Science X-Change

Seminar I

Seminar I

- Building Blocks (polysaccharide, protein, DNA, RNA, lipids)
- ATP-Generation via substrate level phosphorylation, electron transport phosphorylation

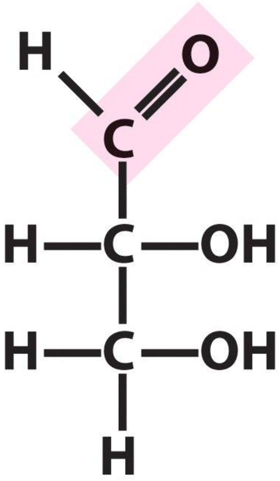
Carbohydrates (Saccharides)

Carbohydrates

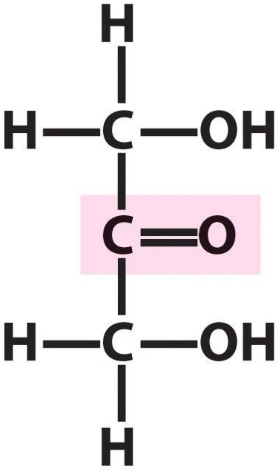
- Name: „hydrated carbon“ = carbohydrates, $(CH_2O)_n$
- Classification according to monomeric units.
- **Monosaccharides** (smallest unit $C_{3\text{-}9}$)
- **Oligosaccharides** (2-20 Monosaccharides) (most abundant disaccharides)
- **Polysaccharides** (>20 Monosaccharides)

Carbohydrates

- Smallest monosaccharides are **trioses.**
- C_1 (e.g. formaldehyde $H_2C{=}O$) or C_2 with the gross fomula $(CH_2O)_n$ are not regarded as sugars, since they miss the typical features (sweet taste, property of crystallisation).
- Glyceraldehyde is an aldehyde: **Aldose** (C_1 highest oxidation level)
- Dihydroxyacetone is a keton: **Ketose** (C_2 highest oxidation level)



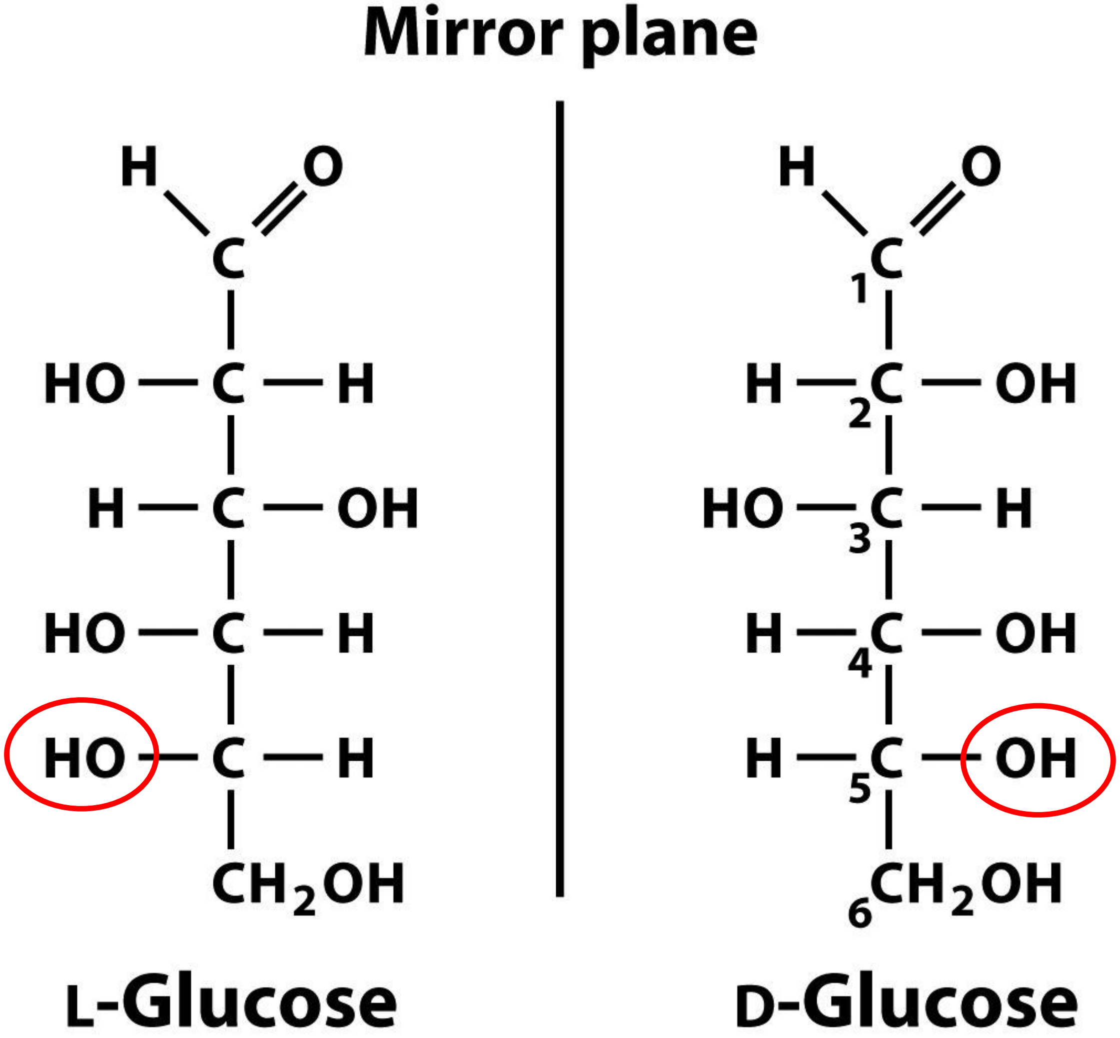
Glyceraldehyde, an aldotriose



Dihydroxyacetone, a ketotriose

Stereoisomers

- In general a molecule with n chiral centers can have 2^n stereoisomers
- Hexoses: 2^4 =16 stereoisomers (8D; 8L)
- C-atom of **most distant chiral center from carbonyl C-atom** decides! (OH group in projection formula on the right D-isomer, on the left L-isomer)



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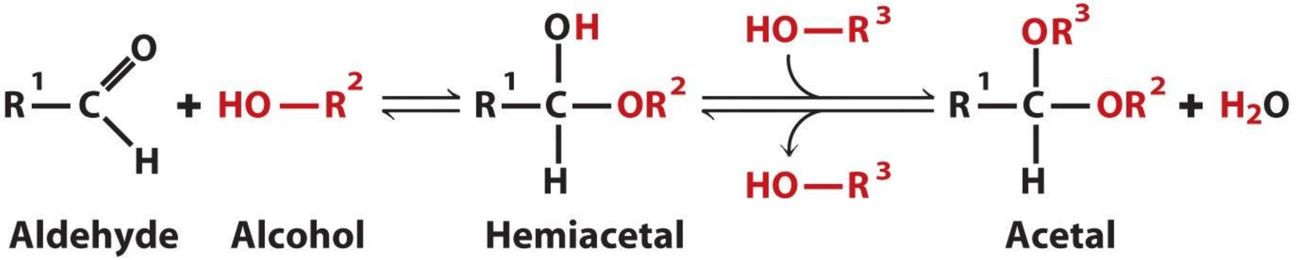
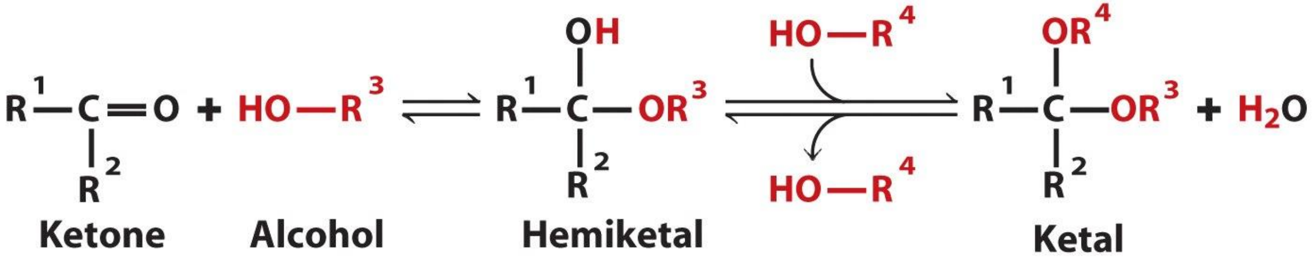
Cyclic structures

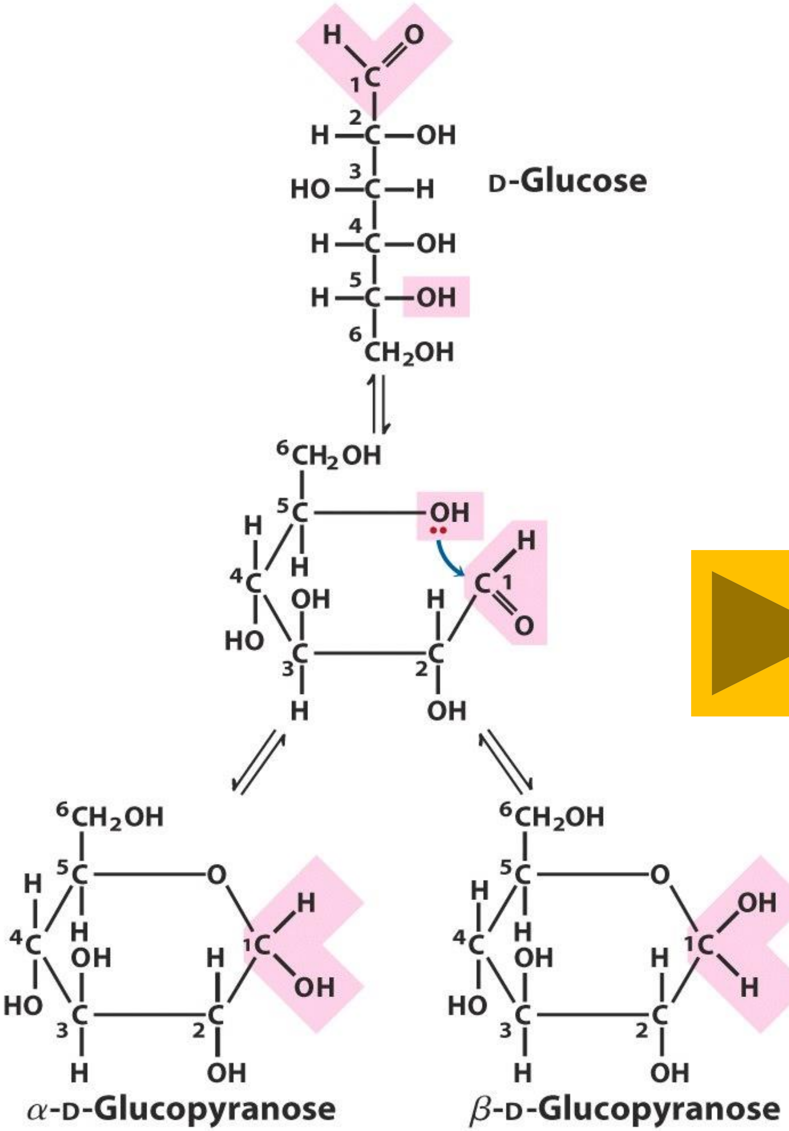
- Fromation of **hemiacetals** and **hemiketals**
  - Aldehyde and ketone carbons are electrophilic
  - Alcohol oxygen atom is a nucleophilic
- **Aldehyde or keton reacts with alcohol** to yield an hemiacetal or hemiketal creating a **new chiral center at the carbonyl carbon**.
- Substitution of **a second alcohol molecules** produces an **acetal** or ketal.
- When the **second alcohol is part of another sugar molecule**, the bond produced is a **gycosidic bond**.





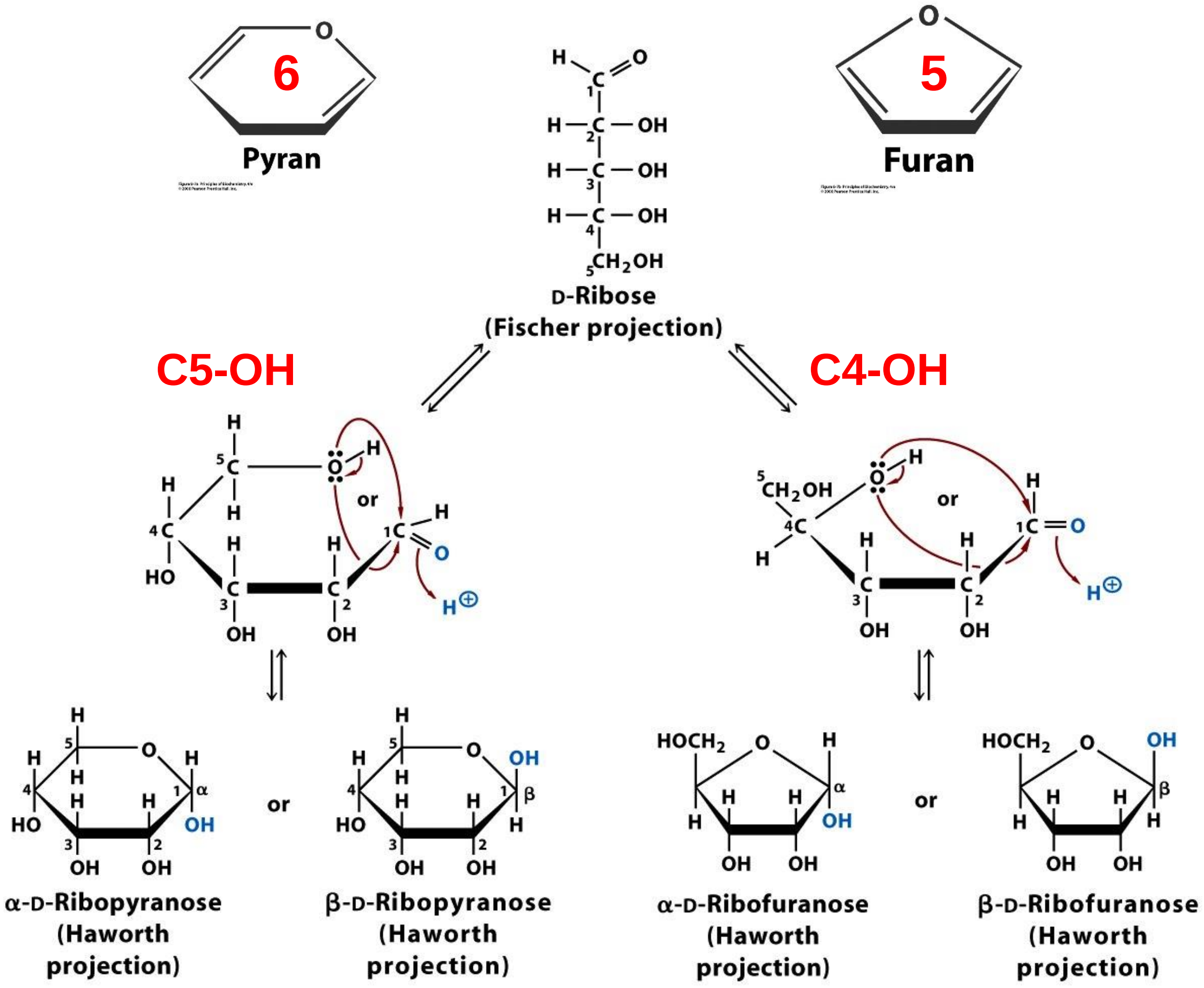
Cyclic structures

- **Carbonyl group** formed a **covalent bond** with the **oxygen of a hydroxyl group** along the chain (hemiketal, hemiacetal)
- D-Glucose: Aldehydic C1 reacts with hydroxyl at C5
- **Addition of new chiral C-atom** results in **two stereoisomers α and β**.



Cyclisierung von D-Ribose

- Can form either a **five-membered furanose ring** or a **six-membered pyranose ring**
- Reaction: formation of hemiacetals from the aldehyde group
- In each case, two enantiomeric forms, α or ß are possible



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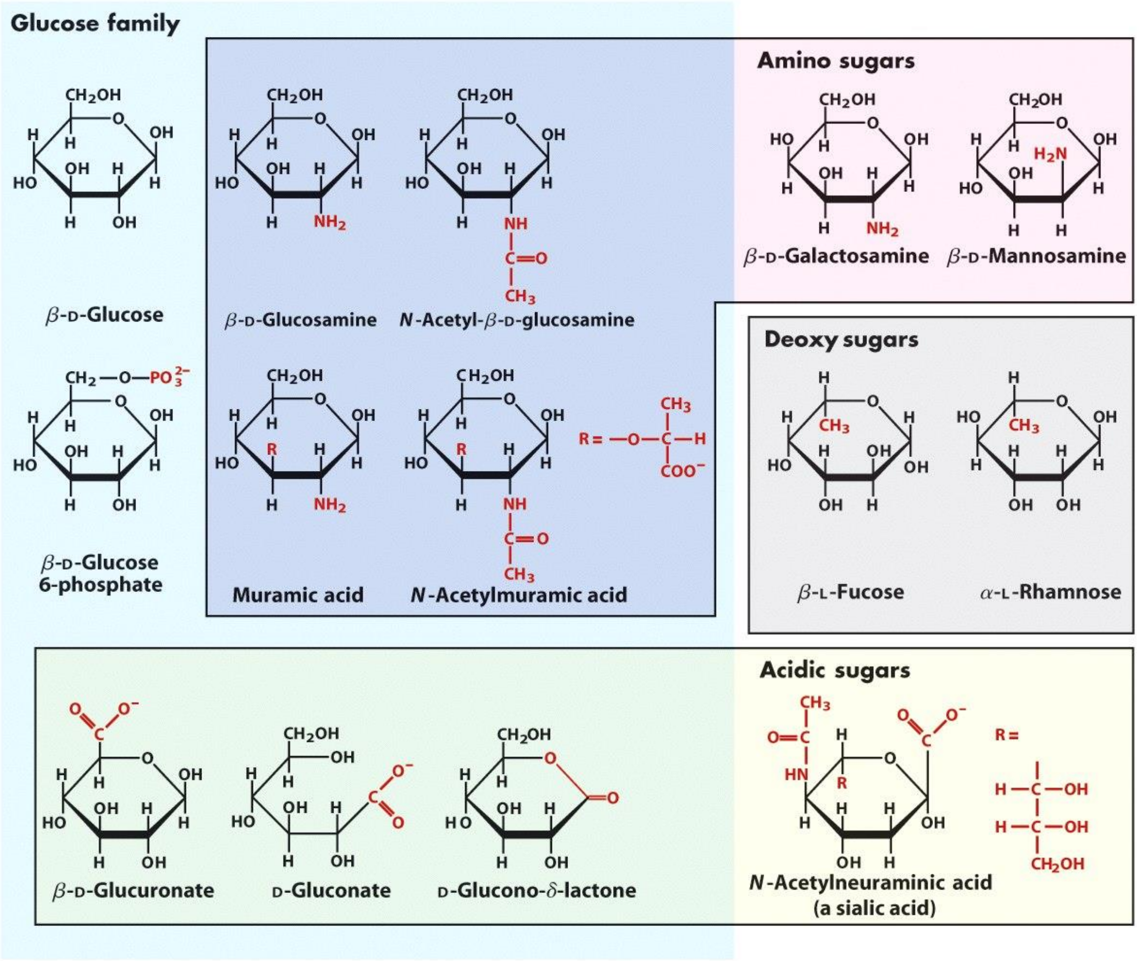
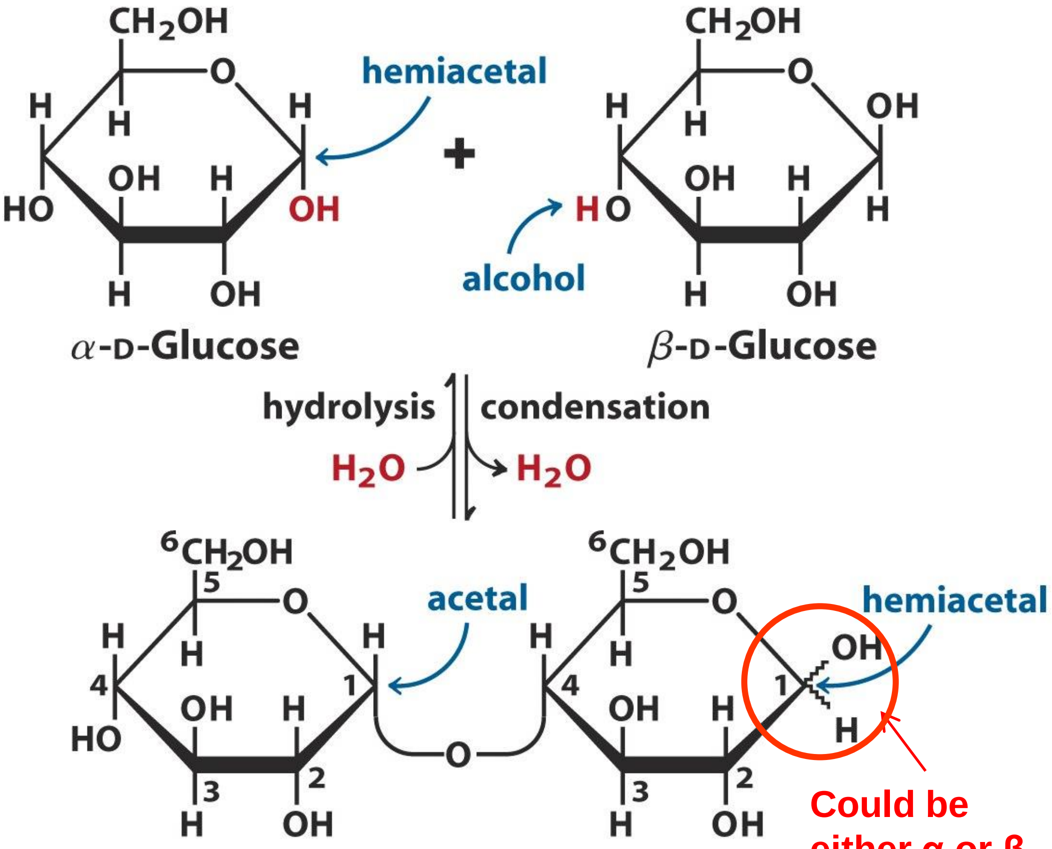
Hexose derivates

- Hydroxyl group in the parent compound is replaced by another substituent.
  - Aminogroup (e.g. glucosamine)
  - Amino group condensed with acetic acid (N-acetylglucosamine)
  - Lactic acid linked to C-4 atom N-acetylmuramic acid
  - Substitution of a hydrogen for hydroxyl group (e.g. fucose)
  - Oxidation of aldehyde group aldonic acids (e.g. gluconic acid)
  - C-6 oxidation uronic acid (e.g. glucuronic acid)
  - Sialic acid C-9 sugar



Glycosidic Bond Formation

- A **reducing end** of a carbohydrate is a carbon atom which can be in equilibrium with the open-chain aldehyde or keto form.
- If the joining of monomers takes place at such a carbon atom, the free hydroxy group of the pyranose or furanose form is exchanged with an OH-side chain of another sugar, yielding a **full acetal**.
- This prevents opening of the chain to the aldehyde or keto form and renders the modified residue **non-reducing**.



Could be either α or β

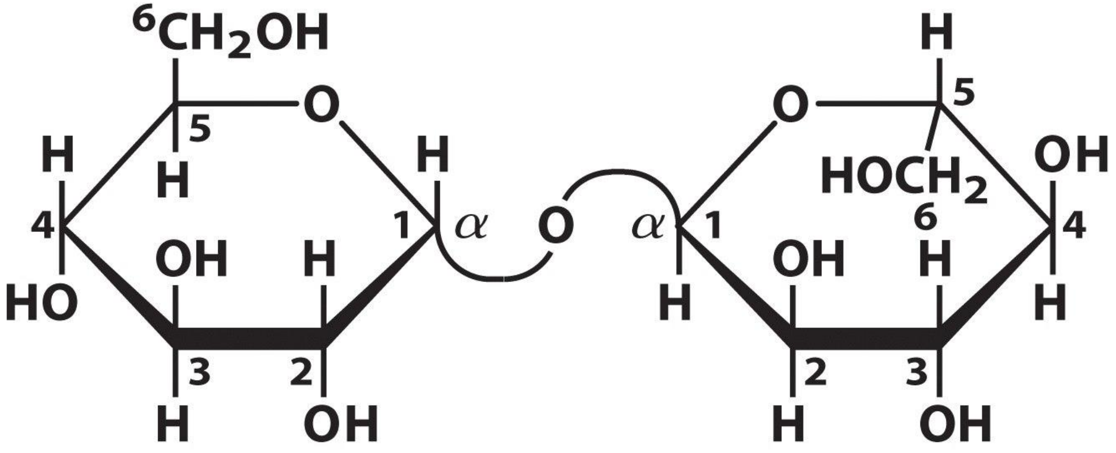
Maltose

α-D-glucopyranosyl-(1→4)-D-glucopyranose

Which is the reducing end?

Trehalose

- **Non reducing sugar**
- **Compatible solute „osmolyte“**; accumulated in high concentration th the cell without interfering with cell metabolism
- Stress response/carbon source



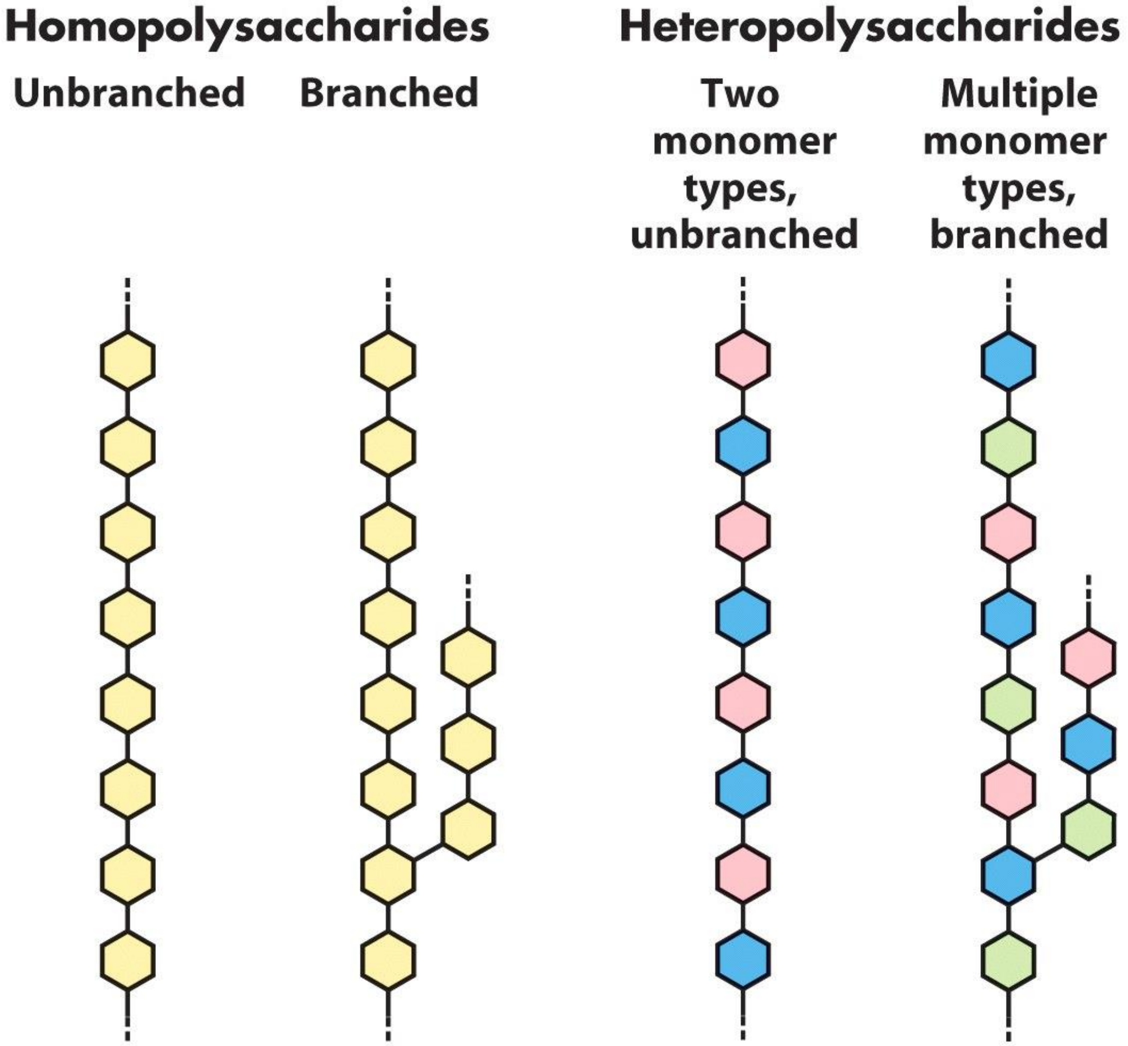
Trehalose

α-D-glucopyranosyl α-D-glucopyranoside

Glc(α1$\leftrightarrow$1α)Glc

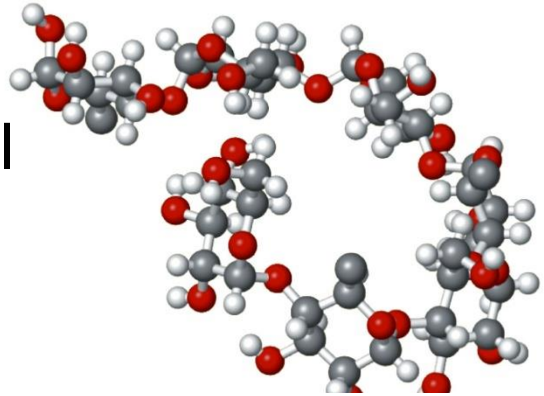
Homo- and Heteropolysaccharides

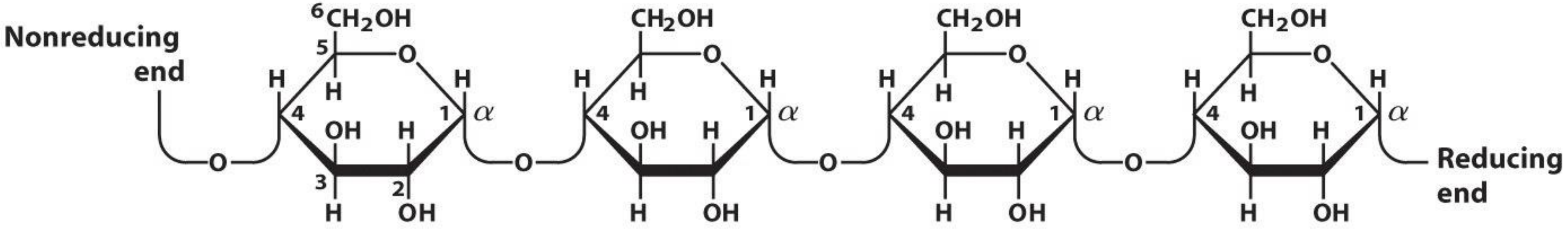
- Polysaccharides or glycans
- Serve as fuels or structural components (e.g. cell wall, animal exo-skeleton)



Starch: Amylose

- Two types of glucose polymers **amylose** & **amylopectin**
- . Amylose is a linear polymer.
  - Glucose residues linked by α(1-->4)-D-glucosidic bonds.
  - Amylose can assume a left-handed helical conformation, which is hydrated on the inside as well as on the outer surface.

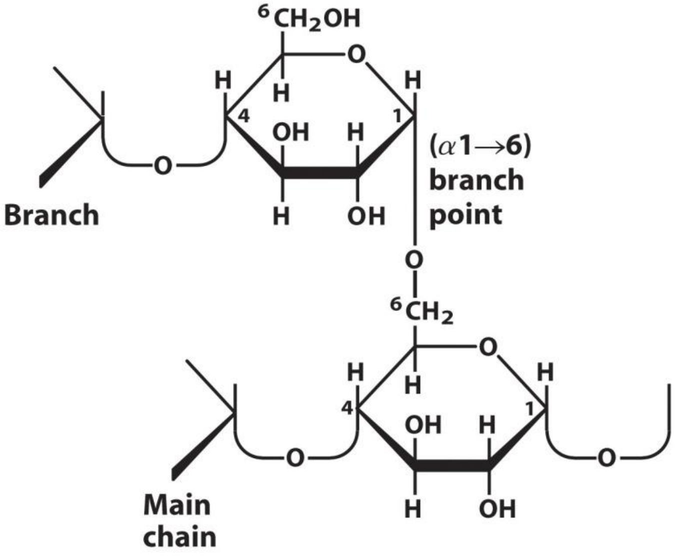


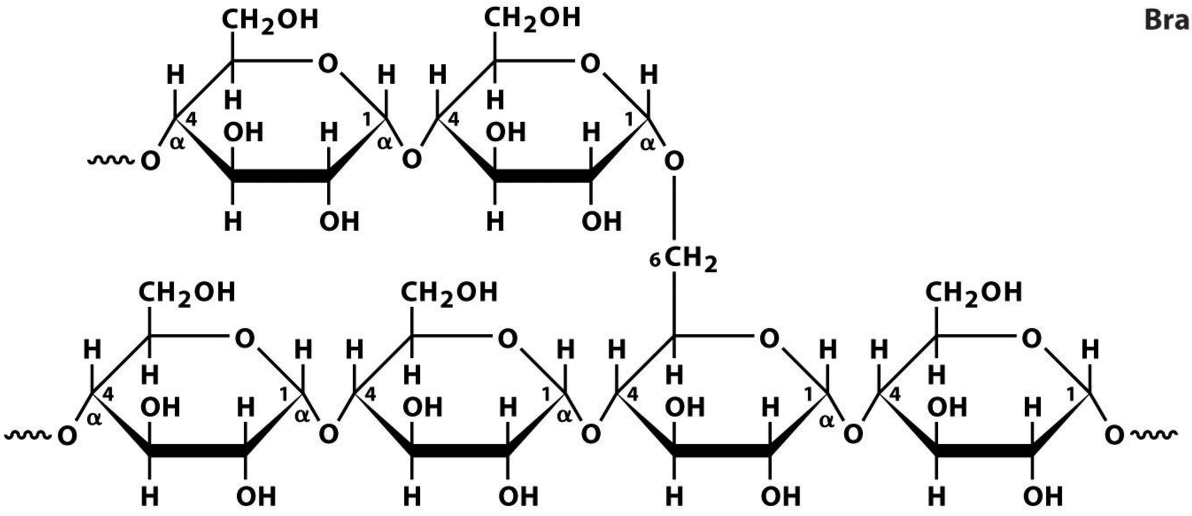


amylose

Starch: Amylopectin

- Amylopectin is a **branched** polymer.
  - The linear glucose residues of the main chain and the side chains of amylopectin are linked by **α(1-->4)-**D-glucosidic bonds
  - **side chains** are linked to the main chain by **α(1-->6)-**D-glucosidic bonds (every 24-30 residues).
  - Size: up to 10^6





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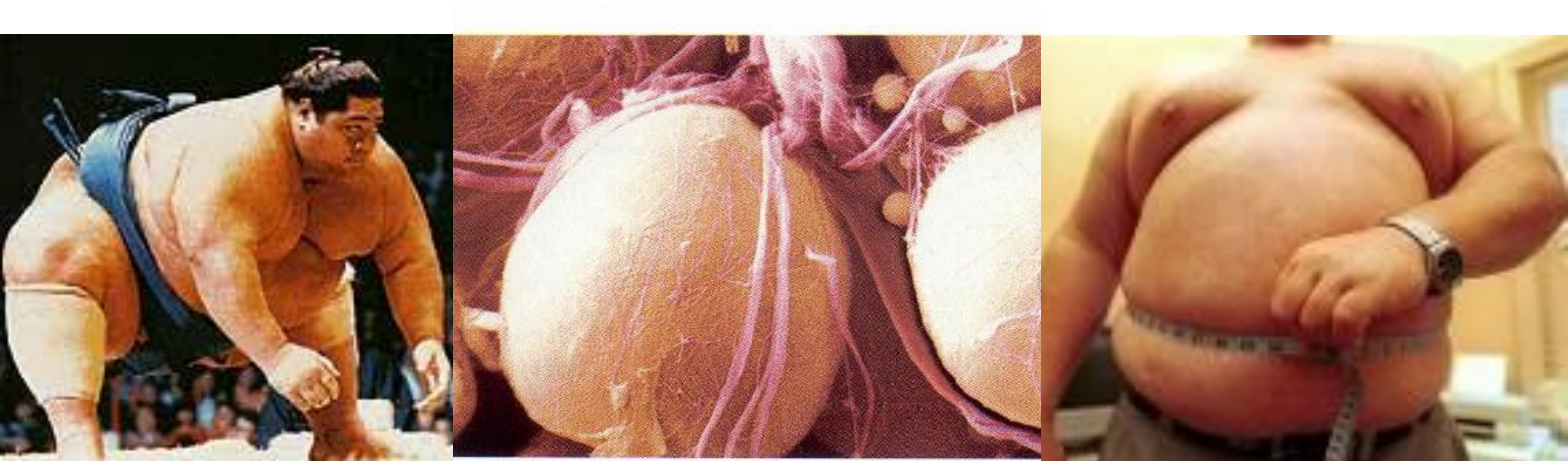
Biomolecules

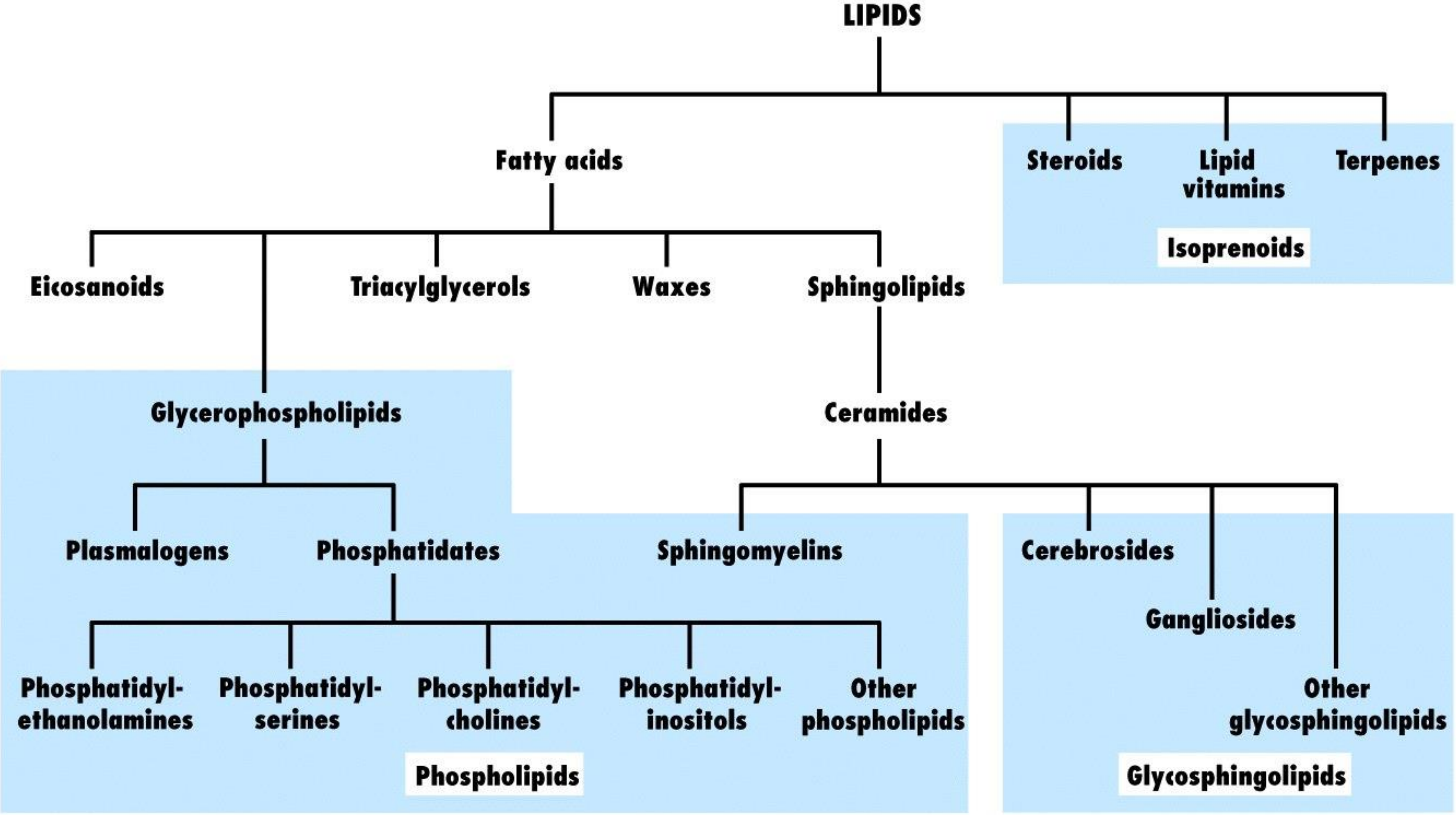
Lipids



Lipids

- **Lipids** are **amphipathic**—they have both hydrophobic (**nonpolar**) and hydrophilic (**polar**) properties.
- Biological lipids are a chemically **diverse** group of compounds
- Common and defining feature - **insolubility in water**
- ***Glycerol bonded to fatty acids and other groups such as phosphate by an ester or ether linkage***

Major Classes of Lipids



LIPIDS

Fatty acids

Steroids

Lipid vitamins

Terpenes

Isoprenoids

Eicosanoids

Triacylglycerols

Waxes

Sphingolipids

Glycerophospholipids

Ceramides

Plasmalogens

Phosphatidates

Sphingomyelins

Cerebrosides

Gangliosides

Phosphatidyl-ethanolamines

Phosphatidyl-serines

Phosphatidyl-cholines

Phosphatidyl-inositols

Other phospholipids

Other glycosphingolipids

Phospholipids

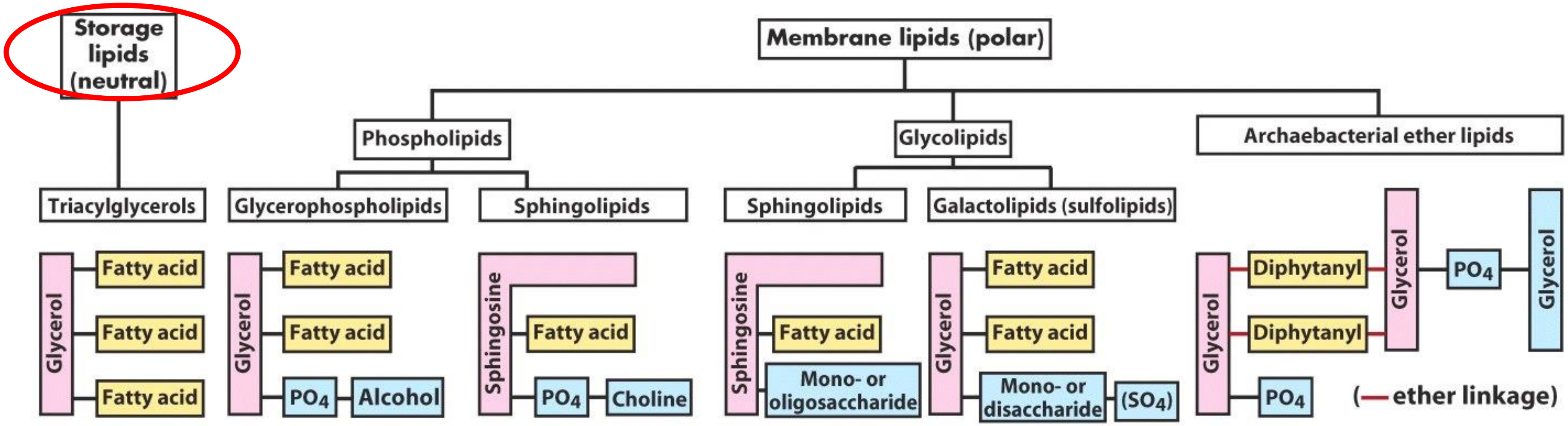
Glycosphingolipids

Figure 9-1 Principles of Biochemistry, 4/e

Major Classes of Lipids

- Structural relationships of the major classes of lipids.
- **Fatty acids** are the simplest lipids. Many other types of lipids either contain or are derived from fatty acids.
- **Glycerophospholipids** and **sphingomyelins** contain phosphate and are classified as **phospholipids**.
- **Cerebrosides** and **gangliosides** contain sphingosine and carbohydrate and are classified as **glycosphingolipids**.
- **Steroids**, **lipid vitamins**, and **terpenes** are called **isoprenoids** because they are related to the five-carbon molecule **isoprene rather than to fatty acids**.

Major Classes of Lipids



Storage Lipids

- Simple lipids (triglycerides)

Simple lipids (triglycerides):
Fatty acids linked to glycerol by ester linkage

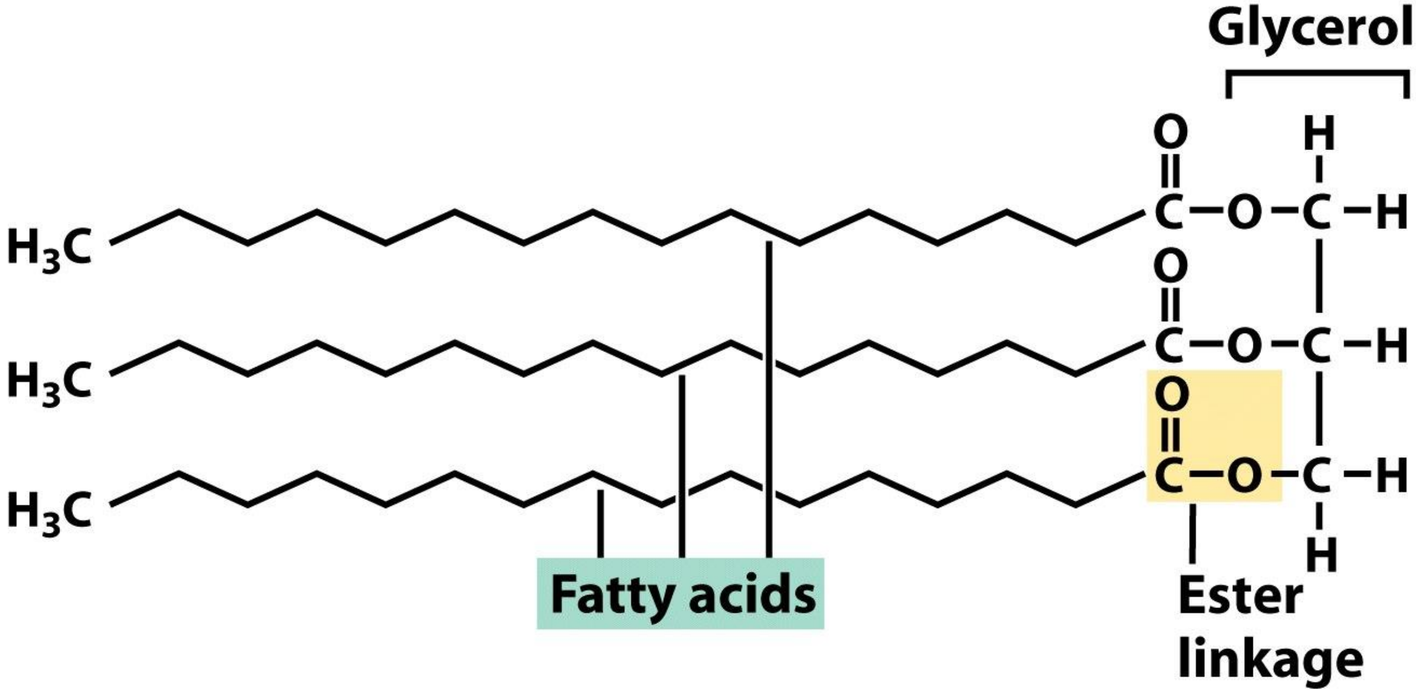


Figure 3-7 part 2 Brock Biology of Microorganisms 11/e
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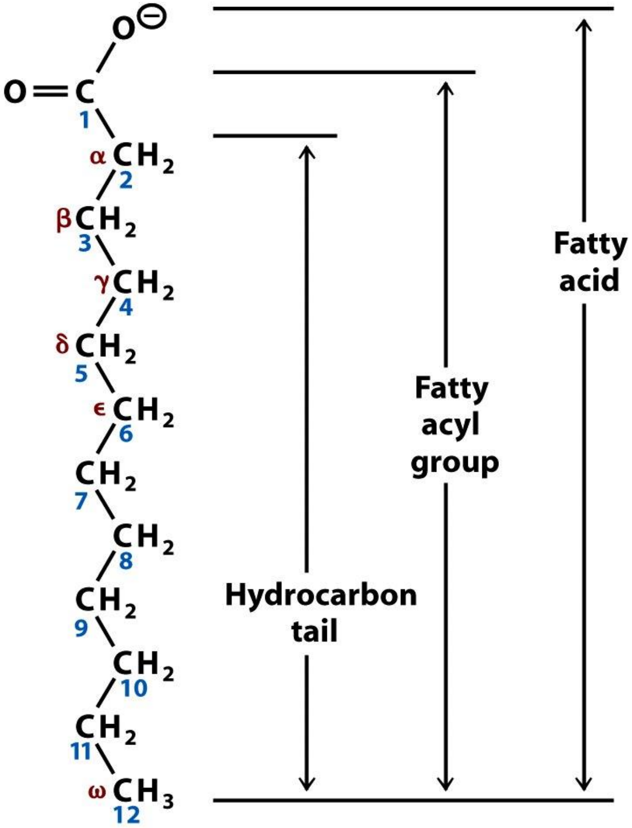
Chemical structures of fatty acids

- Fatty acids consist of a long **hydrocarbon tail** terminating with a **carboxyl group**.
- Since the pKa of the carboxyl group is approximately 4.5 to 5.0, fatty acids are **anionic at physiological pH**.
- In IUPAC nomenclature, carbons are **numbered beginning with the carboxyl carbon**. In common nomenclature, the carbon atom adjacent to the carboxyl carbon is designated α, and the remaining carbons are lettered β, γ, δ, and so on. The carbon atom farthest from the carboxyl carbon is designated the **ω (omega) carbon**, whatever the length of the tail.
- The fatty acid shown, **laurate** (or dodecanoate), has **12 carbon atoms** and contains **no carbon–carbon double bonds**.



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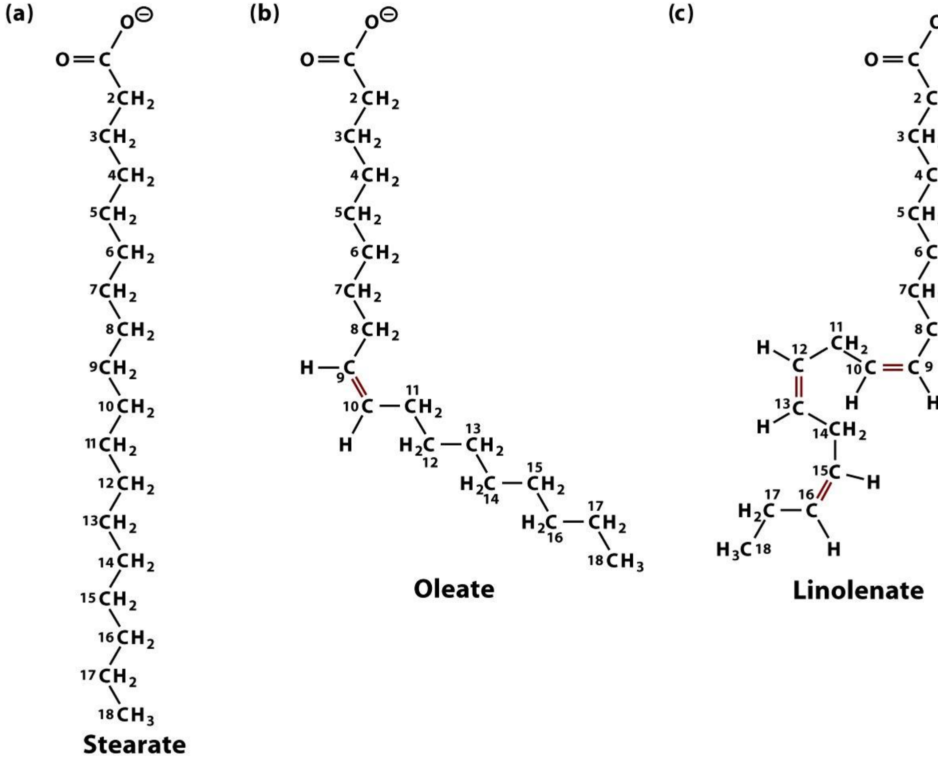
Chemical structures of three C_{18} fatty acids

- (a) **Stearate** (octadecanoate), a **saturated fatty acid**.
- (b) **Oleate** (*cis*-Δ^9-octadecenoate) a **monounsaturated fatty acid**.
- c) **Linolenate** (all-*cis*-$\Delta^{9,12,15}$-octadecatrienoate), a **polyunsaturated fatty acid**. The cis double bonds produce kinks in the tails of the unsaturated fatty acids. Linolenate is a very flexible molecule, and can assume a variety of conformations.

Omega-3-fatty acid can not be synthesized by human must be obtained in the diet.



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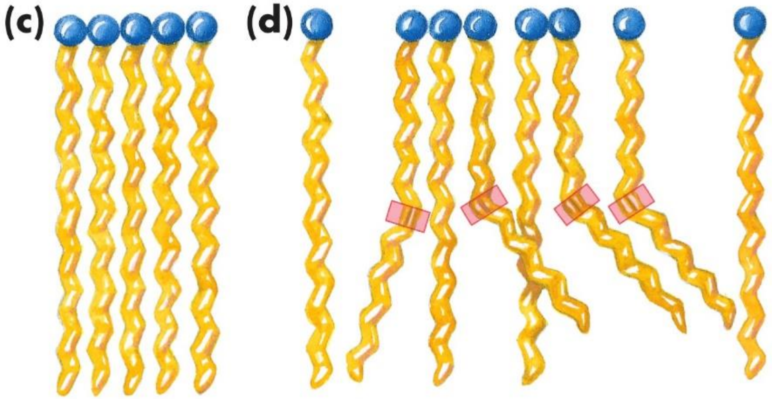
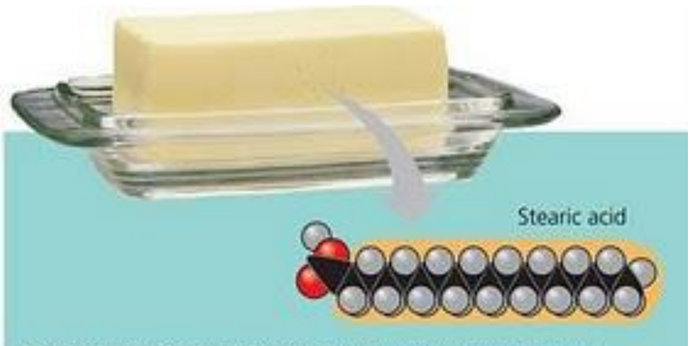
Examples of Fatty Acids



Saturated fatty acids

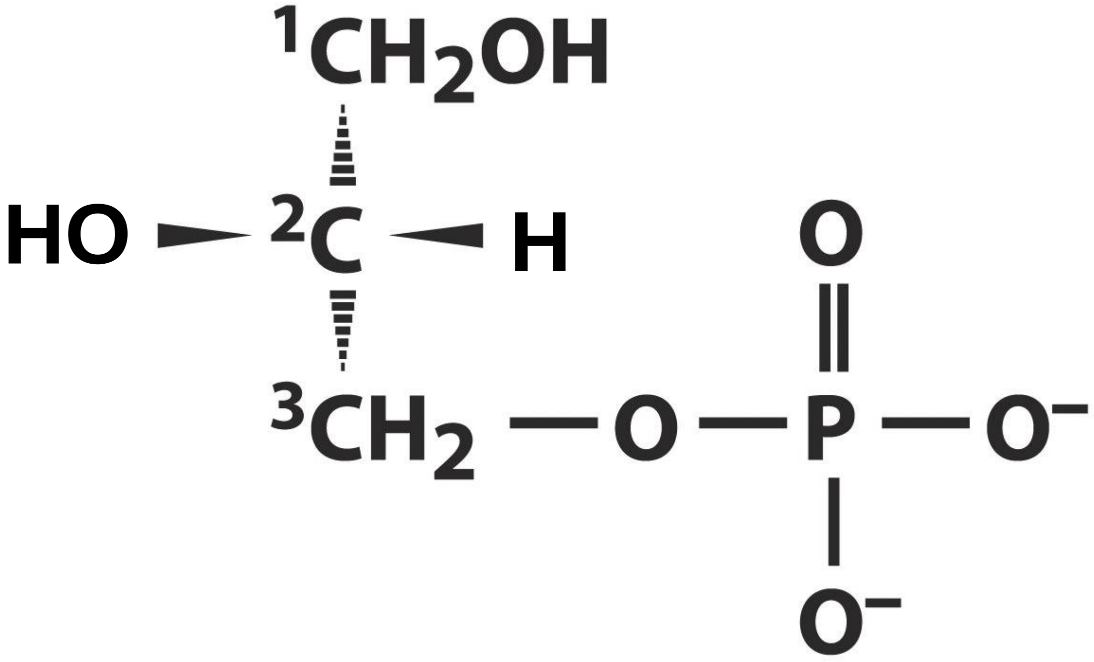
Mixture of saturated and unsaturated fatty acids



(a) Saturated fat and fatty acid. At room temperature, the molecules of a saturated fat such as this butter are packed closely together, forming a solid.

(b) Unsaturated fat and fatty acid. At room temperature, the molecules of an unsaturated fat such as this olive oil cannot pack together closely enough to solidify because of the kinks in their fatty acid tails.

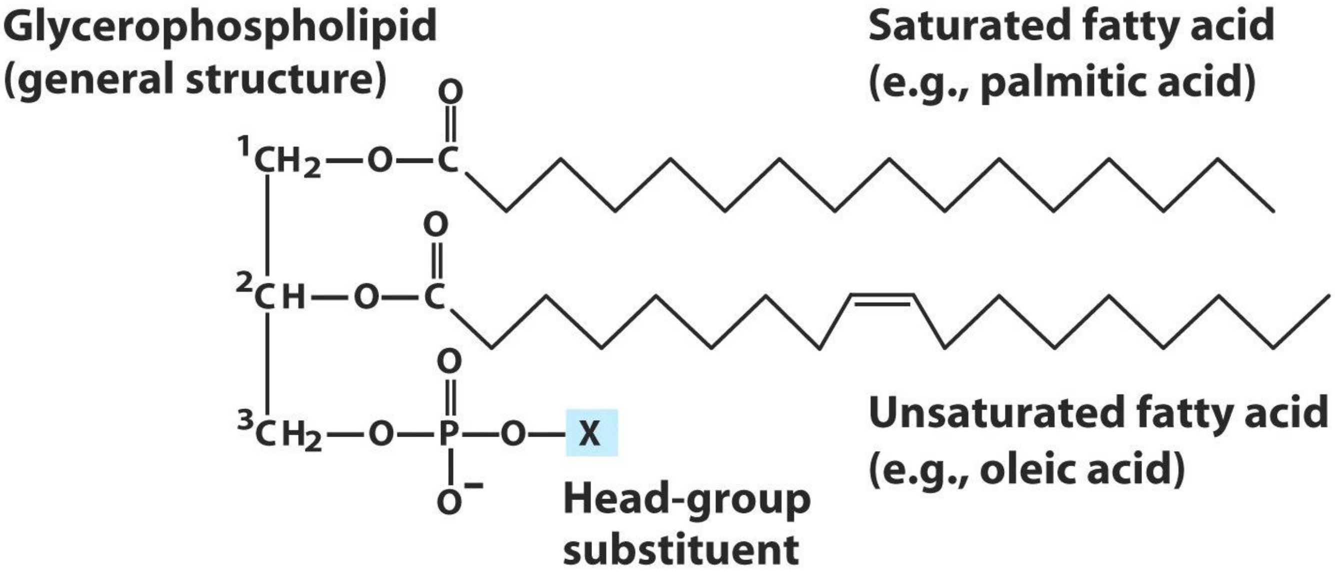
The Backbone of Phospholipids

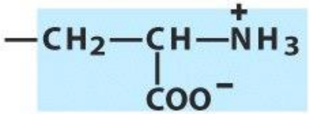
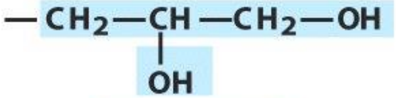
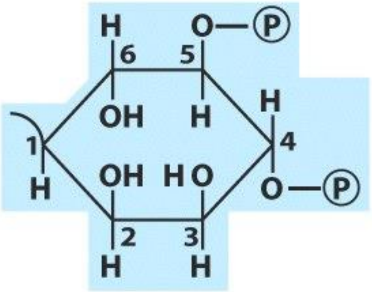
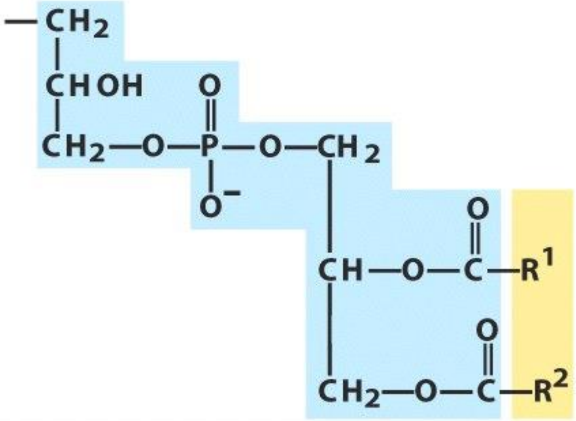


L-Glycerol 3-phosphate
(*sn*-glycerol 3-phosphate)

Glycerophospholipids

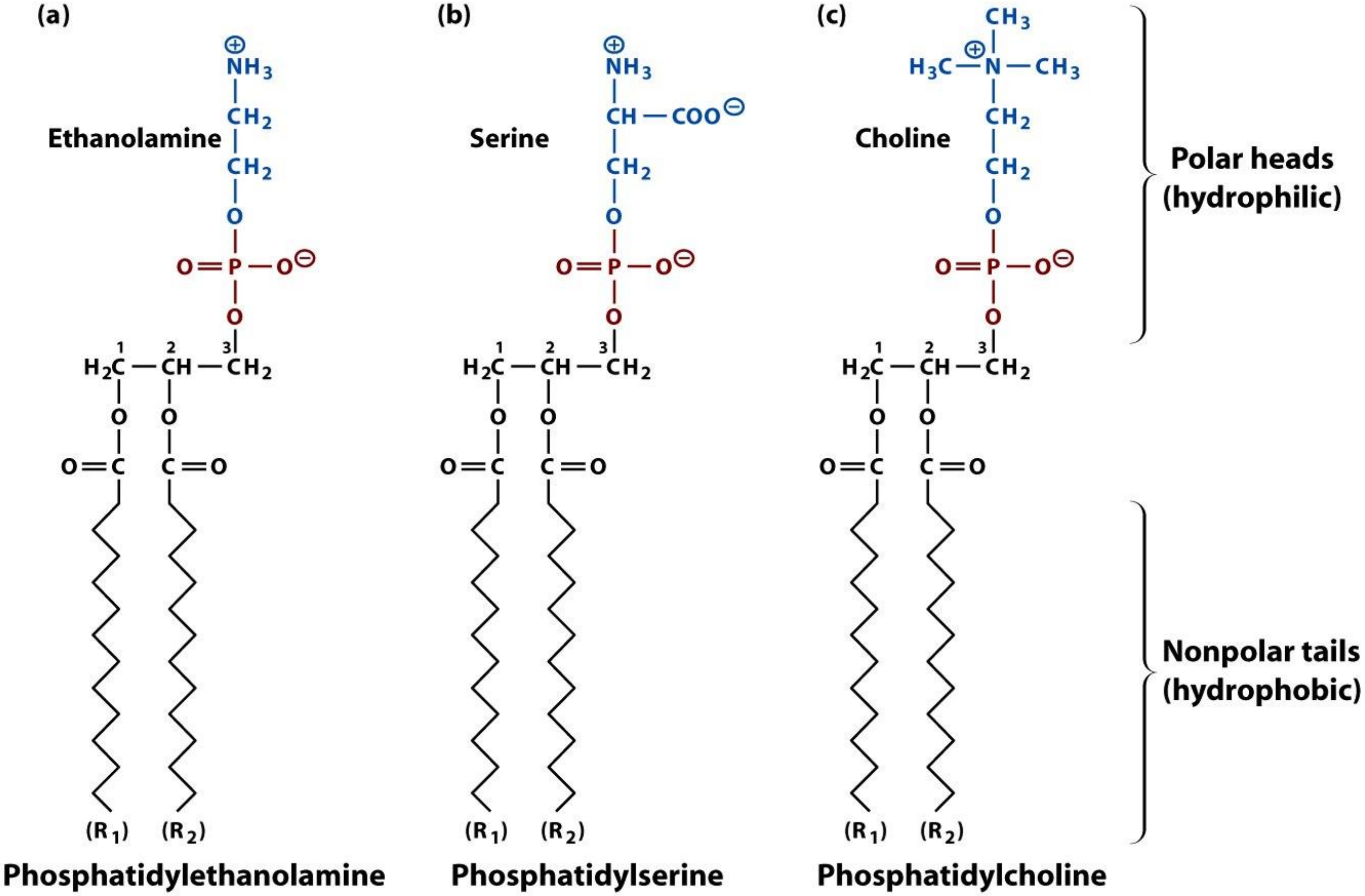
- **Membrane lipids; two fatty acids** are linked to first and second carbon of **glycerol** via **ester linkage;** a **highly polar or charged group** is attached to carbon three via **phosphodiester linkage.**
- **Common glycerophospholipids** are **diacylglycerols** linked to **head-group alcohols** through **a phosphodiester** bond.
- **Phosphatidic acid (X=H)**, a phosphomonoester, is the parent compound.
- Derivatives (x), named for the headgroup alcohol with prefix „phosphatidyl-x“



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	**Phosphatidylglycerol**		**− 2**

Structural Lipids in Membranes

- Functional groups derived from **esterified alcohols** are shown in **blue**.
- Since each of these lipids can contain many combinations of fatty acyl groups, the **general name refers to a family of compounds**, not to a single molecule.



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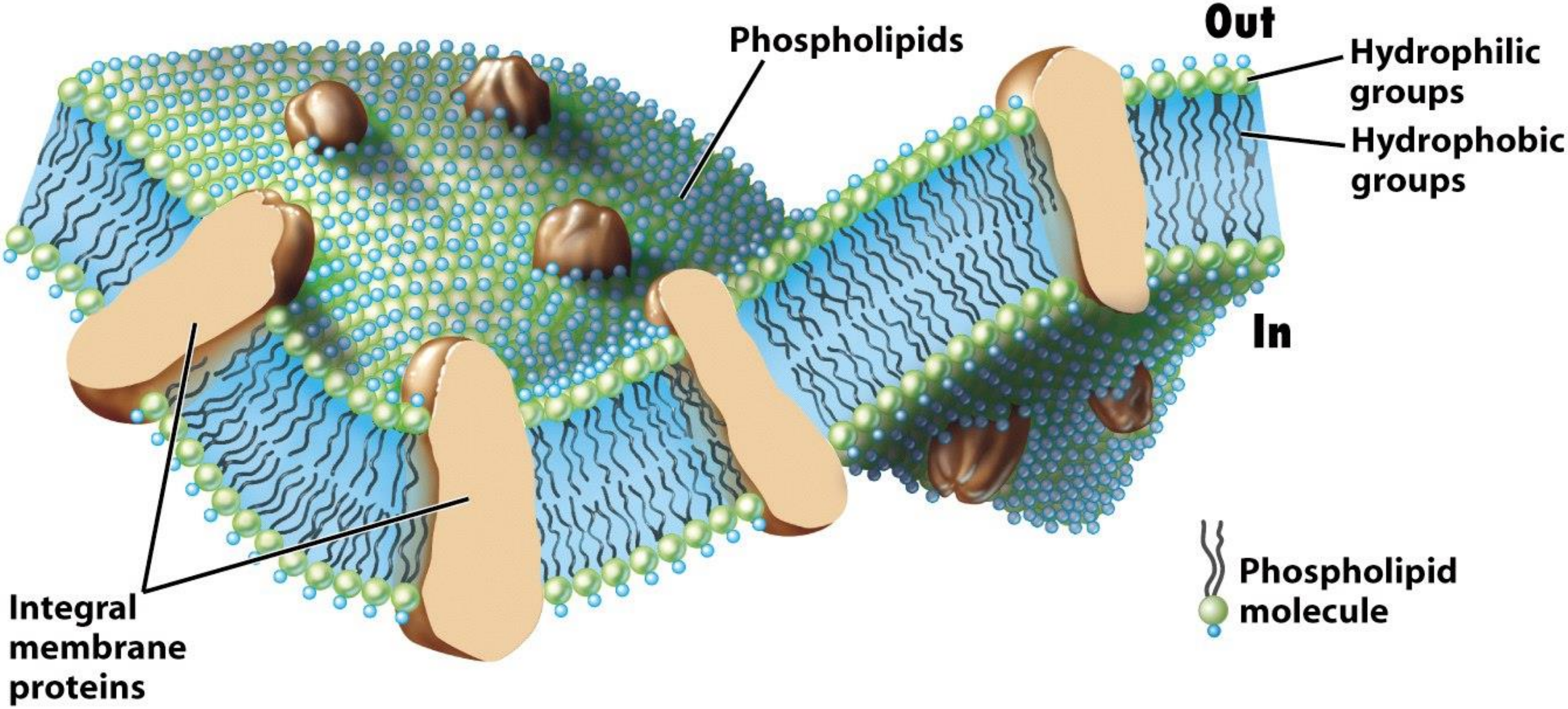
Membranes

- *E. coli* phosphatidylethanolamine & phosphatidylcholine



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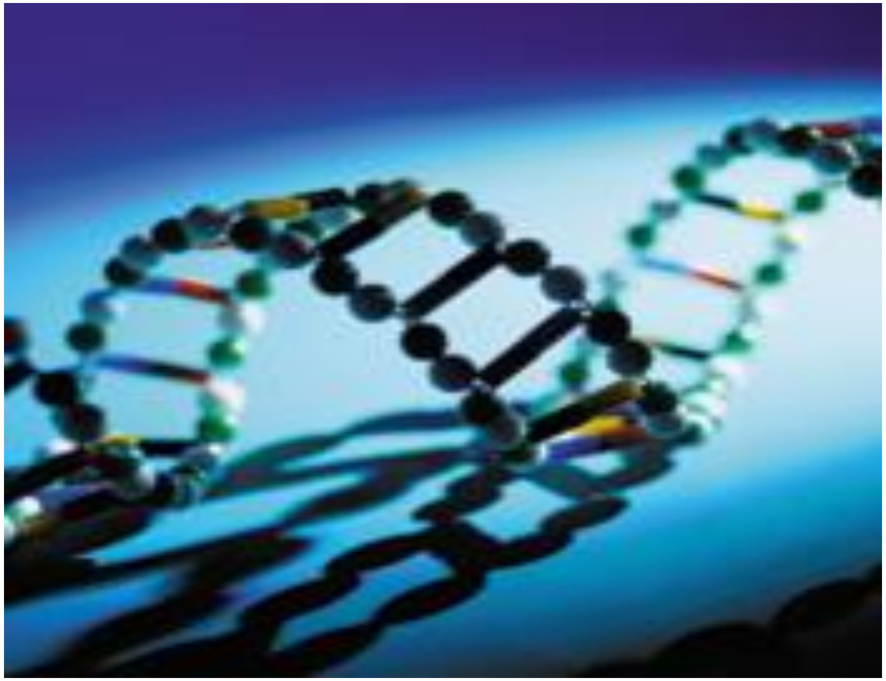
Nucleotides & Nucleic Acids



Nucleotides

- Three building blocks:
  - Nitrogen-containing base
  - Pentose
  - At least one phosphate

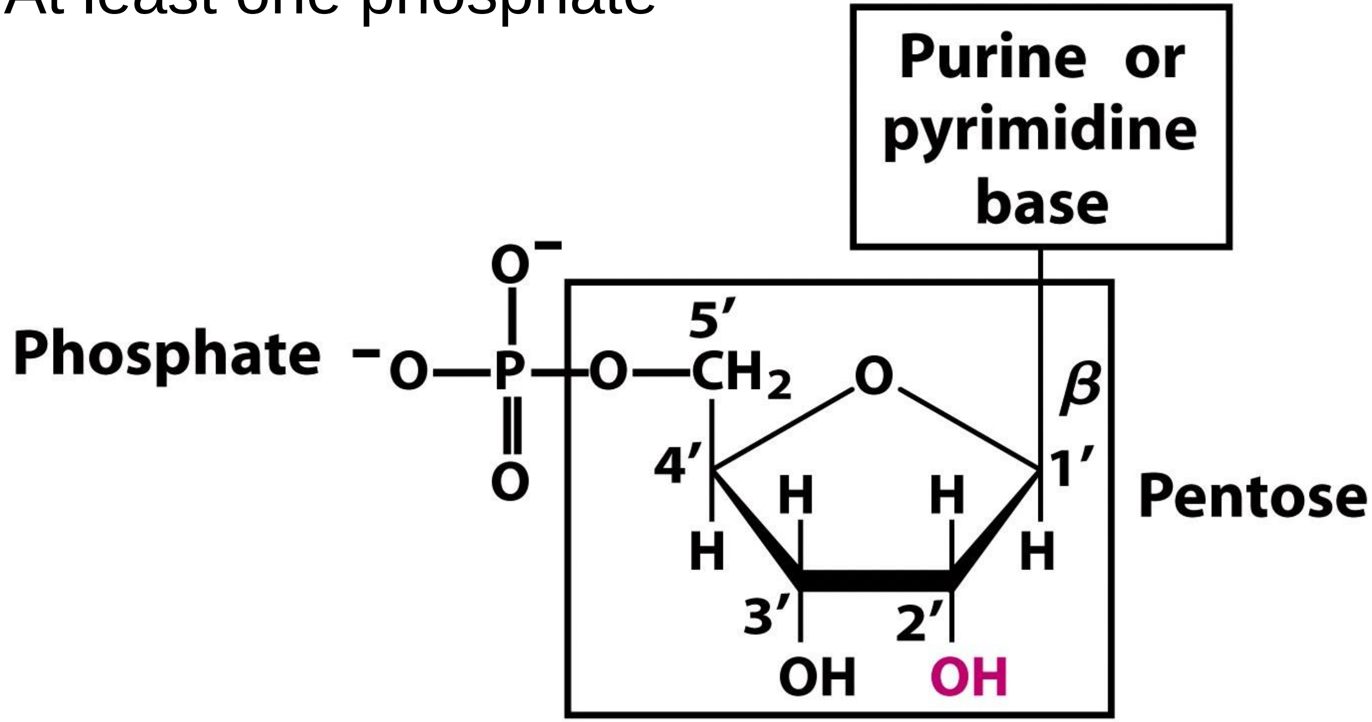


Figure 8-1a
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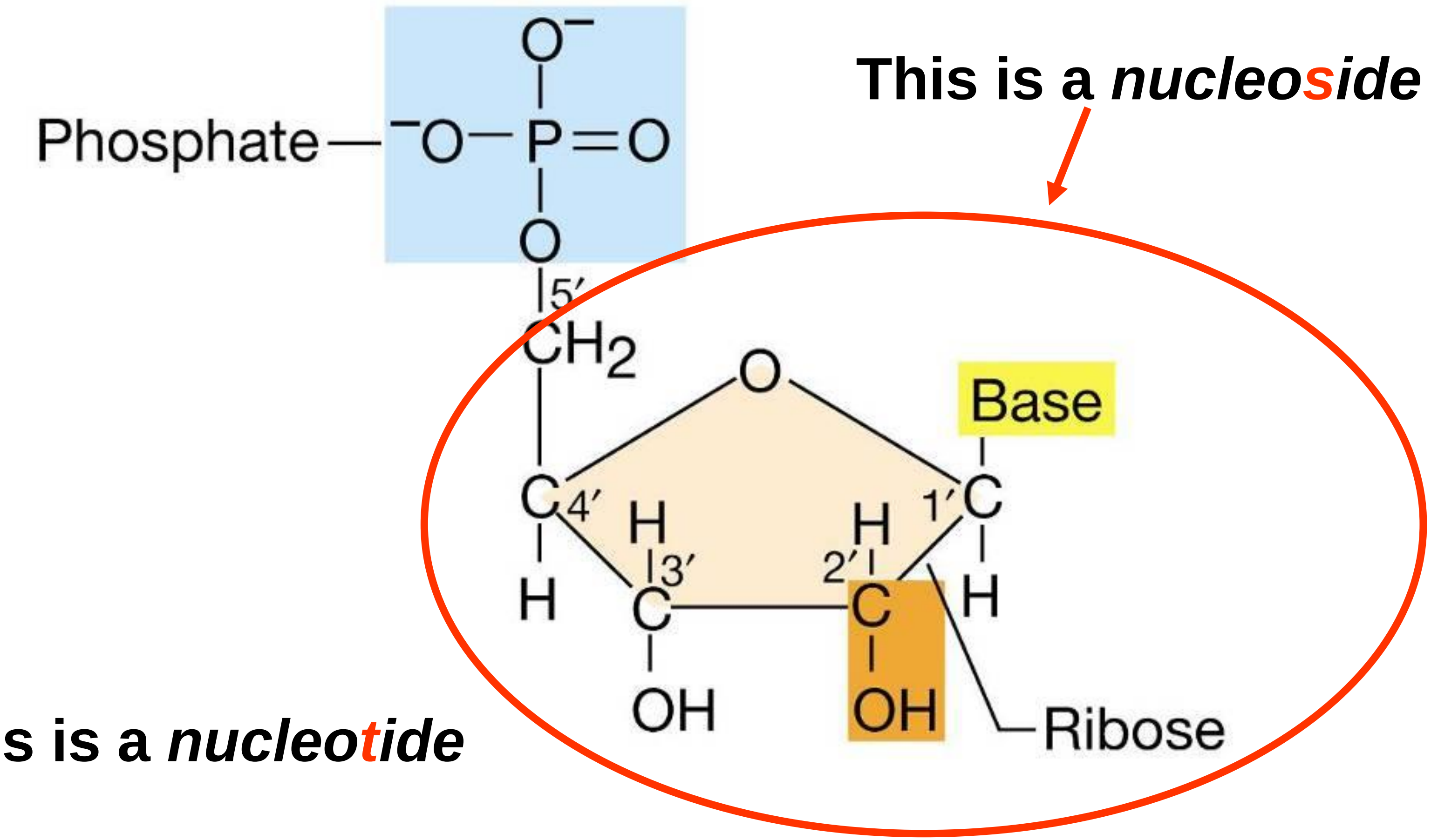
Nucleosides & Nucleotides

- **Nucleotides** (sugar, base and phophate)
- **Nucleoside** (sugar and base, without phosphate)



This is a *nucleoside*

This is a *nucleotide*

Pyrimidine and Purine Bases

- The nitrogenous bases are derivatives of two parent compounds:
  - Glycoside linkage between carbon atom (C1) and nitrogen atom (N1, pyrimidine base, N9 purine base)

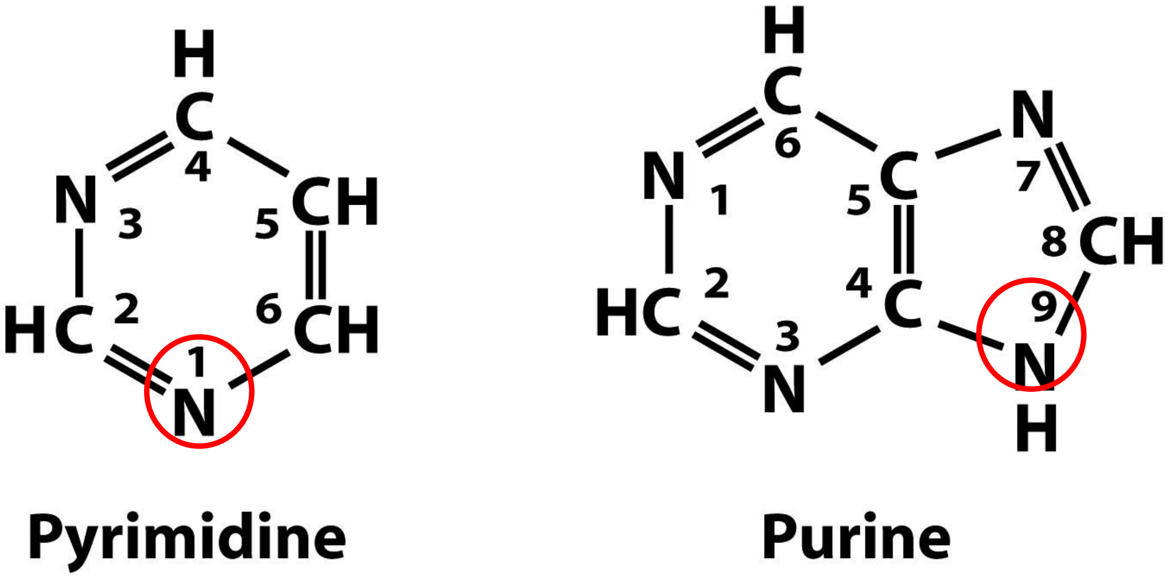
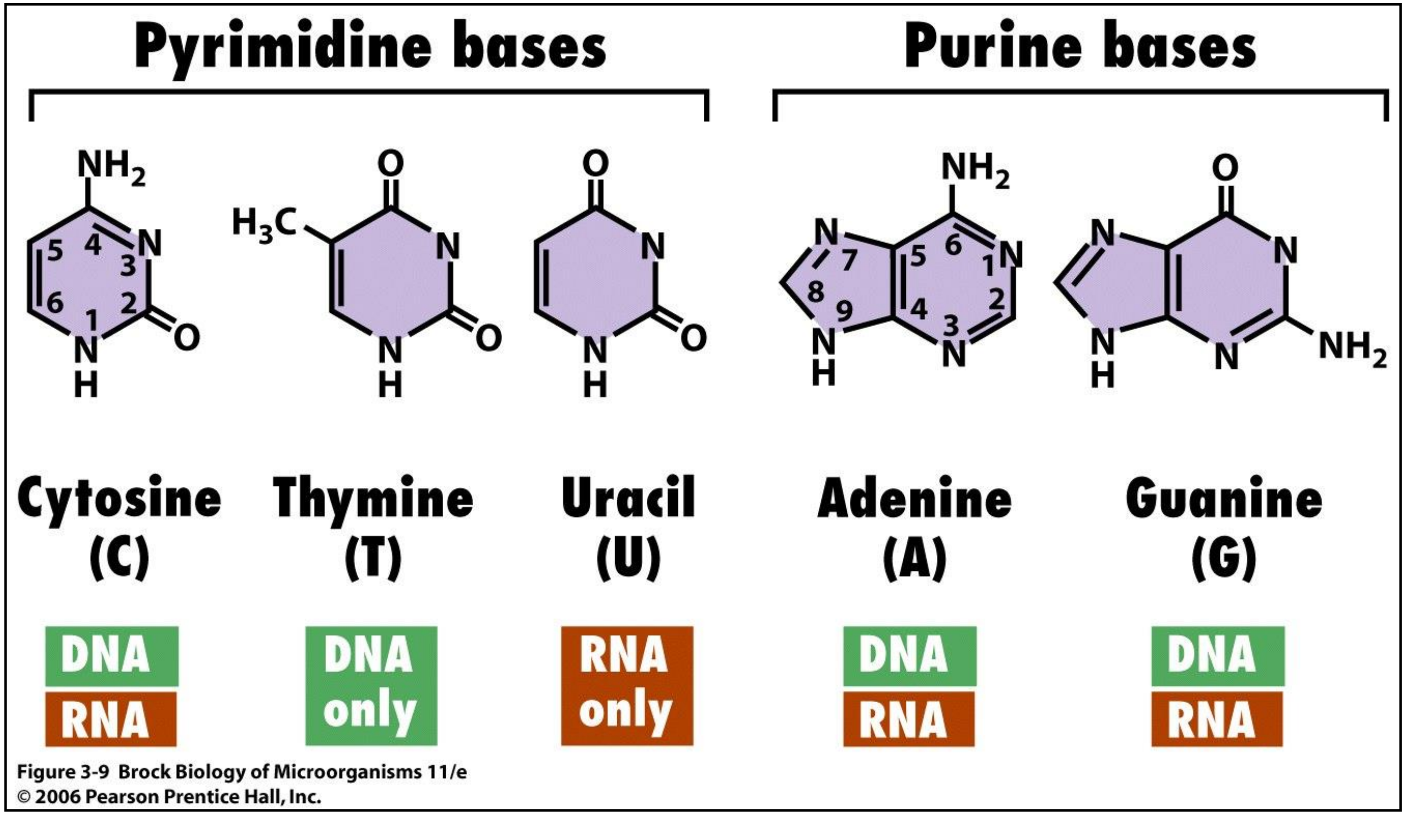


Figure 8-1b
Lehninger Principles of Biochemistry, Fifth Edition

Pyrimidine and Purine Bases

- Major purine and pyrimidine bases of nucleic acids.



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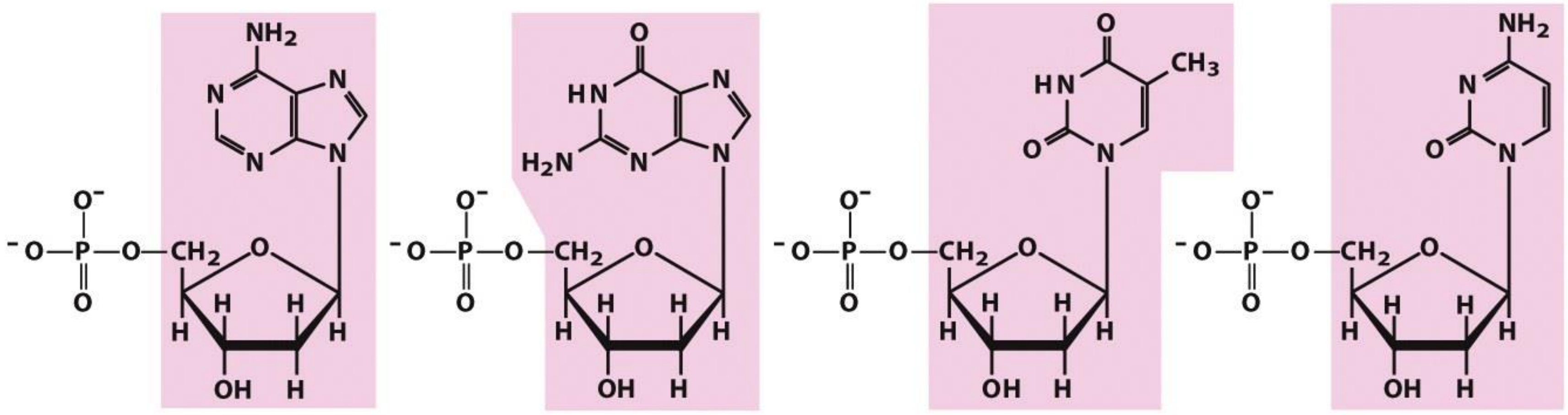
Deoxyribonucleotides of Nucleic Acid



Nucleotide:	**Deoxyadenylate (deoxyadenosine 5′-monophosphate)**	**Deoxyguanylate (deoxyguanosine 5′-monophosphate)**	**Deoxythymidylate (deoxythymidine 5′-monophosphate)**	**Deoxycytidylate (deoxycytidine 5′-monophosphate)**
Symbols:	**A, dA, dAMP**	**G, dG, dGMP**	**T, dT, dTMP**	**C, dC, dCMP**
Nucleoside:	**Deoxyadenosine**	**Deoxyguanosine**	**Deoxythymidine**	**Deoxycytidine**

Deoxyribonucleotides

Figure 8-4a
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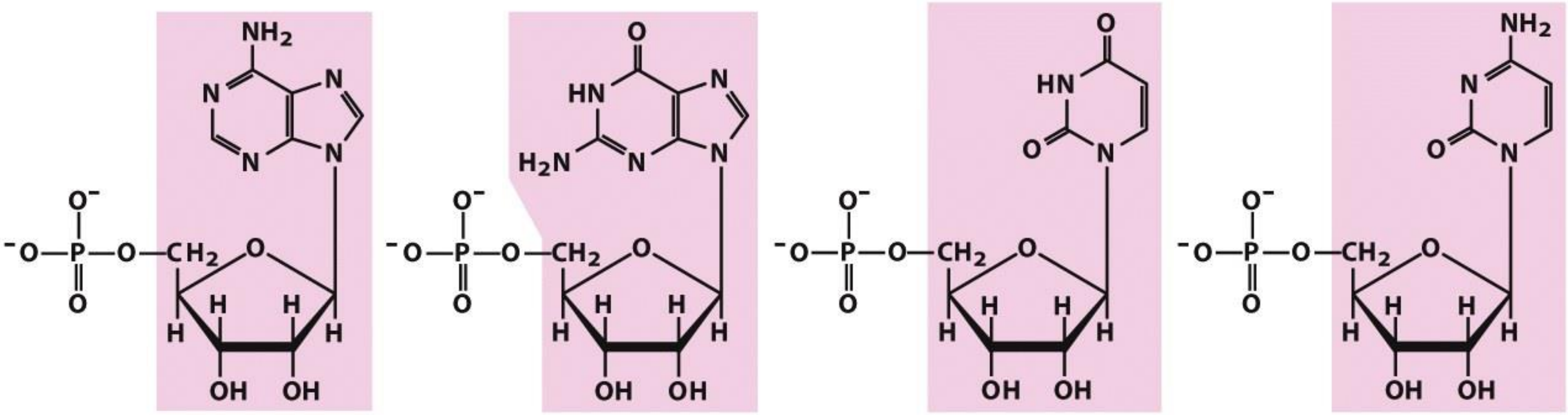
Ribonucleotides of Nucleic Acid



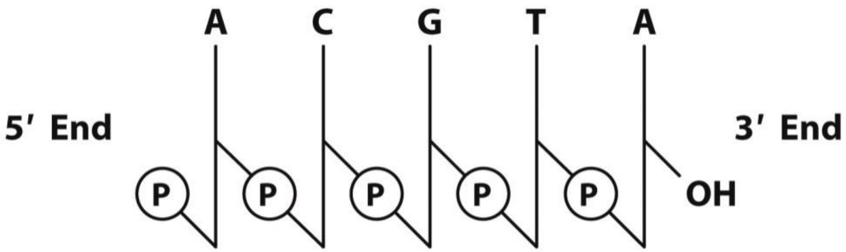
Nucleotide:	Adenylate (adenosine 5′-monophosphate)	Guanylate (guanosine 5′-monophosphate)	Uridylate (uridine 5′-monophosphate)	Cytidylate (cytidine 5′-monophosphate)
Symbols:	A, AMP	G, GMP	U, UMP	C, CMP
Nucleoside:	Adenosine	Guanosine	Uridine	Cytidine

Ribonucleotides

Figure 8-4b
Lehninger Principles of Biochemistry, Fifth Edition

Phosphodiester linkages in the covalent backbone of DNA and RNA

- The **phosphodiester bonds** (one of which is shaded in the DNA) link successive nucleotide units.
- The backbone of alternating pentose and phosphate groups in both types of nucleic acid is **highly polar**.
- The 5′ end of the macromolecule lacks a nucleotide at the 5′ position, and the 3′ end lacks a nucleotide at the 3′ position.



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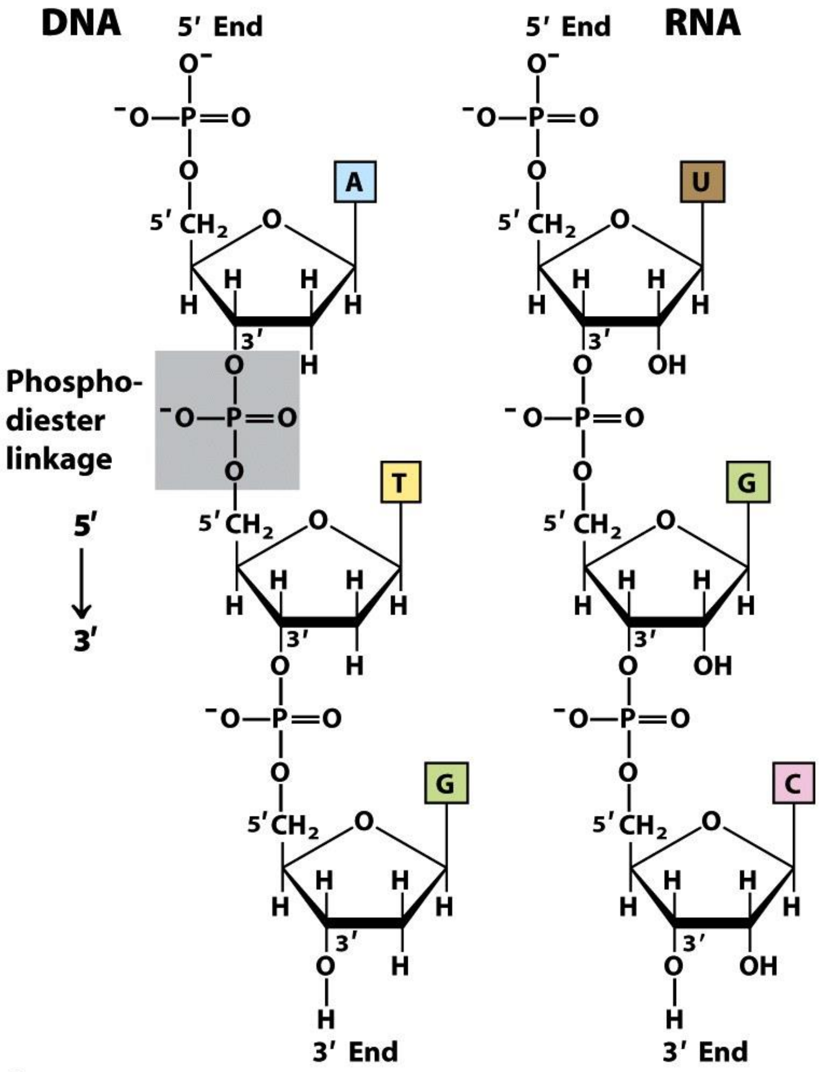

Figure 8-7
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Base Pairing

- Hydrogen-bonding patterns in the base pairs defined by Watson and Crick

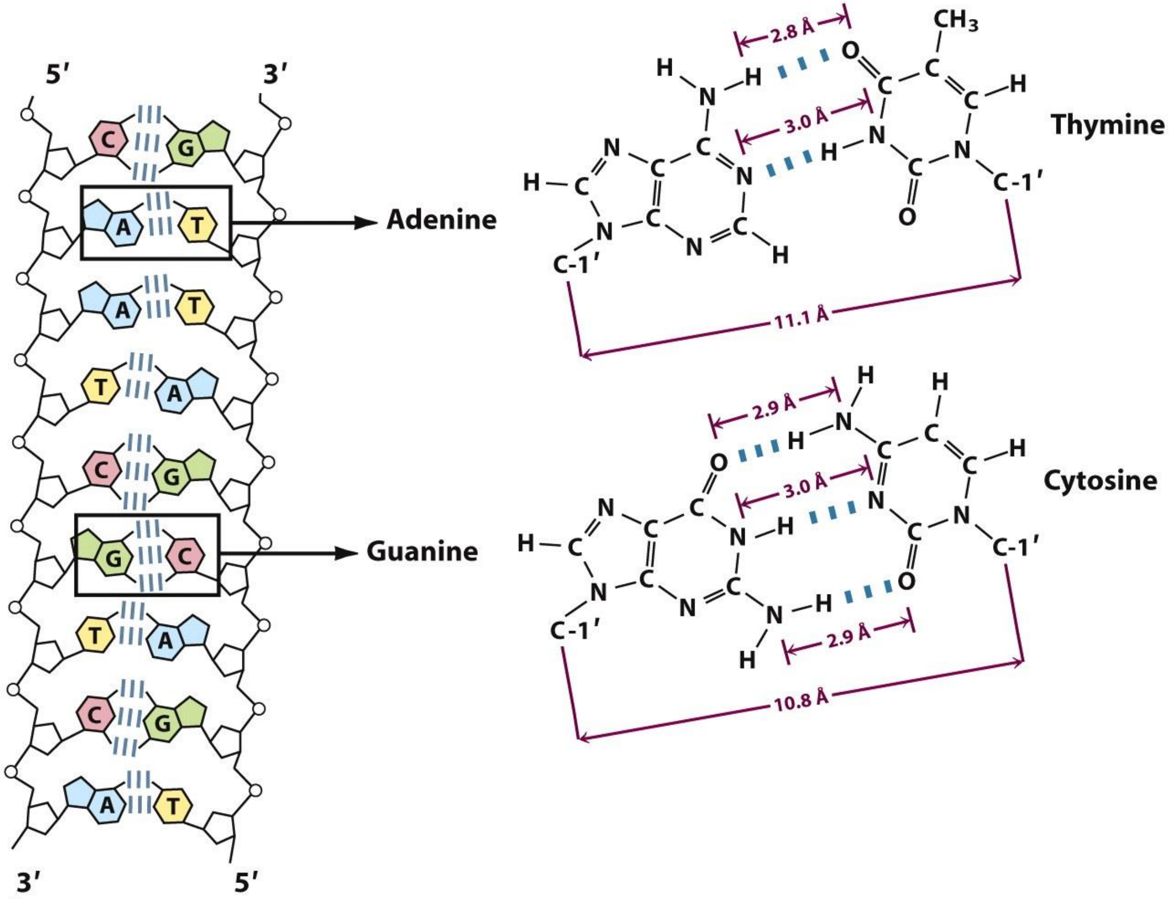

Figure 8-11
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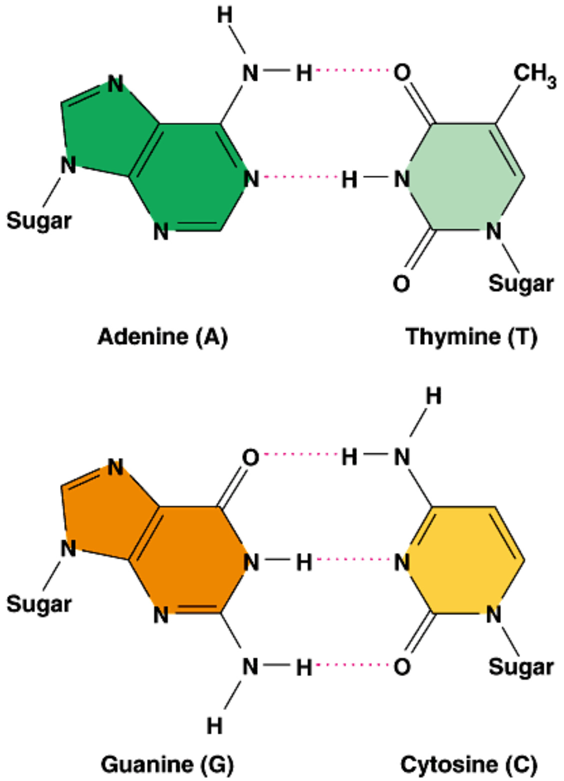
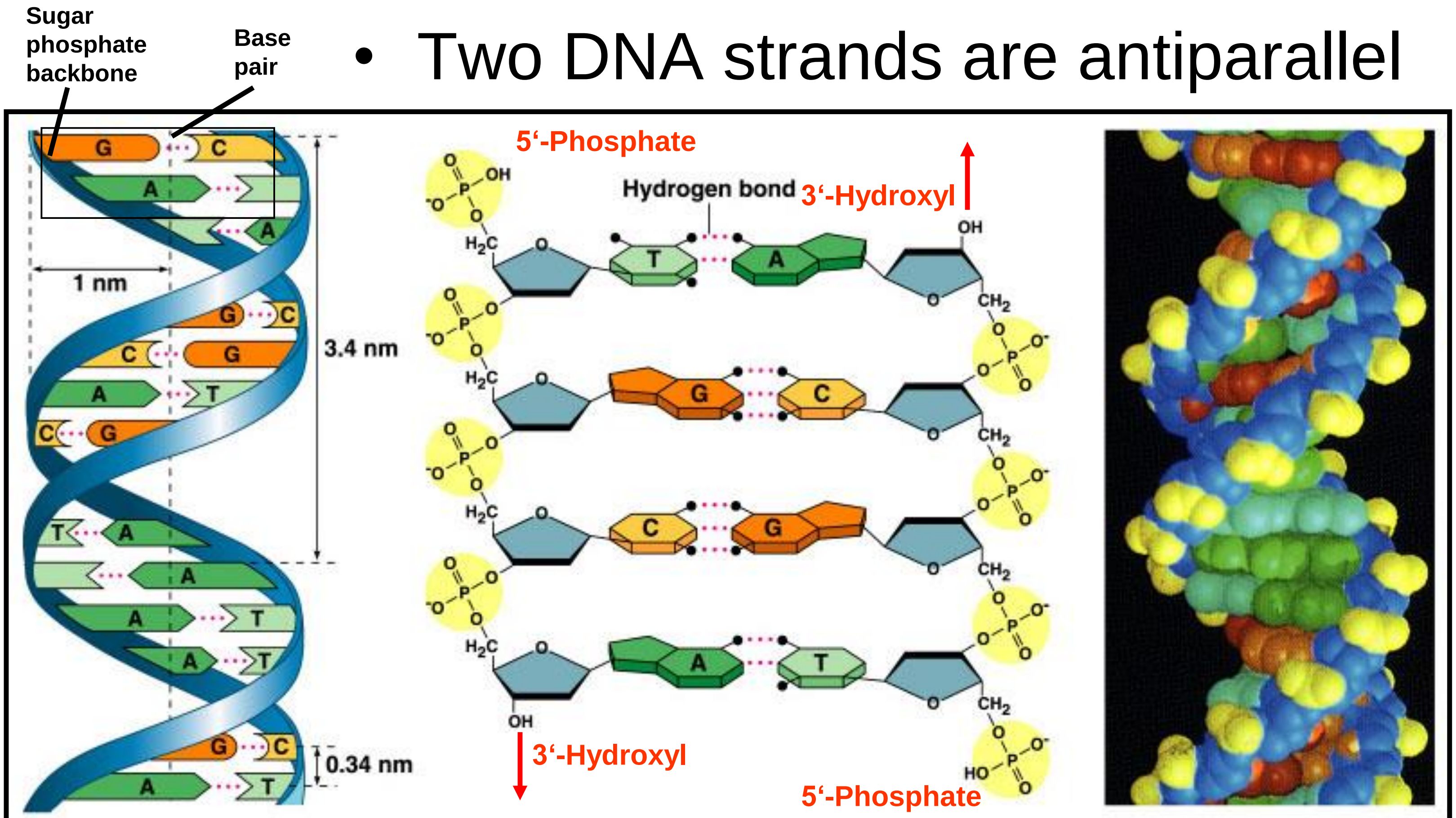


The DNA Double Helix

- Two DNA strands are antiparallel



(a) Key features of DNA structure

(b) Partial chemical structure

(c) Space-filling model

FIGURE 16.5 Biology 6/e

Ribonucleic acid (RNA)

- **Ribose**
- **C, U (no T), A, G,**
- **Base pairing matches DNA (G=C, A=U)**
- **mostly single-stranded, secondary structures**

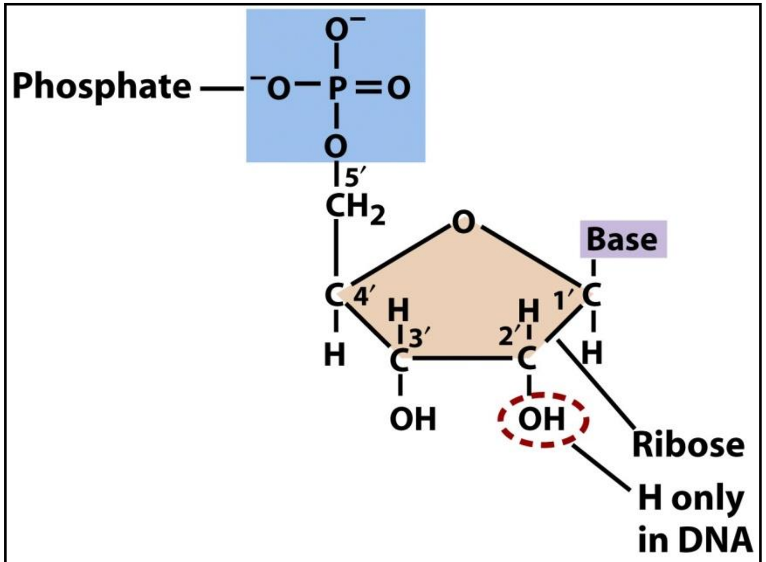


Figure 3-8 Brock Biology of Microorganisms 11/e
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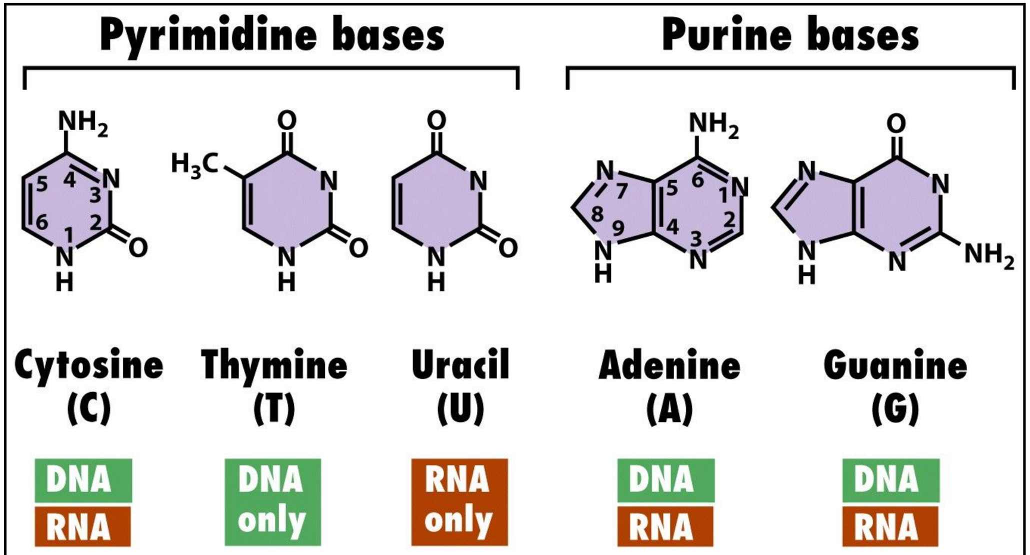

Figure 3-9 Brock Biology of Microorganisms 11/e
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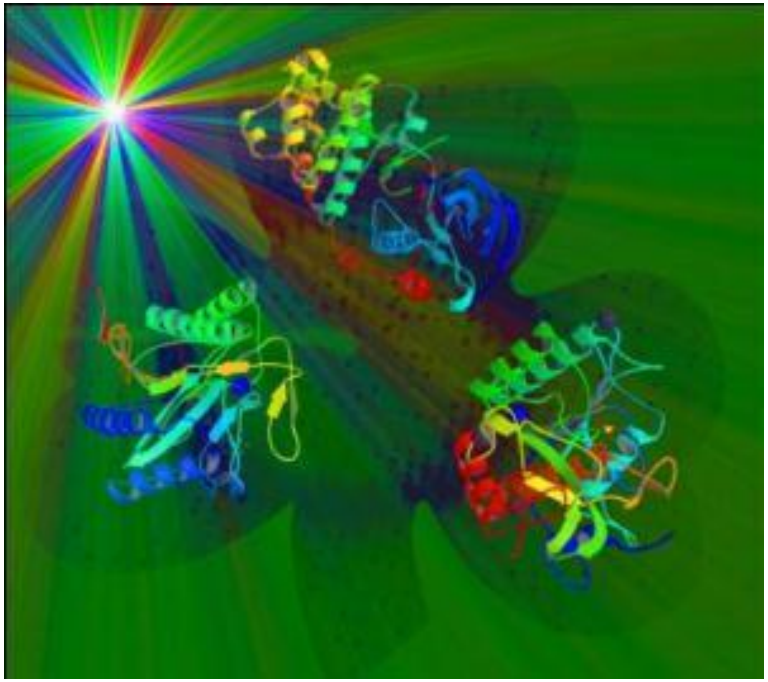
Three major types of RNA

- **messenger RNA (mRNA)**
- **transfer RNA (tRNA)**
- **ribosomal RNA (rRNA)**

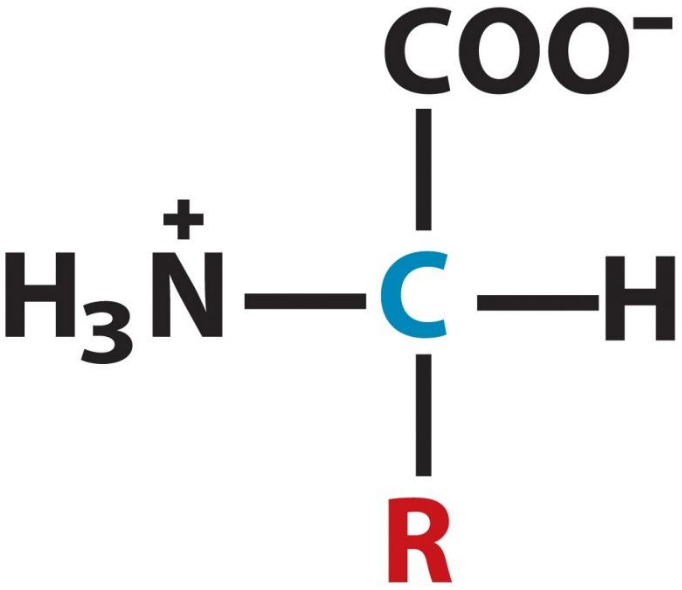
- **Two types of function:**
- **genetic**
  - **carries genetic information of DNA (mRNA)**
- **structural**
  - **e.g. -structural role in ribosome (rRNA),**
  - **amino acid transfer (tRNA),**
  - **catalytic (enzymatic) activity (ribozymes)**

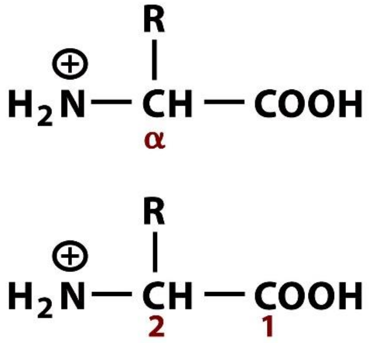
Amino Acids & Proteins



Amino Acid

- General Structure of all but one **α-amino acid** (proline, a cyclic amino acid is the excepteion):
- An amino acid has
- a **carboxylate group** (whose carbon atom is designated C-1),
- an **amino group**,
- a **hydrogen atom**, and
- a **side chain** (or **R** group),
- **all attached to C-2** (the α-**carbon**).





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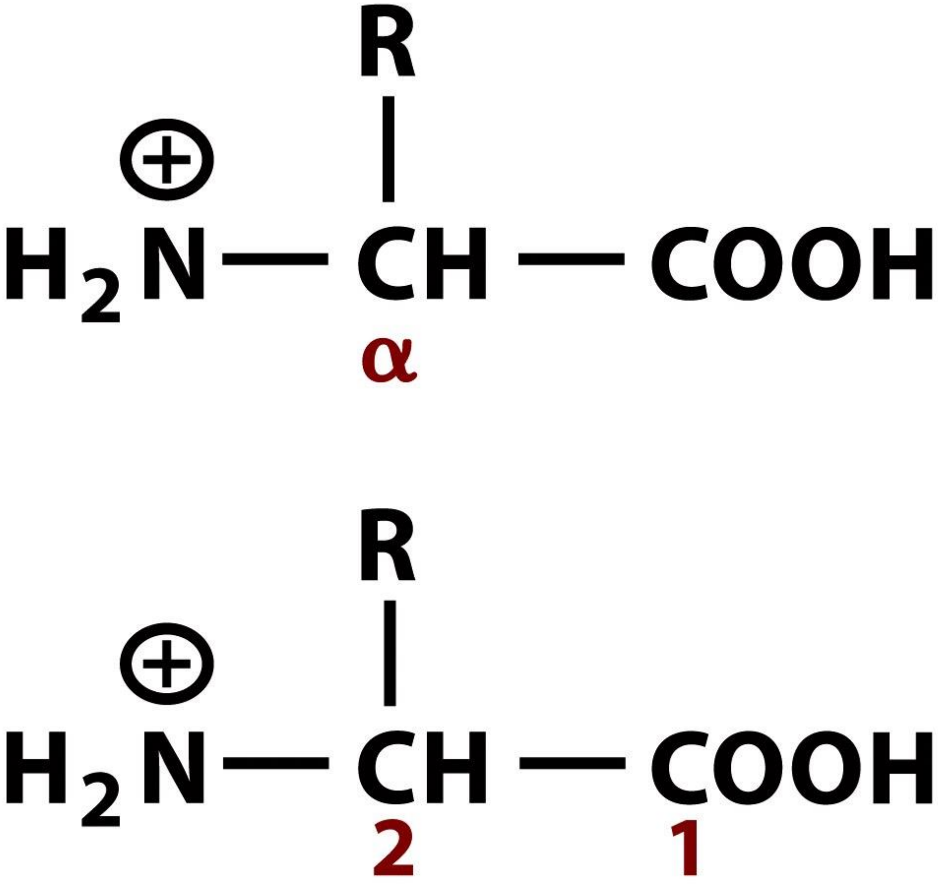
Numbering Conventions of Amino Acids

- In **traditional names**, the carbon atoms adjacent to the carboxyl group are identified by the **Greek letters α, β, γ,** etc.
- In the official IUPAC/IUBMB chemical names or systematic names, **the carbon atom in the carboxyl group is number 1** and the adjacent carbons are numbered sequentially. Thus, the atom in traditional names is the carbon 2 atom in systematic names.



$$H_2\overset{\oplus}{N}-\underset{\alpha}{\overset{\overset{\displaystyle R}{|}}{CH}}-COOH$$

$$H_2\overset{\oplus}{N}-\underset{2}{\overset{\overset{\displaystyle R}{|}}{CH}}-\underset{1}{COOH}$$

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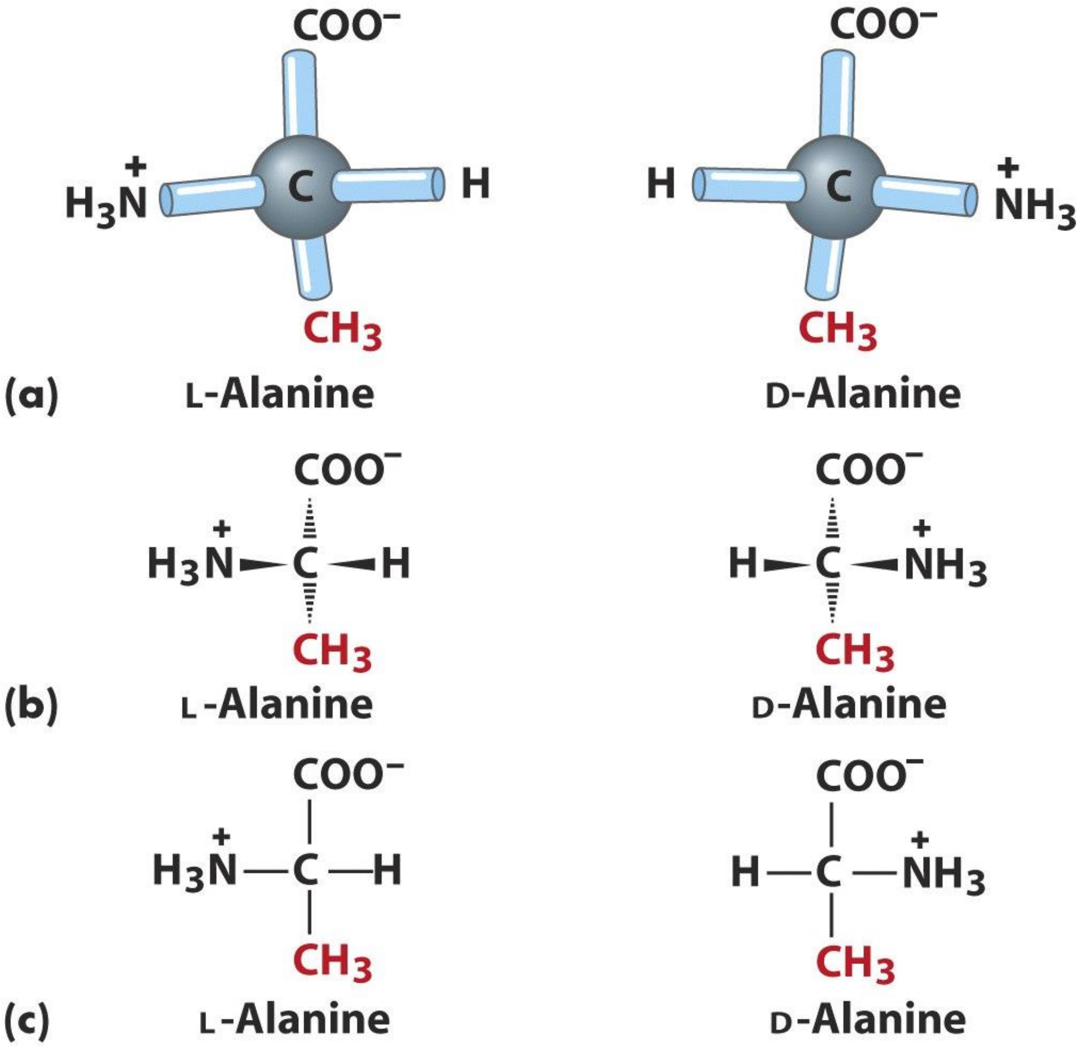
Amino Acid Stereoisomers

- Stereoisomers in **α-amino acids**.
- **Mirror images** of each other **(enantiomers).**
- **Except glycine**, all amino acids are **chiral** (L-, D-isomeres; based on convention of the three-carbon sugar glyceraldehyde)
- In living organisms, they usually occur in the **L-form**.
- Some organisms have **racemases**: D ⇨ L-form.



Amino Acids

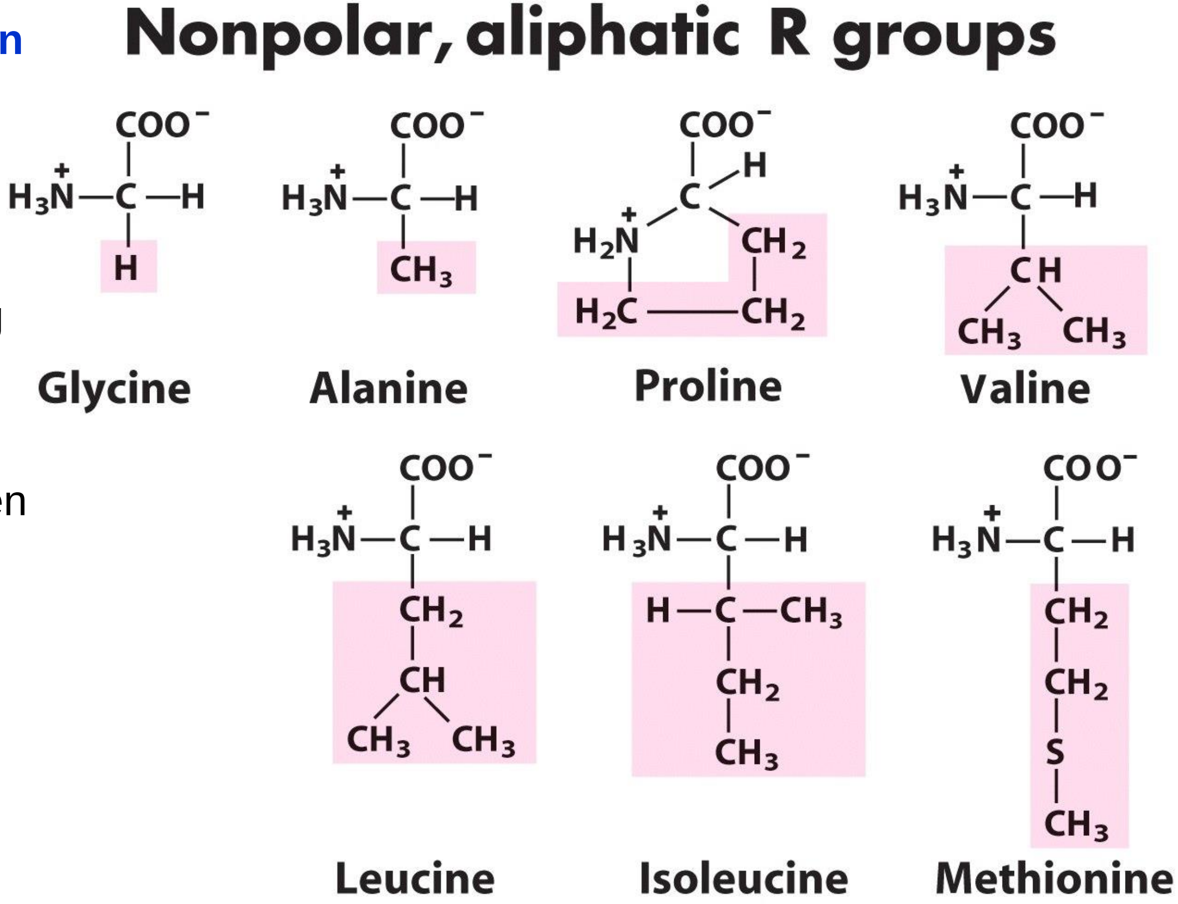
- All common **20 proteinogenic amino aicds** are α-amino acids.
- They **differ in their side chains** (R groups), which vary in structure, size, and electric charge, and which influence the solubility of the amino acid in water.
- In addition to this common ones there are **less common ones**. Some are the result of post-translational modifications, some are amino acids present in living cells but not in proteins.

The 20 Common Amino Acids of Proteins

- 5 groups:
  - Nonpolar, aliphatic R groups
  - Aromatic R groups
  - Polar, uncharged R groups
  - Positively, charged R groups
  - Negatively, charged R goups

The 20 Common Amino Acids of Proteins

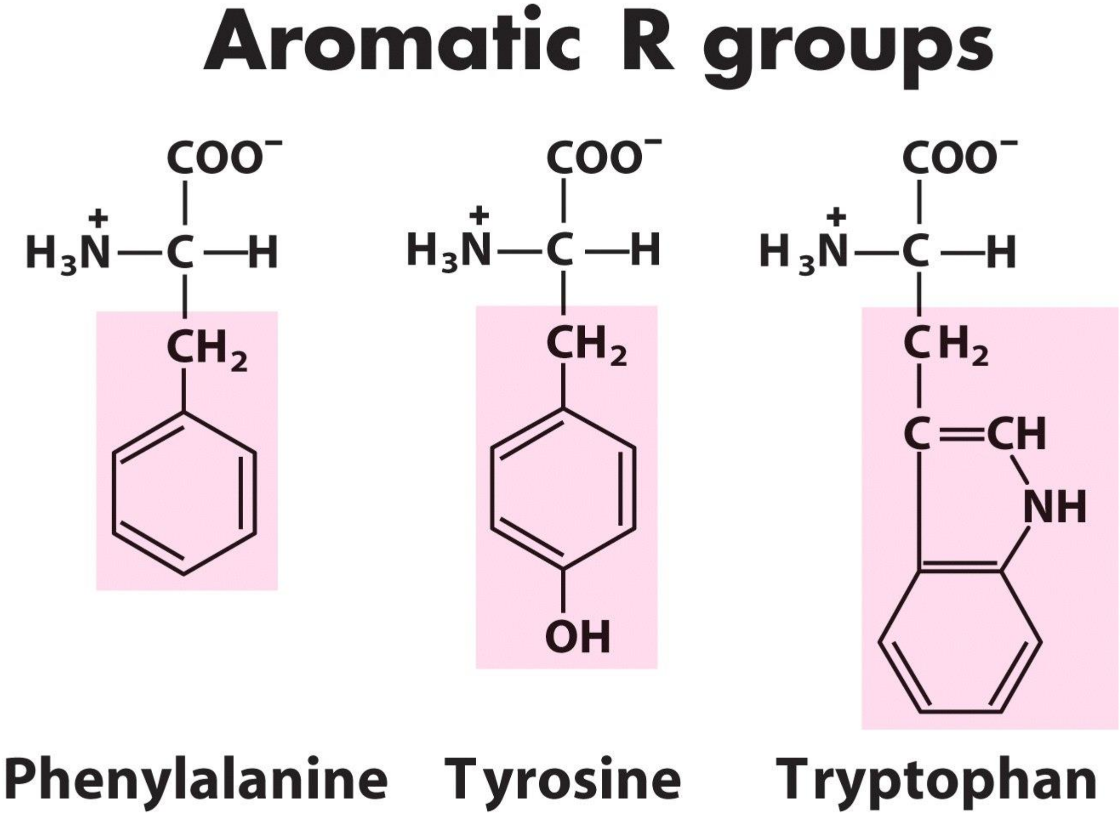
- The nonpolar amino acids are characterised by having **only carbon and hydrogen** in their side chains; R-group nonpolar and hydrophobic .
- Side chains of **alanine, valine, leucine and isoleucine (**saturated hydrocarbon R groups) cluster together **within proteins**, stabilizing protein structure by **hydrophobic interactions**.
- The simplest amino acid is **glycine**, which has a single hydrogen atom as its side chain (**not chiral** !). No real contribution to hydrophobic interactions
- **Methionine**, sulfur-containing amino acid with a **non-polar thioether group** in its side chain.



- **Proline**, has an aliphatic side chain with a **cyclic** structure. The secondary amino (imino) group is held in a rigid conformation that reduces the structural flexibility.
- As the name implies **leucine** and **isoleucine** are **isomers** of each other.

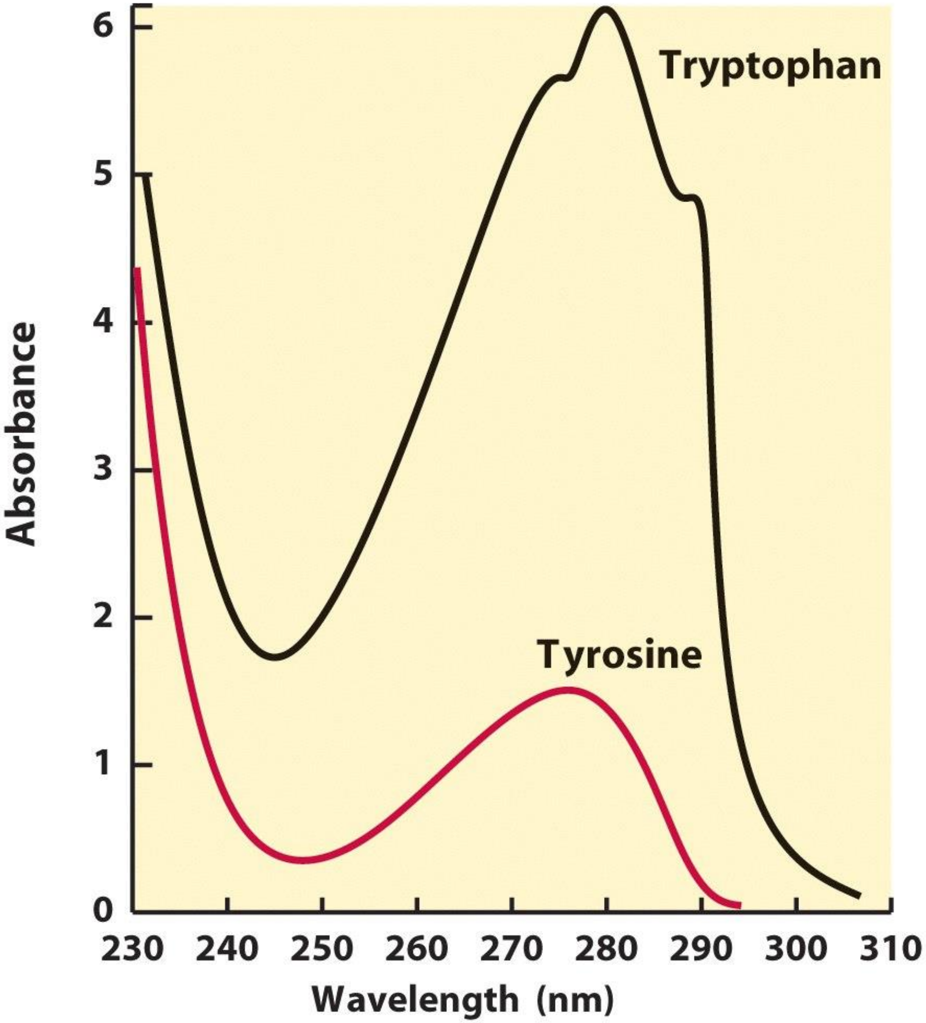
The 20 Common Amino Acids of Proteins

- Aromatic side chains, rel. **nonpolar (hydrophobic)** and parcipitate in hydrophobic interactions.
- **Tyrosine** hydroxyl group can form **hydrogen bonds** and is an important functional group in some enzymes.
- Tyrosine (-OH) and tryptophan (-N/indole ring) are much more polar than phenylalanine.



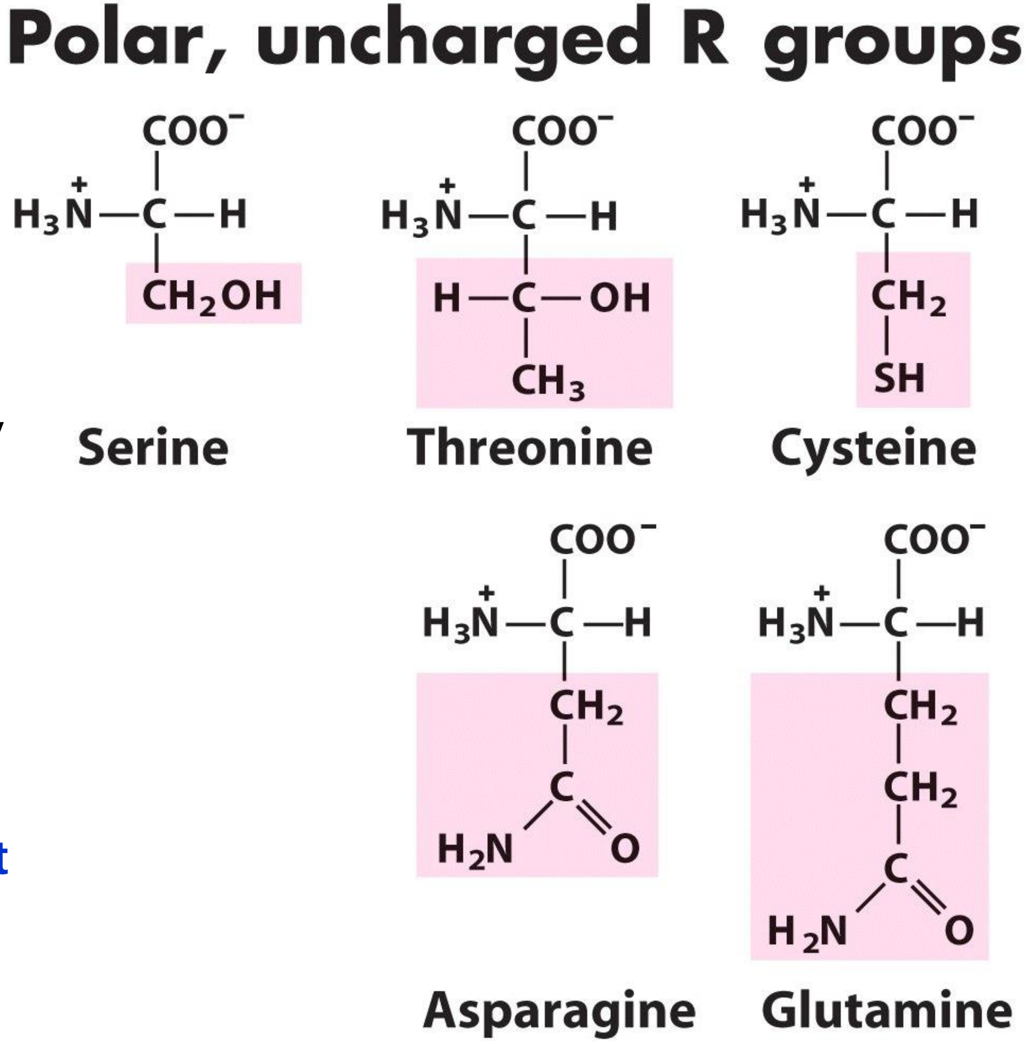
The 20 Common Amino Acids of Proteins

- **Tryptophan and tyrosine** and to a much lesser extent phenylalanine **absorb UV light.**
- Accounts for the characteristic **strong absorbance of light by most proteins** at the wavelength of **280 nm**.
- Property exploited for the detection/characterization of proteins.



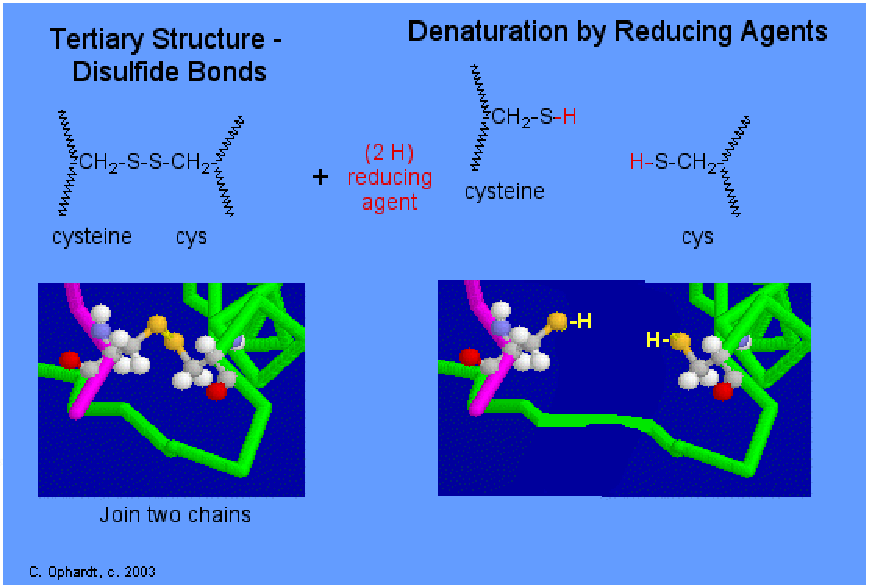
The 20 Common Amino Acids of Proteins

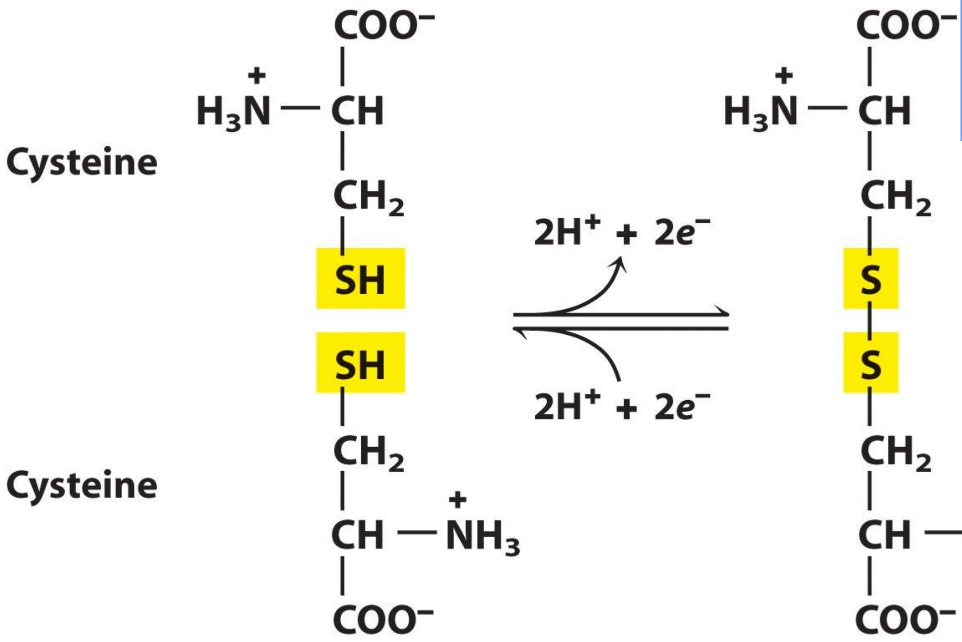
- Polar uncharged R groups are more soluble in water, more **hydrophilic**. These are amino acids that possess **oxygen, sulfur and/or nitrogen** in the side chain and are therefore **polar, but cannot have their R group ionised** and thus do not carry an overall charge.
- **Serine, threonine hydroxyl group**; targets for protein phosphorylation.
- **Cysteine sulfhydryl group** (weak acid, hydrogen bonds with oxygen & nitrogen); readily oxidized to from dimeric amino acid cystine (**kovalent disulfide bond** formation).
- **Asparagine, glutamine amide group**, (amides of aspartate and glutamate).



Disulfide Bond

- **Reversible formation** of a disulfide bond by the **oxidation of two molecules of cysteine**.
- Disulfide bonds between Cys residues **stabilize the structures of many proteins**.

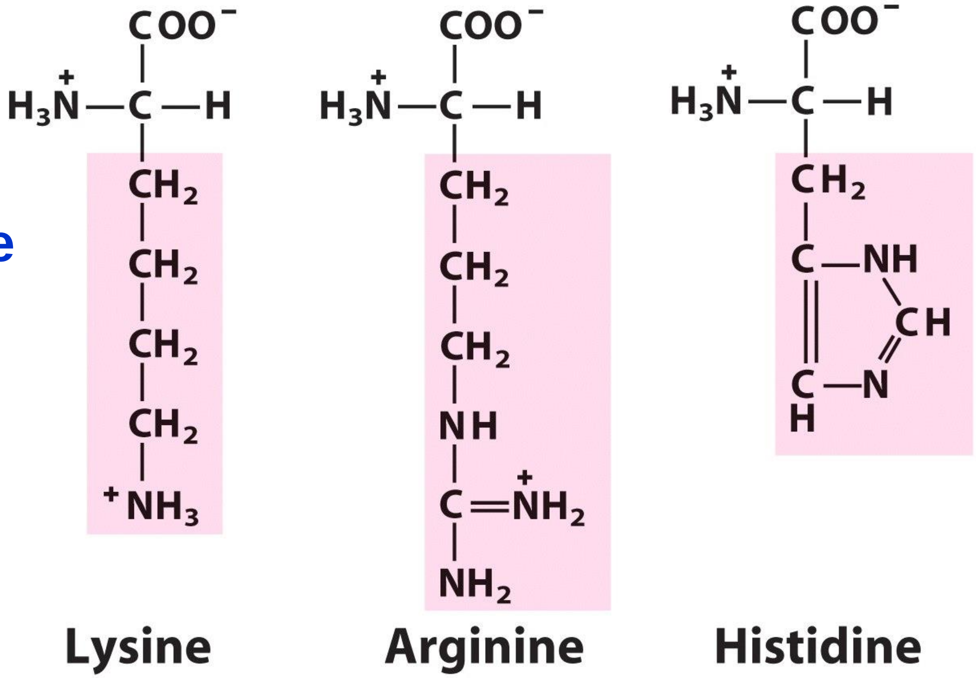




The 20 Common Amino Acids of Proteins

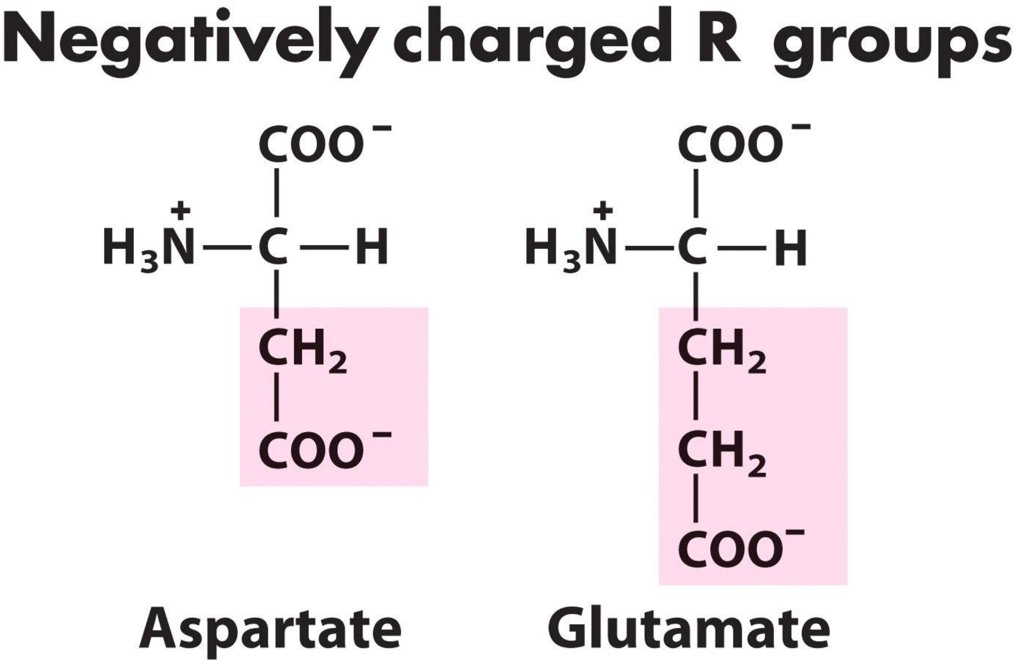
- **Most hydrophilic** R groups are those that are **positively or negatively charged**.
- **Lysine** with second primary **amino group at ε position.**
- **Arginine** with positively charged **guanidiniumgroup**.
- **Histidine** with **aromatic imidazole** group. Only common amino acid with **ionizable side chain with pK_a near neutrality**, histidine may be positively charged (protonated form) or uncharged at pH 7.0.
- His residues **facilitate many enzyme-catalyzed reactions by serving as proton donors or acceptors**.

Positively charged R groups



The 20 Common Amino Acids of Proteins

- Negative charge at pH 7.0.
- Both have a **second carboxyl group.**



Overview on Properties of Amino Acids

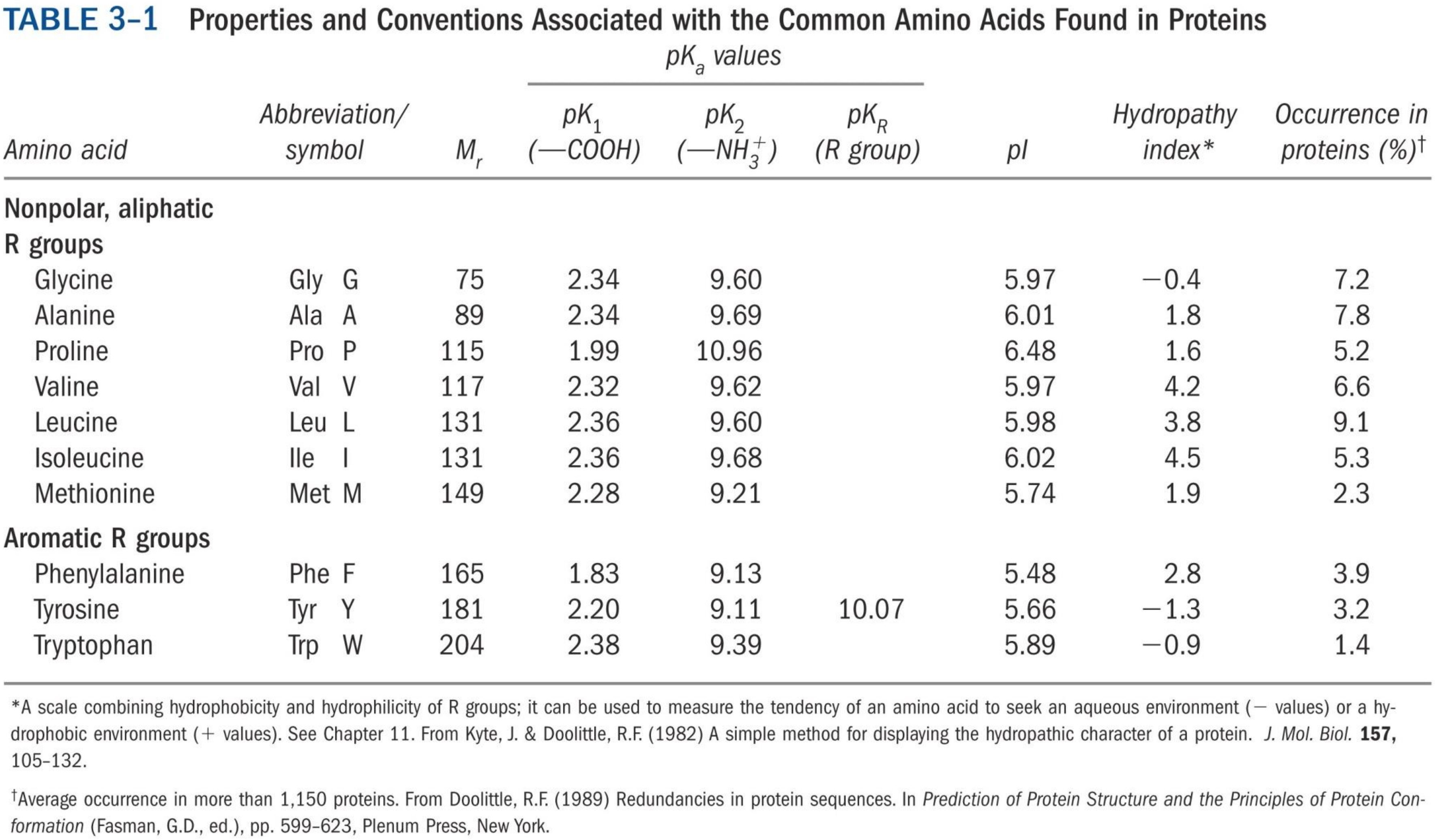


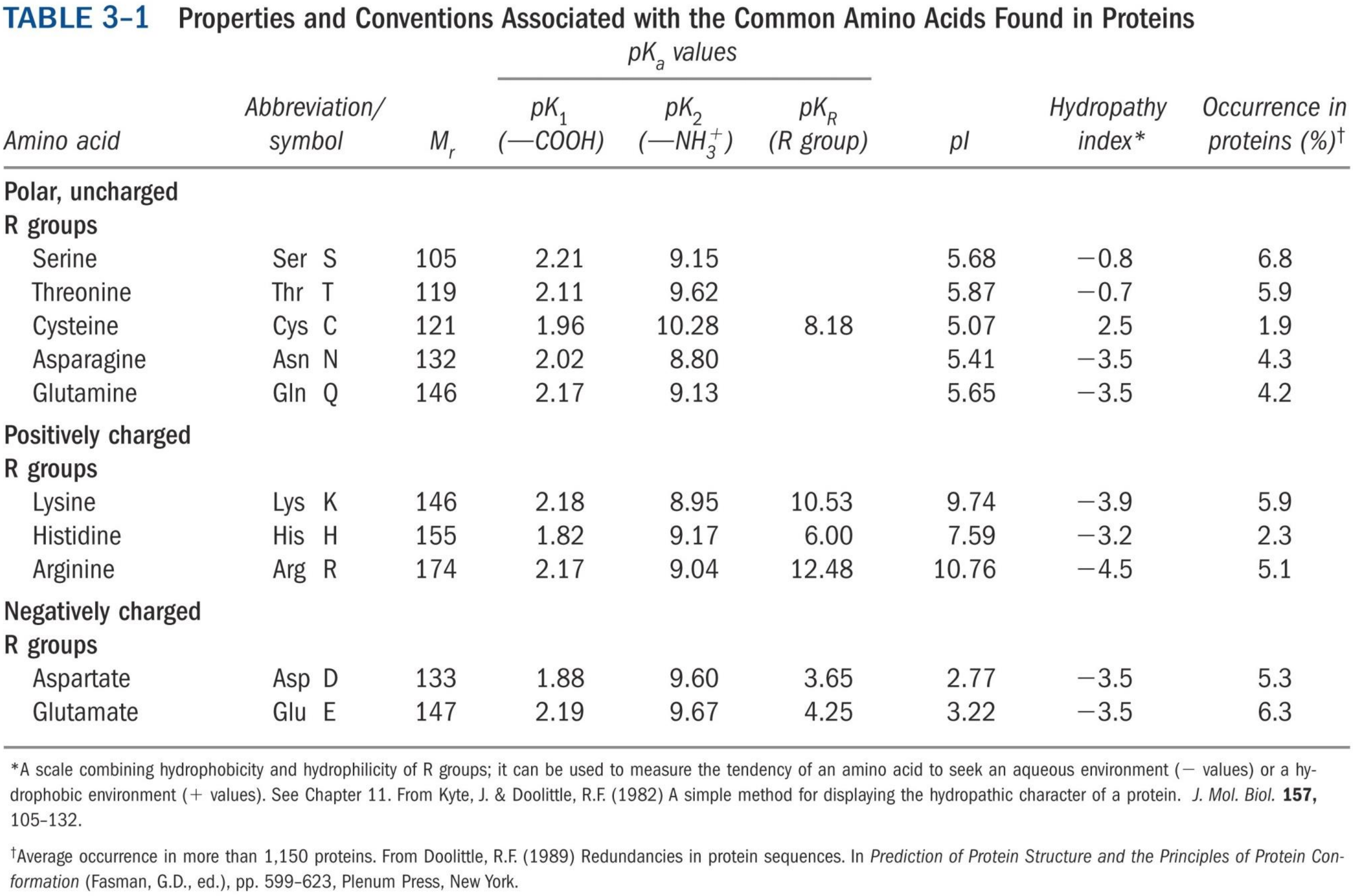
TABLE 3–1 **Properties and Conventions Associated with the Common Amino Acids Found in Proteins**

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

*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 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.

Overview on Properties of Amino Acids



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			pK_a values					
Amino acid	*Abbreviation/ symbol*	M_r	pK_1 (—COOH)	pK_2 (—NH_3^+)	pK_R (R group)	*pI*	*Hydropathy index**	*Occurrence in proteins (%)*†
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 hydropathic character of a protein. *J. Mol. Biol.* **157,** 105–132.

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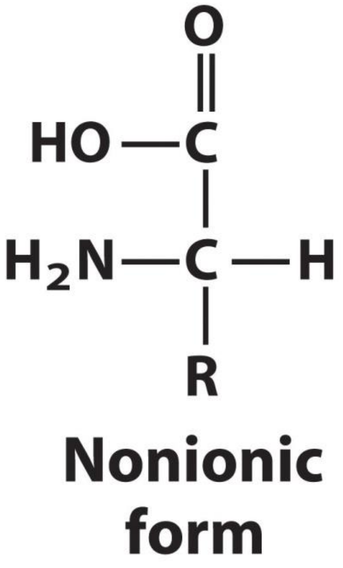
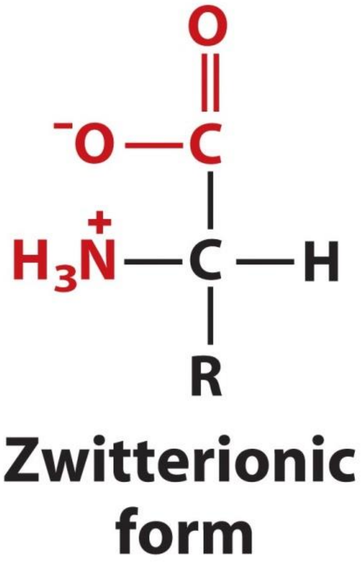
Nonionic and Zwitterionic Forms of Amino Acids

- The **amino and carboxylgroups** of amino acids and the **ionizable R groups** of some amino acids function as **weak acids and bases**.
- When an amino acid (without ionizable R) is dissoved in water at **neutral pH**, it exists in solution as a **dipolar ion „zwitterion**“
- **Ampholytes** are substances that exhibit this **dual (acid/base) nature**. They are amphoteric.





Characteristic Titration Curves

- Titration curve for **alanine**. **Titration = gradual addition or removal of protons**.
- **p*K*$_a$ value**; is the pH value where the concentration of **protonated and deprotonated form of the specific residue are equal**. Is the pH of the solution below the p*K*$_a$ value the residue is **protonated (acid)** if it is above it is **deprotonated (basic)**.
- The first p*K*$_a$ value is 2.4; the second is 9.9.
- pI$_{Ala}$ represents the **isoelectric point** of alanine "**zwitterion**".

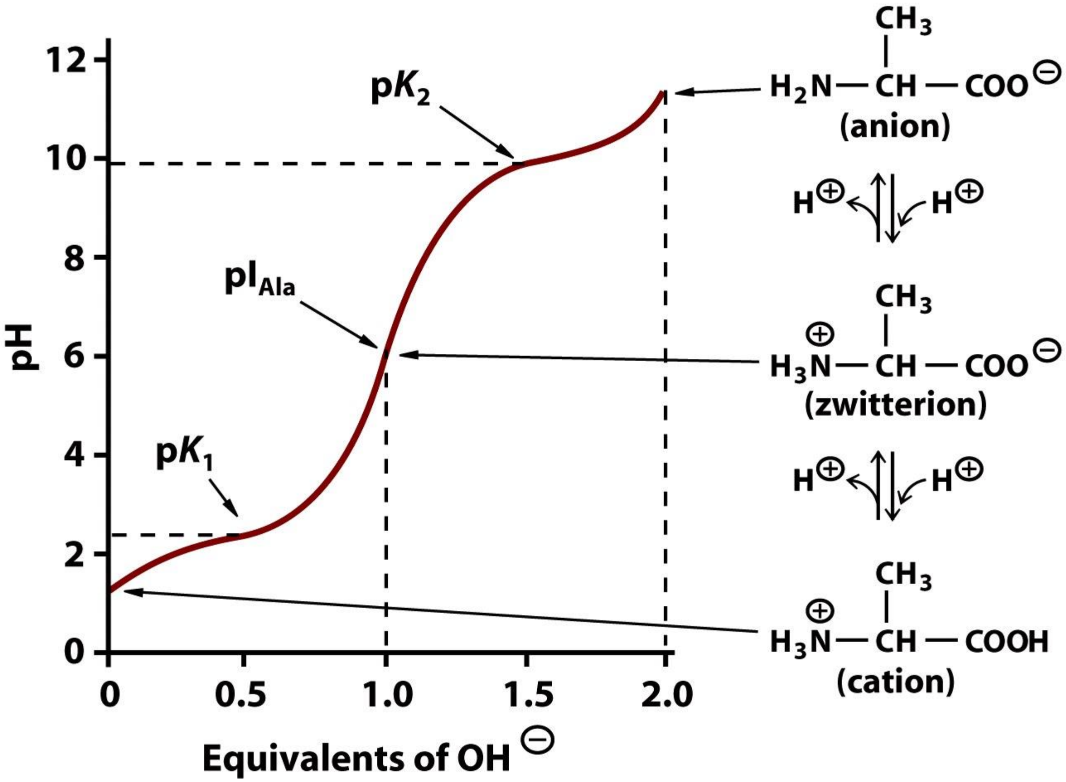


Figure 3-6 Principles of Biochemistry, 4/e
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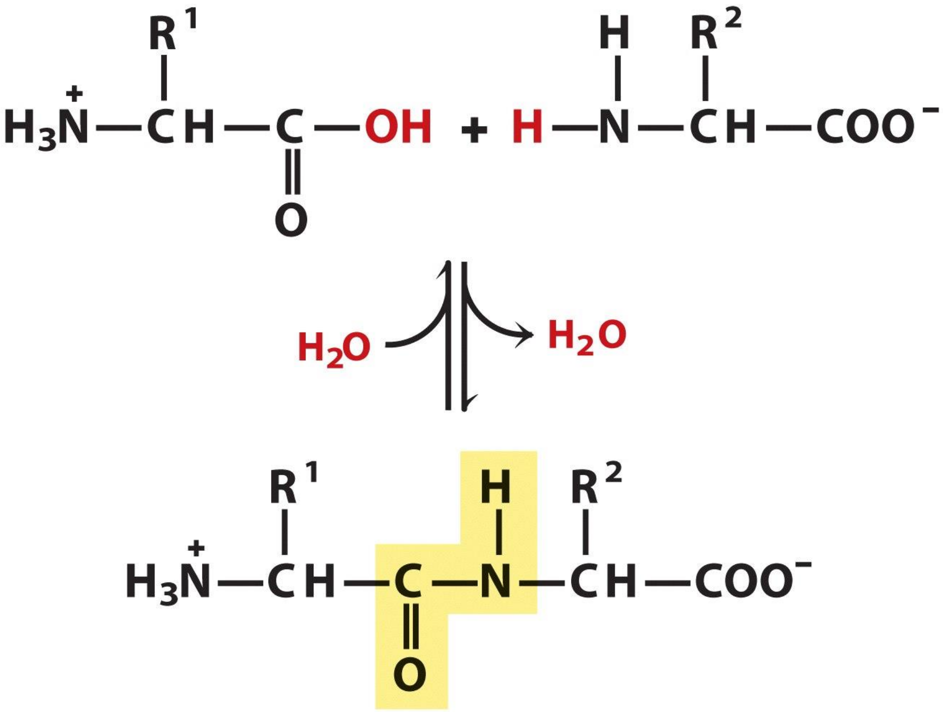
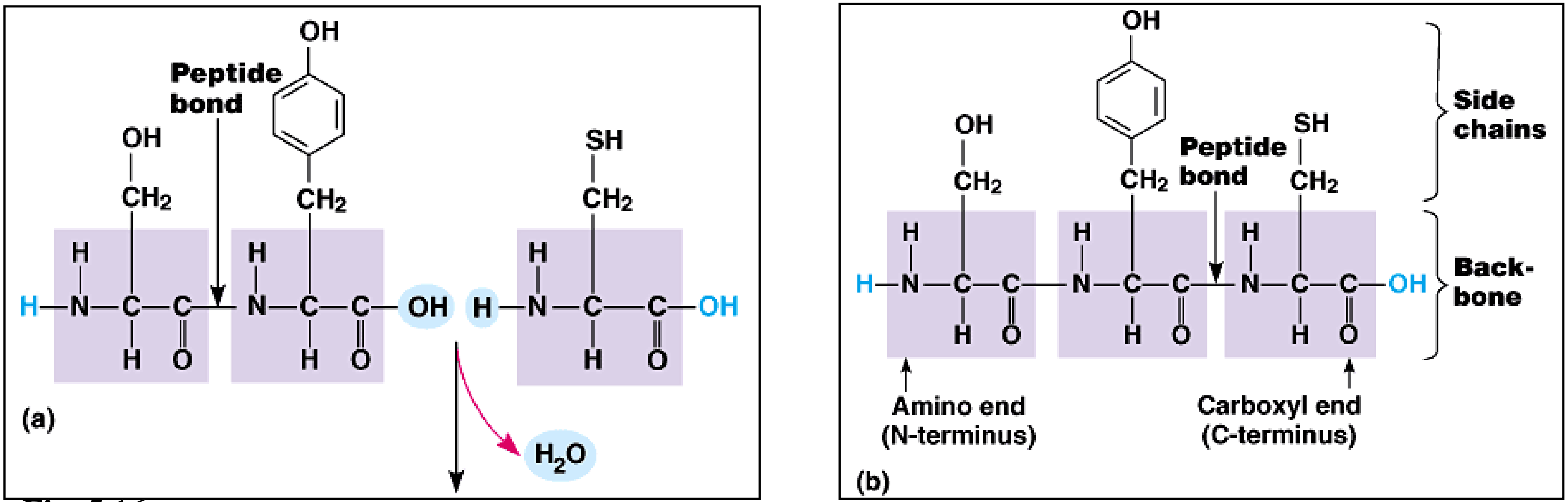
Peptide bond formation

- Aminoacids can be linked through a substituted amide linkage, termed **peptide bond**, to yield a dipeptide.
- The linkage is formed by the **removal of water** (**dehydration**) between the **α-carboxyl** group of one amino acid and the **α-amino** group of a second amino acids in a **condensation** reaction.
- The repeated sequence (**N-C-C**) is the **polypeptide backbone**.
- Dipeptide, tripeptide, oligopeptide, polypeptide
- **Polpeptides** molecular weights <10,000 ; **Proteins** > 10,000



Peptide bond formation

- Amino acids are joined together when a **dehydration reaction** removes a hydroxyl group from the carboxyl end of one amino acid and a hydrogen from the amino group of another (H_2O).
- The resulting covalent bond is called a **peptide bond**.
- The repeated sequence (**N-C-C**) is the polypeptide **backbone**.
- Attached to the backbone are the **various R groups**.
- Polypeptides range in size from a few monomers to thousands.



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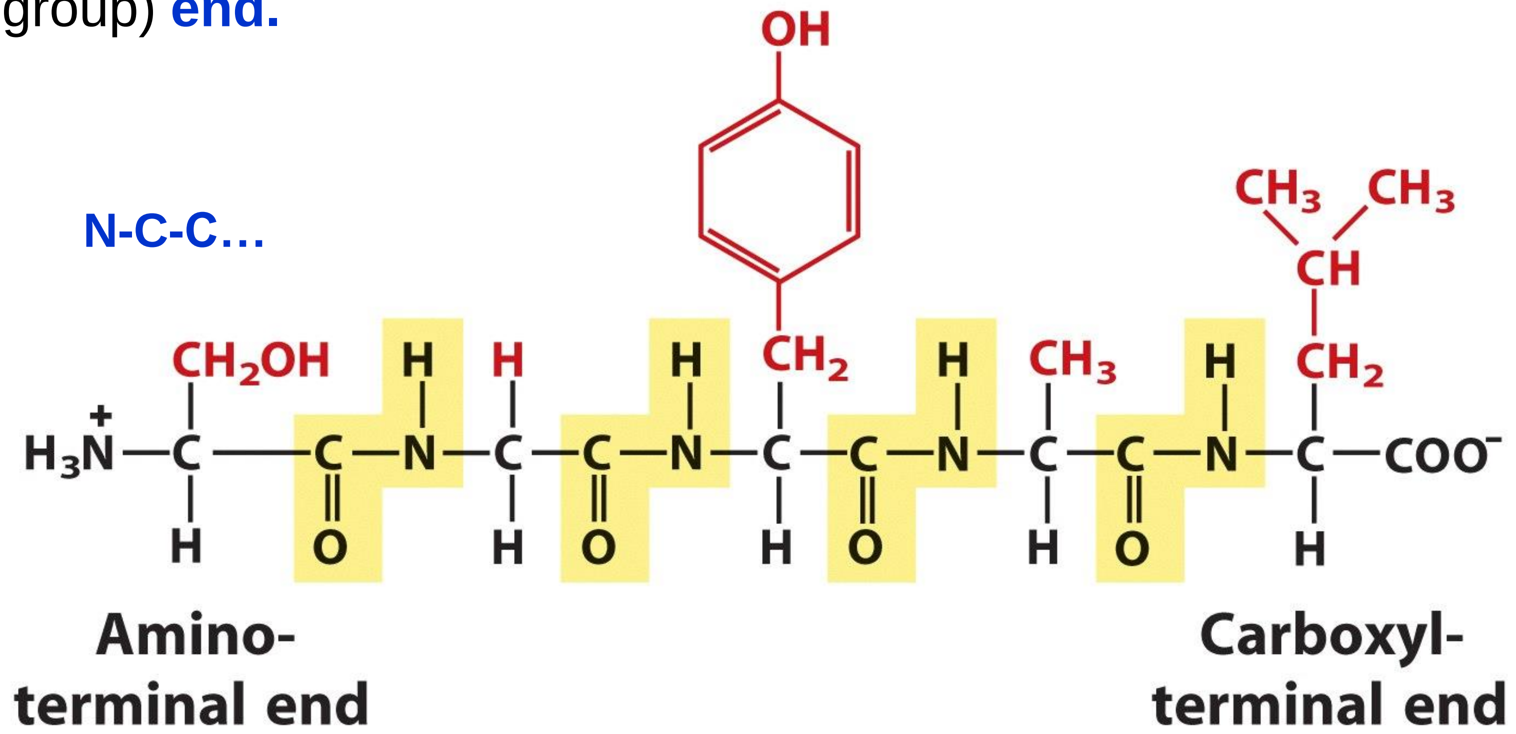
Pentapeptide

- Serylglycyltyrosylalanylleucine (Ser-Gly-Tyr-Ala-Leu)
- Named beginning with the N-terminal residue (by convention placed at the left)
- Every peptide/protein has an **amino-terminal** (or N-terminal, free amino group) and a **carboxy-terminal** (or C-terminal, free carboxyl group) **end.**

N-C-C…



Proteins

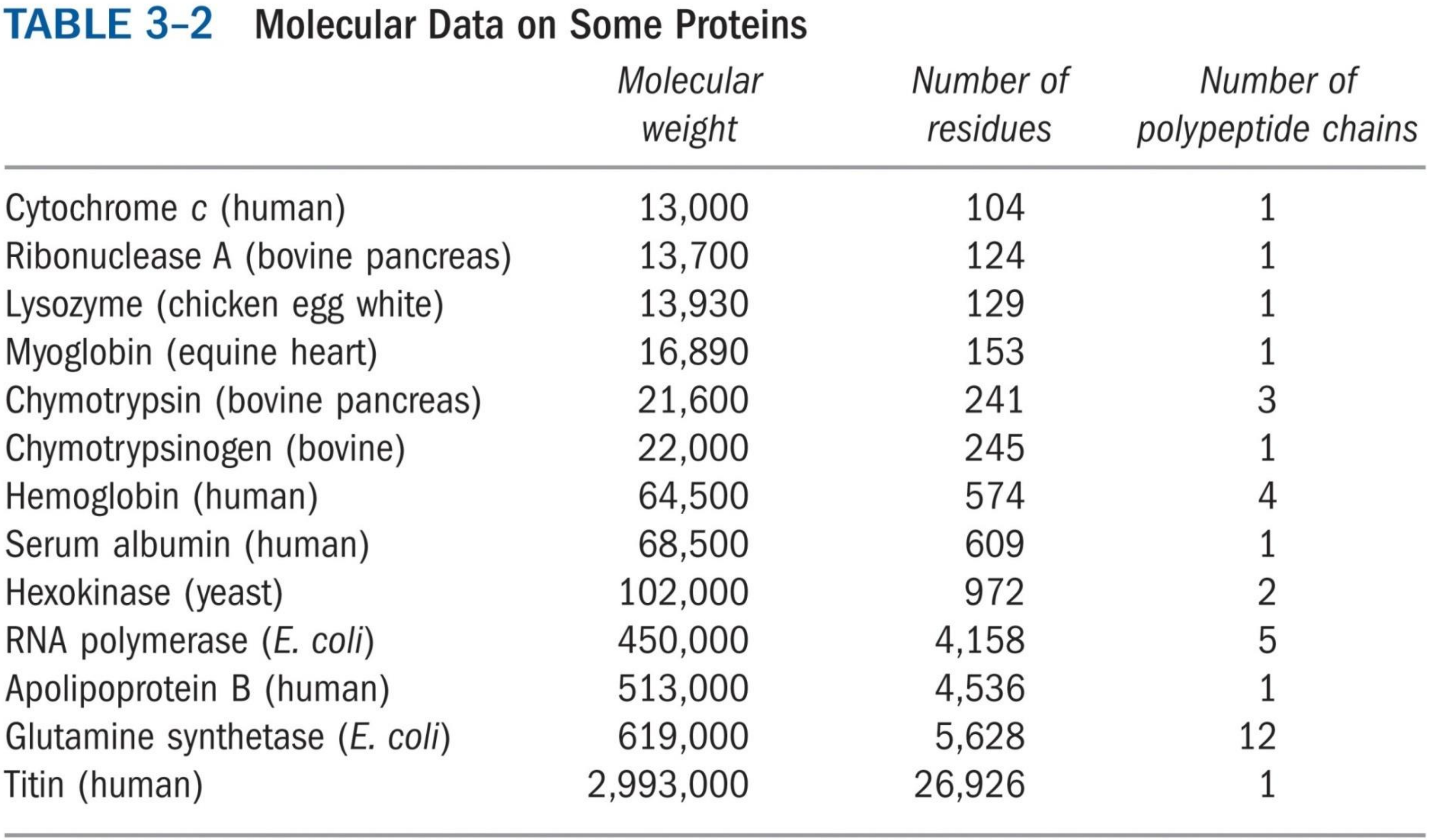
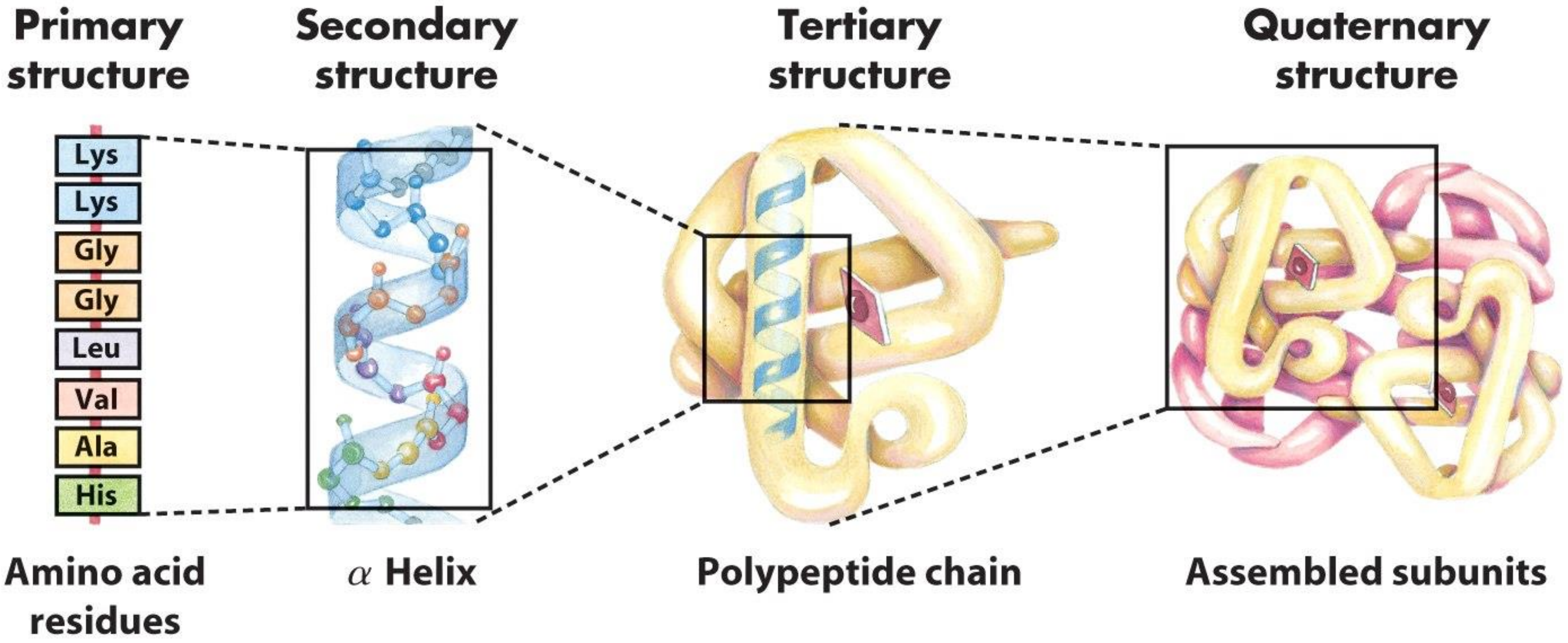


TABLE 3–2 Molecular Data on Some Proteins

	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

Level of Structures in Proteins

- Primary structure, **sequence** of amino acid residues.
- Secondary structure, particulary stable arrangements of amino acids giving rise to recuring **structural patterns**.
- Tertiary structures describes all aspects of the **three-dimensional folding** of a polypeptide.
- Quarternary structrue, describes the arragement in space of **two or more polypeptides subunits.**



Protein Folding

- The **information is stored in the primary sequence information**.
- The **spatial arrangement of atoms in a protein** is called **conformation**.
- A protein‘s conformation is **stabilized largely by weak interactions**, where **hydrophobic interactions** generally predominate.
- In water the optimal arrangement of hydrogen bonds results in a structured shell or **solvation layer**.

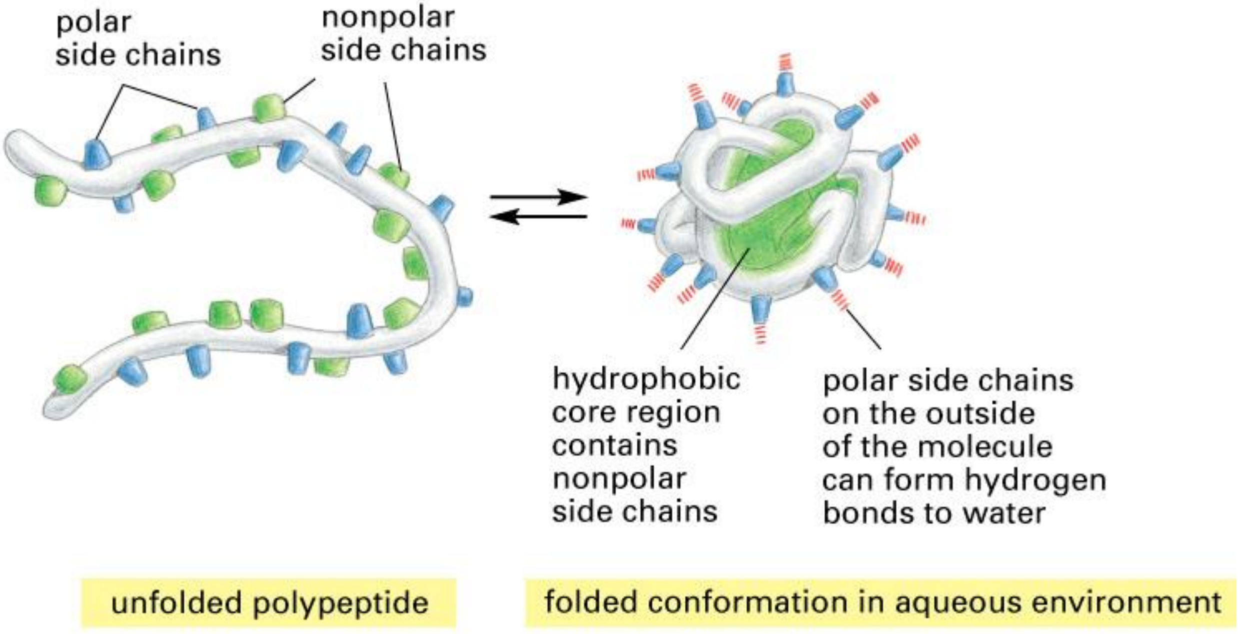


Figure 3–6. Molecular Biology of the Cell, 4th Edition.

Protein Folding

- Noncovalent interactions

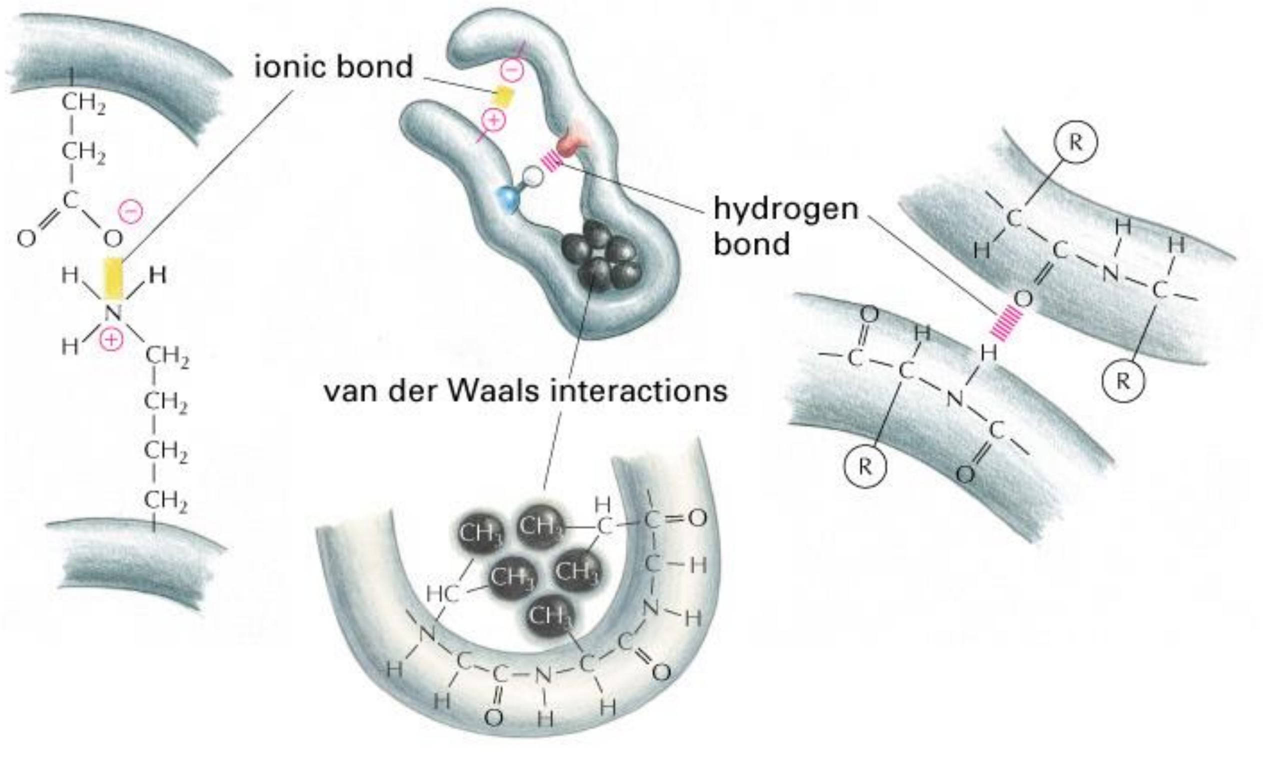
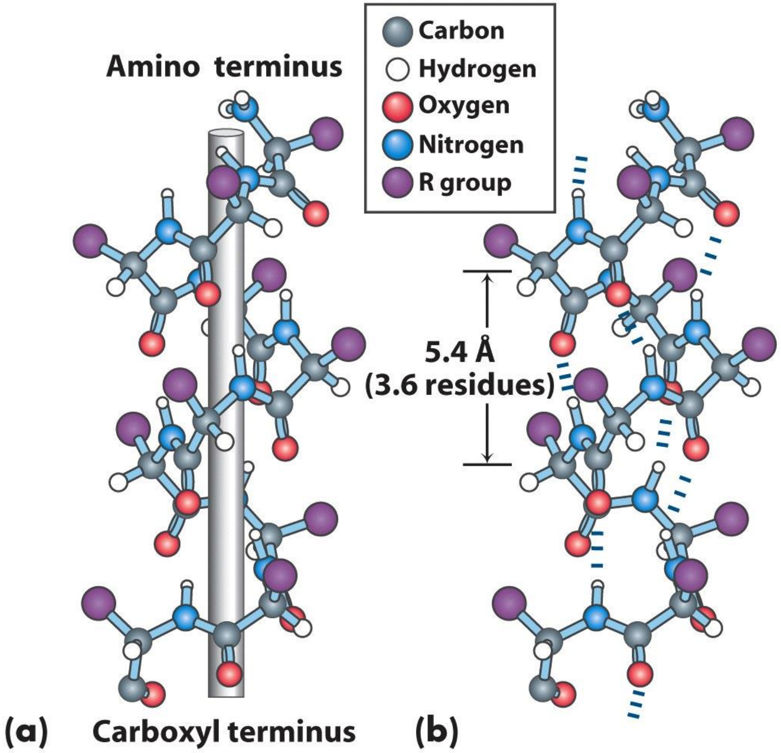


Figure 4-4 **Essential Cell Biology, 2/e. (© 2004 Garland Science)**

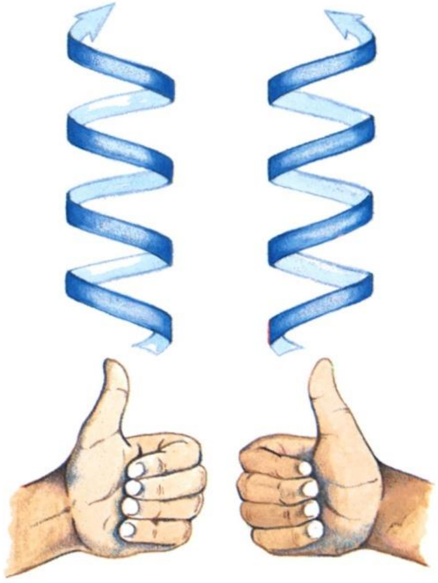
Secondary Structure: The α Helix

- In all proteins the **α helix is right handed**.
- The repeat unit is a single turn of the helix, **3.6 residues**.
- This facilitates the formation **hydrogen bonds** between **amino group AS$_n$** and **carboxyl group As$_{n+4}$** as stabilizing factor.



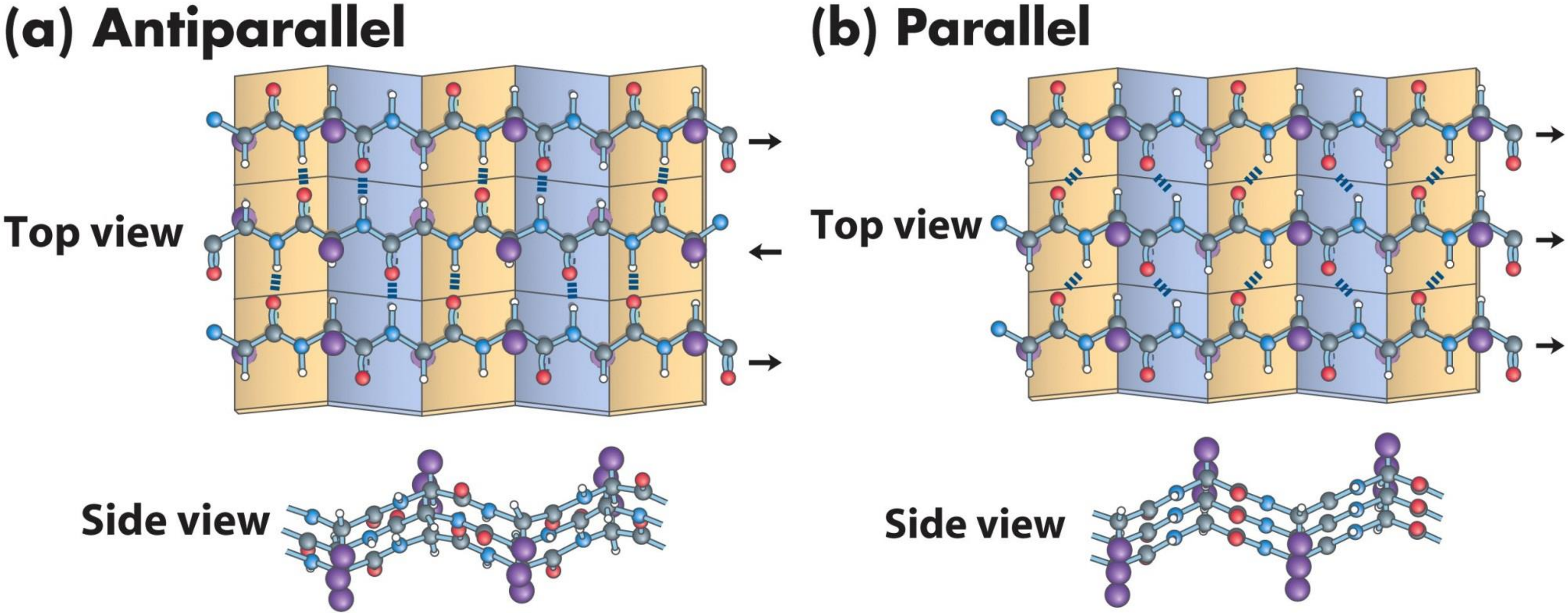
Left-handed helix

Right-handed helix



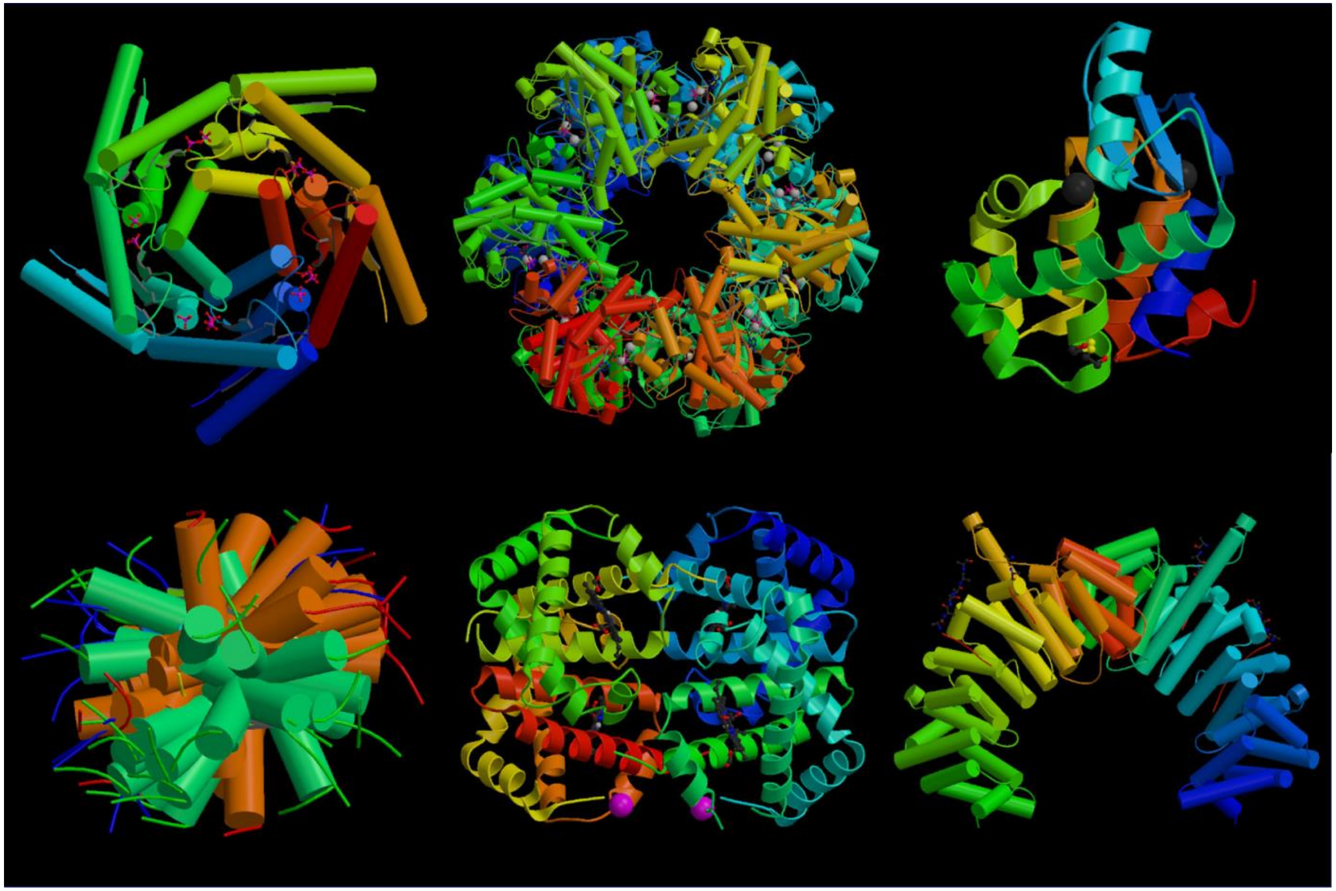
Secondary Structure: The β Sheet

- **Hydrogen bonds** form between adjacent segments of polypeptide chain.
- **Parallel or antiparallel** orientation of two chains within a sheet are possible
- In **parallel** β sheets the H-bonded strands run in the same direction
- In **antiparallel** β sheets the H-bonded strands run in opposite directions

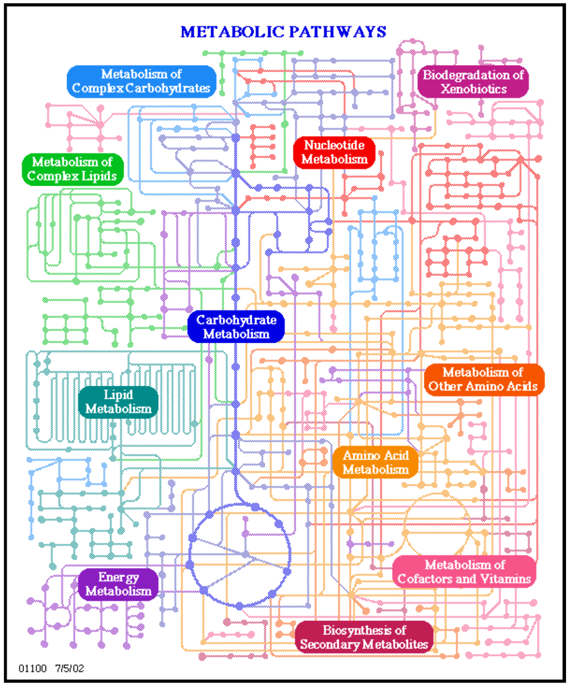


Protein Structure and Function

- The multiplicity of functions performed by proteins arises from the huge number of different shapes they adopt.
- **Structure dictates function !**



Principles of Metabolism
-Energy generation-



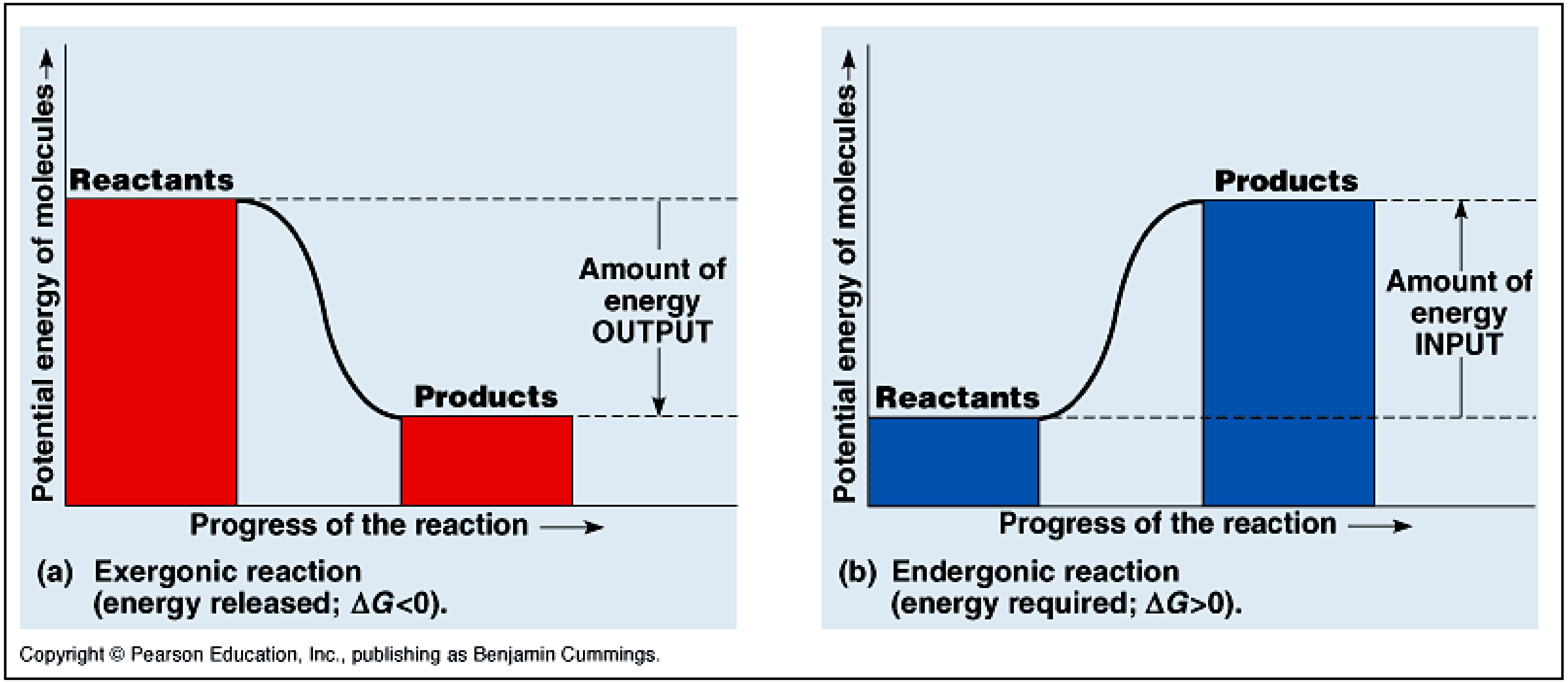
Laws of Thermodynamics Apply to Living Organisms

- Living organisms cannot create energy from nothing
- Living organisms cannot destroy energy into nothing
- Living organism may transform energy from one form to another

- **In the process of transforming energy, living organisms must increase the entropy of the universe**
- **In order to maintain organization within the themselves, living systems must be able to extract useable energy from the surrounding, and release useless energy (heat) back to the surrounding**

Energy Change in Exergonic und Endergonic Reactions

- **Change of free energy (ΔG Gibbs free energy (enthalpie)) indicates if a reaction runs spontaneous or not.**
- **$\Delta G^{0\prime}$:** standard conditions, pH 7, 25°C, all reaction compounds at 1M
- Reaction runs spontaneous, **ΔG<0 (exergonic reaction)**
- Reaction can not run spontaneous **ΔG>0 (endergonic reaction)**



(a) Exergonic reaction (energy released; ΔG<0).

(b) Endergonic reaction (energy required; ΔG>0).

Fig. 6.5 Biology (6th edition, Campbell & Reece)

Chemical Principles

Example Cellular Respiration

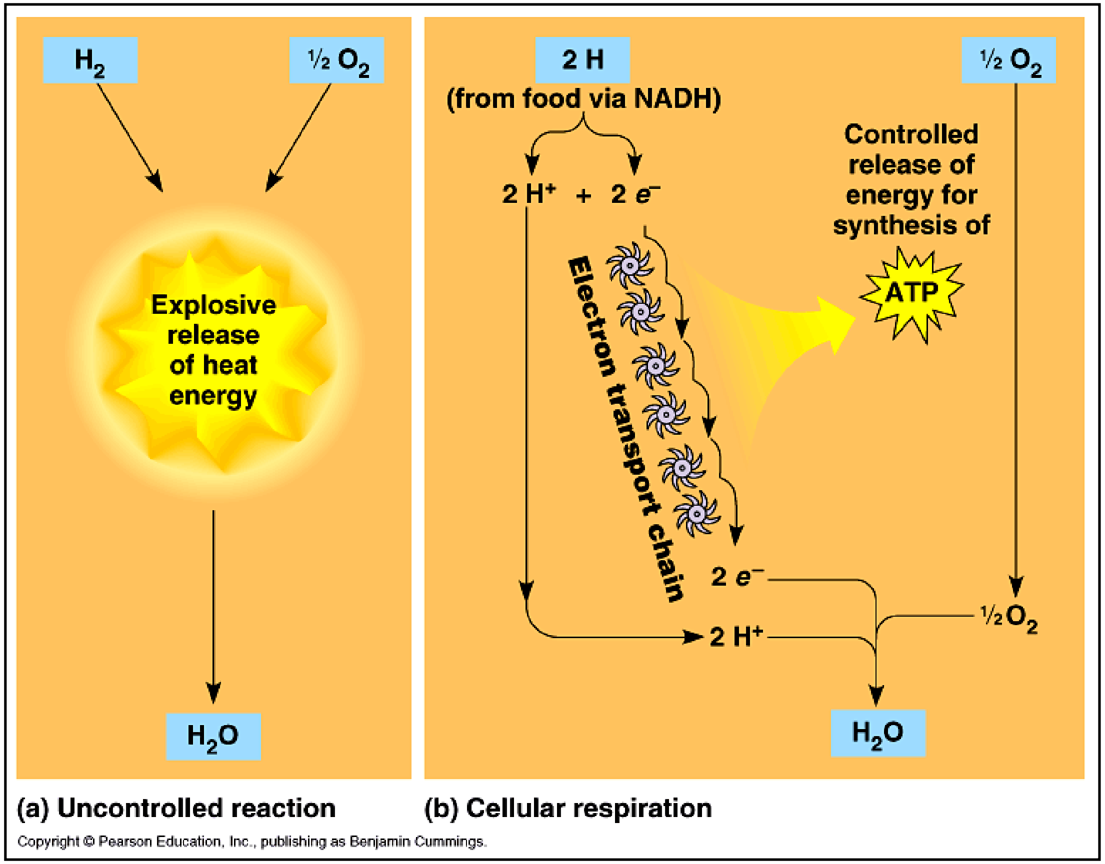


Fig. 9.5 Biology (6th edition, Campbell & Reece)

Electron Transfer in Metabolism

Oxidation-Reduction „Redox“-reactionen
Oxidation: donation/release of electrons
Reduktion: acception/uptake of electrons

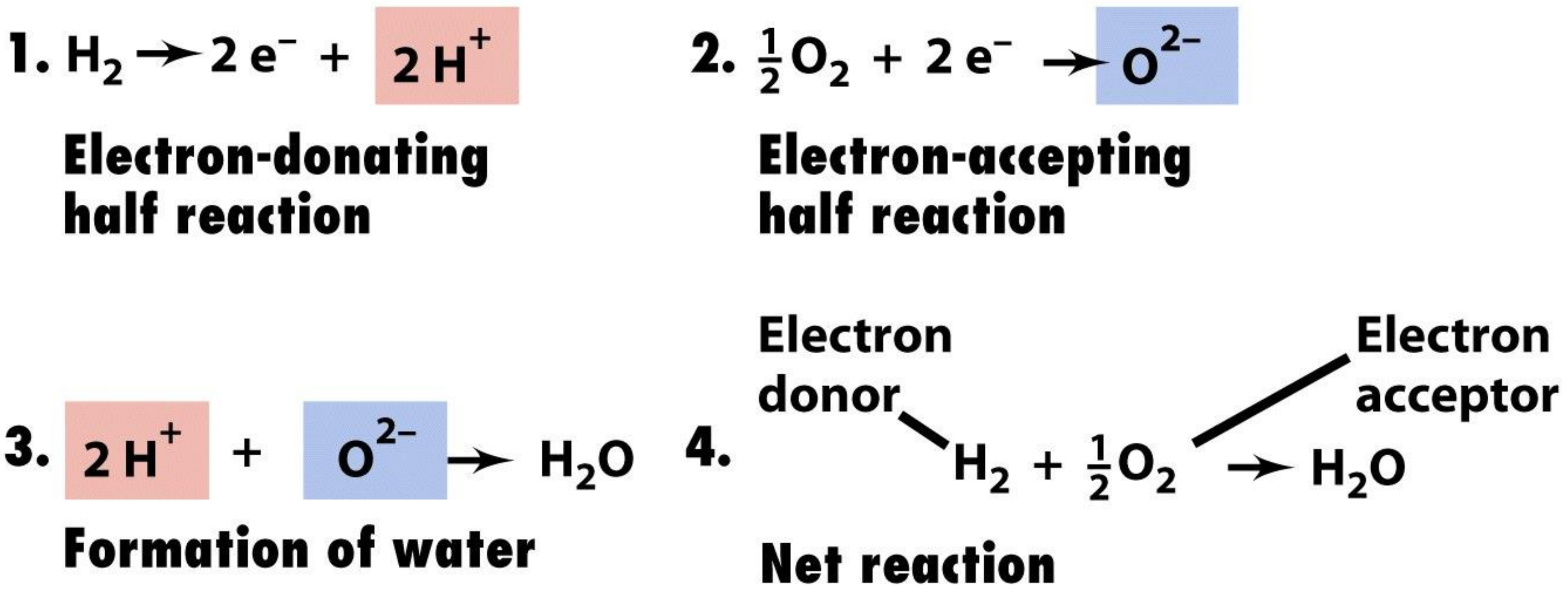


Figure 5-8 Brock Biology of Microorganisms 11/e

Redoxreaktionen & Redoxpotential

$H_2 + ½ O_2 \rightarrow H_2O$

$H_2 \rightarrow 2 e^- + 2 H^+$
Electron-donor

$½ O_2 + 2 e^- \rightarrow O^{2-}$
Electron-acceptor

Reduction (Redox) potential: Substrates vary in their tendency to be oxidized or reduced, wich is expressed as reduction potential (E_0') in volts (V). The free energy ($\Delta G^{0'}$) of the redox reaction is proportional to the difference of the reduction potential (E_0', standard conditions) of both half reactions.

$$\Delta G^{0'} = -n \cdot F \cdot \Delta E_0' = -n \cdot 96,5 \cdot \Delta E_0' \text{ (kJ/mol)}$$

n = number of transferred electrons
F = Faraday constant

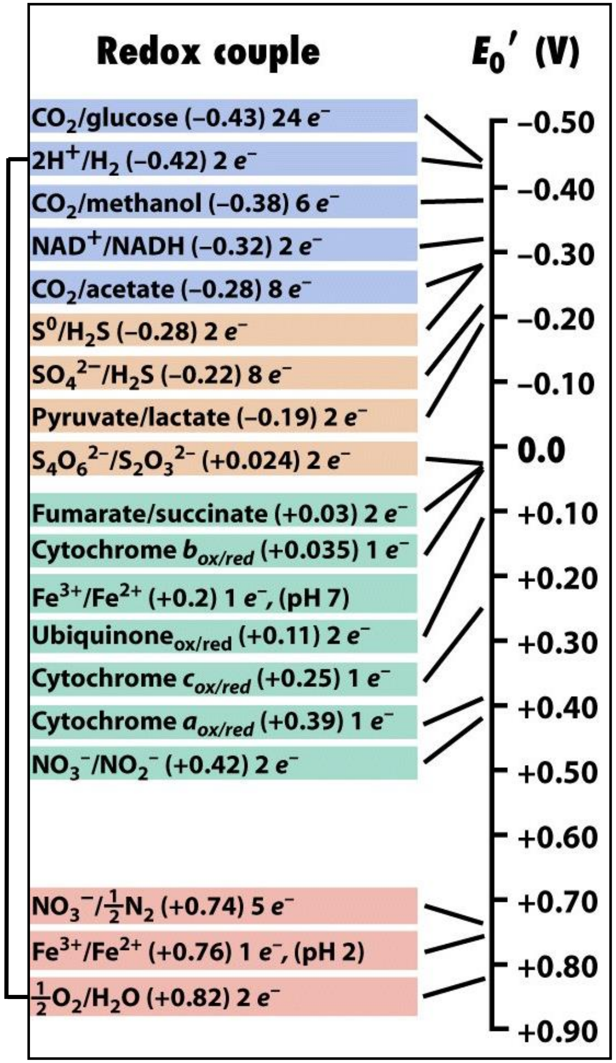


Fig. 5.8, 5.9 Brock Biology of Microorganisms (10th edition) (Madigan et al.)

The Electronen Tower

$\Delta G^{0'}$ of ATP synthesis or hydrolysis = 32 kJ/mol

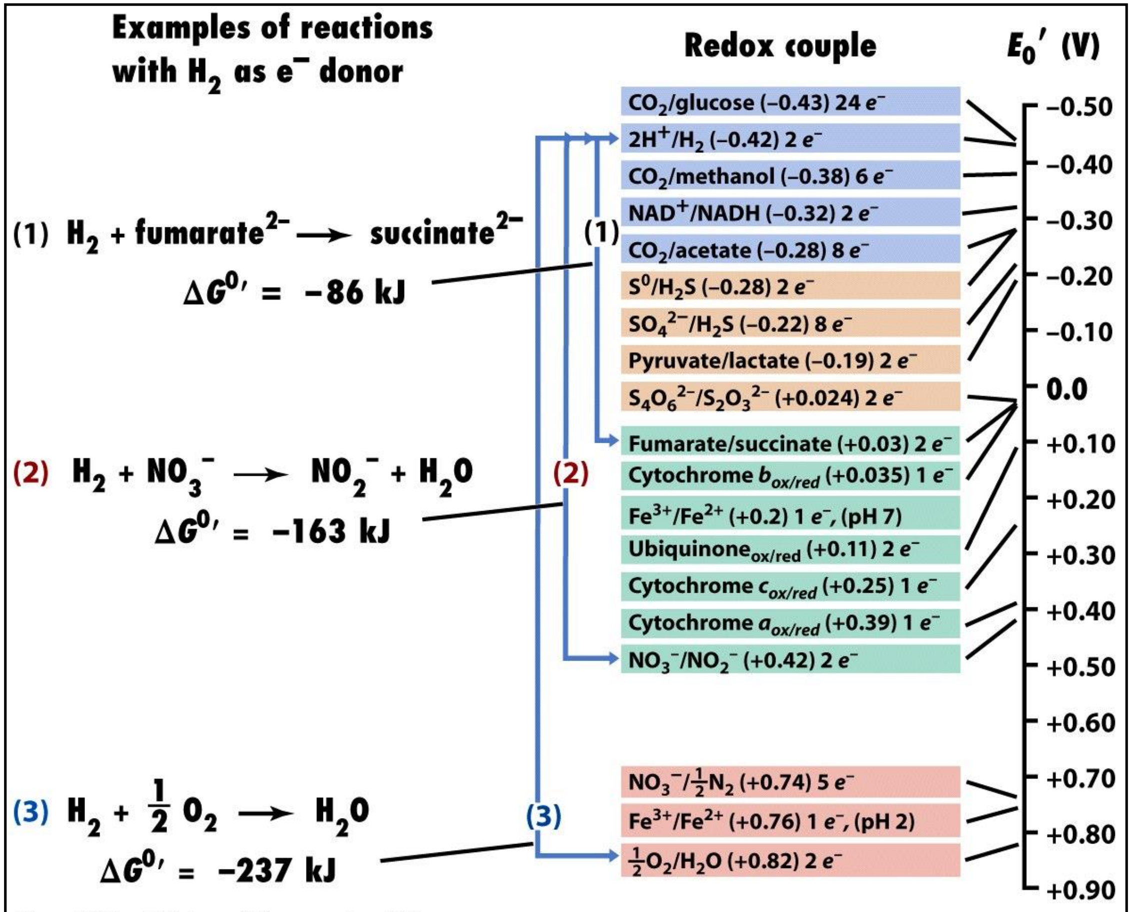


Figure 5-9 Brock Biology of Microorganisms 11/e
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Redoxpairs arranged from the strongest reductants (neg. reduction potential, at the top) to the strongest oxidants (positive reduction potential, at the bottom).

Electronen Carriers

Nicotinamide adenine dinucleotide (NAD(P)$^+$/NAD(P)H + H$^+$)
Free „carrier“ (coenzyme)

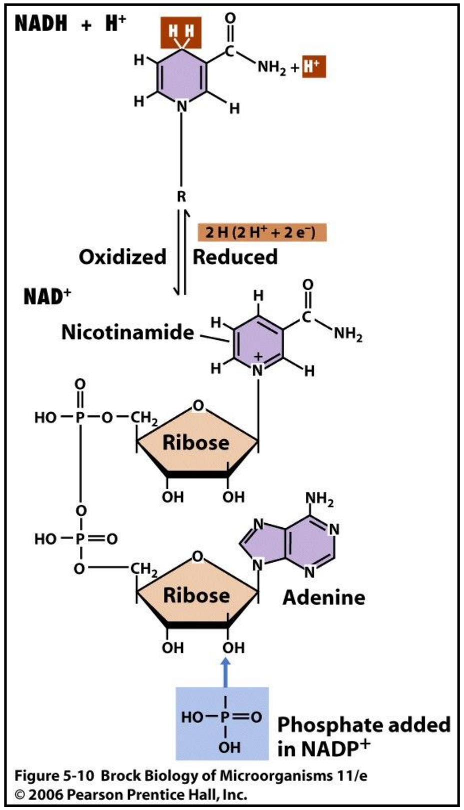

Figure 5-10 Brock Biology of Microorganisms 11/e
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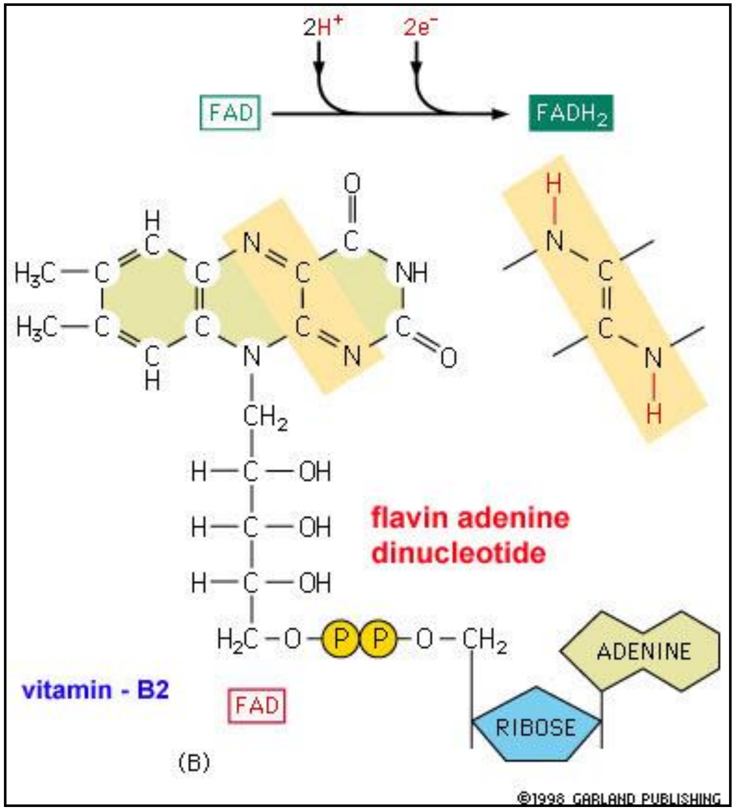
Flavin adenine dinucleotide (FAD) (FAD$^+$/FADH$_2$)
Bound „Carrier“ (prostethic group, e.g. succinate dehydrogenase)



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<u>Glyceraldehyde-3-phosphate dehydrogenase</u>:

Glyceraldehyde-3-phosphate + NAD$^+$ + P$_i$ ↔1,3-Diphosphoglycerate + NADH + H$^+$

Energy Currency of all Cells „ATP“

Energy provided by redoxreactions in the cell must be conserved, i.e. stored „Energy-Rich Phosphatebounds (Phophoanhydrides)“

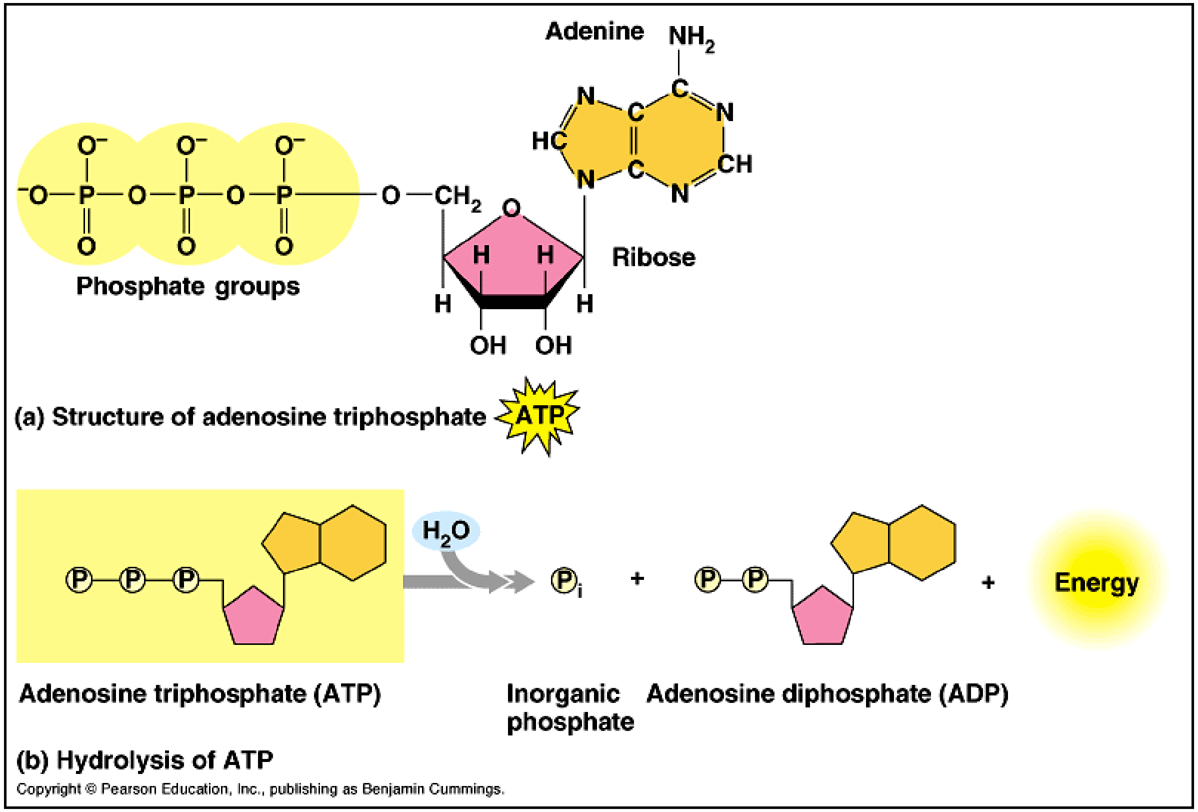

Fig. 6.8 Die Struktur und Hydrolyse von ATP.
Biology (6th edition, Campbell & Reece)

Energy Currency of all Cells „ATP“

$\Delta G^{0'}$ of ATP synthesis or hydrolysis = 32 kJ/mol

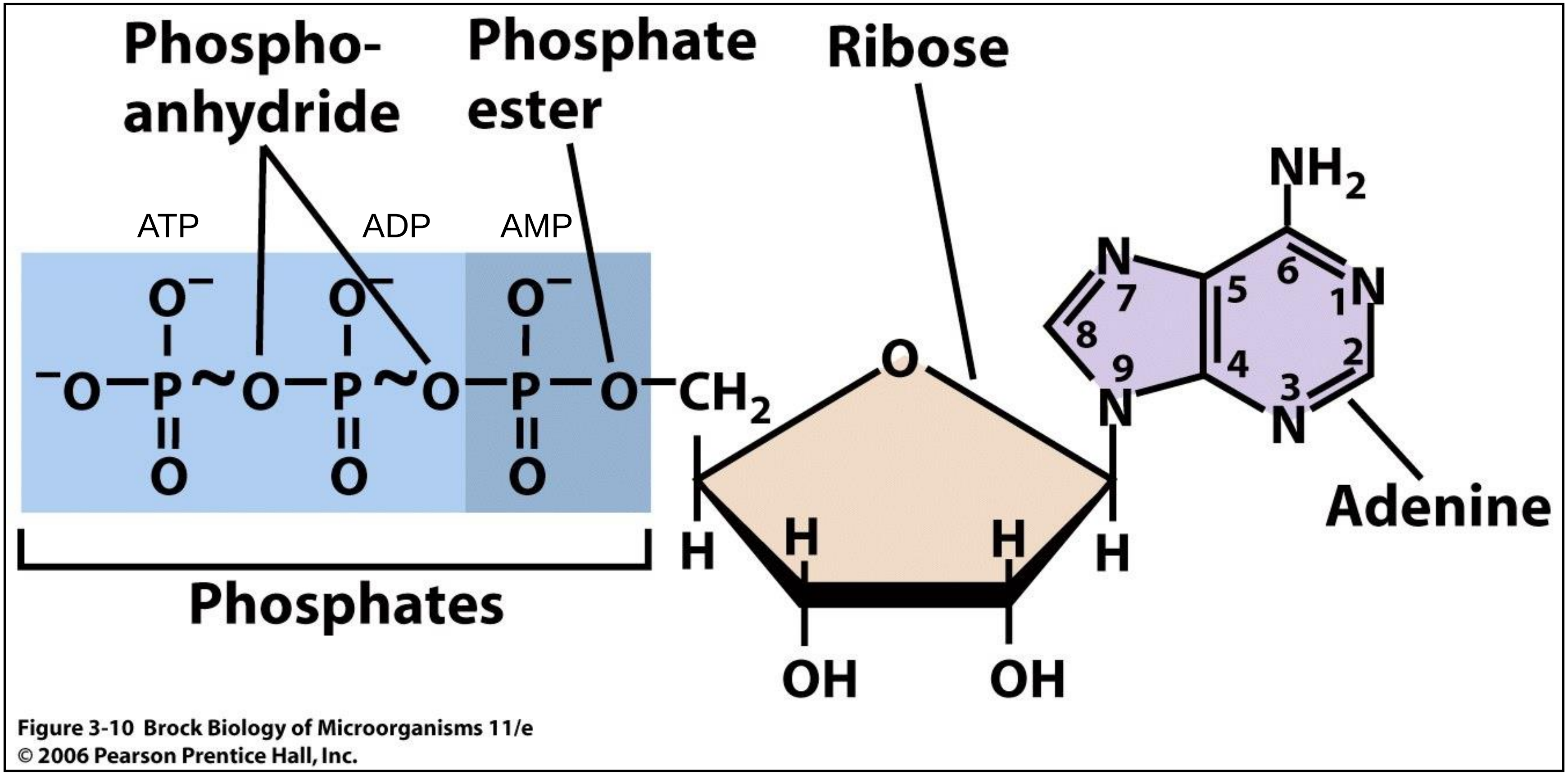

Figure 3-10 Brock Biology of Microorganisms 11/e
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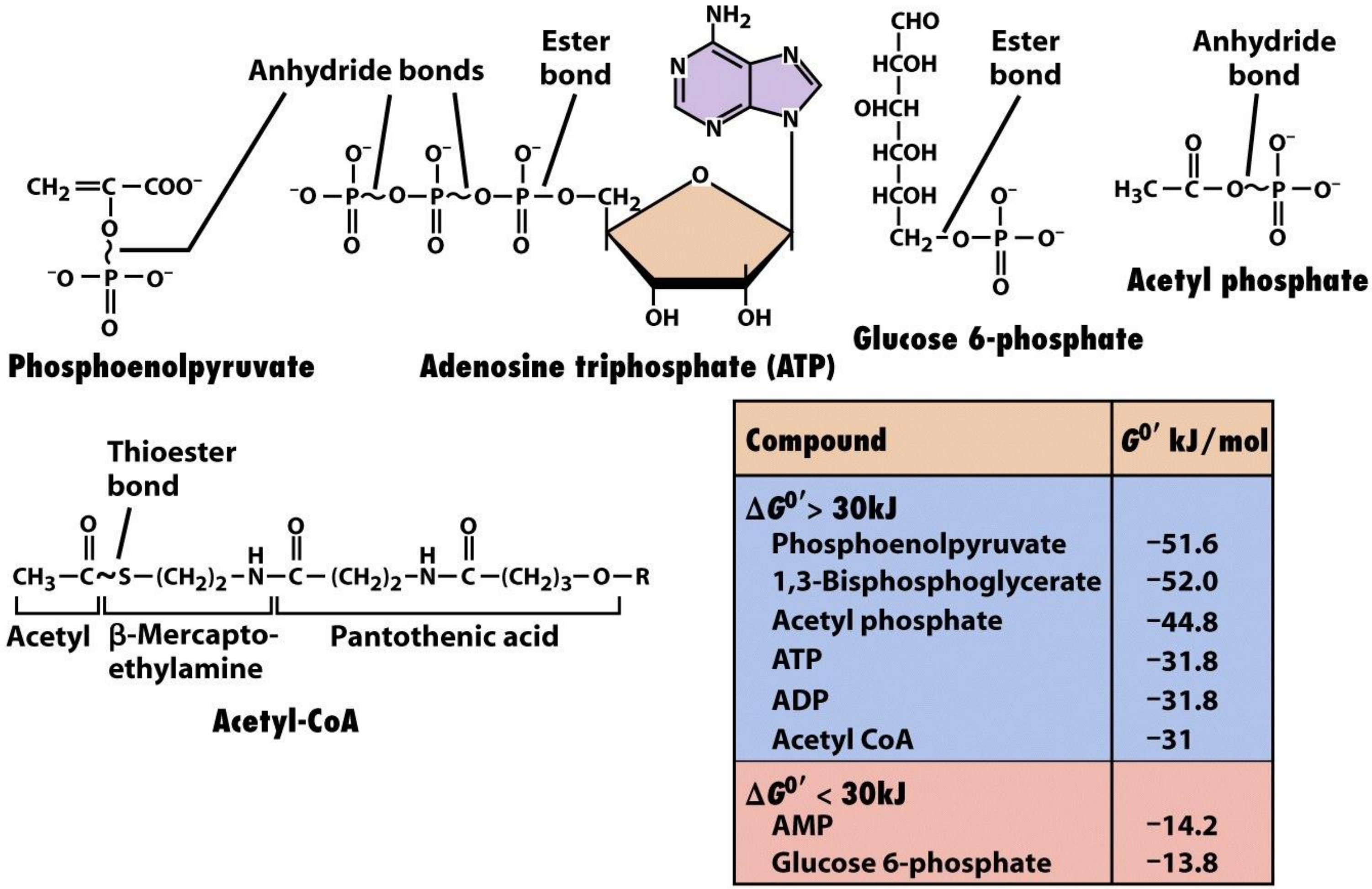
Energy-Rich Compounds



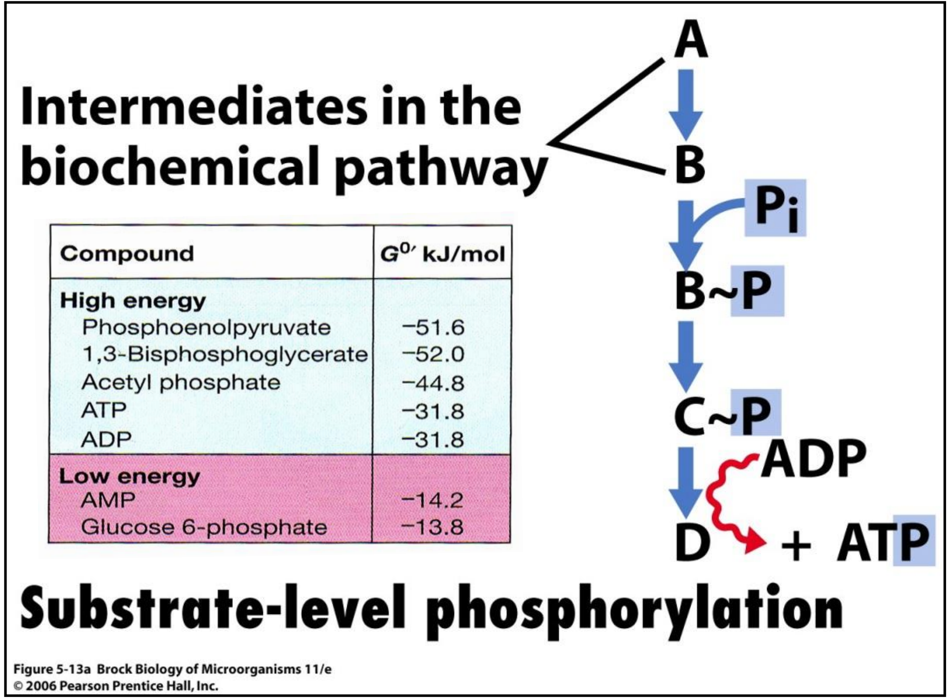
Compound	$G^{0\prime}$ kJ/mol
$\Delta G^{0\prime} > 30$kJ	
Phosphoenolpyruvate	−51.6
1,3-Bisphosphoglycerate	−52.0
Acetyl phosphate	−44.8
ATP	−31.8
ADP	−31.8
Acetyl CoA	−31
$\Delta G^{0\prime} < 30$kJ	
AMP	−14.2
Glucose 6-phosphate	−13.8

Figure 5-12 Brock Biology of Microorganisms 11/e

Basic Mechanisms of Energy Conservation

Substrate-level phosphorylation
Formation of energy-rich intermediates produces ATP

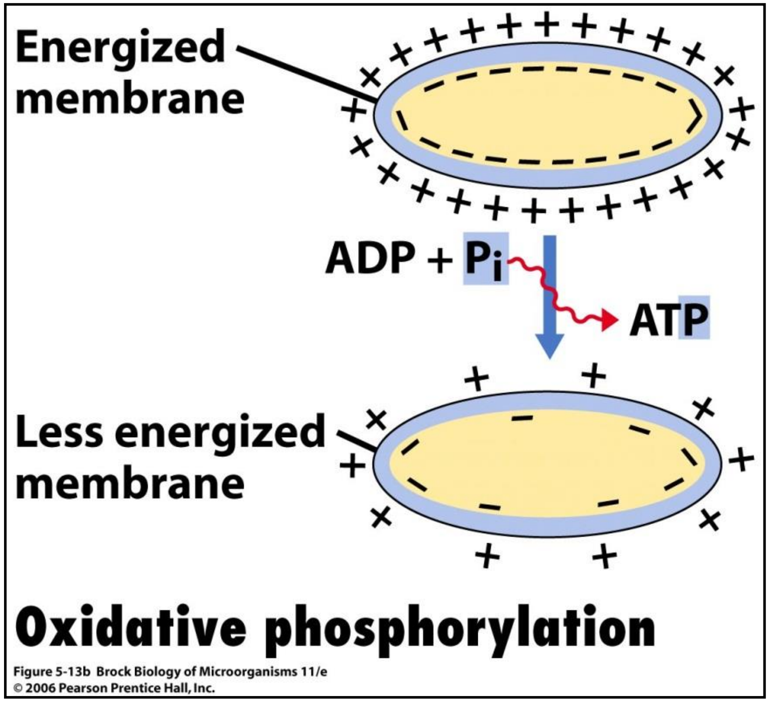
Elektron-transport phosphorylation
(Oxidative Phosphorylation)



Compound	$G^{0\prime}$ kJ/mol
High energy	
Phosphoenolpyruvate	−51.6
1,3-Bisphosphoglycerate	−52.0
Acetyl phosphate	−44.8
ATP	−31.8
ADP	−31.8
Low energy	
AMP	−14.2
Glucose 6-phosphate	−13.8

Substrate-level phosphorylation

Figure 5-13a Brock Biology of Microorganisms 11/e



Oxidative phosphorylation

Figure 5-13b Brock Biology of Microorganisms 11/e

Fig. 5.13 Brock Biology of Microorganisms (11th edition) (Madigan et al.)

EMP-Weg (Glycolysis)

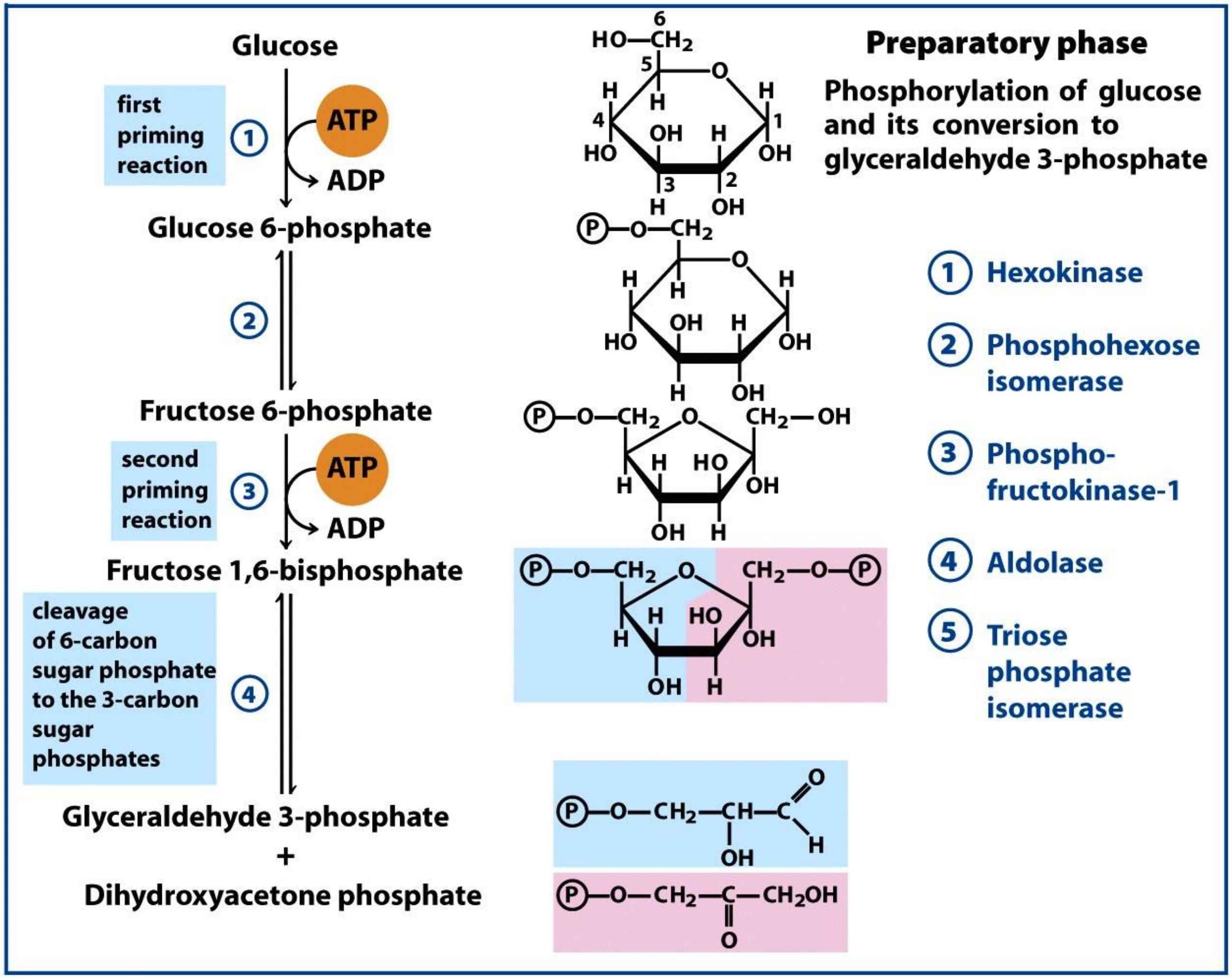
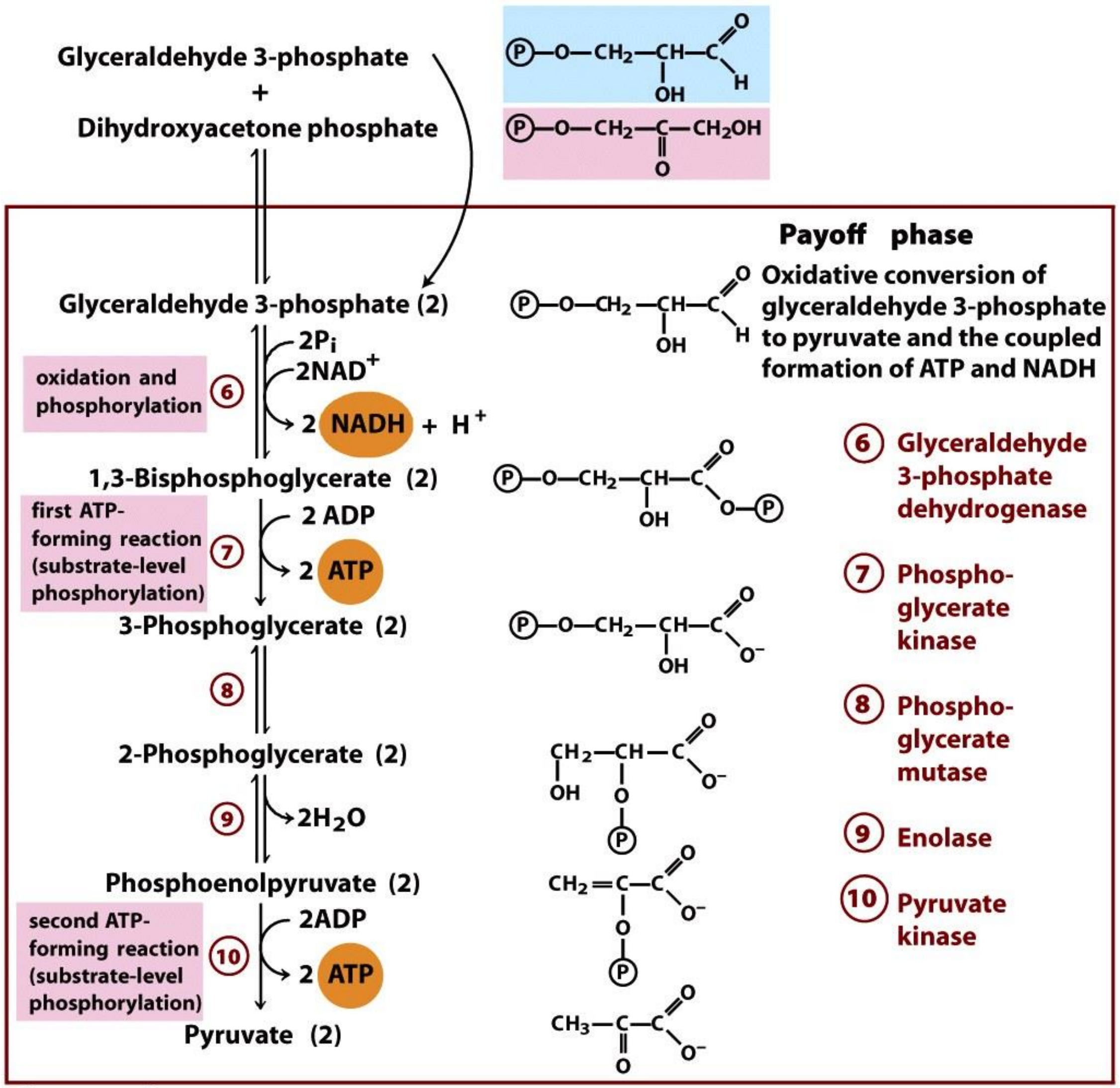


Figure 14-2a

Lehninger Principles of Biochemistry, Fifth Edition

EMP-Weg (Glycolysis)



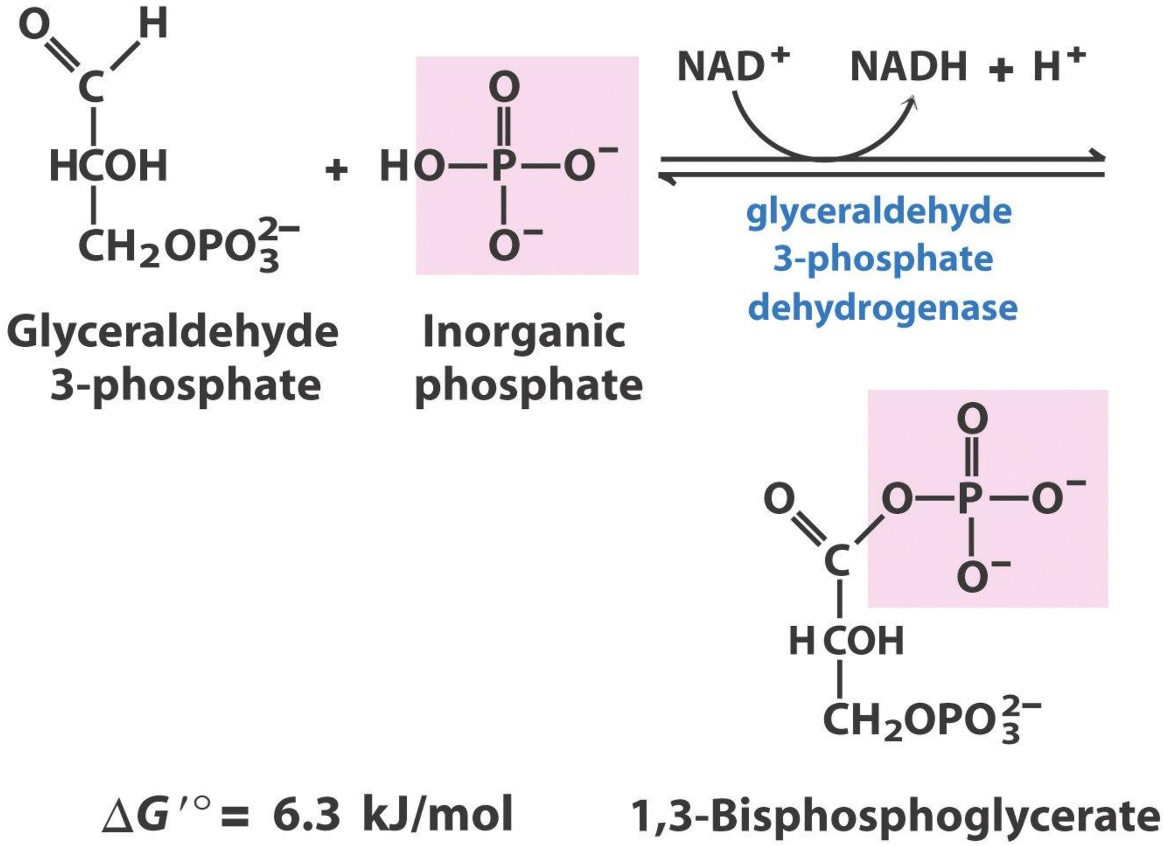
Oxidative conversion of glyceraldehyde 3-phosphate to pyruvate and the coupled formation of ATP and NADH

Figure 14-2b

Lehninger Principles of Biochemistry, Fifth Edition

Glyceraldehyde-3-phosphate dehydrogenase

- Which compound is oxidized/reduced?



Energetics of Glycolysis

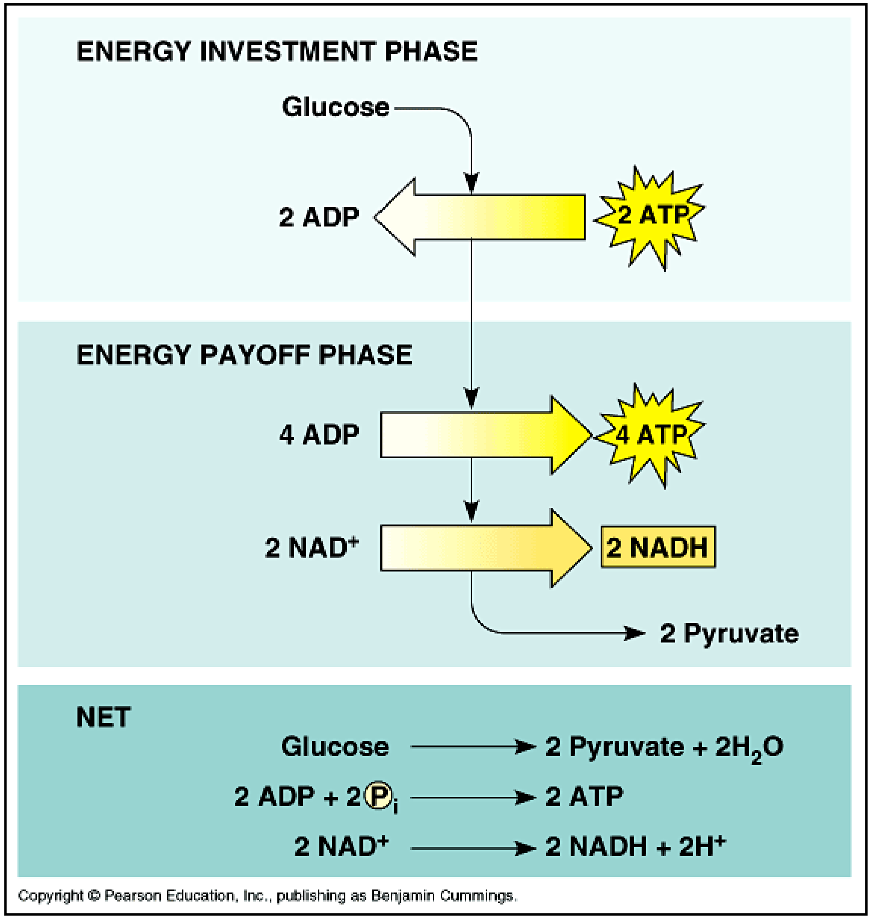


Fig. 9.8 **Die Glycolyse im Überblick.**
Biology (6th edition, Campbell & Reece)

Pyruvat Dehydrogenase and Citric Acid Cycle

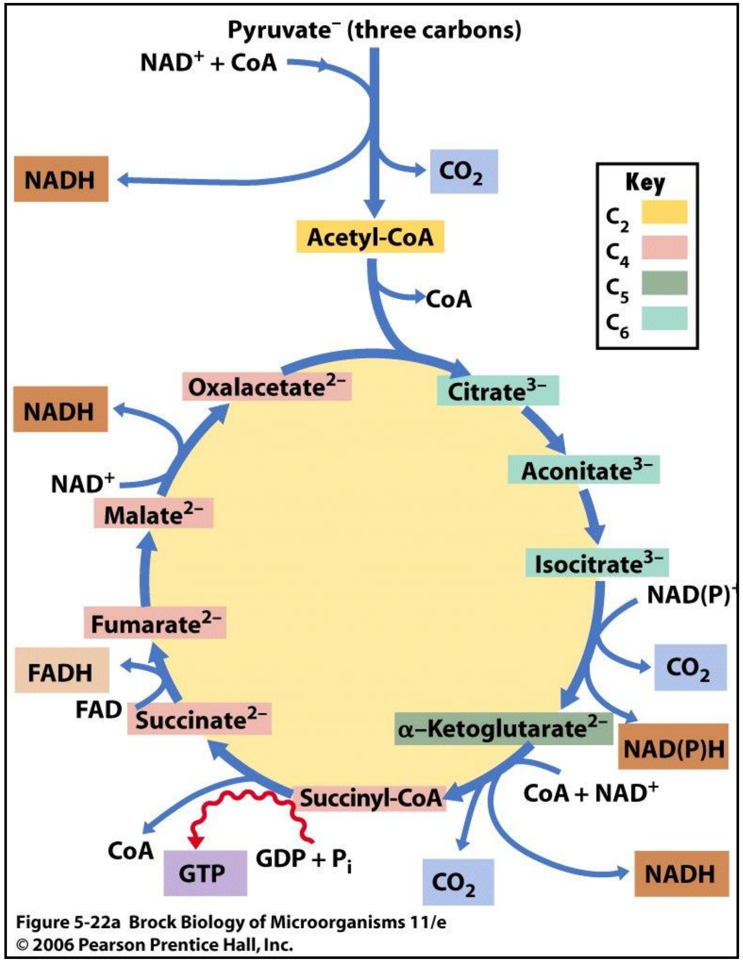


Figure 5-22a Brock Biology of Microorganisms 11/e
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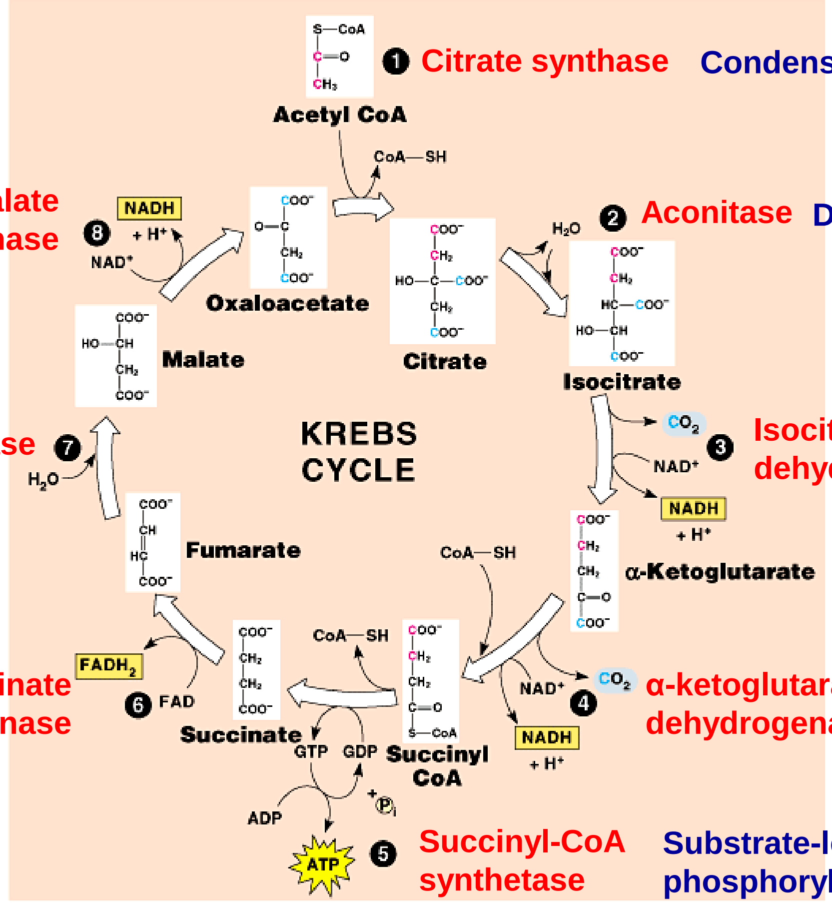
Citric Acid Cycle



① Citrate synthase Condensation

② Aconitase Dehydration/Hydration

③ Isocitrate dehydrogenase Oxidative decarboxylation

④ α-ketoglutarate dehydrogenase complex Oxidative decarboxylation

⑤ Succinyl-CoA synthetase Substrate-level phosphorylation

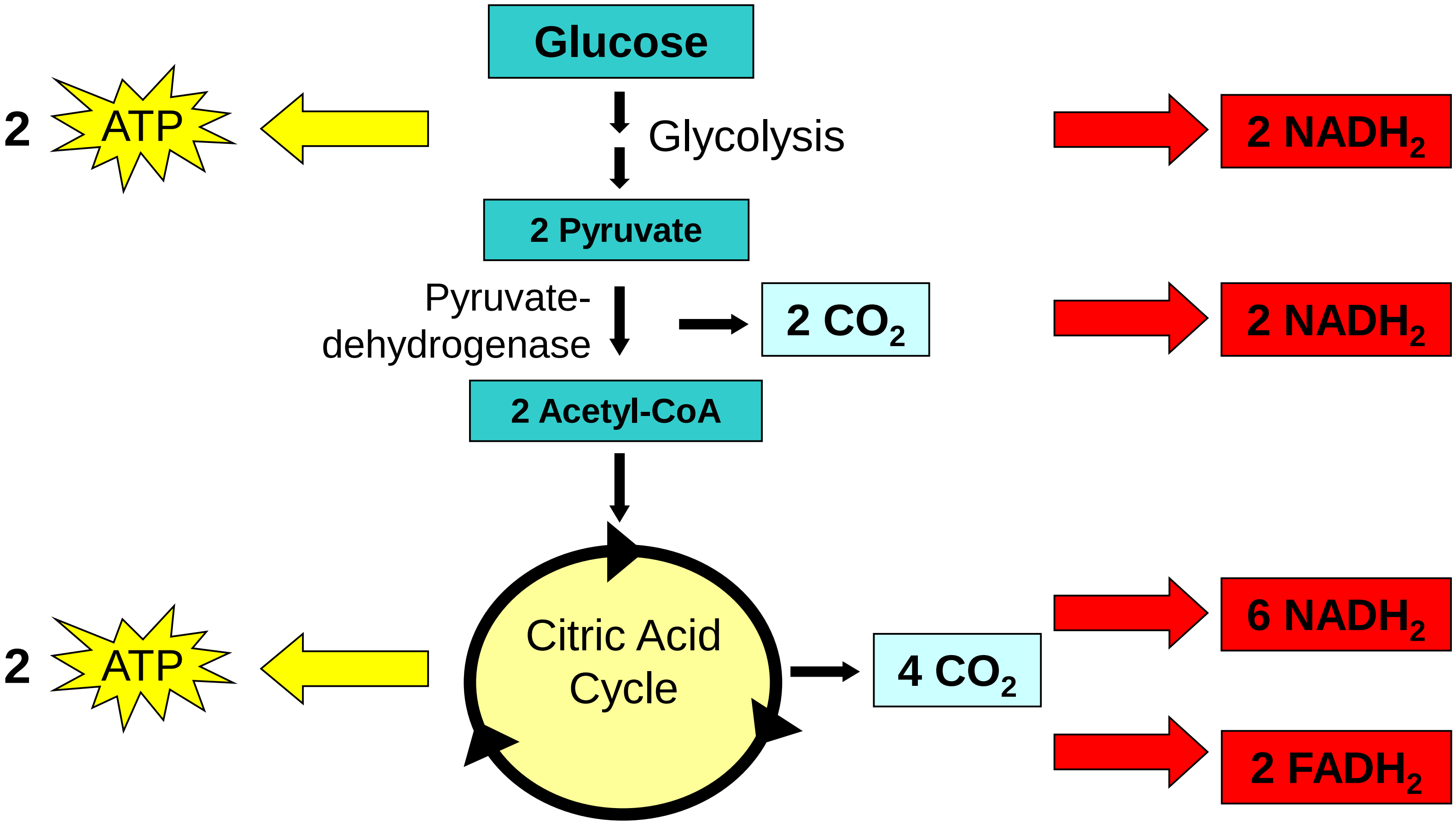
⑥ Succinate dehydrogenase Dehydrogenation

⑦ Fumarase Hydration

⑧ Malate dehydrogenase Dehydrogenation

Fig. 9.11 **The citric acid cycle.**
Biology (6th edition, Campbell & Reece)

Energetics of Carbohydrate Metabolism



Glucose

Glycolysis

2 Pyruvate

Pyruvate-dehydrogenase

2 Acetyl-CoA

Citric Acid Cycle

2 ATP

2 ATP

2 CO_2

4 CO_2

2 $NADH_2$

2 $NADH_2$

6 $NADH_2$

2 $FADH_2$

$$C_6H_{12}O_6 + 6\ H_2O + 4\ ADP + 4\ P_i \rightarrow 6\ CO_2 + 24\ [H] + 4\ ATP$$

Electron Transport Chain

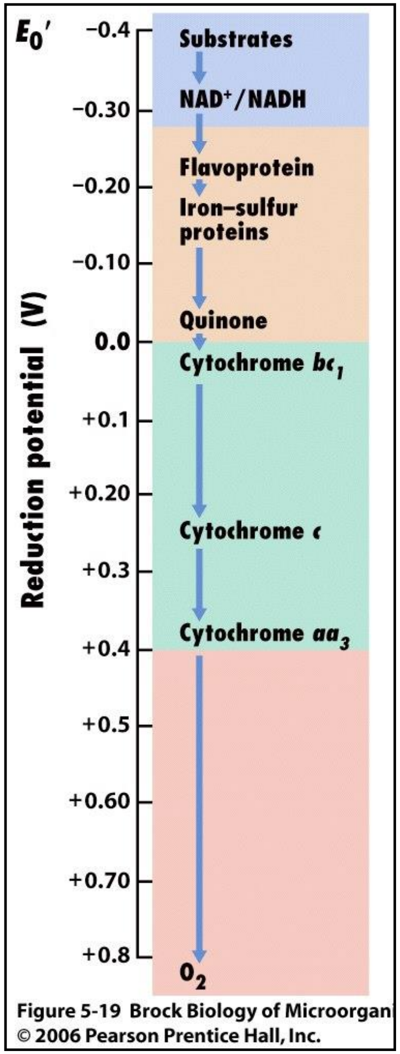


Figure 5-19 Brock Biology of Microorgani
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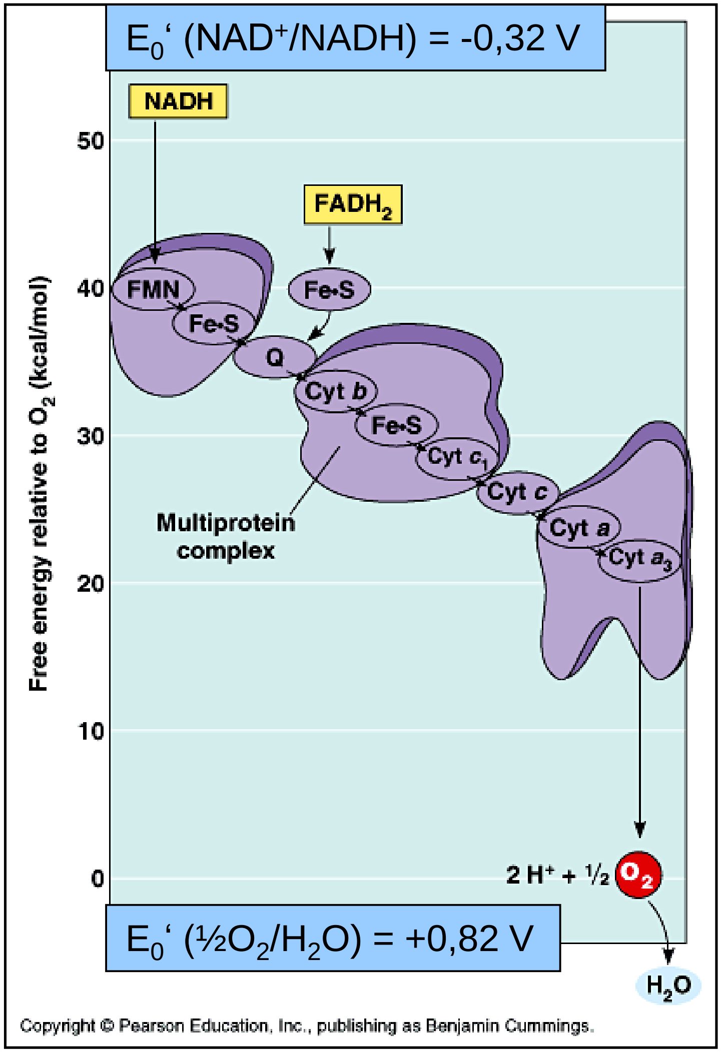
Fig. 5.19 Brock Biology of Microorganisms
(10th edition) (Madigan et al.)


E_0' ($NAD^+/NADH$) = -0,32 V

E_0' (½O_2/H_2O) = +0,82 V

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Fig. 9.13 Biology (6th edition, Campbell & Reece)

- The mitochondrial or bacterial electron transport chain (ETC) = a series of e^- carriers, operating together to transfer e^- from NADH and $FADH_2$ to a terminal e^- acceptor, O_2
- E^- flow from carriers with more negative reduction potentials (E_0) to carriers with more positive E_0

Atmungskette

(*Paracoccus denitrificans*)

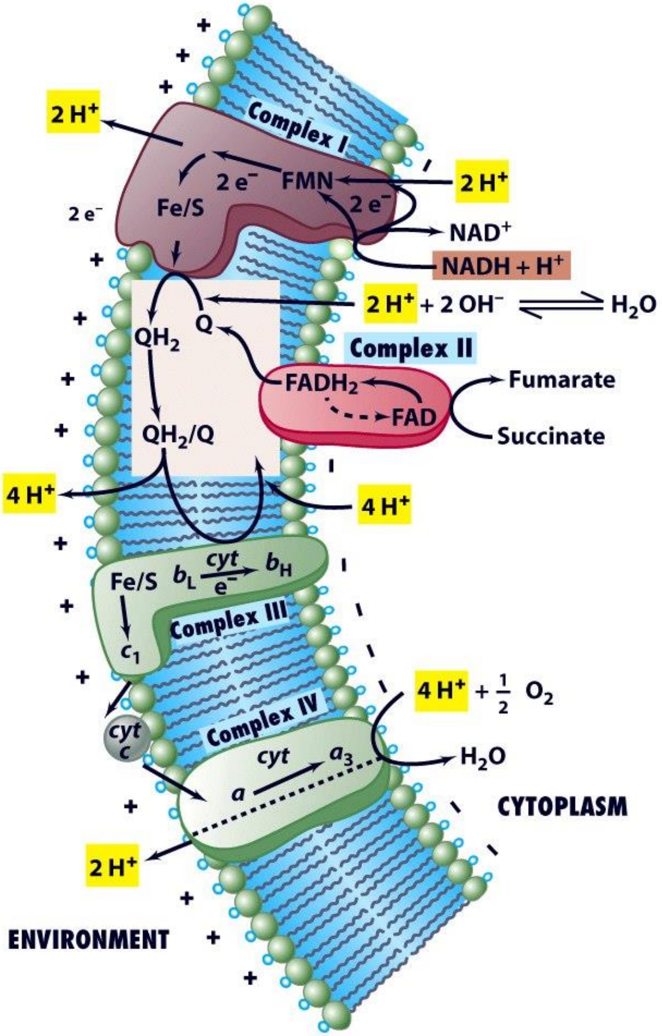

Figure 5-20 Brock Biology of Microorganisms 11/e
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Komplex I (**NADH + H^+**)
NADH-Chinon-Oxidoreductase,
NADH Dehydrogenase
FMN, FeS

Komplex II (**$FADH_2$**)
Succinate-Chinon-Oxidoreductase,
Succinat Dehydrogenase
FeS

Q – Coenzyme Q (Chinon)

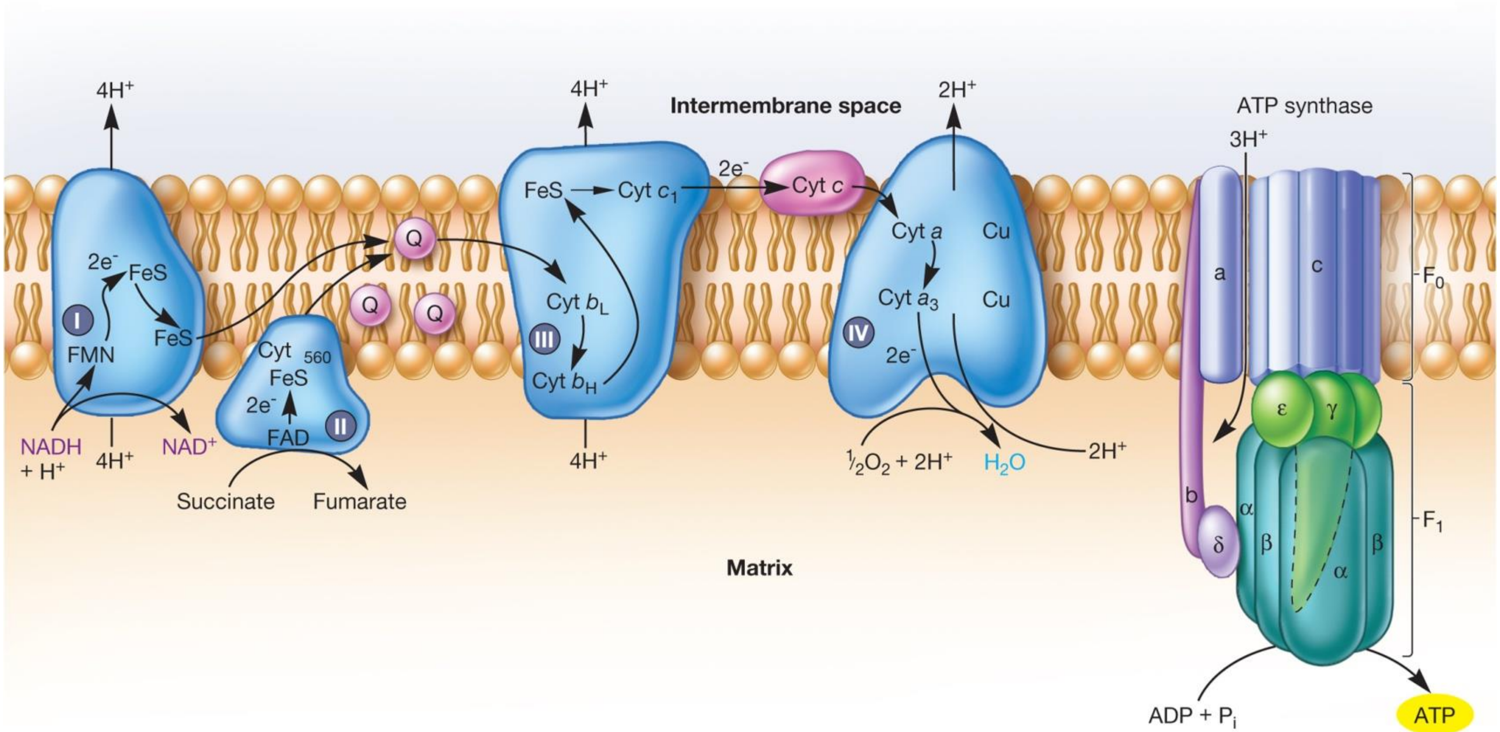
Komplex III
Cytochrom c-Reduktase (Cyt bc_1-Komplex)
Cytb, $Cytc_1$, FeS

Cyt c – Cytochrom c

Komplex IV
Cytochrom c-Oxidase (Cyt aa_3-Komplex)
Cyta, $Cytaa_3$, Kupfer (CuA, CuB)

Elektron Transport Chain

- In eukaryotes the e⁻ transport chain carriers are in the inner mitochondrial membrane, connected by coenzyme Q and cytochrome c
- E⁻ transfer accompanied by proton movement across inner mitochondrial membrane (**proton pumps**)



Chemiosmotic Model

- In this simple representation of the chemiosmotic theory applied to mitochondria, electrons from NADH and other oxidizable substrates pass through a chain of carriers arranged asymmetrically in the inner membrane.
- Electron flow is accompanied by proton transfer across the membrane, producing both a chemical gradient (ΔpH) and an electrical gradient (Δψ).
- The inner mitochondrial membrane is impermeable to protons; protons can reenter the matrix only through proton-specific channels (F_o). The **proton-motive force (PMF)** that drives protons back into the matrix provides the energy for ATP synthesis, catalyzed by the F_1 complex associated with F

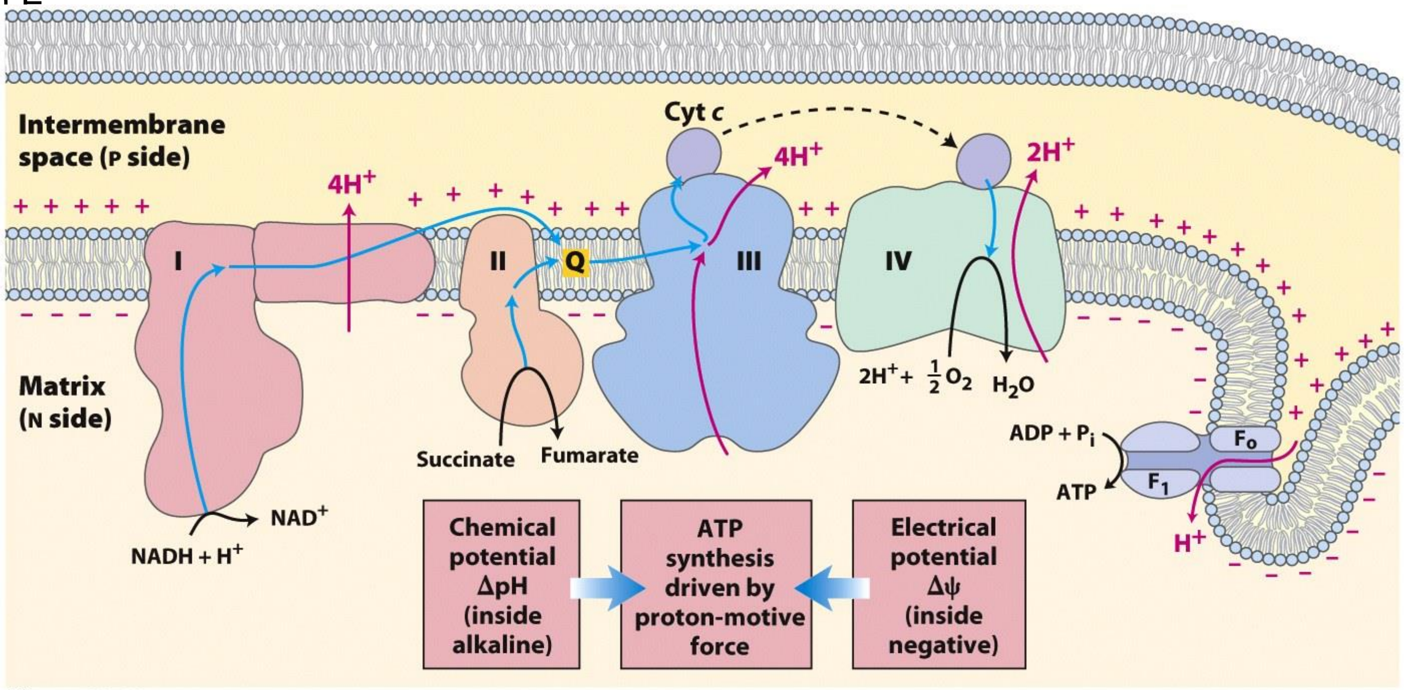
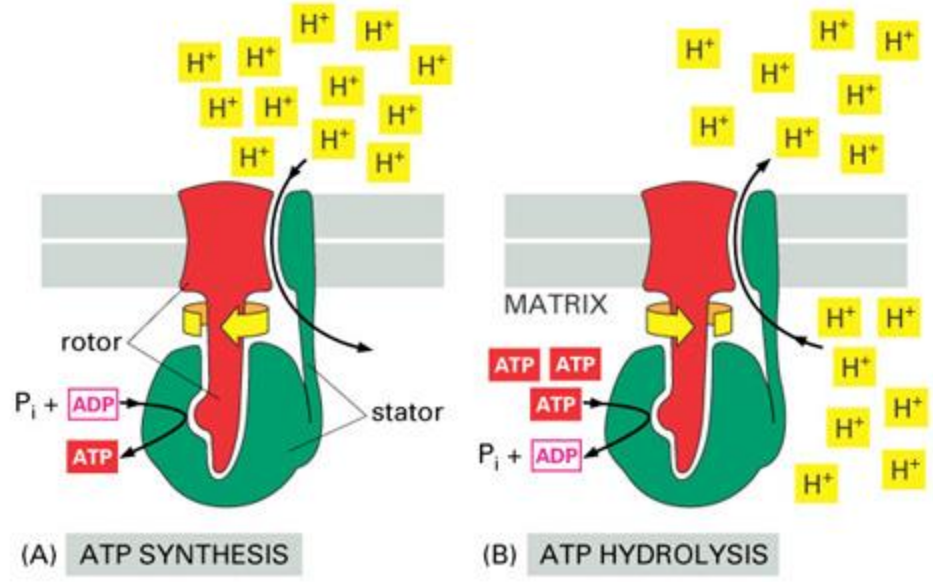


Figure 19-19
Lehninger Principles of Biochemistry, Fifth Edition

ATP-Synthase/ATPase

-reversibel



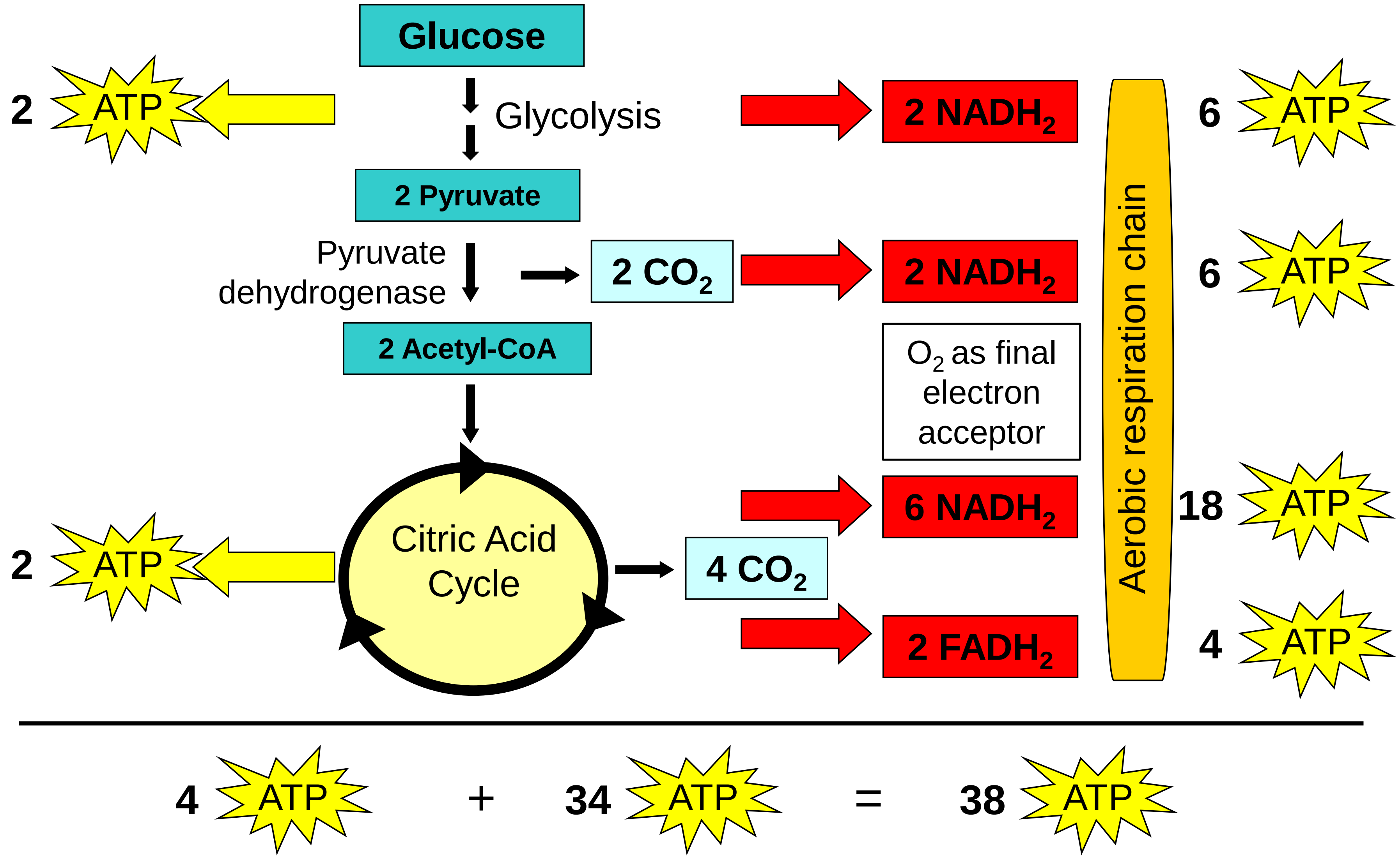
(A) ATP SYNTHESIS

(B) ATP HYDROLYSIS

Figure 14-15 Essential Cell Biology, 2/e. (© 2004 Garland Science)

Fig. 14.15 Essential Cell Biology (2nd edition, Alberts, Bray et al.)

Energetics of Carbohydrate Metabolism (Aerobic Respiration)



Glucose

Glycolysis

2 Pyruvate

Pyruvate dehydrogenase

2 CO_2

2 Acetyl-CoA

Citric Acid Cycle

4 CO_2

2 ATP

2 ATP

2 $NADH_2$

2 $NADH_2$

O_2 as final electron acceptor

6 $NADH_2$

2 $FADH_2$

Aerobic respiration chain

6 ATP

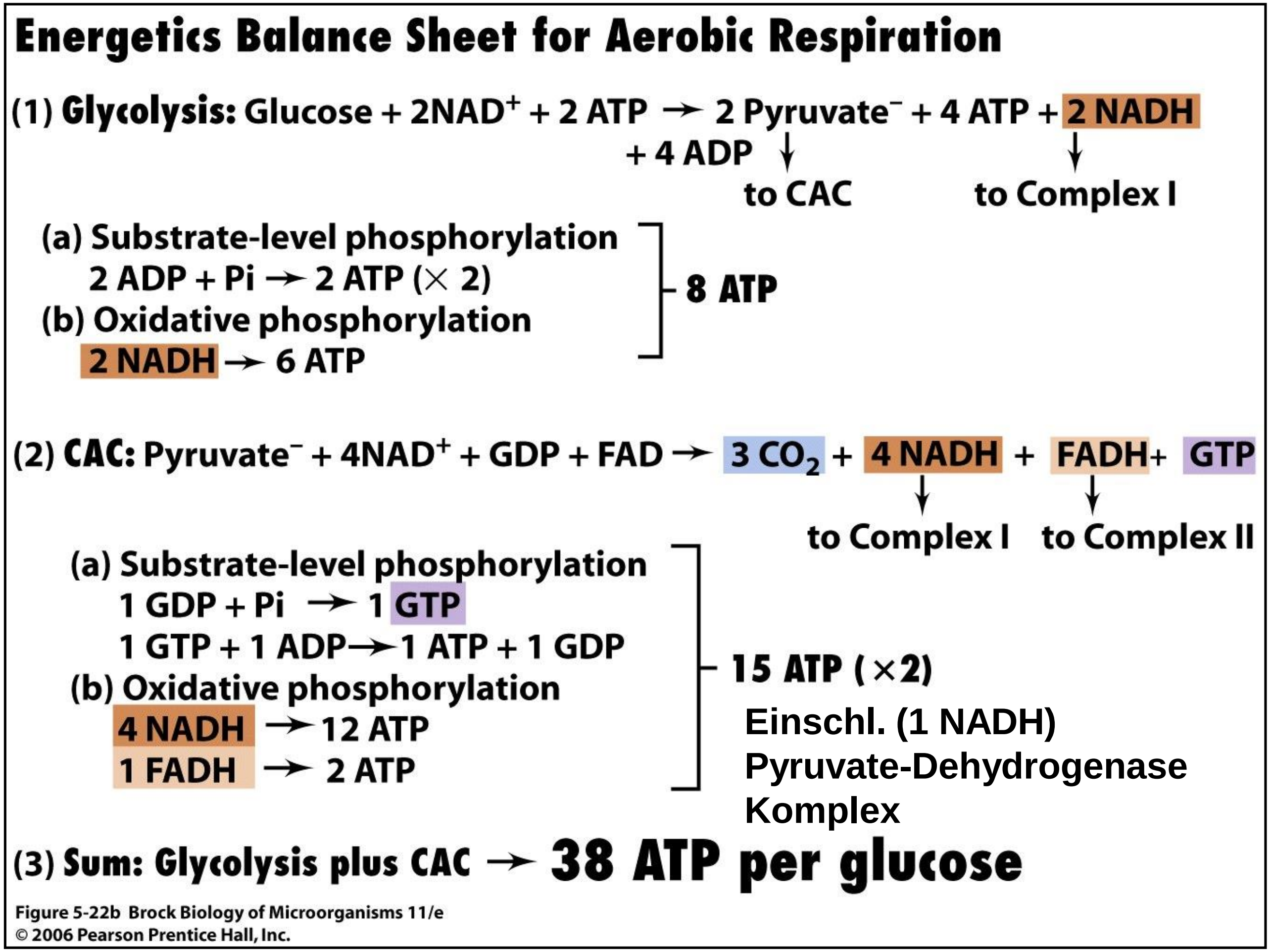
6 ATP

18 ATP

4 ATP

4 ATP + **34** ATP = **38** ATP

Energetics Balance Aerobic Respiration



Energetics Balance Sheet for Aerobic Respiration

(1) **Glycolysis:** Glucose + $2NAD^+$ + 2 ATP → 2 $Pyruvate^-$ + 4 ATP + 2 NADH
+ 4 ADP
Pyruvate ↓ to CAC
2 NADH ↓ to Complex I

(a) Substrate-level phosphorylation
2 ADP + Pi → 2 ATP (× 2)
(b) Oxidative phosphorylation
2 NADH → 6 ATP

→ **8 ATP**

(2) **CAC:** $Pyruvate^-$ + $4NAD^+$ + GDP + FAD → 3 CO_2 + 4 NADH + FADH+ GTP
4 NADH ↓ to Complex I
FADH ↓ to Complex II

(a) Substrate-level phosphorylation
1 GDP + Pi → 1 GTP
1 GTP + 1 ADP → 1 ATP + 1 GDP
(b) Oxidative phosphorylation
4 NADH → 12 ATP
1 FADH → 2 ATP

→ **15 ATP (×2)**

Einschl. (1 NADH)
Pyruvate-Dehydrogenase
Komplex

(3) **Sum: Glycolysis plus CAC → 38 ATP per glucose**

Figure 5-22b Brock Biology of Microorganisms 11/e
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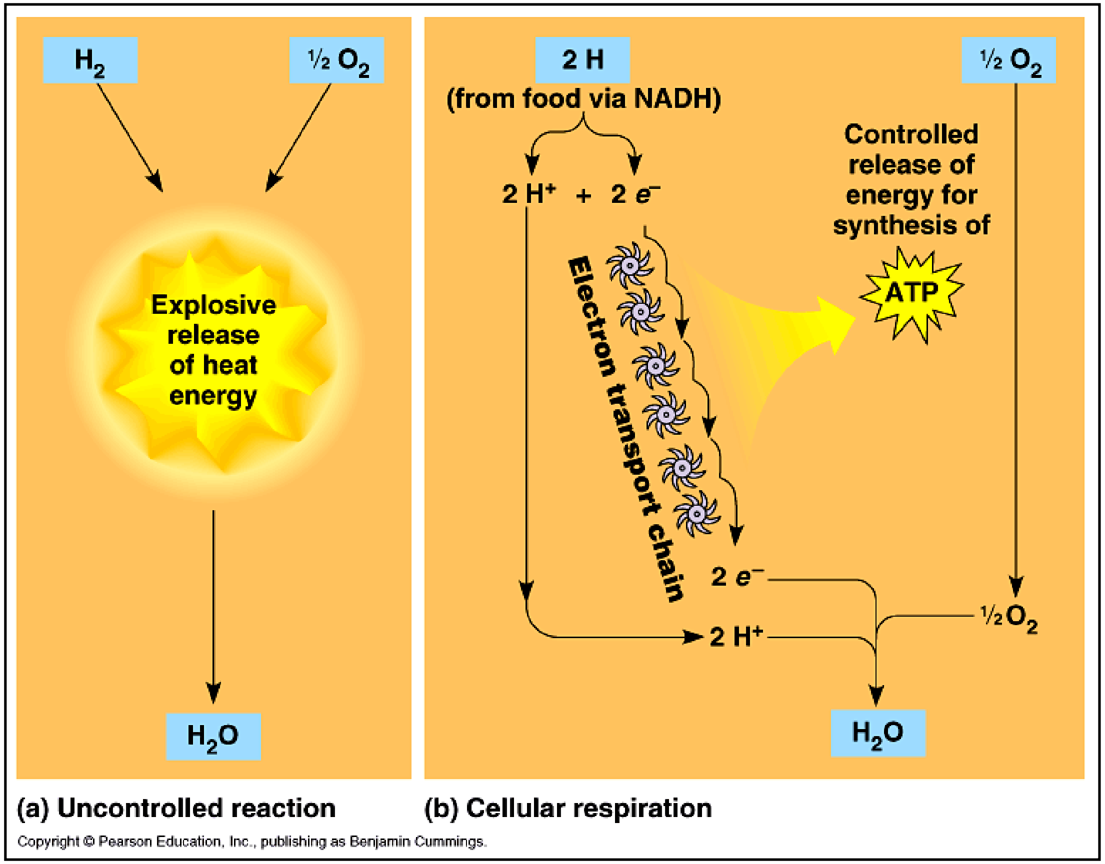
ATP-Synthese (ΔG^{0}‘=-31,8 KJ/mol)

Chemical Principles

Example Cellular Respiration



(a) Uncontrolled reaction **(b) Cellular respiration**

Fig. 9.5 Biology (6th edition, Campbell & Reece)

PMF Energized Membrane

Proton-motive force (PMF)

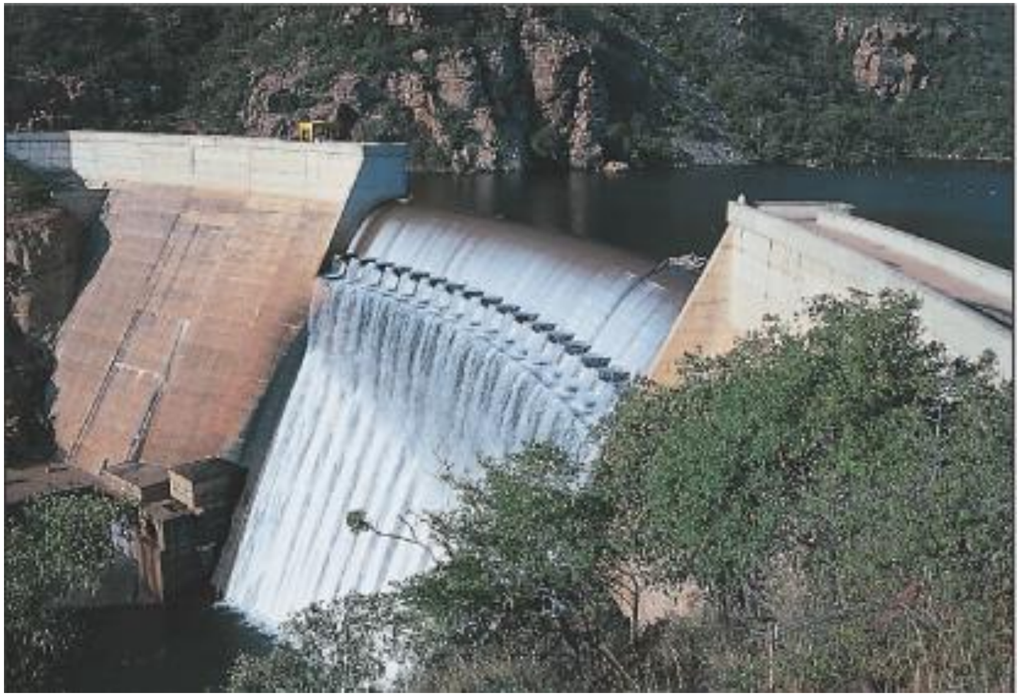


Figure 12-11 Essential Cell Biology, 2/e. (© 2004 Garland Science)

Fermentation

Atmung/Fermentation

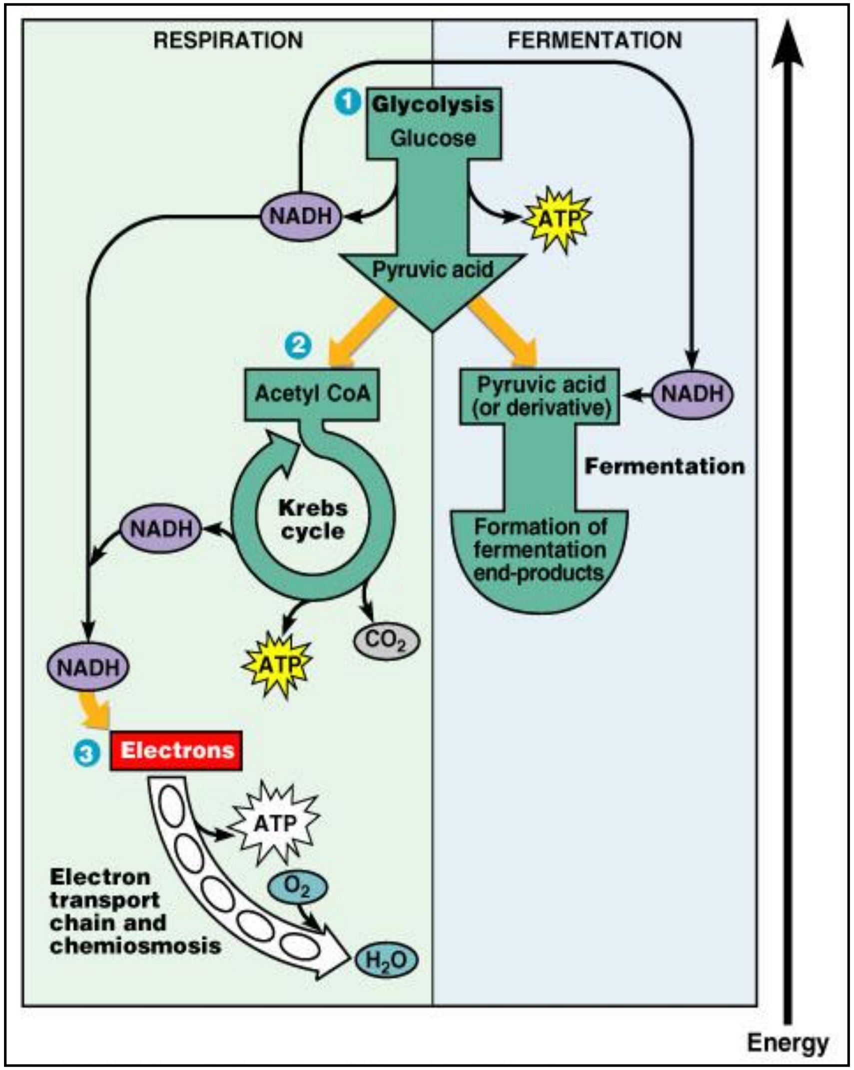
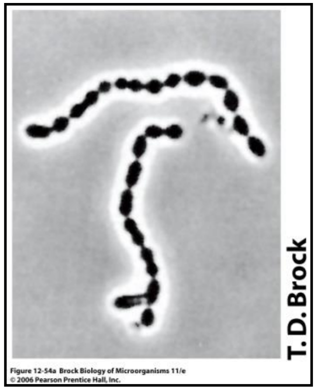
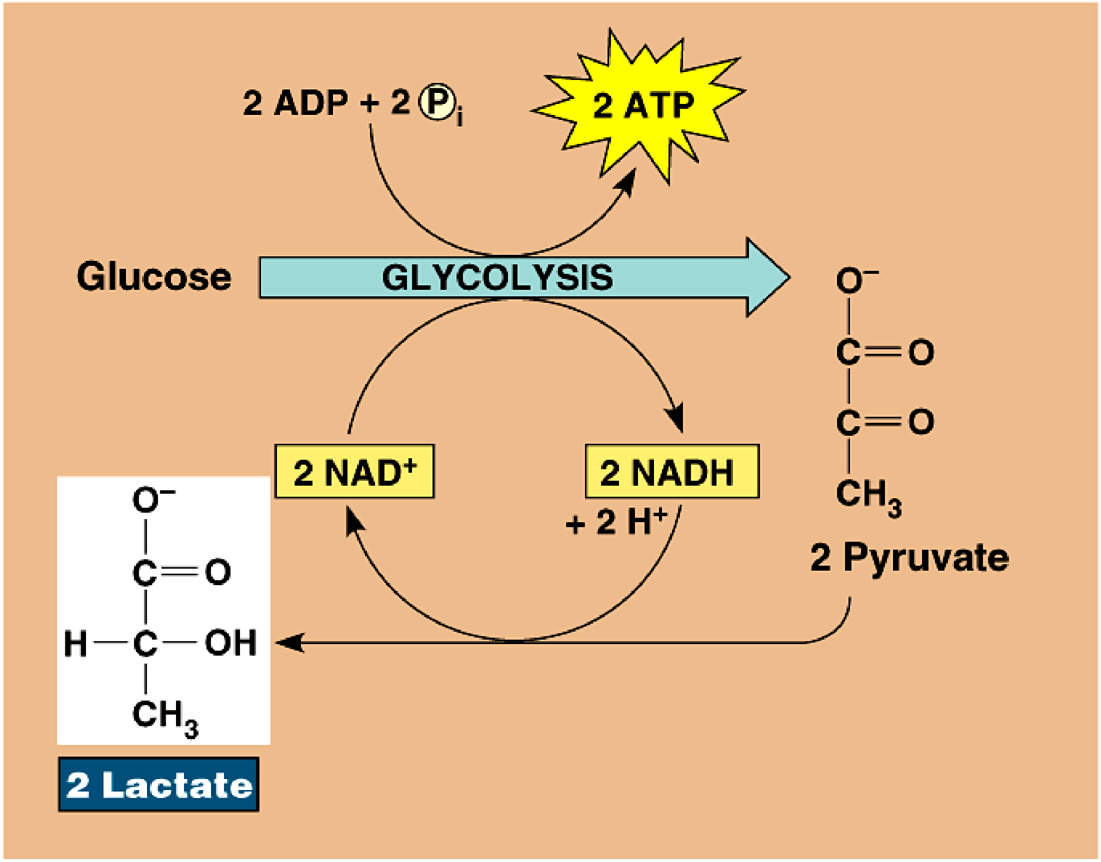


Fig. 5.14 Microbiology: An Introduction (Tortora, Funke, Case)

Lacitc Acid Fermentation



Lactococcus lactis



(b) Lactic acid fermentation

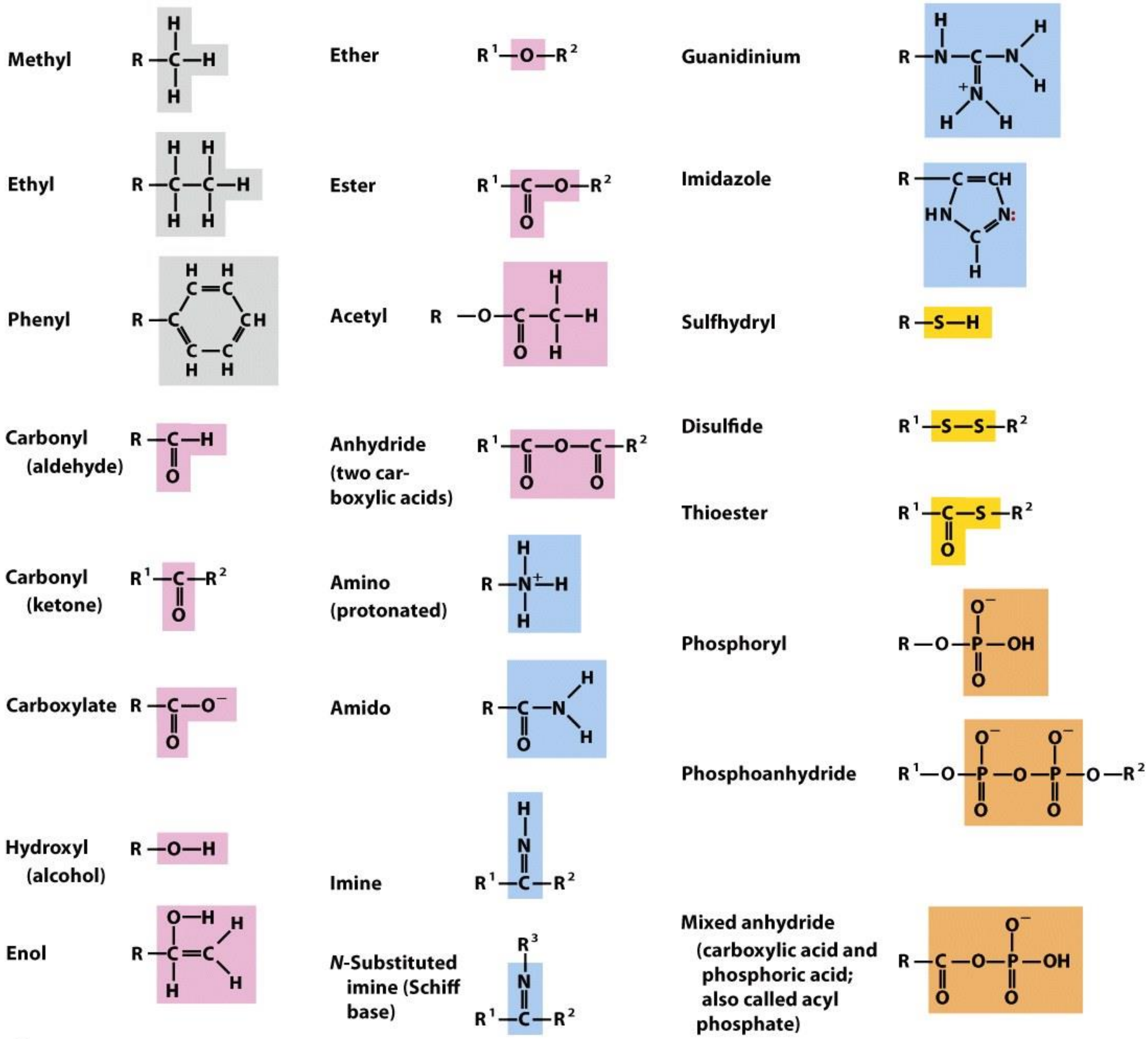


Figure 1-15

Lehninger Principles of Biochemistry, Fifth Edition

TABLE 1.1 SI units commonly used in biochemistry

Physical quantity	*SI unit*	*Symbol*
Length	meter	m
Mass	gram	g
Amount	mole	mol
Volume	liter[a]	L
Energy	joule	J
Electric potential	volt	V
Time	second	s
Temperature	kelvin[b]	K

---

[d] 1 liter = centimeter.

[b] 273K = 0°C

Table 1-1 Principles of Biochemistry, 4/e

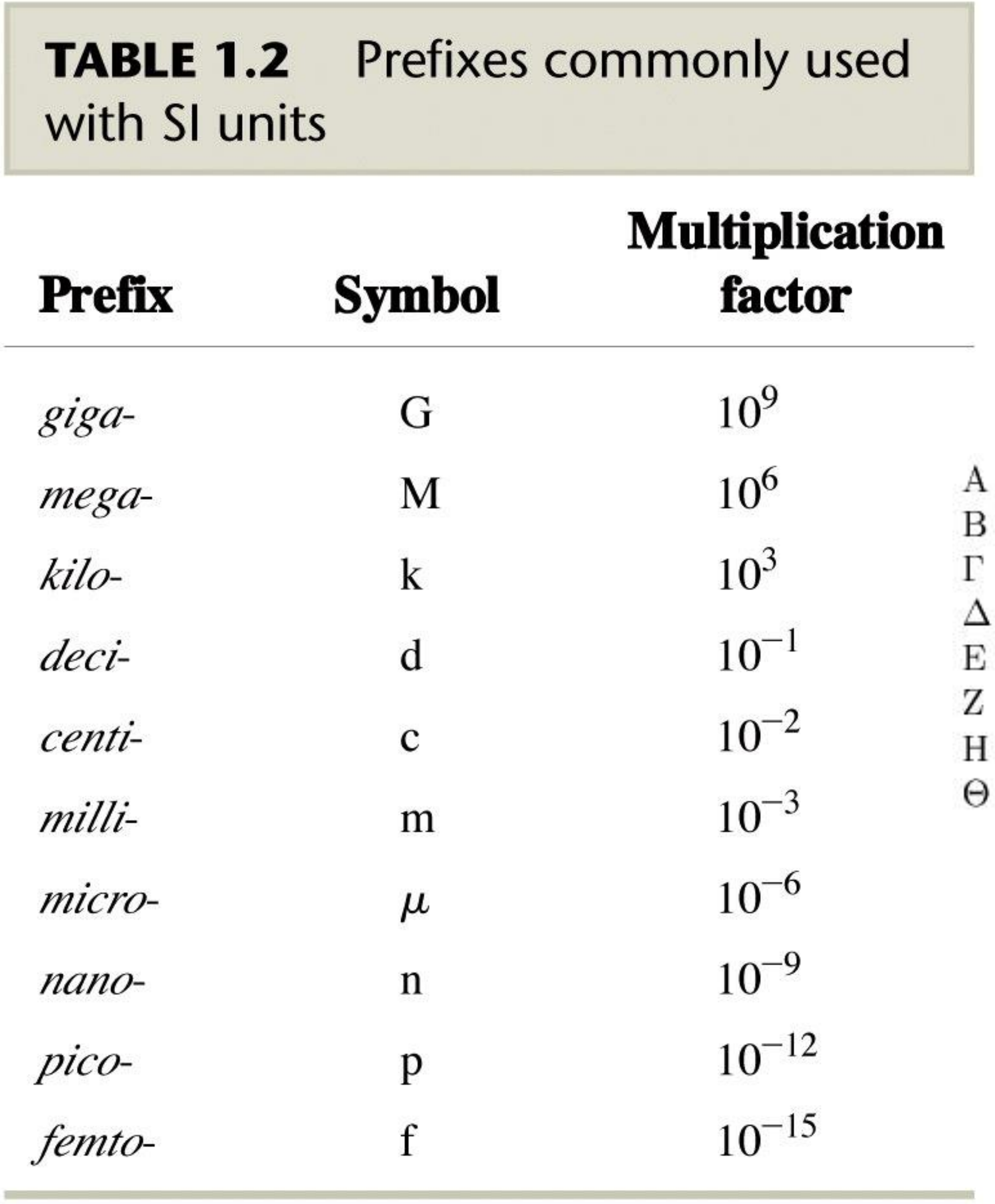
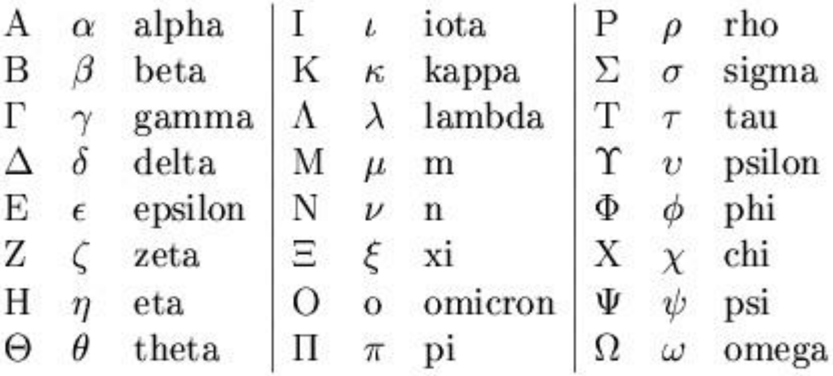


TABLE 1.2 Prefixes commonly used with SI units

Prefix	Symbol	Multiplication factor
giga-	G	10^{9}
mega-	M	10^{6}
kilo-	k	10^{3}
deci-	d	10^{-1}
centi-	c	10^{-2}
milli-	m	10^{-3}
micro-	μ	10^{-6}
nano-	n	10^{-9}
pico-	p	10^{-12}
femto-	f	10^{-15}

Table 1-2 Principles of Biochemistry, 4/e

Das griechische Alphabet



A	α	alpha	I	ι	iota	P	ρ	rho
B	β	beta	K	κ	kappa	Σ	σ	sigma
Γ	γ	gamma	Λ	λ	lambda	T	τ	tau
Δ	δ	delta	M	μ	m	Υ	υ	psilon
E	ϵ	epsilon	N	ν	n	Φ	ϕ	phi
Z	ζ	zeta	Ξ	ξ	xi	X	χ	chi
H	η	eta	O	o	omicron	Ψ	ψ	psi
Θ	θ	theta	Π	π	pi	Ω	ω	omega