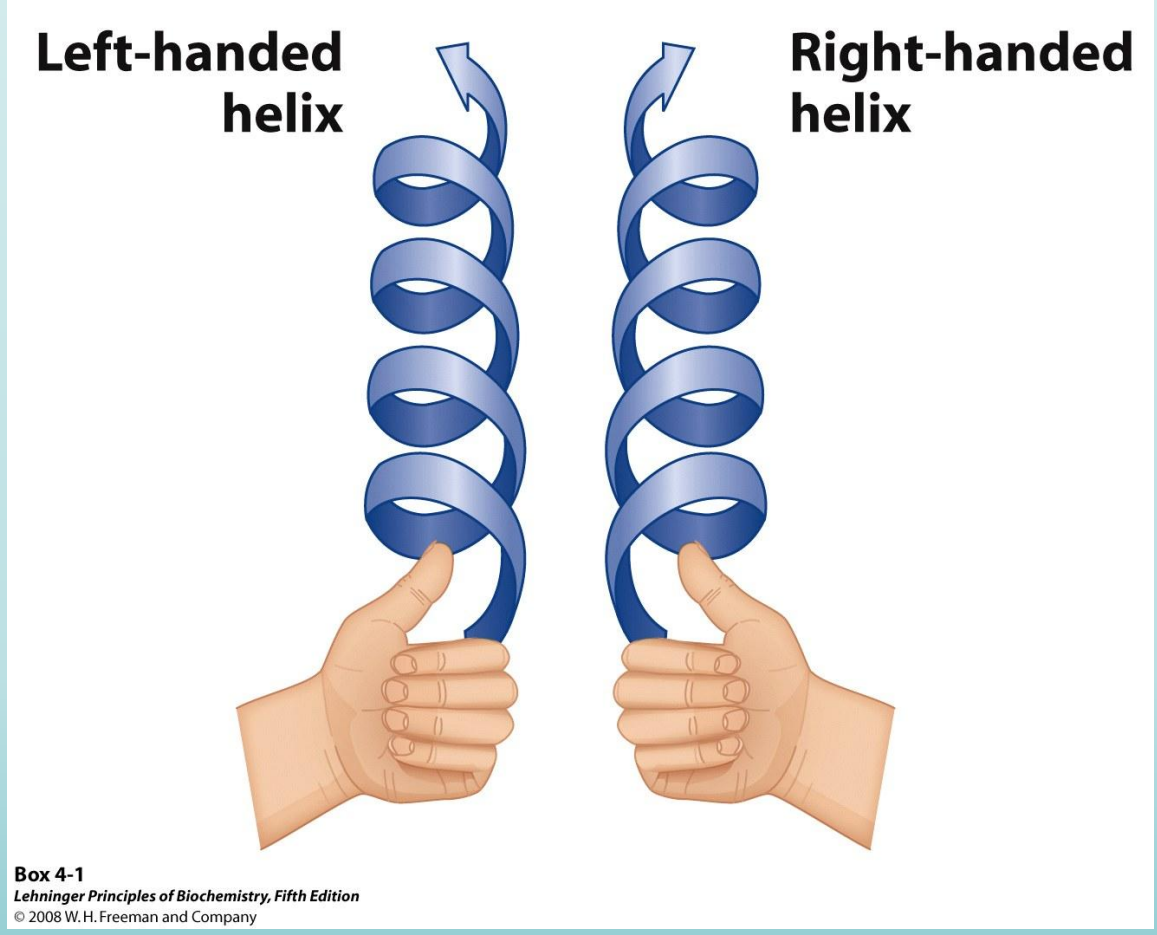


Figure 8-11 **The right-handed α helix.** Hydrogen bonds between the N—H groups and the C=O groups that are four residues back along the polypeptide chain are indicated by dashed lines. [Illustration, Irving Geis. Image from the Irving Geis Collection, Howard Hughes Medical Institute. Reprinted with permission.]



Box 4-1
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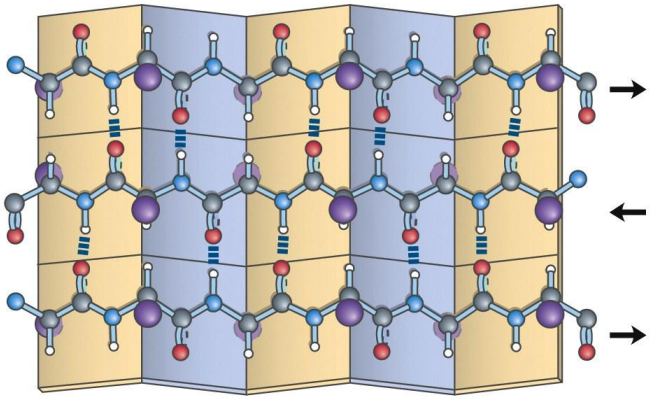
α-helix: p = 5.4 A, n= 3.6 helical rise = 1.5 A

Antiparallel

Top view



Side view

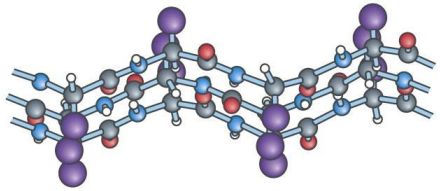


Figure 4-6a
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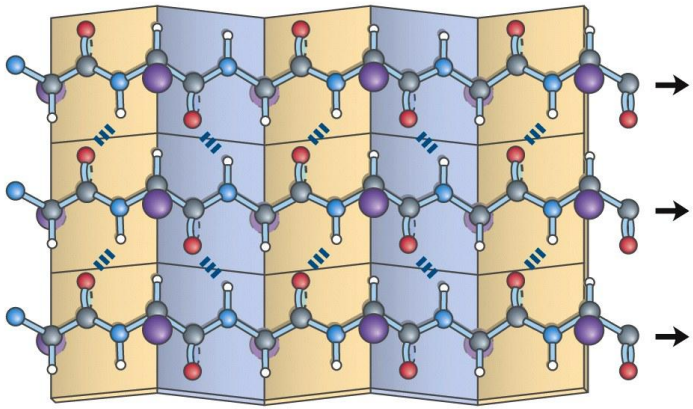
Parallel

Top view



Side view

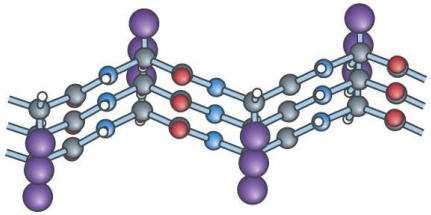


Figure 4-6b
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Fatty acids

TABLE 10–1 Some Naturally Occurring Fatty Acids: Structure, Properties, and Nomenclature

Carbon skeleton	Structure*	Systematic name†	Common name (derivation)	Melting point (°C)	Solubility at 30 °C (mg/g solvent)	
					Water	Benzene
12:0	$CH_3(CH_2)_{10}COOH$	*n*-Dodecanoic acid	Lauric acid (Latin *laurus*, "laurel plant")	44.2	0.063	2,600
14:0	$CH_3(CH_2)_{12}COOH$	*n*-Tetradecanoic acid	Myristic acid (Latin *Myristica*, nutmeg genus)	53.9	0.024	874
16:0	$CH_3(CH_2)_{14}COOH$	*n*-Hexadecanoic acid	Palmitic acid (Latin *palma*, "palm tree")	63.1	0.0083	348
18:0	$CH_3(CH_2)_{16}COOH$	*n*-Octadecanoic acid	Stearic acid (Greek *stear*, "hard fat")	69.6	0.0034	124
20:0	$CH_3(CH_2)_{18}COOH$	*n*-Eicosanoic acid	Arachidic acid (Latin *Arachis*, legume genus)	76.5		
24:0	$CH_3(CH_2)_{22}COOH$	*n*-Tetracosanoic acid	Lignoceric acid (Latin *lignum*, "wood" + *cera*, "wax")	86.0		
16:1(Δ^9)	$CH_3(CH_2)_5CH{=}CH(CH_2)_7COOH$	*cis*-9-Hexadecenoic acid	Palmitoleic acid	1 to –0.5		
18:1(Δ^9)	$CH_3(CH_2)_7CH{=}CH(CH_2)_7COOH$	*cis*-9-Octadecenoic acid	Oleic acid (Latin *oleum*, "oil")	13.4		
18:2($\Delta^{9,12}$)	$CH_3(CH_2)_4CH{=}CHCH_2CH{=}CH(CH_2)_7COOH$	*cis*-,*cis*-9,12-Octadecadienoic acid	Linoleic acid (Greek *linon*, "flax")	1–5		
18:3($\Delta^{9,12,15}$)	$CH_3CH_2CH{=}CHCH_2CH{=}CHCH_2CH{=}CH(CH_2)_7COOH$	*cis*-,*cis*-,*cis*-9,12,15-Octadecatrienoic acid	α-Linolenic acid	−11		
20:4($\Delta^{5,8,11,14}$)	$CH_3(CH_2)_4CH{=}CHCH_2CH{=}CHCH_2CH{=}CHCH_2CH{=}CH(CH_2)_3COOH$	*cis*-,*cis*-,*cis*-,*cis*-5, 8,11, 14- Icosatetraenoic acid	Arachidonic acid	−49.5		

*All acids are shown in their nonionized form. At pH 7, all free fatty acids have an ionized carboxylate. Note that numbering of carbon atoms begins at the carboxyl carbon.

†The prefix *n*- indicates the "normal" unbranched structure. For instance, "dodecanoic" simply indicates 12 carbon atoms, which could be arranged in a variety of branched forms; "*n*-dodecanoic" specifies the linear, unbranched form. For unsaturated fatty acids, the configuration of each double bond is indicated; in biological fatty acids the configuration is almost always cis.

Table 10-1

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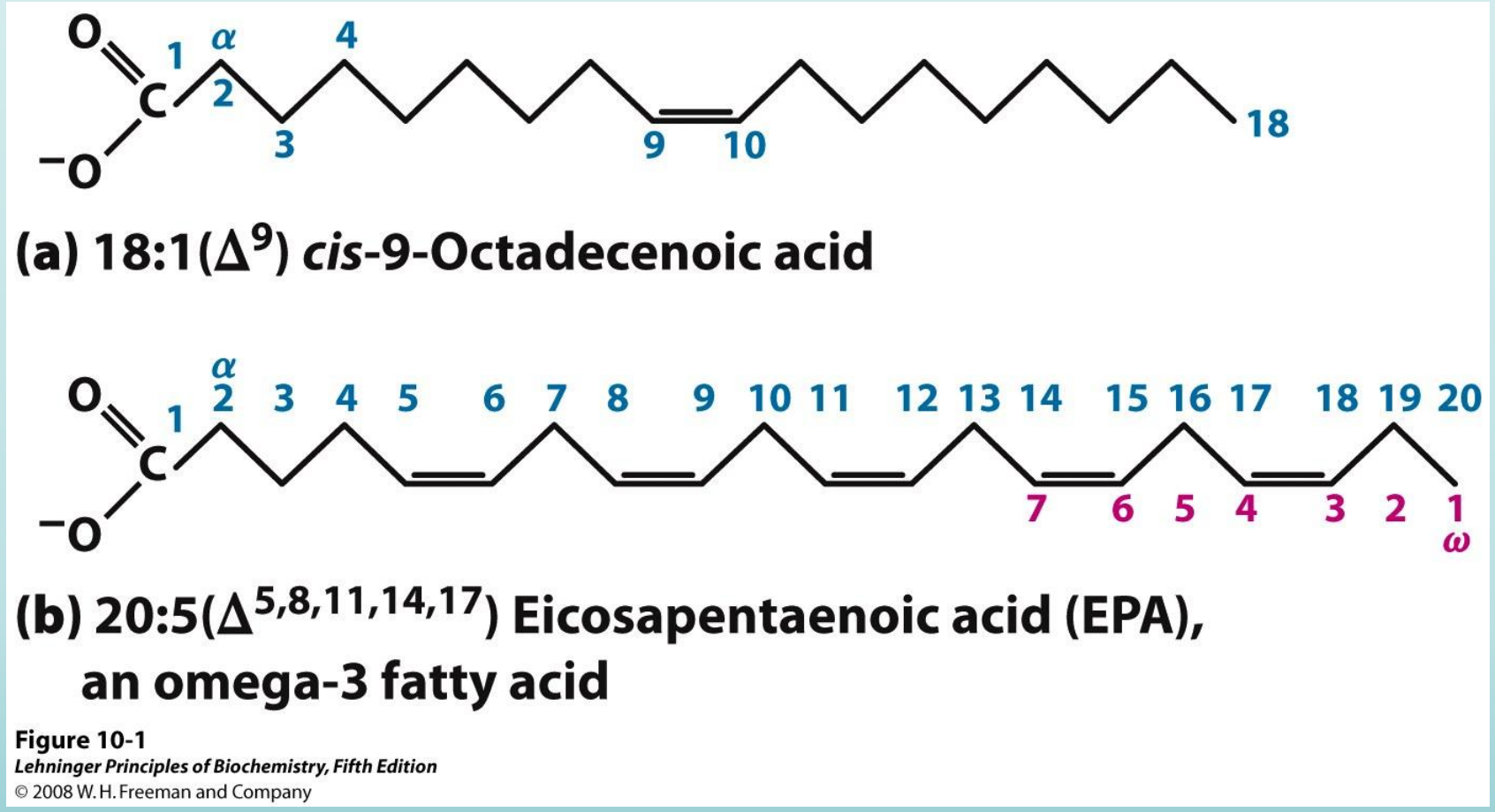

Figure 10-1
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Two conventions for naming fatty acids. (a) Standard nomenclature assigns the number 1 to the carboxyl carbon (C-1), and *α* to the carbon next to it. The position of any double bond(s) is indicated by Δ followed by a superscript number indicating the lower-numbered carbon in the double bond. (b) For polyunsaturated fatty acids (PUFAs), an alternative convention numbers the carbons in the opposite direction, assigning the number 1 to the methyl carbon at the other end of the chain; this carbon is also designated Ω (omega; the last letter in the Greek alphabet). The positions of the double bonds are indicated relative to the Ω carbon.

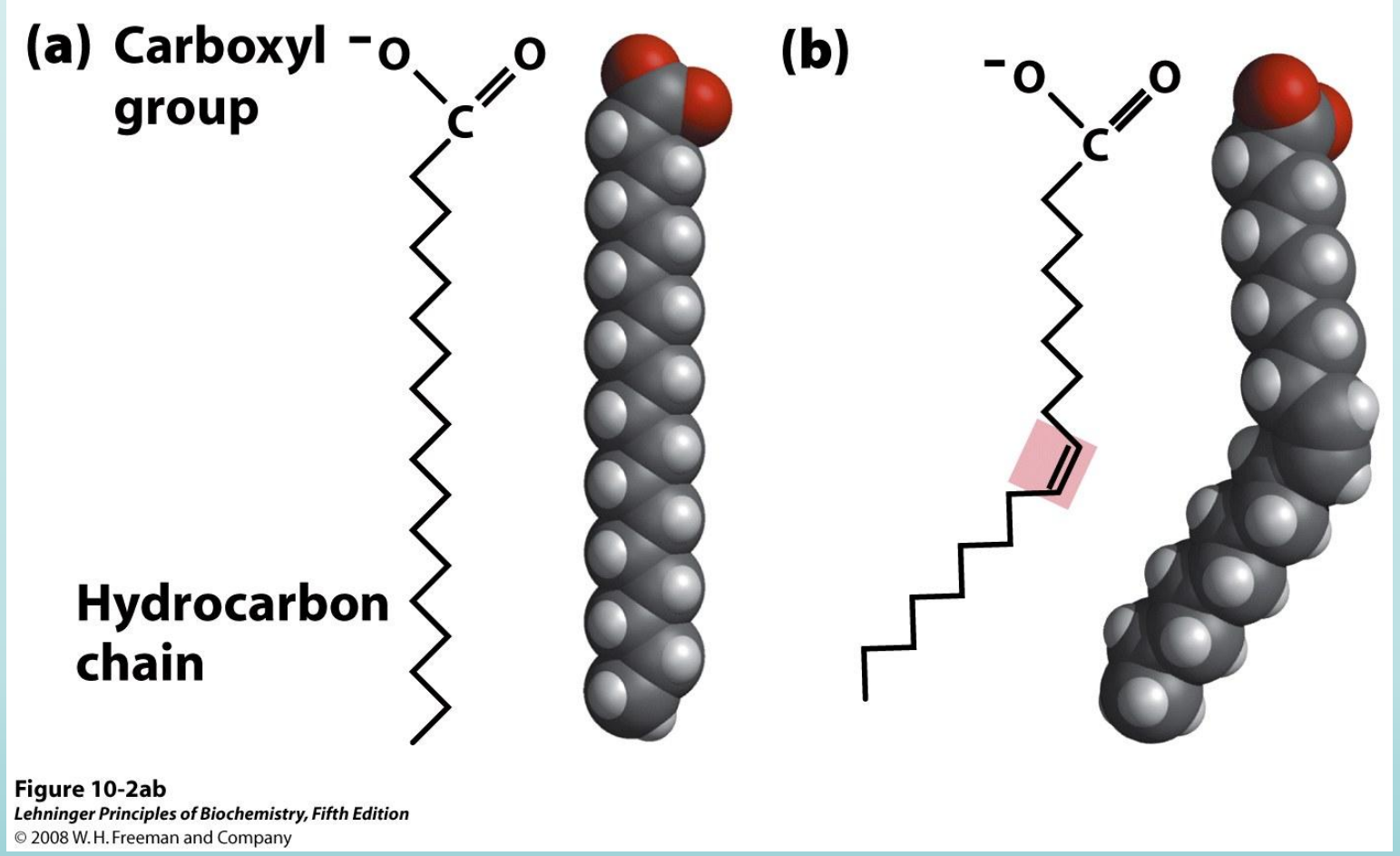

Figure 10-2ab
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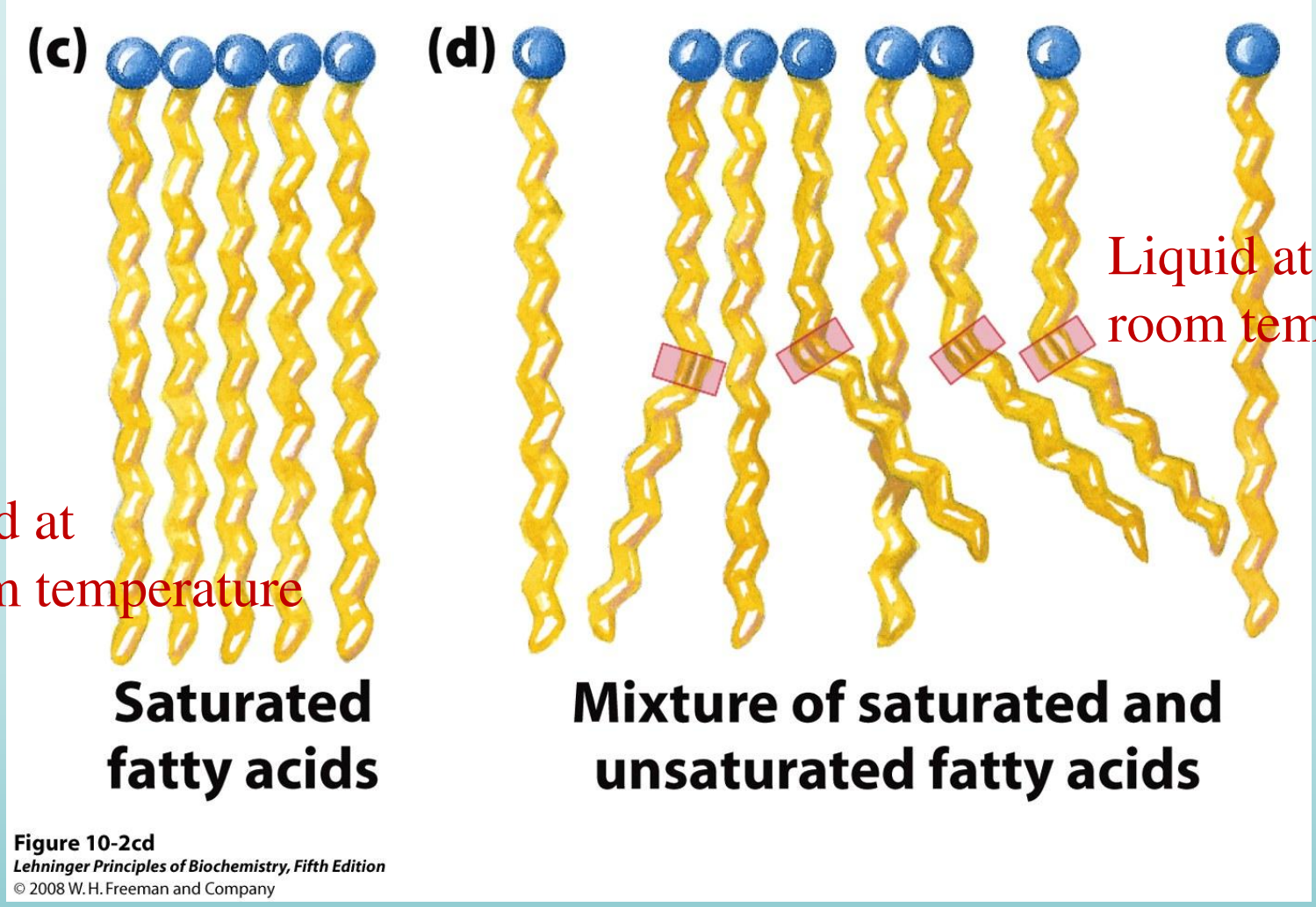
The packing of fatty acids into stable aggregates. The extent of packing depends on the degree of saturation. (a) Two representations of the fully saturated acid stearic acid, 18:0 (stearate at pH 7), in its usual extended conformation. Each line segment of the zigzag represents a single bond between adjacent carbons. (b) The cis double bond (shaded) in oleic acid, 18:1(Δ^9) (oleate), restricts rotation and introduces a rigid bend in the hydrocarbon tail. All other bonds in the chain are free to rotate



Solid at room temperature

Liquid at room temperature

Figure 10-2cd
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The packing of fatty acids into stable aggregates. The extent of packing depends on the degree of saturation. (c) Fully saturated fatty acids in the extended form pack into nearly crystalline arrays, stabilized by many hydrophobic interactions. (d) The presence of one or more fatty acids with cis double bonds interferes with this tight packing and results in less stable aggregates.

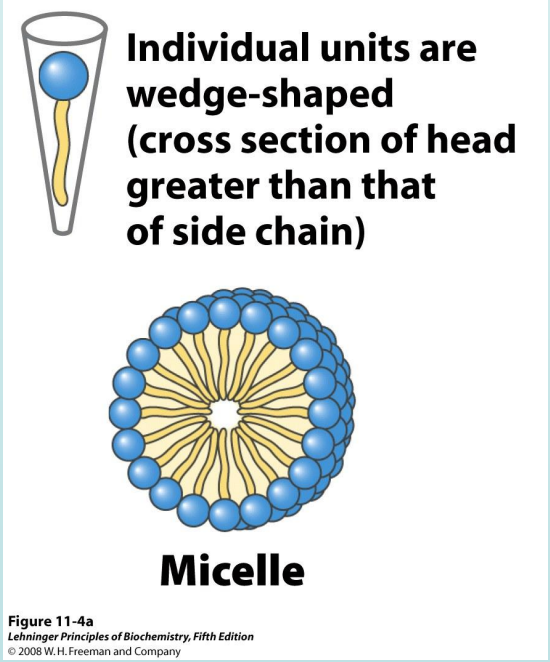

Figure 11-4a
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Amphipathic lipid aggregates that form in water. (a) In micelles, the hydrophobic chains of the fatty acids are sequestered at the core of the sphere. There is virtually no water in the hydrophobic interior.

Amphipathic lipid aggregates that form in water. (b) In an open bilayer, all acyl side chains except those at the edges of the sheet are protected from interaction with water.

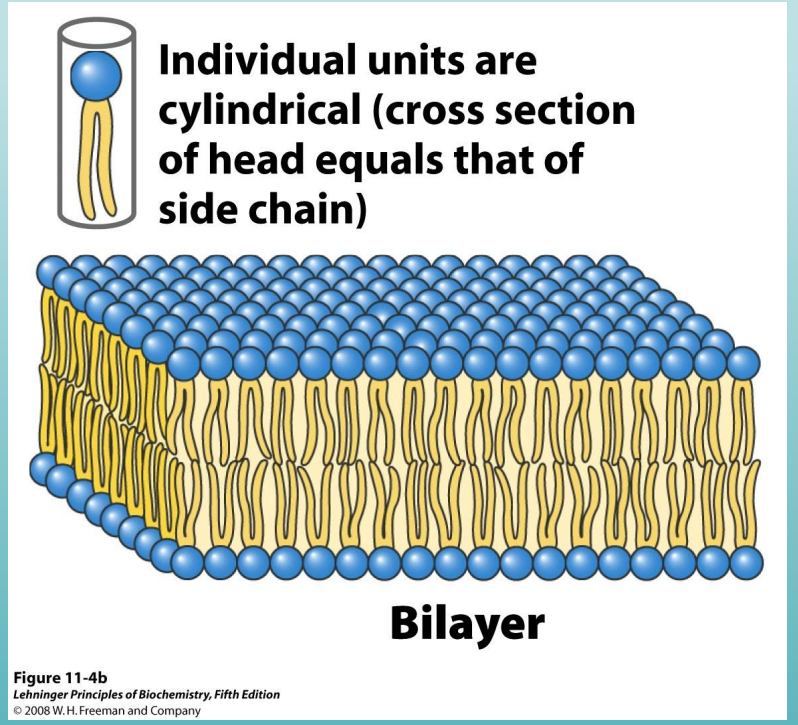

Figure 11-4b
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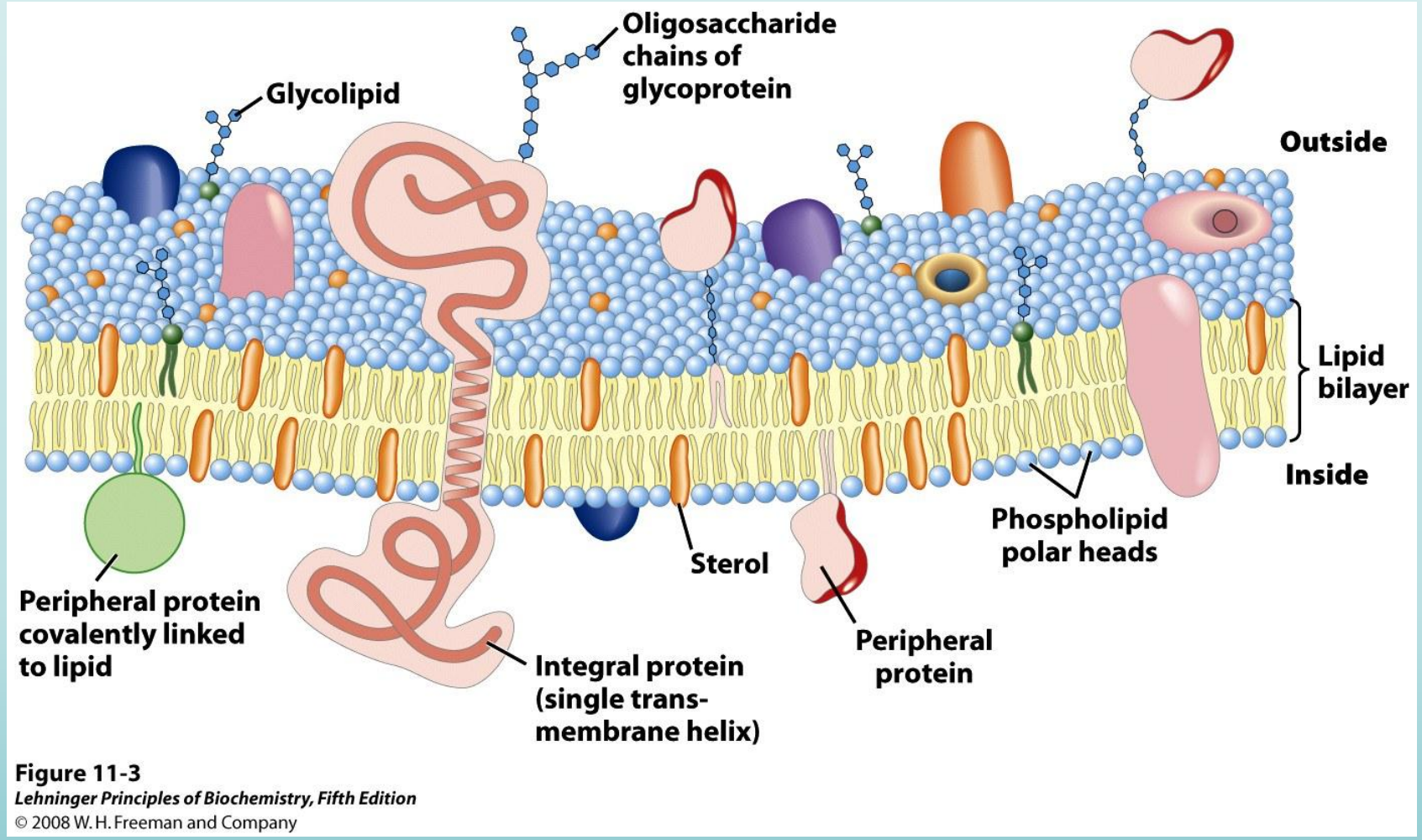

Figure 11-3
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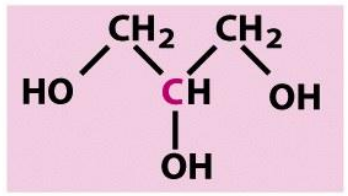
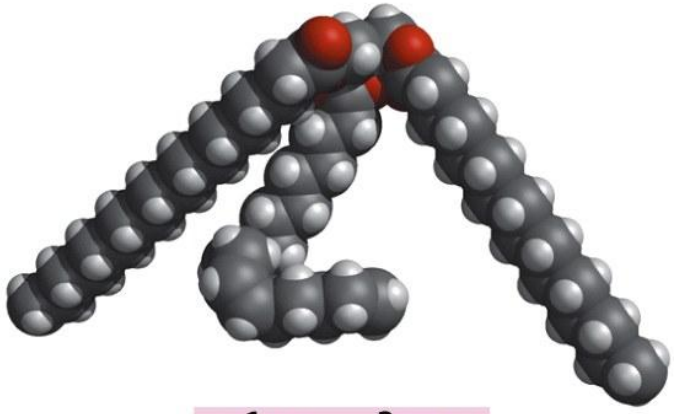
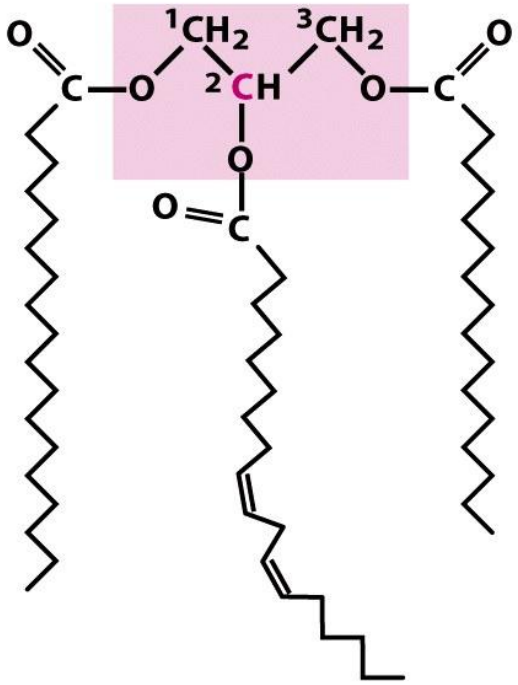
Fluid mosaic model for membrane structure. The fatty acyl chains in the interior of the membrane form a fluid, hydrophobic region. Integral proteins float in this sea of lipid, held by hydrophobic interactions with their nonpolar amino acid side chains. Both proteins and lipids are free to move laterally in the plane of the bilayer, but movement of either from one leaflet of the bilayer to the other is restricted. The carbohydrate moieties attached to some proteins and lipids of the plasma membrane are exposed on the extracellular surface of the membrane.

Lipids



Glycerol





1-Stearoyl, 2-linoleoyl, 3-palmitoyl glycerol,
a mixed triacylglycerol

Figure 10-3
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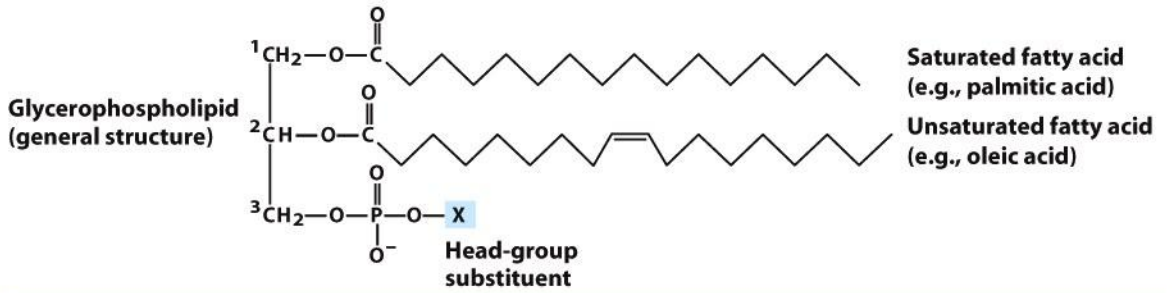
Glycerol and a triacylglycerol. The mixed triacylglycerol shown here has three different fatty acids attached to the glycerol backbone. When glycerol has different fatty acids at C-1 and C-3, C-2 is a chiral center



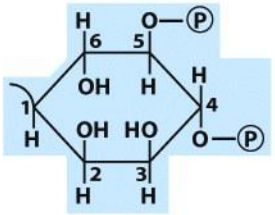
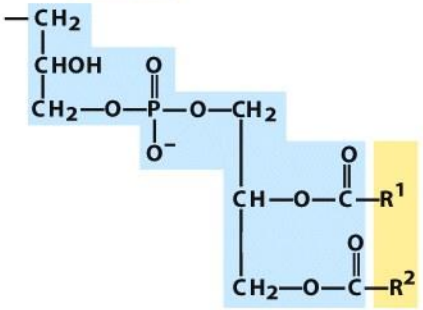
Name of glycerophospholipid	Name of X	Formula of X	Net charge (at pH 7)
Phosphatidic acid	—	—H	−1
Phosphatidylethanolamine	Ethanolamine	$-CH_2-CH_2-\overset{+}{N}H_3$	0
Phosphatidylcholine	Choline	$-CH_2-CH_2-\overset{+}{N}(CH_3)_3$	0
Phosphatidylserine	Serine	$-CH_2-\underset{COO^-}{CH}-\overset{+}{N}H_3$	−1
Phosphatidylglycerol	Glycerol	$-CH_2-\underset{OH}{CH}-CH_2-OH$	−1
Phosphatidylinositol 4,5-bisphosphate	*myo*-Inositol 4,5-bisphosphate		−4
Cardiolipin	Phosphatidyl-glycerol		−2

Figure 10-9
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Glycerophospholipids. The common glycerophospholipids are diacylglycerols linked to head-group alcohols through a phosphodiester bond. Phosphatidic acid, a phosphomonoester, is the parent compound. Each derivative is named for the head-group alcohol (X), with the prefix "phosphatidyl-." In cardiolipin, two phosphatidic acids share a single glycerol (R^1 and R^2 are fatty acyl groups).

Carbohydrates

Carbohydrates (monosaccharides, oligo- or poly-saccharides): polyhydroxy aldehides or ketones

- Carbohydrates are the most abundant biomolecules on earth.
- Photosynthesis.
- Oxidation of carbohydrates is the central **energy-yelding** pathway in most non-photosynthetic organisms.
- **Glycogoniugates**
- Non-linear polymers

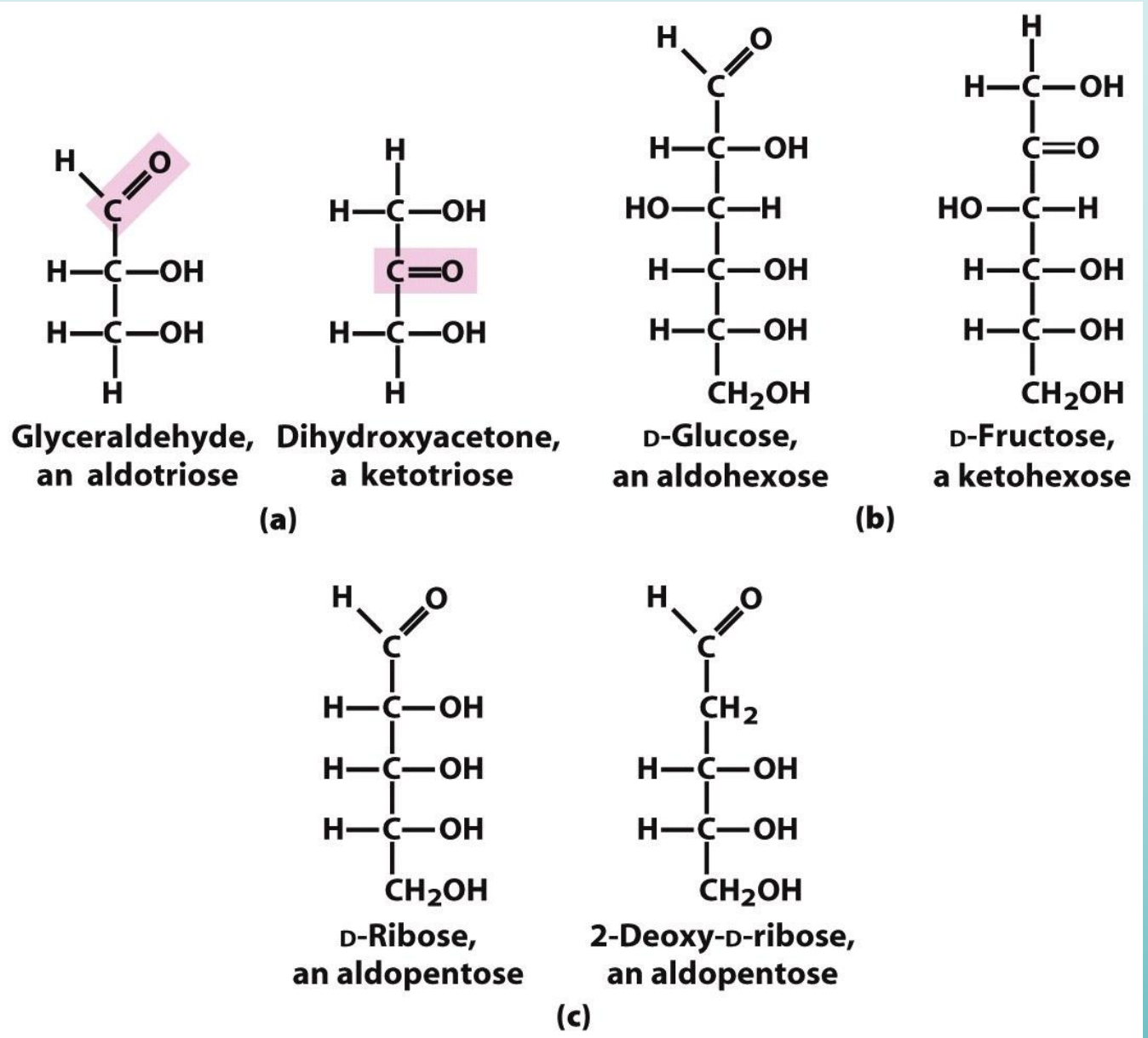

Figure 7-1
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Representative monosaccharides. (a)Two trioses, an aldose and a ketose. The carbonyl group in each is shaded. (b) Two common hexoses. (c) The pentose components of nucleic acids. D-Ribose is a component of ribonucleic acid (RNA), and 2-deoxy-D-ribose is a component of deoxyribonucleic acid (DNA).

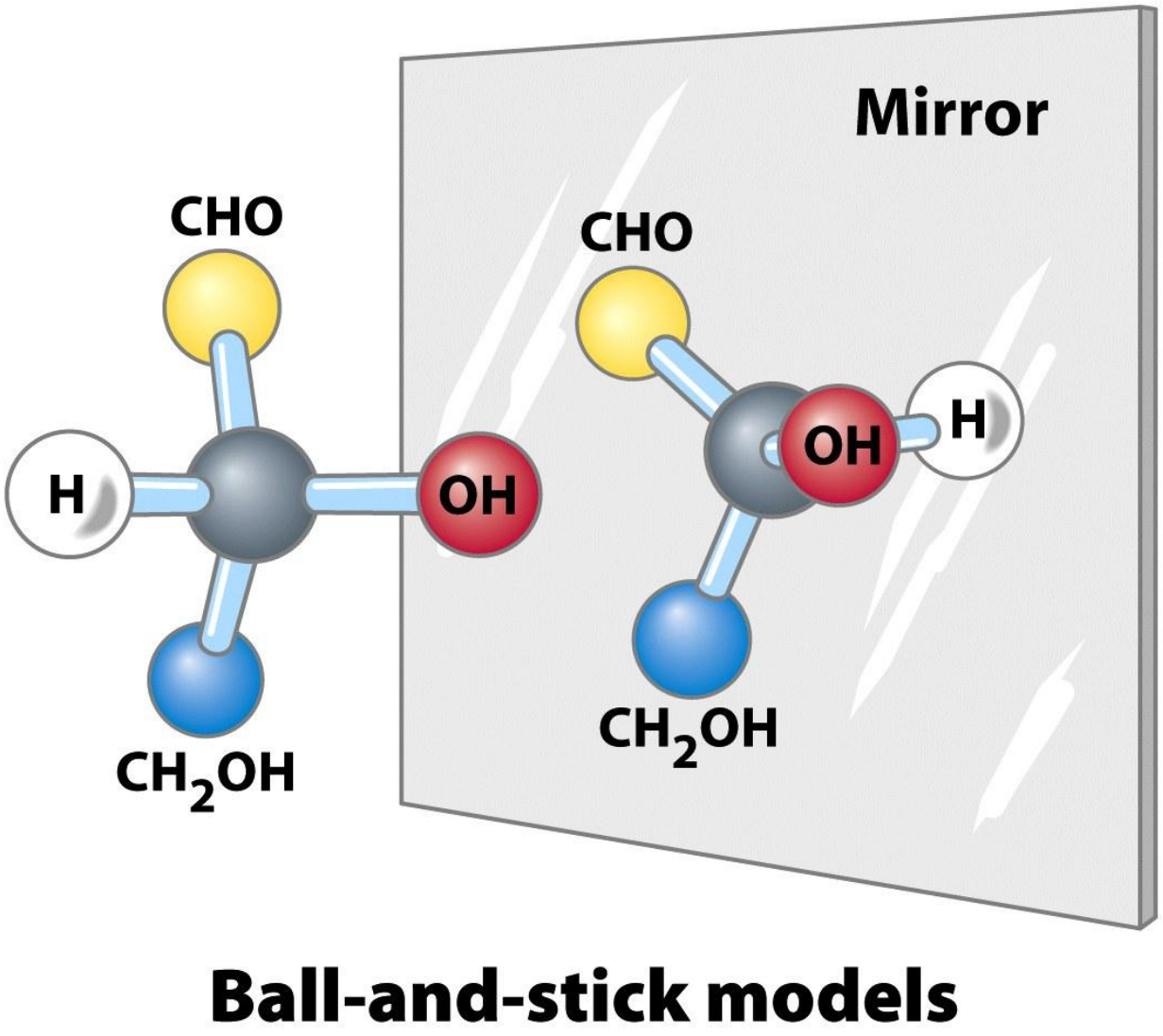

Figure 7-2 part 1
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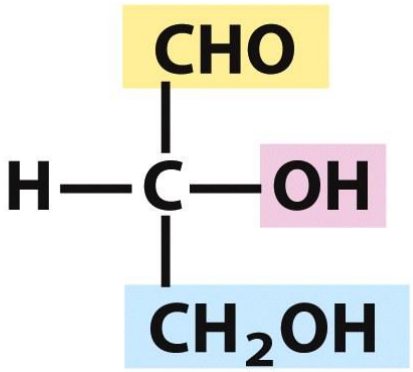
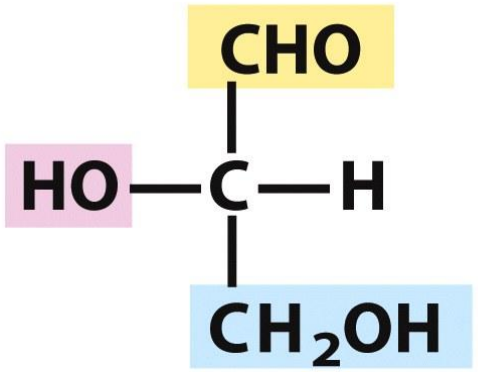
Three ways to represent the two enantiomers of glyceraldehyde. The enantiomers are mirror images of each other. Ball-and-stick models show the actual configuration of molecules. Recall (see Figure 1-17) that in perspective formulas, solid wedge-shaped bonds point toward the reader, dashed wedges point away.

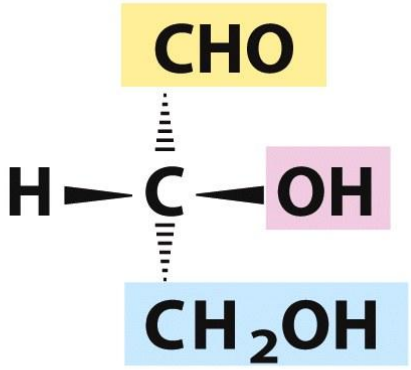


D-Glyceraldehyde

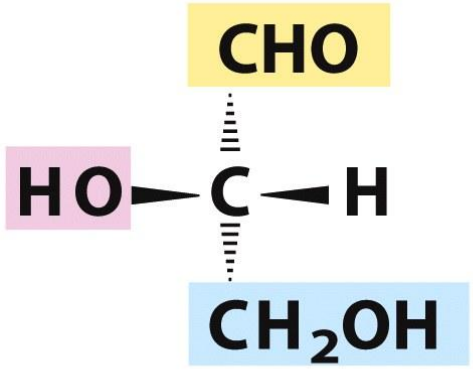


L-Glyceraldehyde

Fischer projection formulas



D-Glyceraldehyde



L-Glyceraldehyde

Perspective formulas

Figure 7-2 part 3
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***n* chiral centers □ 2^n stereoisomers**

Glyceraldehide □ 2 stereoisomers

Aldohexoses □ 2^4 = 16 stereoisomers

The stereoisomers of monosaccharides of each carbon-chain length can be divided into two groups that differ in the configuration about the chiral center most distant from the carbonyl carbon. Those in which the configuration at this reference carbon is the same as that of **D -glyceraldehyde** are designated **D isomers**, and those with the same configuration as L glyceraldehyde are **L isomers**.

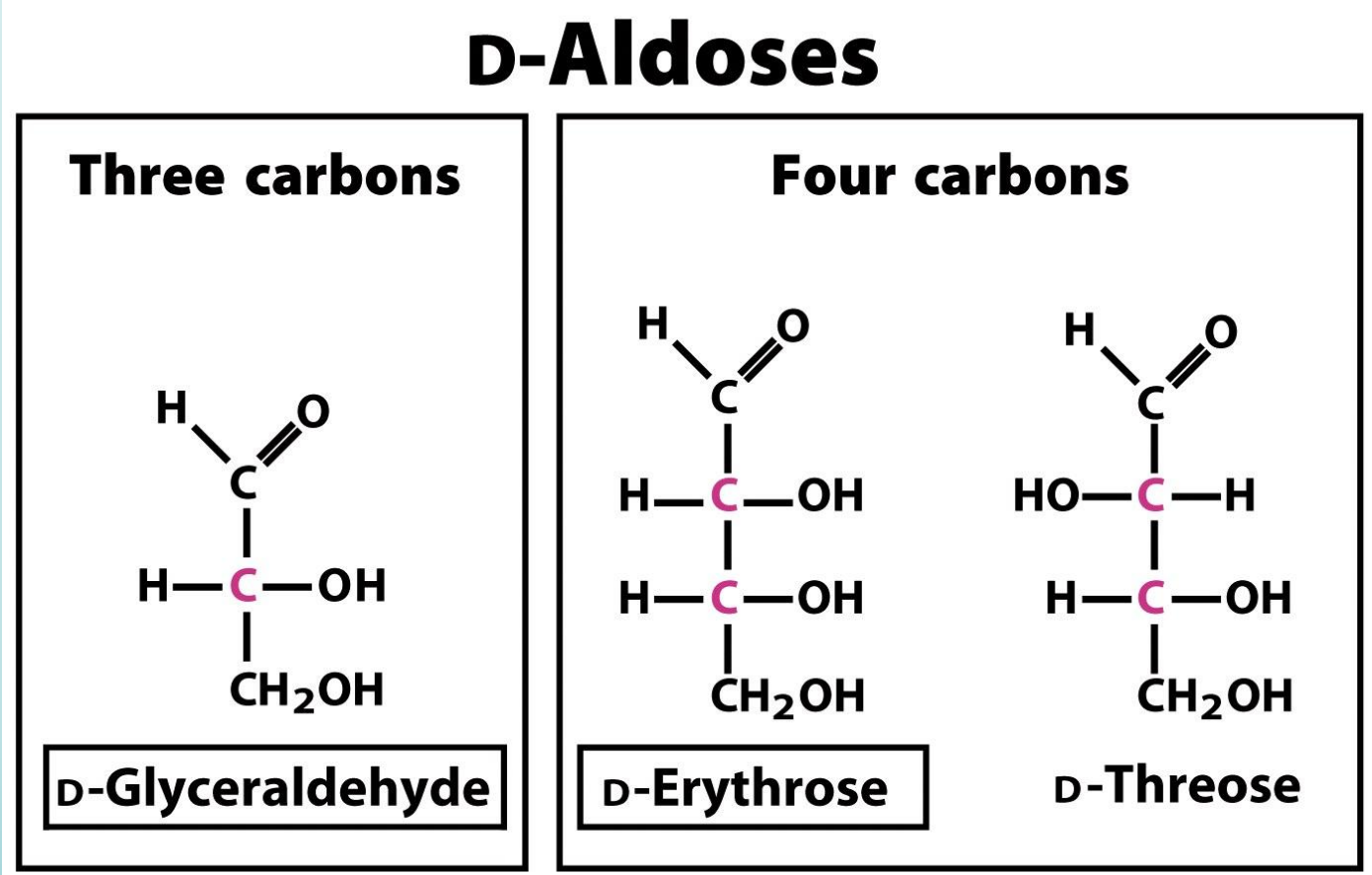

Figure 7-3a part 1
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Aldoses and ketoses. The series of (a) D-aldoses and (b) D-ketoses having from three to six carbon atoms, shown as projection formulas. The carbon atoms in red are chiral centers. In all these D isomers, the chiral carbon *most distant from the carbonyl carbon* has the same configuration as the chiral carbon in D-glyceraldehyde. The sugars named in boxes are the most common in nature; you will encounter these again in this and later chapters.

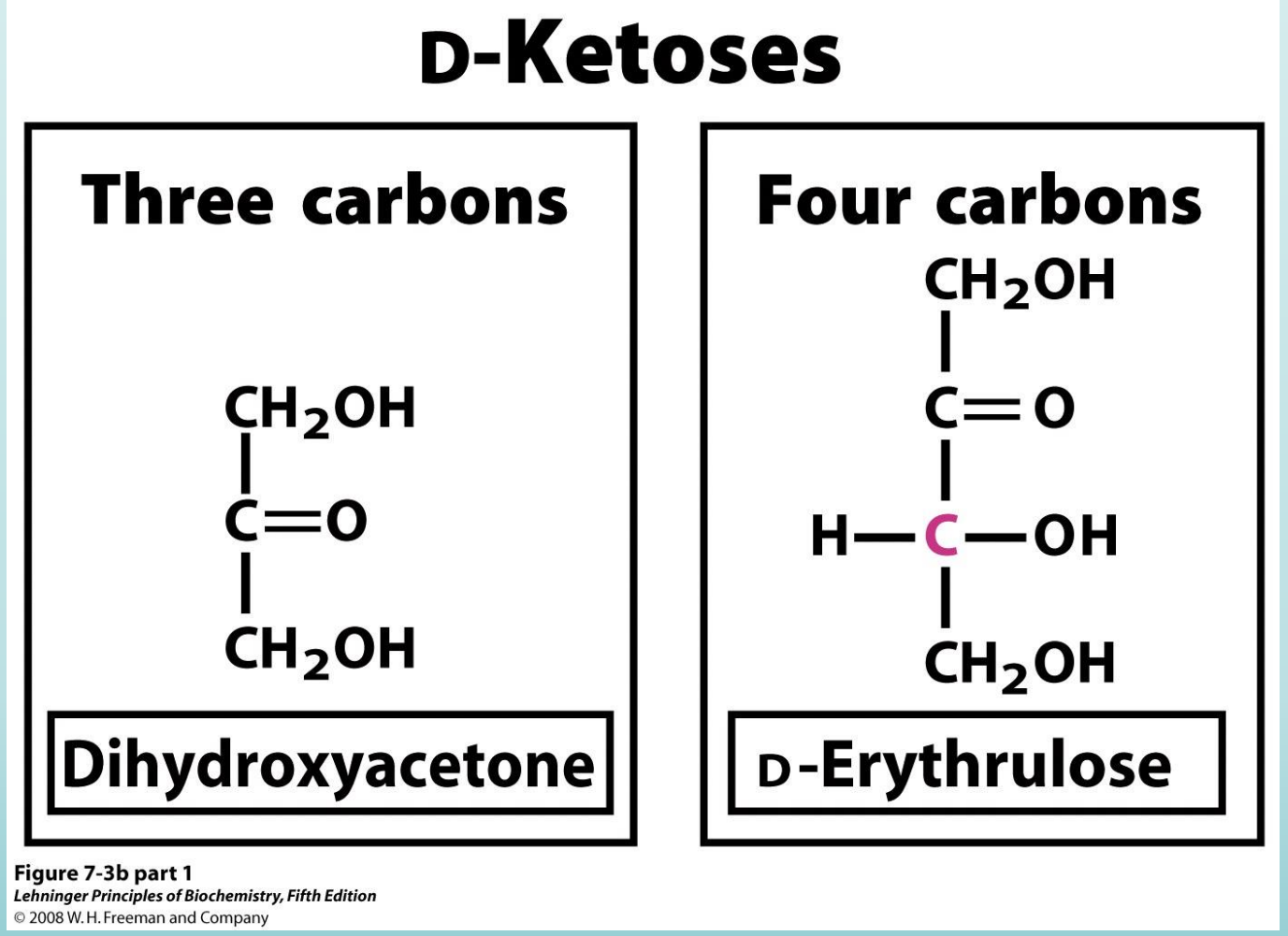

Figure 7-3b part 1
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Aldoses and ketoses. The series of (a) D-aldoses and (b) D-ketoses having from three to six carbon atoms, shown as projection formulas. The carbon atoms in red are chiral centers. In all these D isomers, the chiral carbon *most distant from the carbonyl carbon* has the same configuration as the chiral carbon in D-glyceraldehyde. The sugars named in boxes are the most common in nature; you will encounter these again in this and later chapters.

Forme lineari
e
cicliche

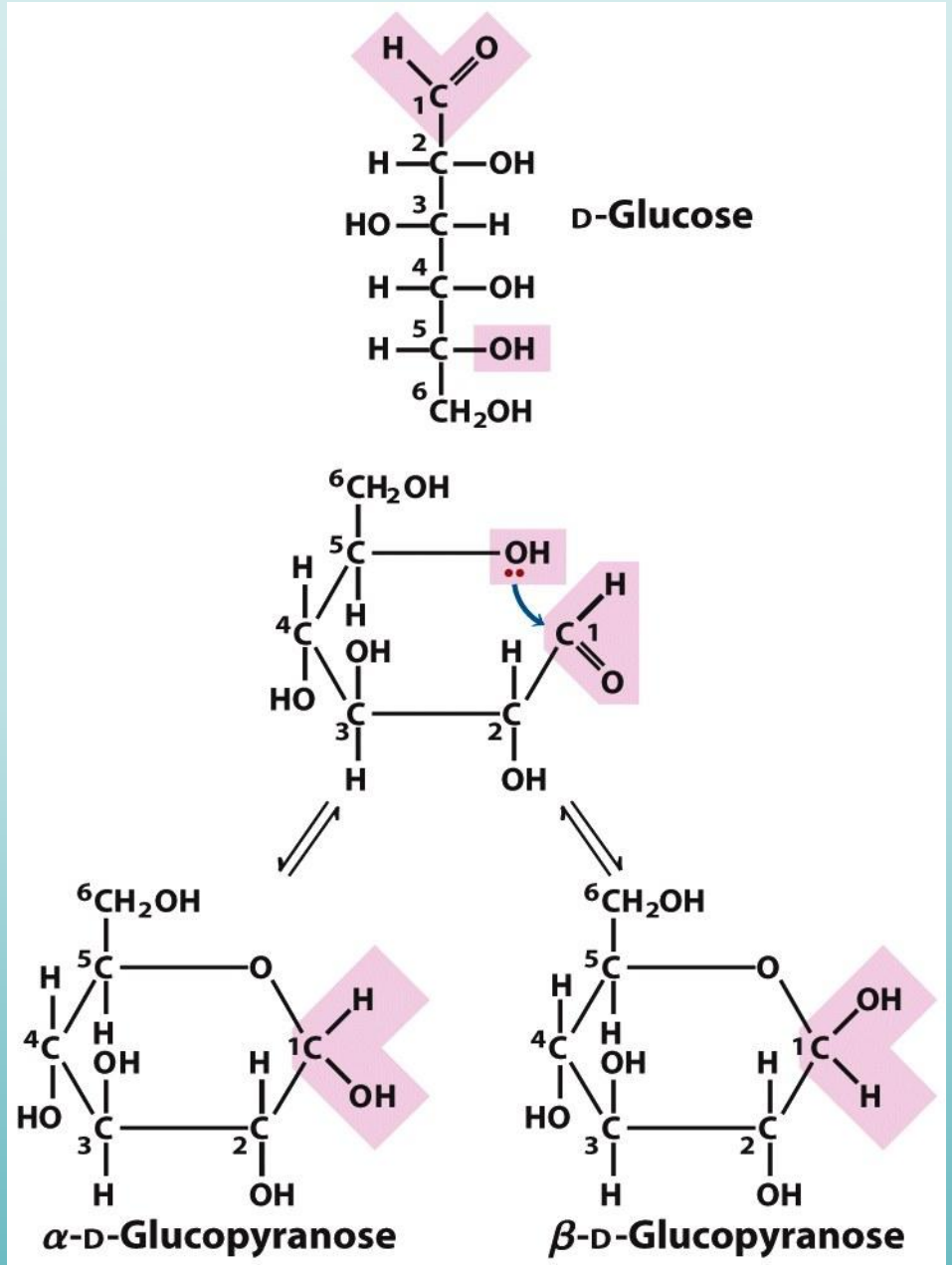

Figure 7-6
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Formation of the two cyclic forms of D-glucose. Reaction between the aldehyde group at C-1 and the hydroxyl group at C-5 forms a hemiacetal linkage, producing either of two stereoisomers, the *α* and *β* **anomers**, which differ only in the stereochemistry around the hemiacetal carbon. The interconversion of *α* and *β* anomers is called **mutarotation**.

Polisaccaridi

(glicani)

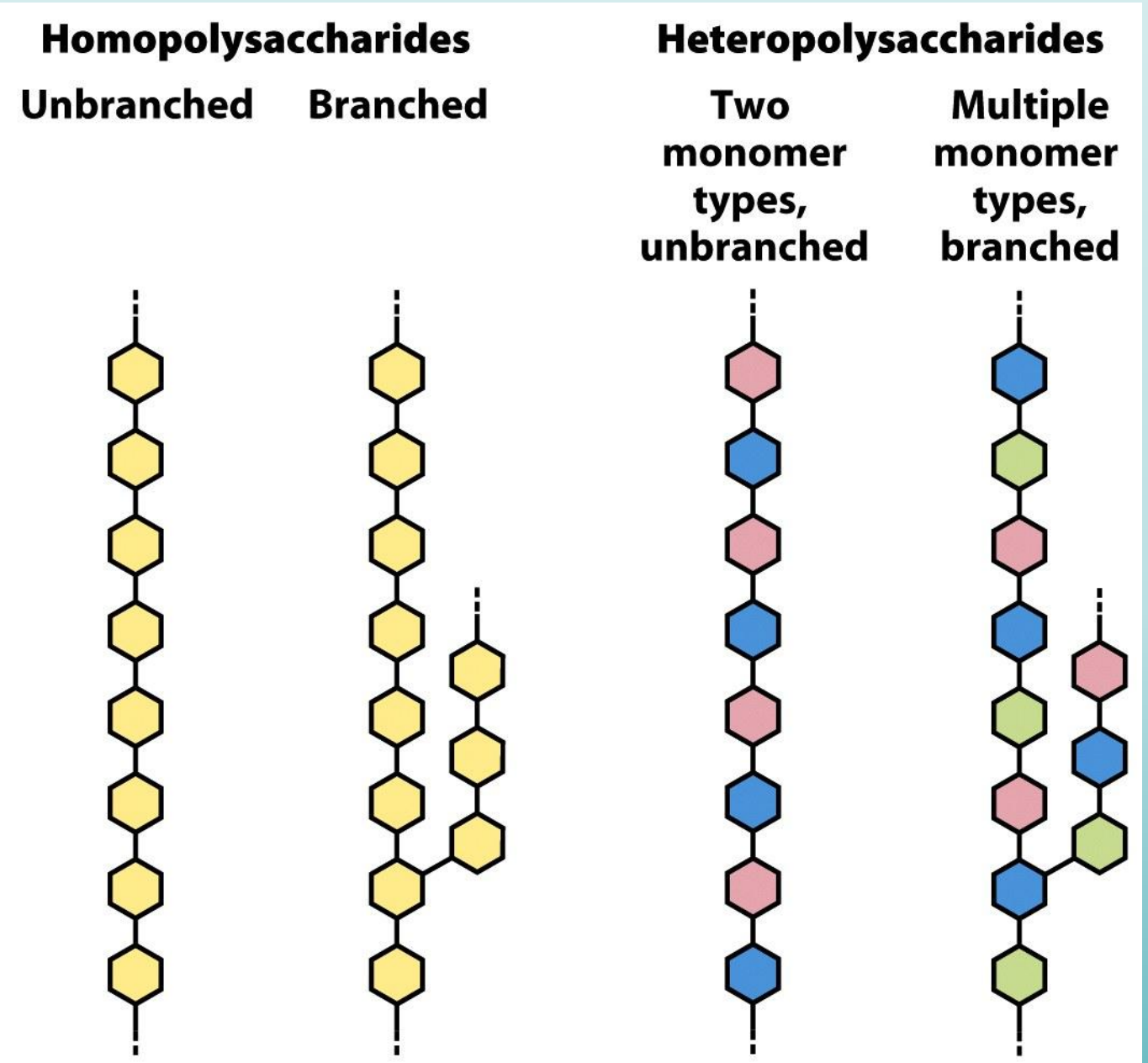

Figure 7-13
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Homo- and heteropolysaccharides. Polysaccharides may be composed of one, two, or several different monosaccharides, in straight or branched chains of varying length.

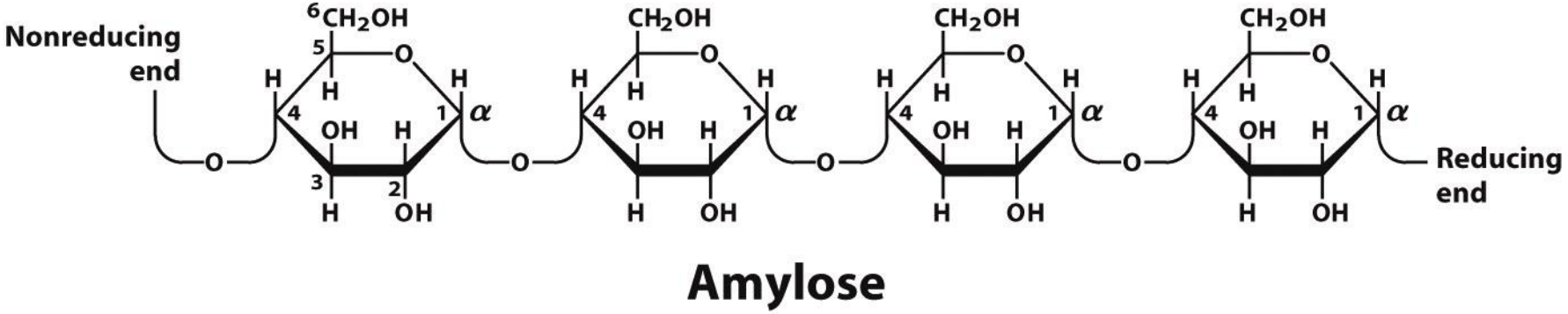

Figure 7-14a
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Glycogen and starch. (a) A short segment of **amylose**, a **linear polymer of D-glucose** residues in **(α1→4)** linkage. A single chain can contain several thousand glucose residues. **Amylopectin** has stretches of similarly linked residues between branch points. Glycogen has the same basic structure, but has more branching than amylopectin.

Starch (amido)

Amylose: unbranched

Amylopectin: branched

Glycogen: more branched than amylopectin

(α1→4) linear polymer

(α1→6) branch point of glycogen or amylopectin.