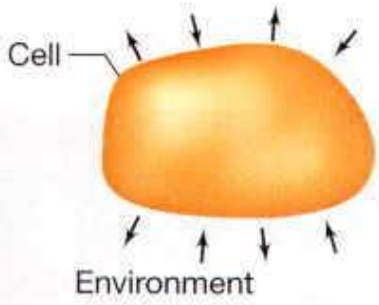
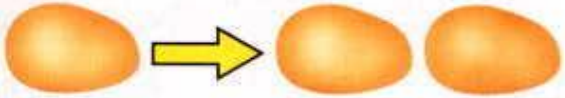
Die Zellfabrik

Aufbau
Moleküle – Strukturen
Nährstoffversorgung
Lebensbedingungen

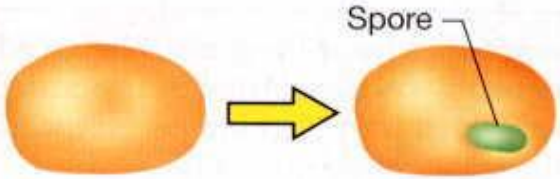
Basisfunktionen der Zelle



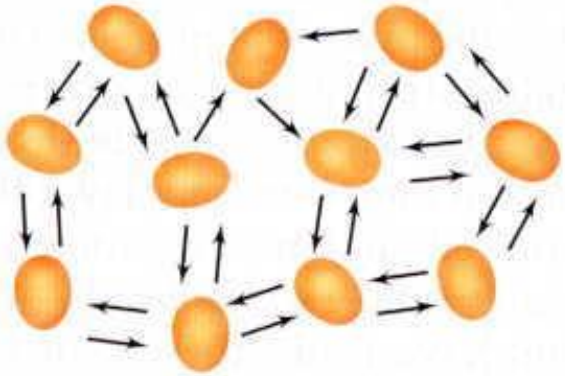
1. Metabolism
Uptake of chemicals from the environment, their transformation within the cell, and elimination of wastes into the environment. The cell is thus an *open* system.



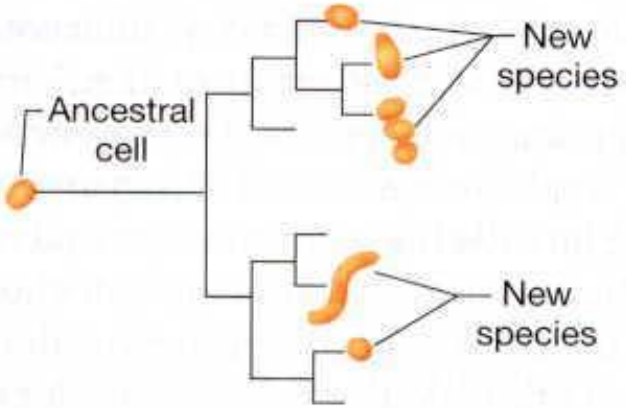
2. Reproduction (growth)
Chemicals from the environment are turned into new cells under the direction of preexisting cells.



3. Differentiation
Formation of a new cell structure such as a spore, usually as part of a cellular *life cycle*.

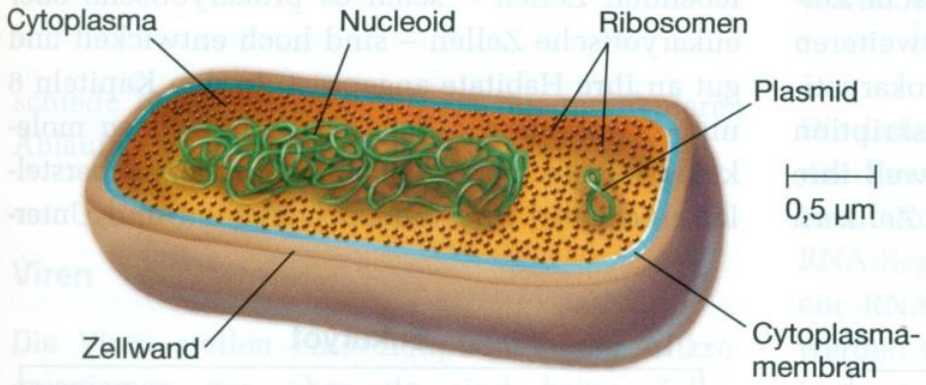


4. Communication
Cells *communicate* or *interact* primarily by means of chemicals that are released or taken up.

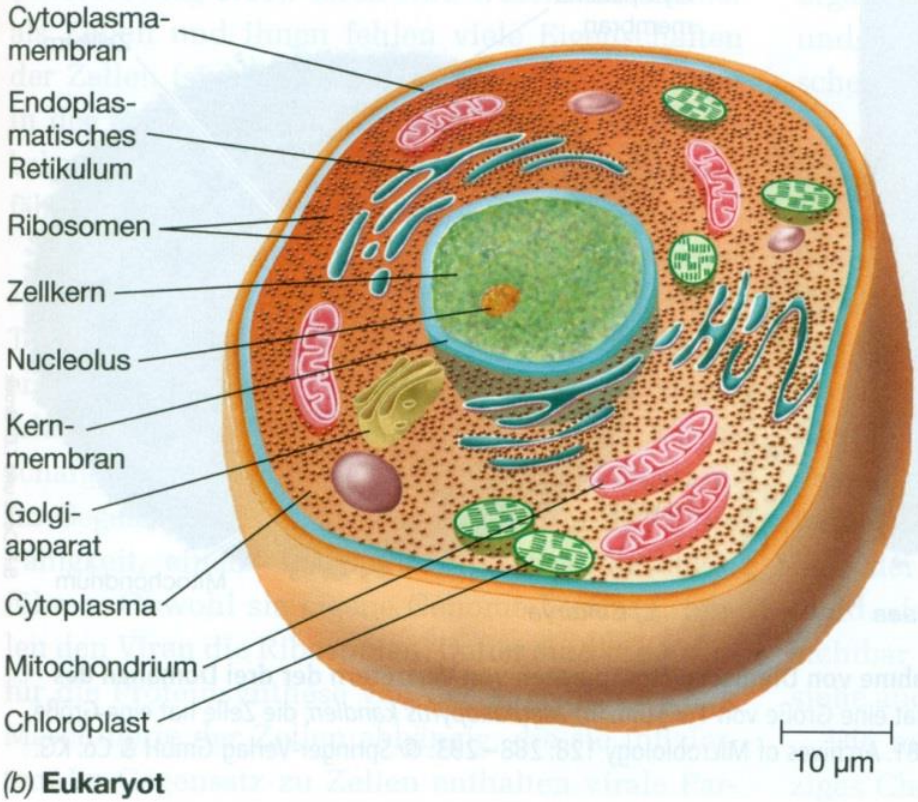


5. Evolution
Cells *evolve* to display new biological properties. Phylogenetic trees show the evolutionary relationships between cells.

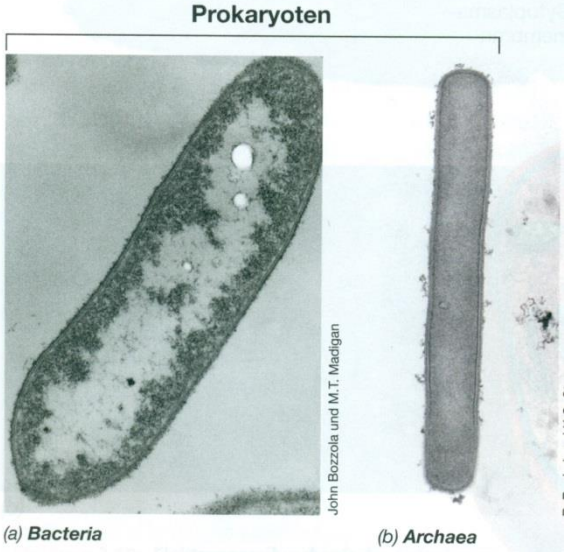
Zellstrukturen



(a) **Prokaryot**



(b) **Eukaryot**



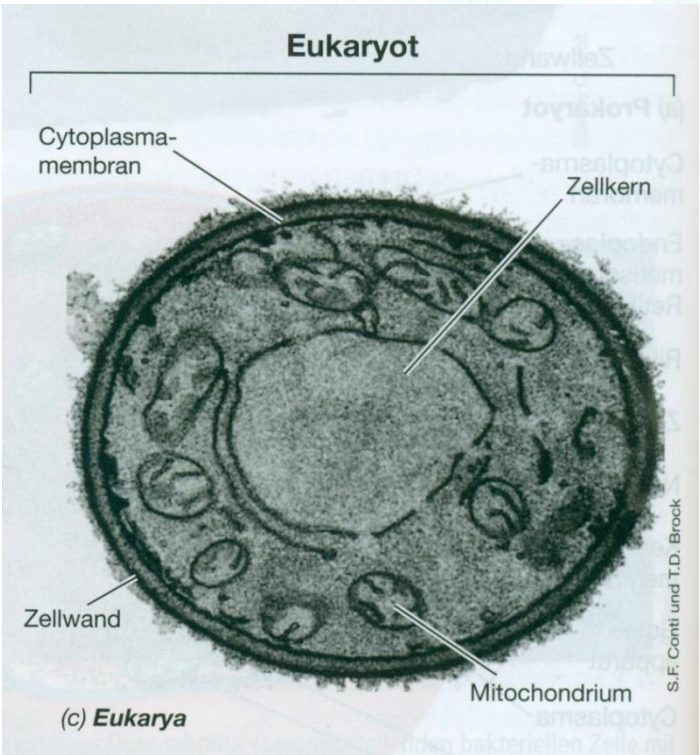


TABLE 2.2 Chemical composition of a prokaryotic cell[a]

Molecule	Percent of dry weight[b]	Molecules per cell	Different kinds
Total macromolecules	96	24,610,000	~2500
Protein	55	2,350,000	~1850
Polysaccharide	5	4,300	2[c]
Lipid	9.1	22,000,000	4[d]
Lipopolysaccharide	3.4	1,430,000	1
DNA	3.1	2.1	1
RNA	20.5	255,500	~660
Total monomers	3.0		~350
Amino acids and precursors	0.5		~100
Sugars and precursors	2		~50
Nucleotides and precursors	0.5		~200
Inorganic ions	1		18
Total	100%		

a Data from Neidhardt, F. C., et al. (eds.), 1996. *Escherichia coli* and *Salmonella typhimurium—Cellular and Molecular Biology*, 2nd edition. American Society for Microbiology, Washington, DC.

b Dry weight of an actively growing cell of *E. coli* $\cong 2.8 \times 10^{-13}$ g; total weight (70% water) $\approx 9.5 \times 10^{-13}$ g.

c Assuming peptidoglycan and glycogen to be the major polysaccharides present.

d There are several classes of phospholipids, each of which exists in many kinds because of variability in fatty acid composition between species and because of different growth conditions.

Grundmoleküle Kohlenhydrate

Hauptsächlich

Pentosen

+

Hexosen

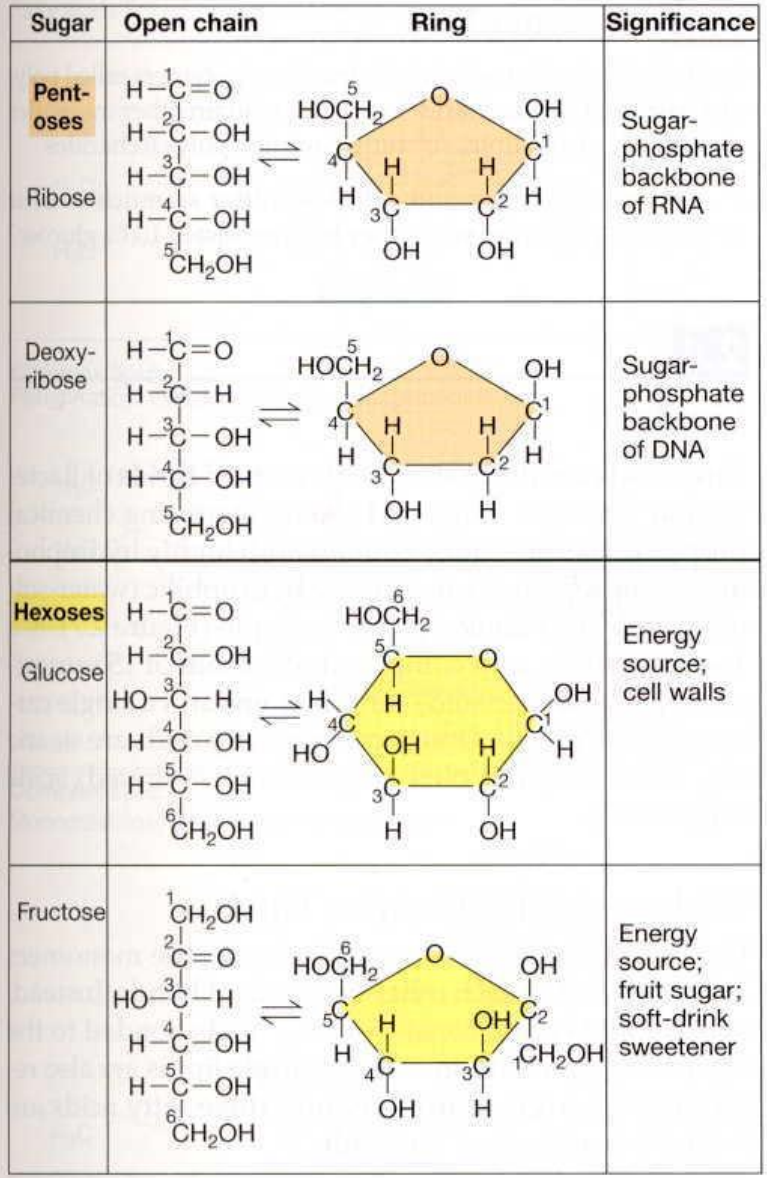
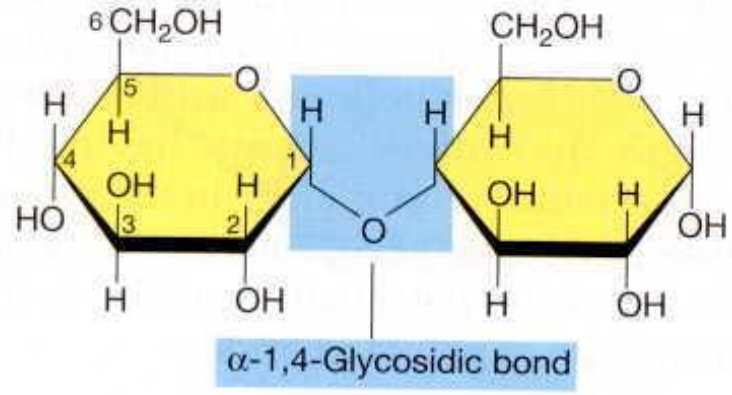
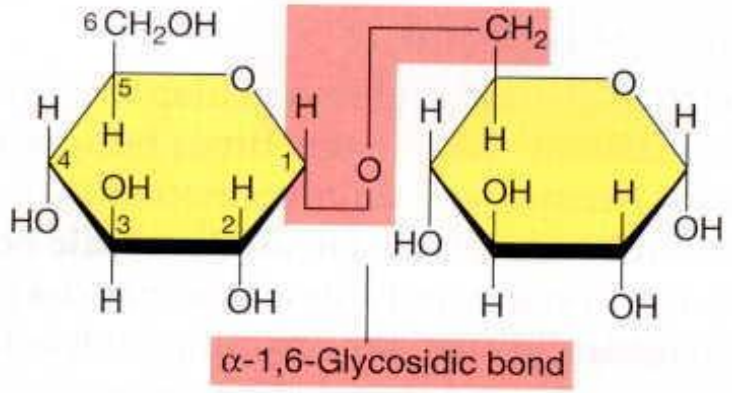
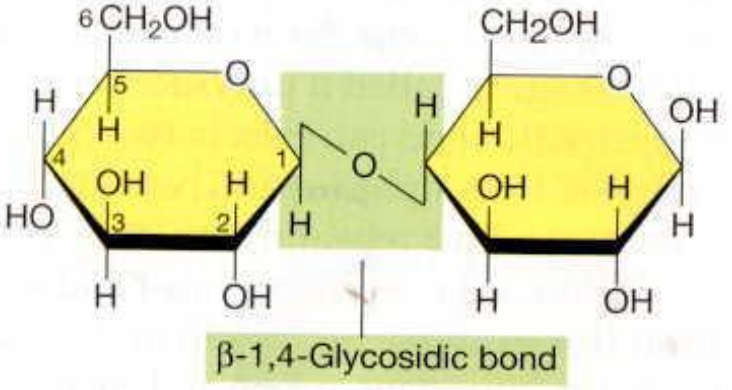


FIGURE 2.4 Structural formulas of a few common sugars. The formulas can be represented in two alternate ways, open chain and ring. The open chain is easier to visualize, but the ring form is the commonly used structure. Note the numbering system on the ring.

Struktur ←→ Funktion







(a)

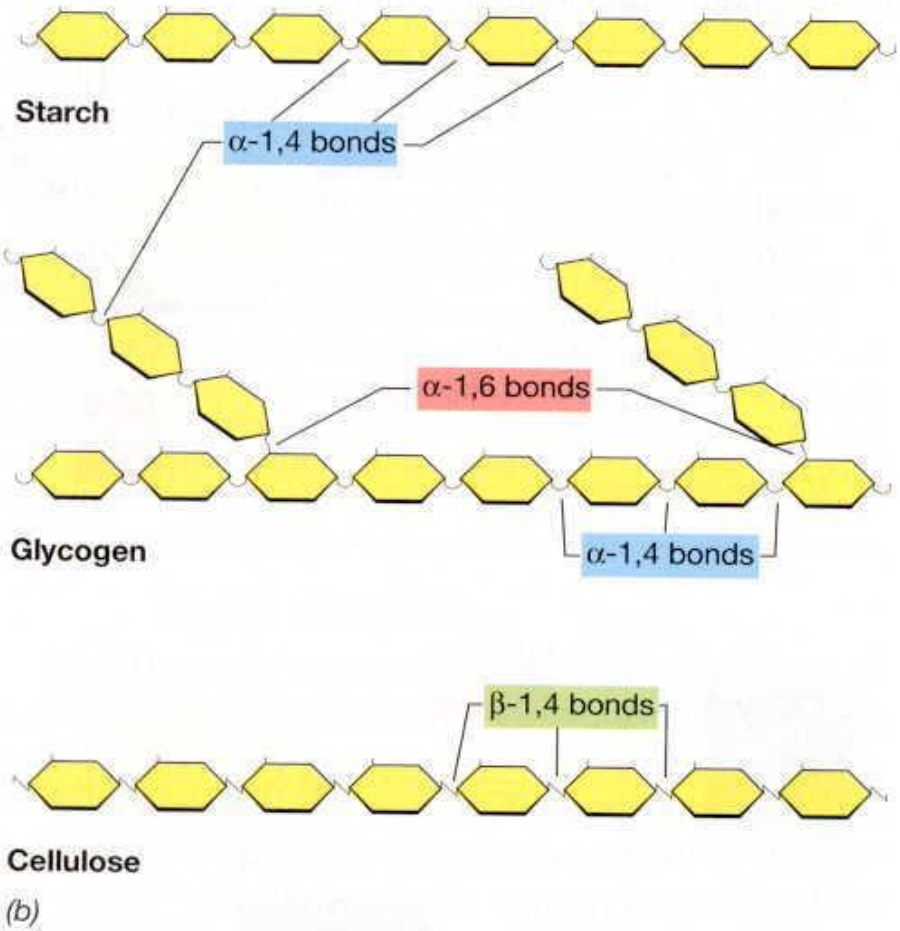


FIGURE 2.6 Polysaccharides (a) Structure of different glycosidic bonds. Note that both the *linkage* and the *geometry* of the linkage can vary about the glycosidic bond. (b) General structures of some common polysaccharides. Note color coding to (a).

Funktionalisierte Kohlenhydrate

N → amino

COOH → acid

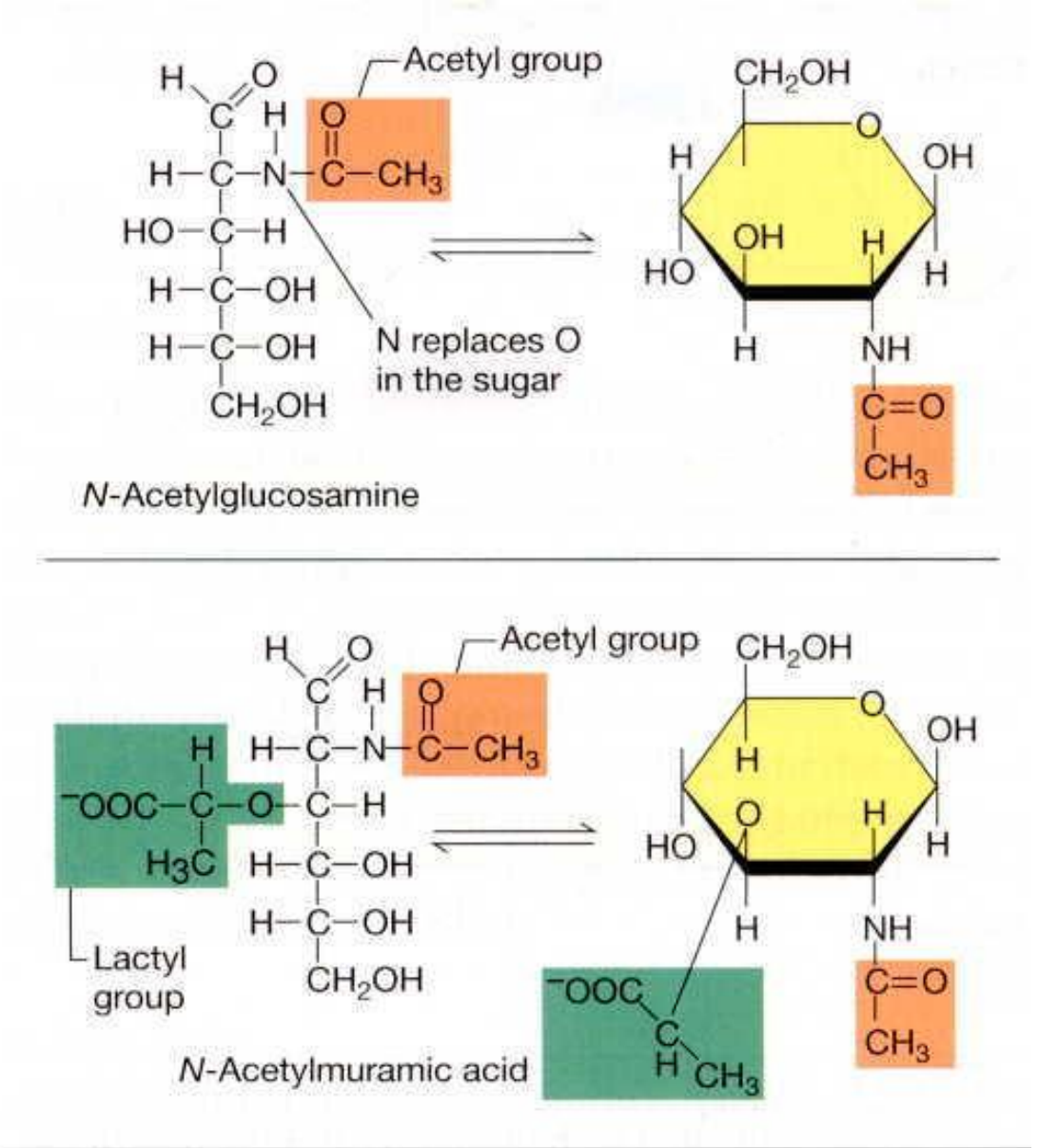
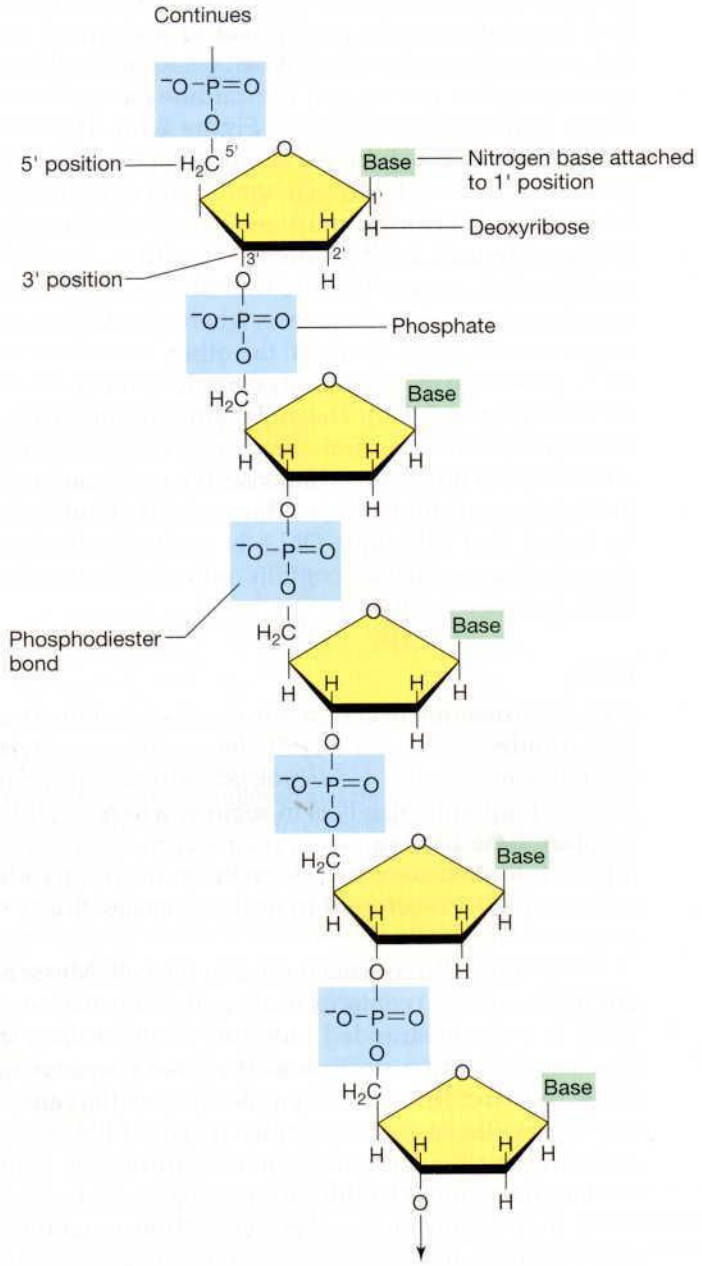


FIGURE 2.5 Sugar derivatives found in the cell walls of most Bacteria, in the polysaccharide called *peptidoglycan*. Note that the parent structure is *glucose* in both cases.



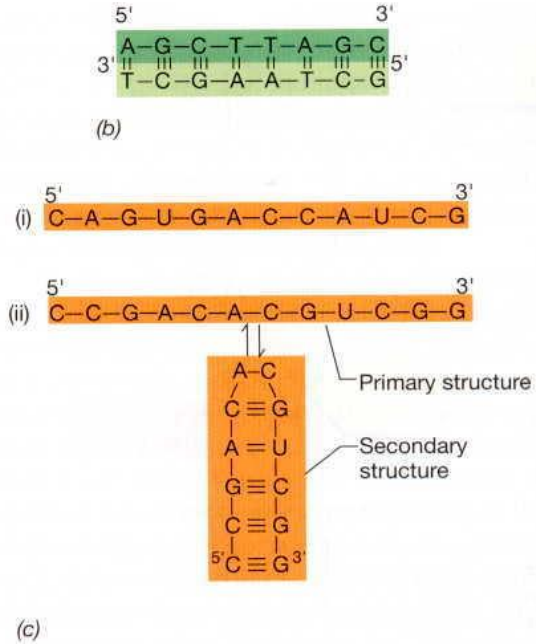


FIGURE 2.11 Structure of part of a DNA chain. (a) The nitrogen bases can be adenine, guanine, cytosine, or thymine. In RNA, an OH group is present on the 2′ carbon of the pentose sugar (see Figure 2.8), and uracil replaces thymine. (b) Simplified structure of DNA in which only the nitrogen bases are shown. Note how the two strands are complementary in base sequence (A═T; G≡C) and bonded by hydrogen bonds. Note also how the two strands of DNA are shown in two different shades of green; this convention is used throughout this book. (c) RNA: (i) A sequence showing only primary structure; (ii) A sequence that allows for secondary structure. RNA is shown in orange throughout this

Macomolecules

→ complex structures
→ Interactions

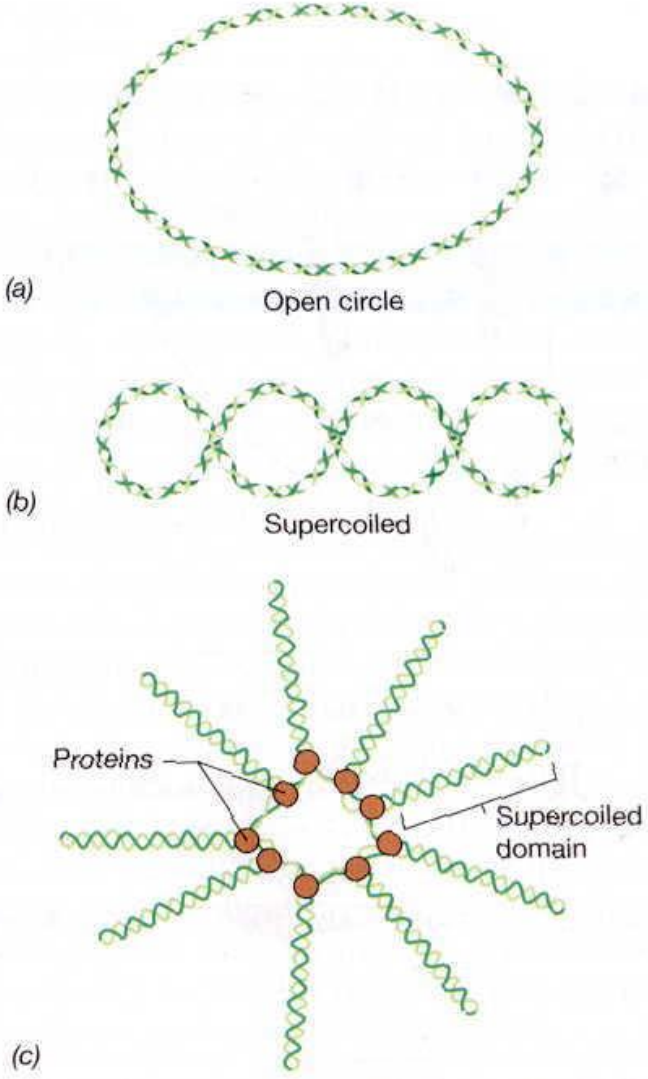


FIGURE 3.44 The bacterial chromosome and supercoiling. (a) Open circular form of the bacterial chromosome. (b) Supercoiled form. (c) In actuality, the double-stranded DNA in the bacterial chromosome is arranged not in one supercoil but in several *supercoiled domains*, as shown here. In *Escherichia coli* over 50 supercoiled domains are thought to exist, each of which is stabilized by binding to specific proteins.

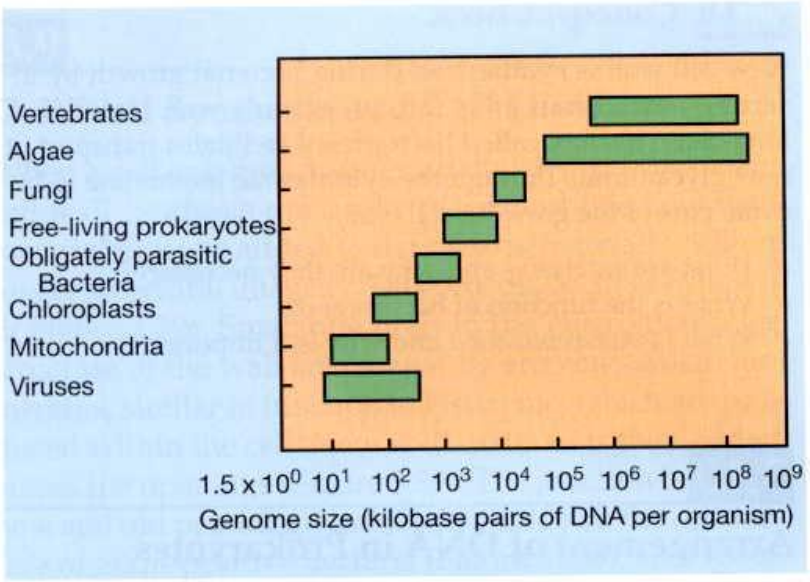
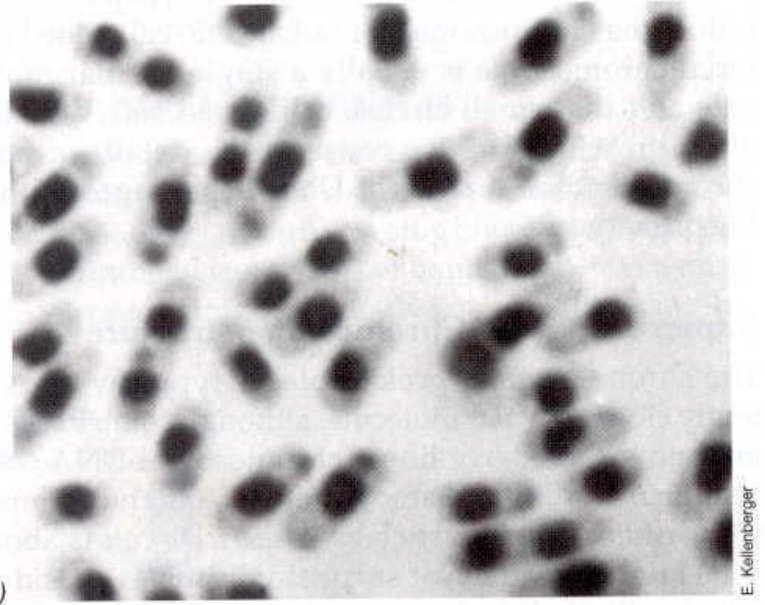
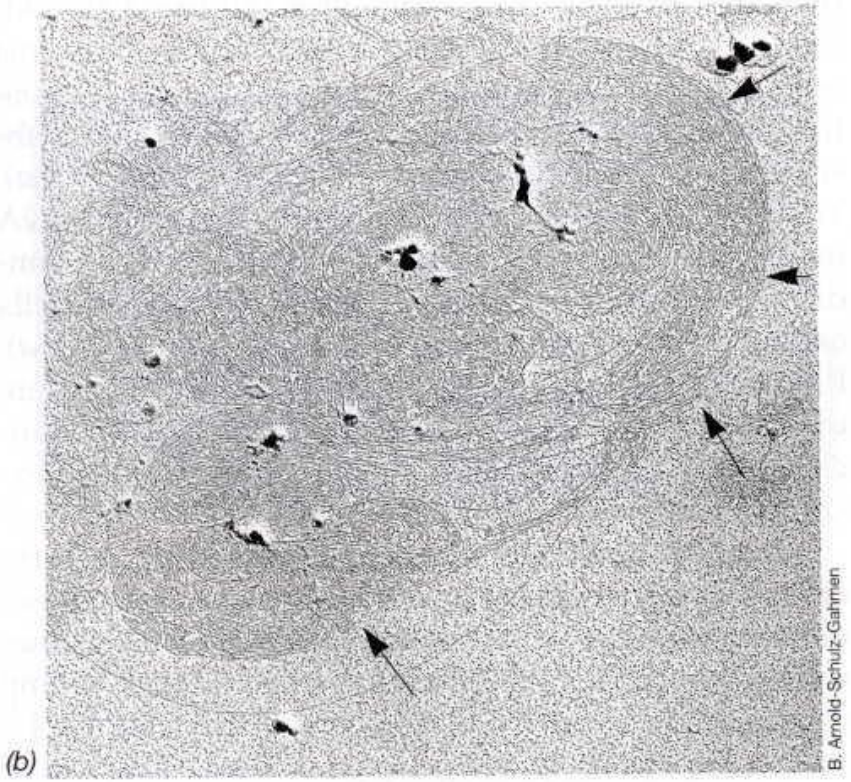


FIGURE 3.42 Range of genome sizes in various groups of organisms and the organelles of Eukarya.





Amino Acids

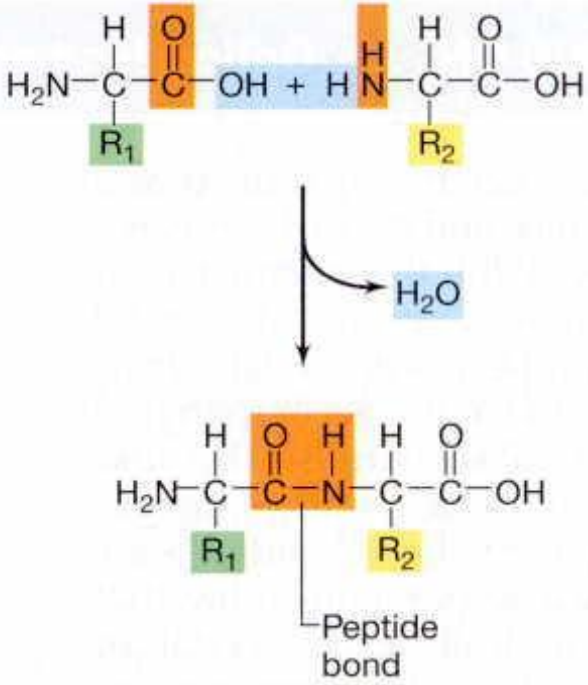


FIGURE 2.13 Peptide bond formation. R_1 and R_2 refer to the variable portion (side chain) of the amino acid (see Figure 2.12).

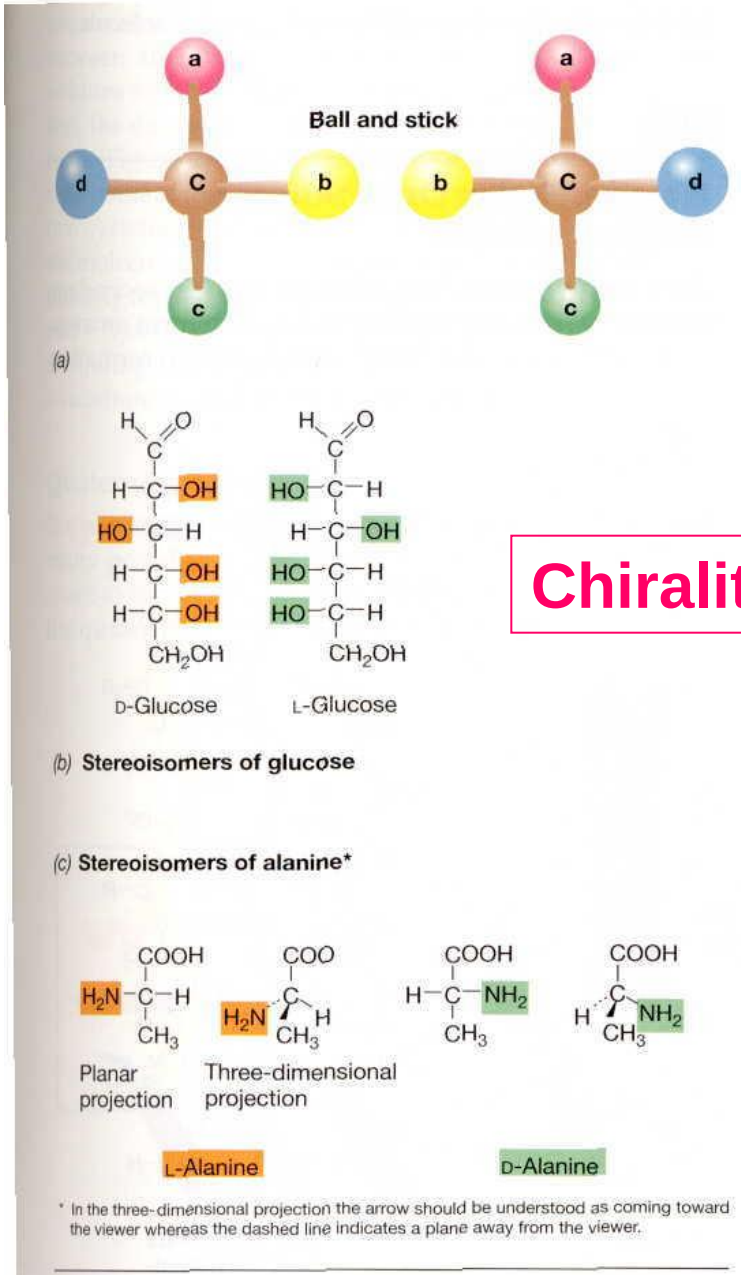
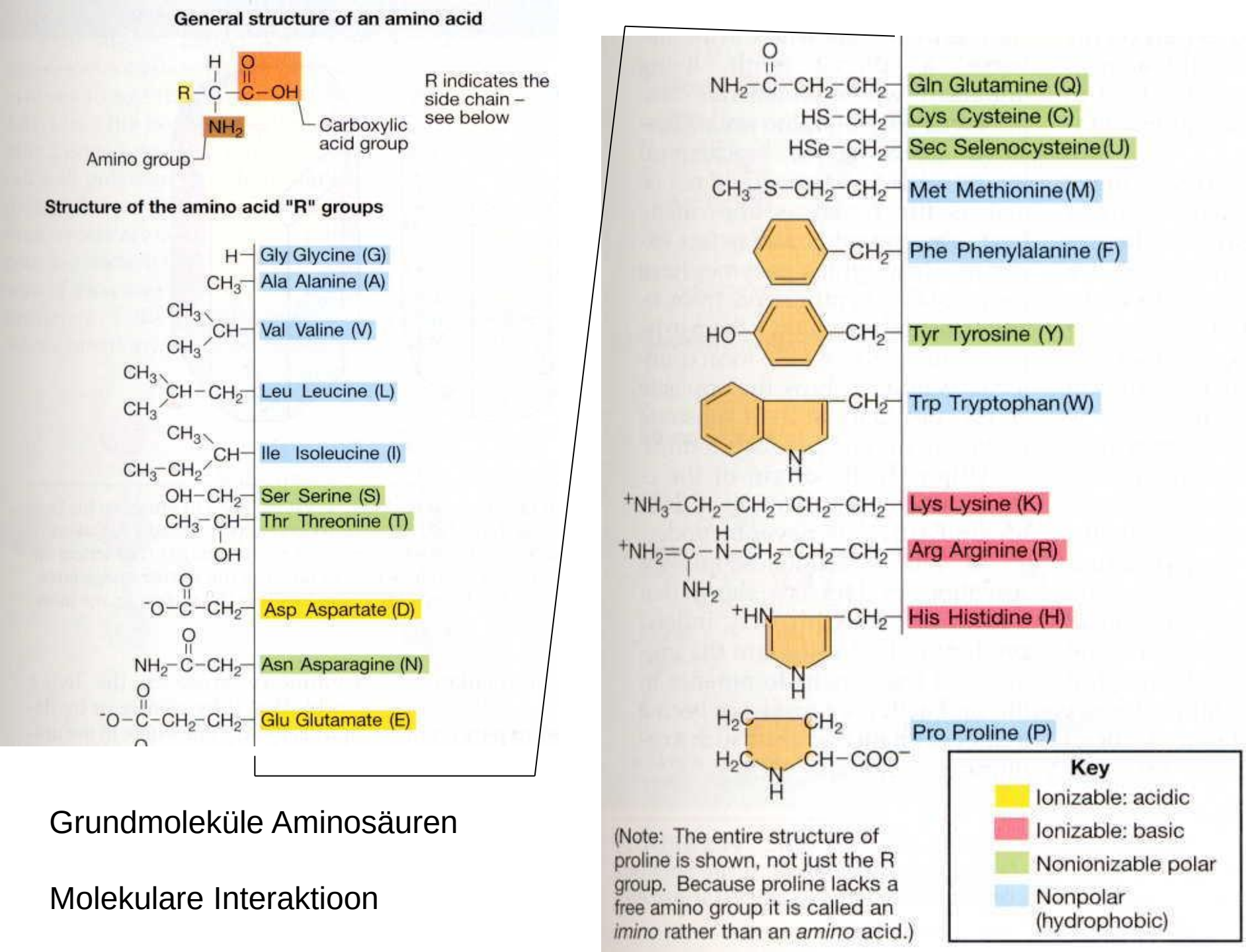


FIGURE 2.14 Stereoisomers. (a) Ball-and-stick model showing mirror images (stereoisomers). (b) Stereoisomers of glucose. (c) Stereoisomers of the amino acid alanine.

Chirality



Grundmoleküle Aminosäuren

Molekulare Interaktioon

Proteine
Struktur - Funktion

Aminosäureketten von Proteinen falten sich durch die Kräfte von verschiedenen Interaktionen (chemische Bindungen – Disulfid, ionische Wechselwirkungen, hydrophobe Interaktionen, Wasserstoffbrückenbindungen. Van der Waals Kräfte) zu übergeordneten Strukturen

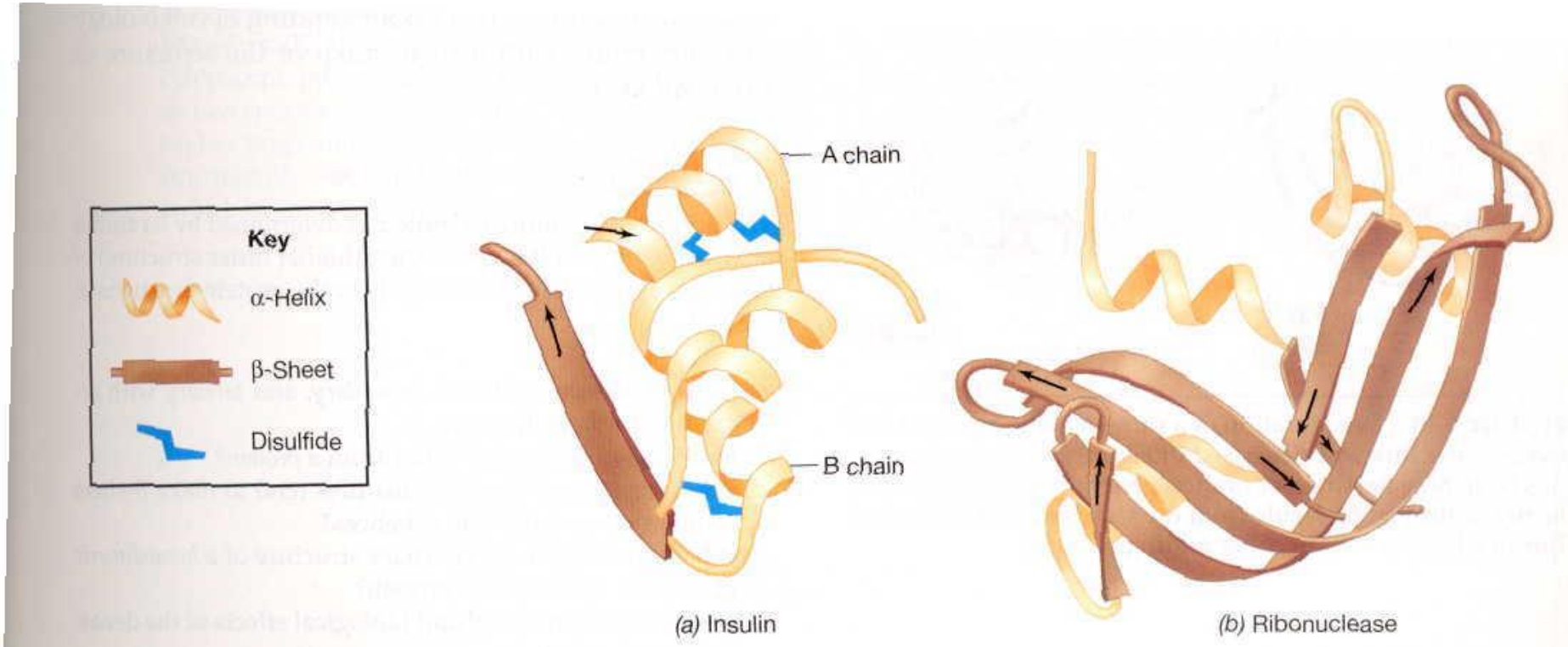


FIGURE 2.16 Tertiary structure of polypeptides showing where regions of α-helix or β-sheet secondary structure might be located. (a) Insulin, a protein containing two polypeptide chains; note how the B chain contains both α-helix and β-sheet secondary structure and how disulfide linkages (—S—S—) may help in dictating folding patterns (tertiary structure). (b) Ribonuclease, a large protein with several regions of α-helix and β-sheet.

Richtige Faltung und Aufbau der 3-dimensionalen Struktur ist Voraussetzung für Funktion

Die meisten Proteine sind erst in höhergeordneten Komplexen aktiv

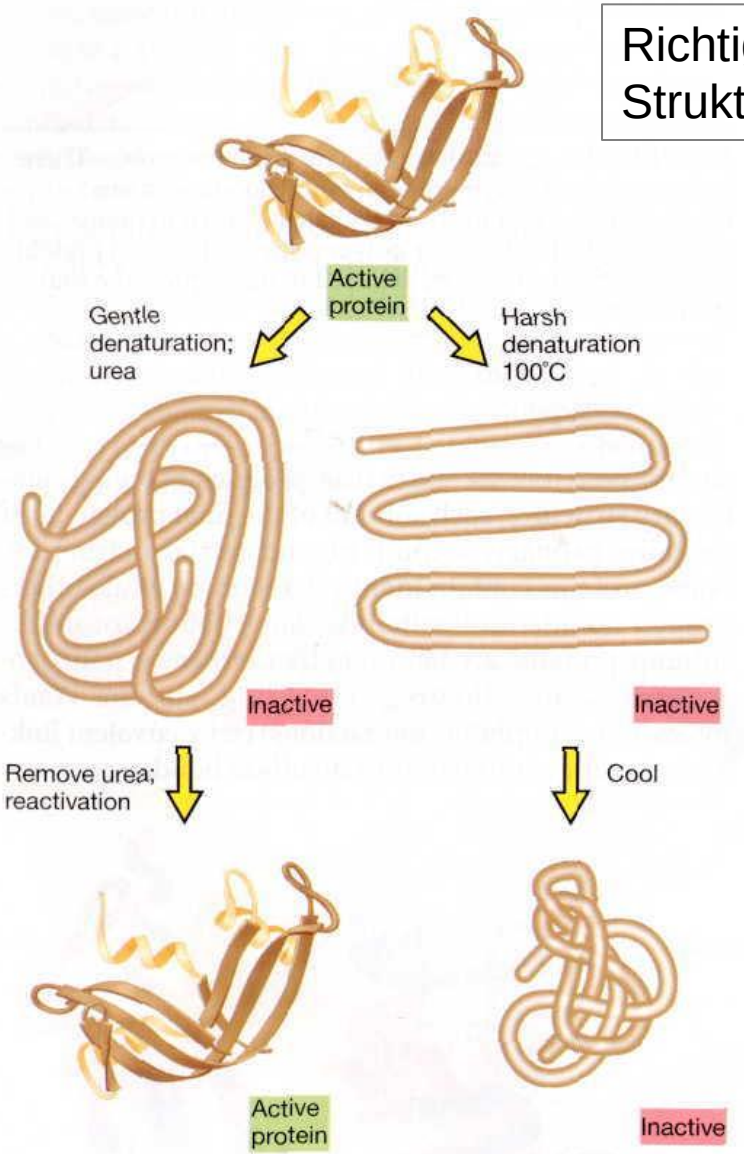


FIGURE 2.18 Denaturation of a protein using ribonuclease (whose structure was discussed in Figure 2.16*b*) as an example. Note how harsh denaturation generally yields a permanently destroyed molecule from the standpoint of biological function because of improper folding.

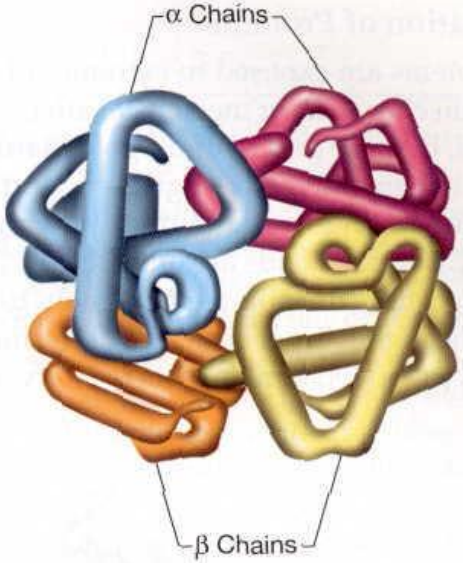
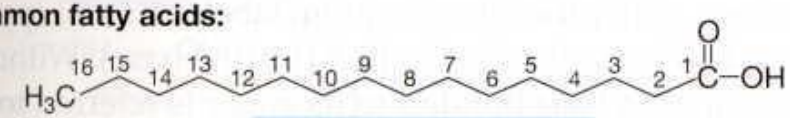


FIGURE 2.17 Quaternary structure of hemoglobin. There are two *kinds* of polypeptide in hemoglobin, α chains (shown in blue and red) and β chains (shown in orange and yellow), but a total of four polypeptides in the final protein molecule. Separate colors are used to distinguish the four distinct chains.

Proteine sind keine starren Körper:
→ Motilität ist wichtig für Funktion

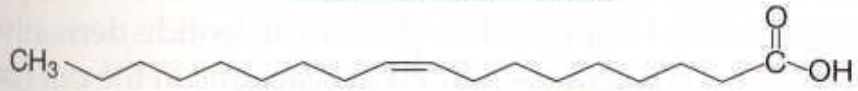
Common fatty acids:



C_{16} saturated (palmitic)

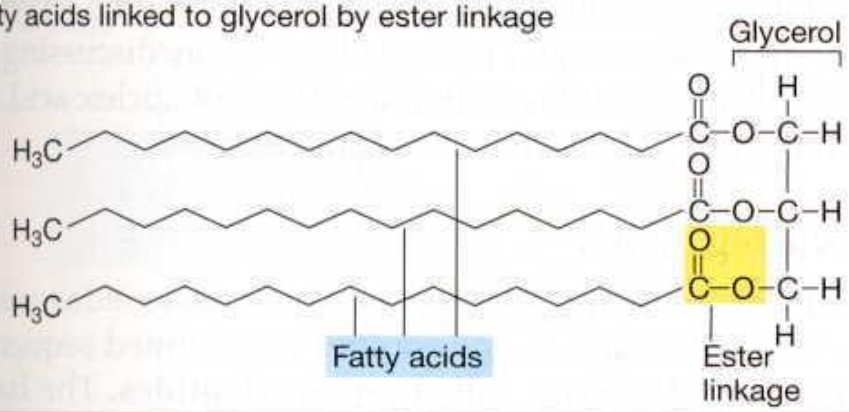
C_{16} monounsaturated (palmitoleic)

C_{18} saturated (stearic)

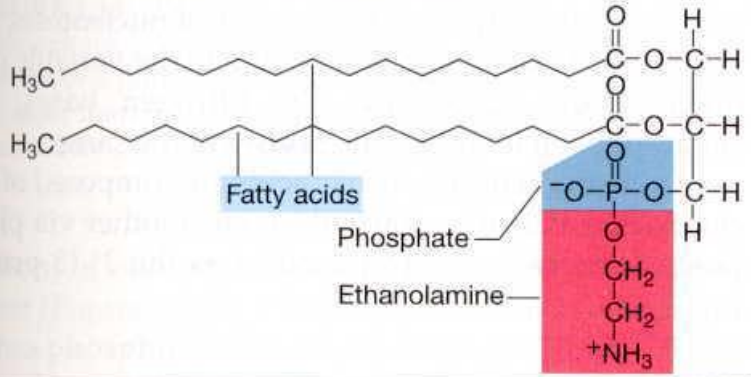


C_{18} monounsaturated (oleic)

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



Complex lipid:
Phosphatidyl ethanolamine (a phospholipid)



Complex lipid:
Monogalactosyl diglyceride (a glycolipid)

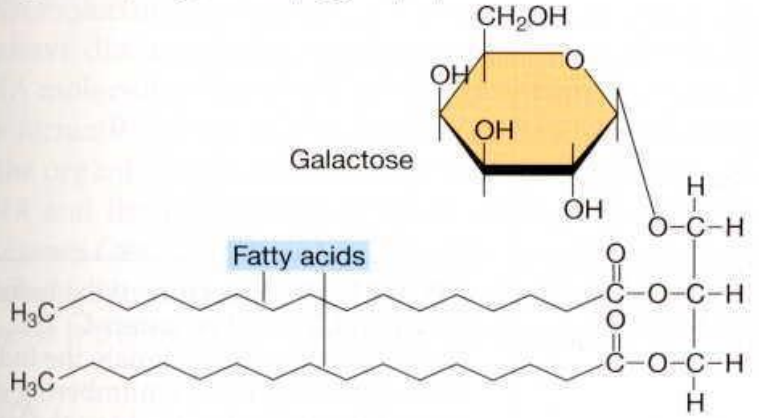


FIGURE 2.7 Fatty acids, simple lipids (fats), and complex lipids. Simple lipids are formed by a dehydration reaction between fatty acids and glycerol to yield the ester linkage.

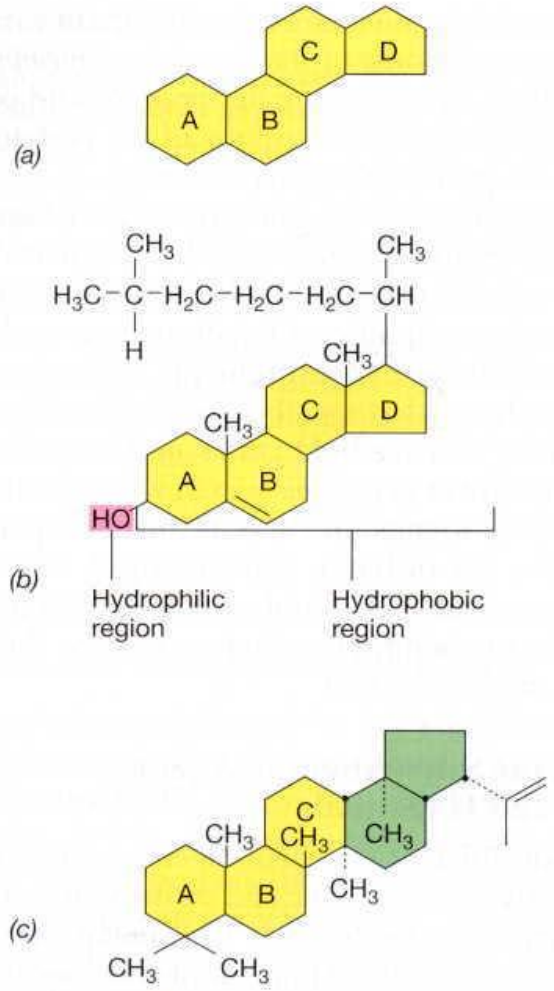


FIGURE 3.19 Sterols and hopanoids. (a) The general structure of a sterol. All sterols contain the same four rings, labeled A, B, C, and D. (b) The structure of cholesterol. (c) The structure of the hopanoid diploptene. Note the structural resemblance to cholesterol in rings A through C. Sterols are found in the membranes of eukaryotes and hopanoids in the membranes of some prokaryotes.

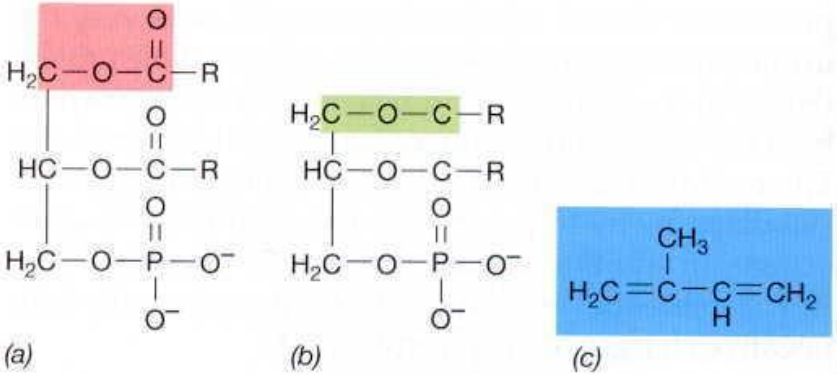


FIGURE 3.20 Chemical bonds in lipids. (a) The *ester* linkage as found in the lipids of Bacteria and Eukarya. (b) The *ether* linkage of lipids from Archaea. (c) Isoprene, the parent structure of the hydrophobic side chains (R) of archaeal lipids. By contrast, in lipids of Bacteria and Eukarya, R are fatty acids.

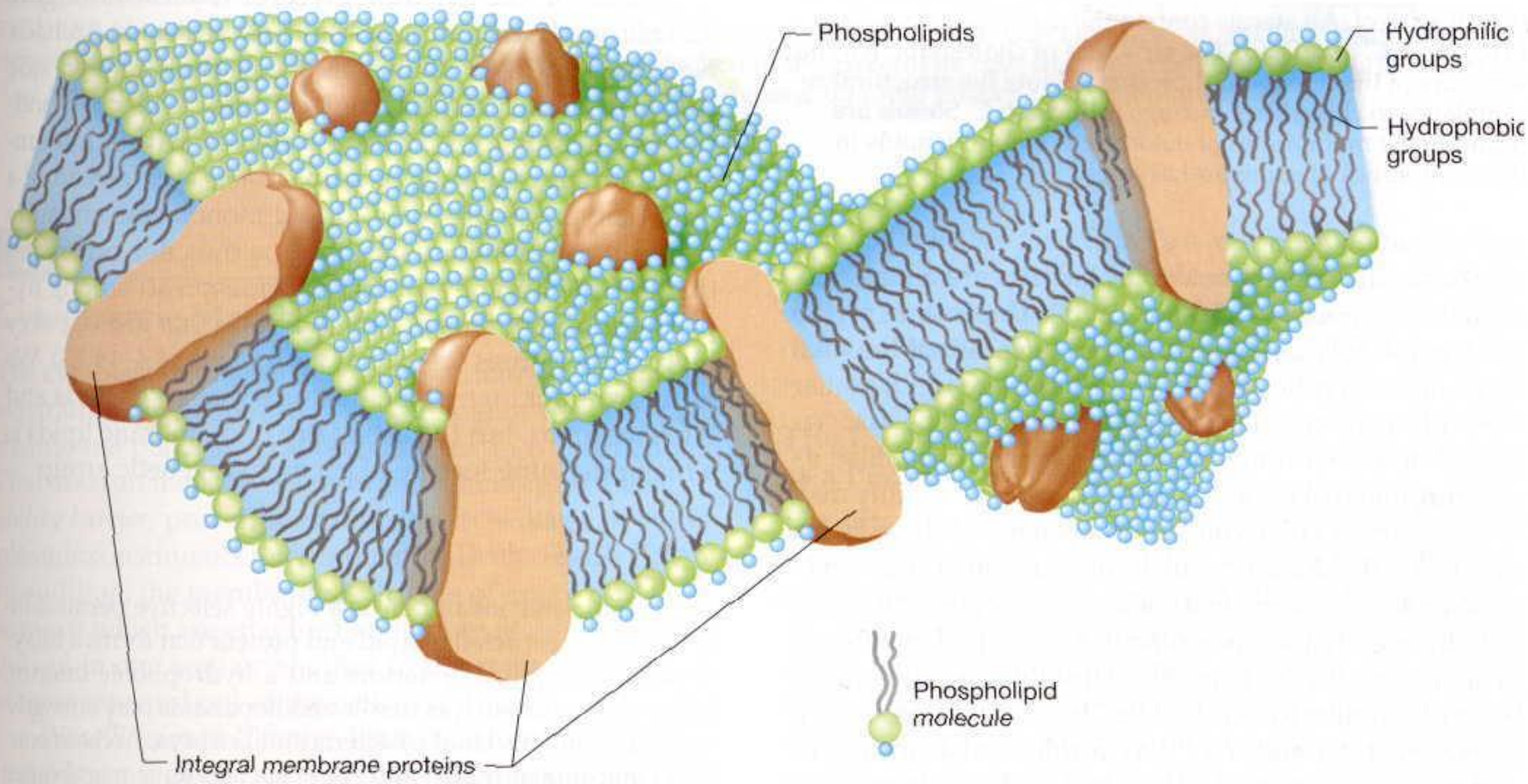
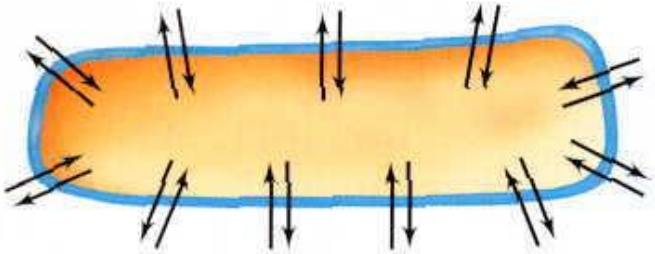
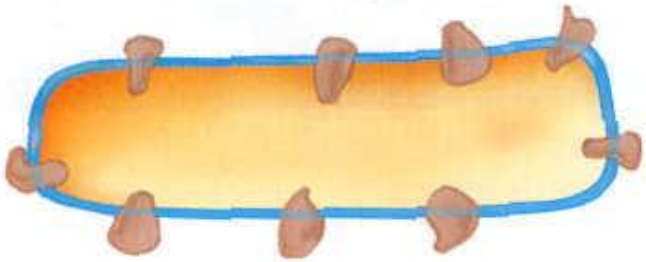


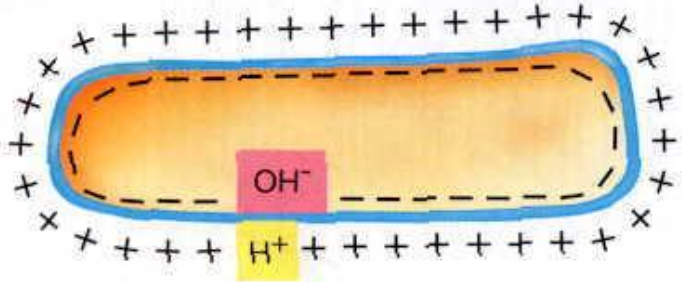
FIGURE 3.18 Diagram of the structure of the cytoplasmic membrane. The matrix of the unit membrane is composed of phospholipids, with the hydrophobic groups directed inward and the hydrophilic groups toward the outside, where they associate with water. Embedded in the matrix are proteins that have considerable hydrophobic character in the region that traverses the fatty acid bilayer. Hydrophilic proteins and other charged substances, such as metal ions, may be attached to the hydrophilic surfaces. Although there are some chemical differences, the overall structure of the cytoplasmic membrane shown is similar in both prokaryotes and eukaryotes (but see an exception to the bilayer design in Figure 3.21).



Permeability Barrier — Prevents leakage and functions as a gateway for transport of nutrients into and out of the cell



Protein Anchor — Site of many proteins involved in transport, bioenergetics, and chemotaxis



Energy Conservation — Site of generation and use of the proton motive force

FIGURE 3.22 The major functions of the cytoplasmic membrane.

TABLE 3.1 Comparative permeability of membranes to various molecules

Substance	Rate of permeability[a]
Water	100
Glycerol	0.1
Tryptophan	0.001
Glucose	0.001
Chloride ion (Cl^-)	0.000001
Potassium ion (K^+)	0.0000001
Sodium ion (Na^+)	0.00000001

a Relative scale—permeability with respect to permeability of water, given as 100.

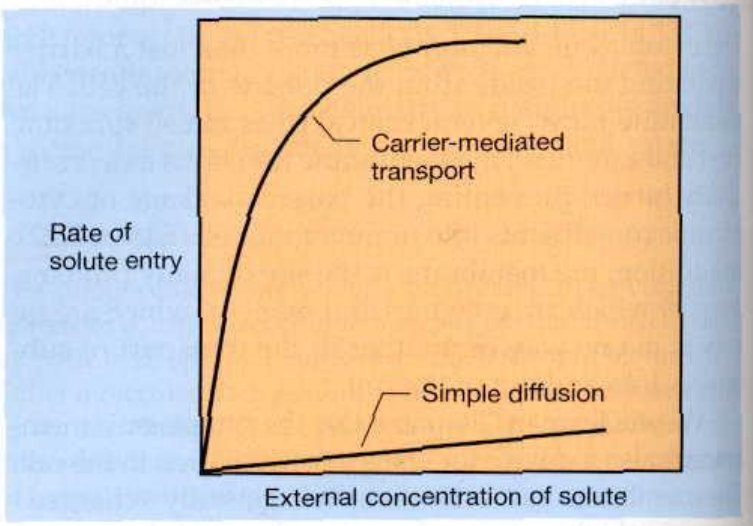


FIGURE 3.23 Relationship between uptake rate and external concentration in diffusion and transport. Note that in the carrier-mediated process the uptake rate shows saturation at relatively low external concentrations.

Passive transport driven by concentration gradients

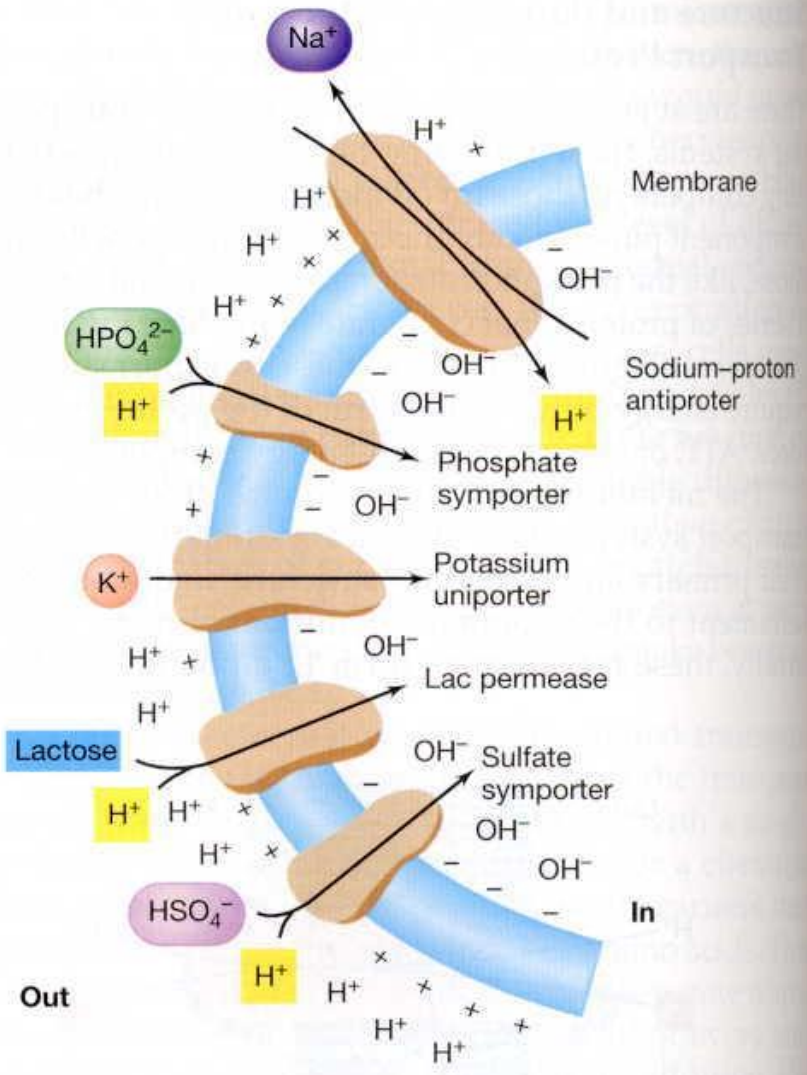
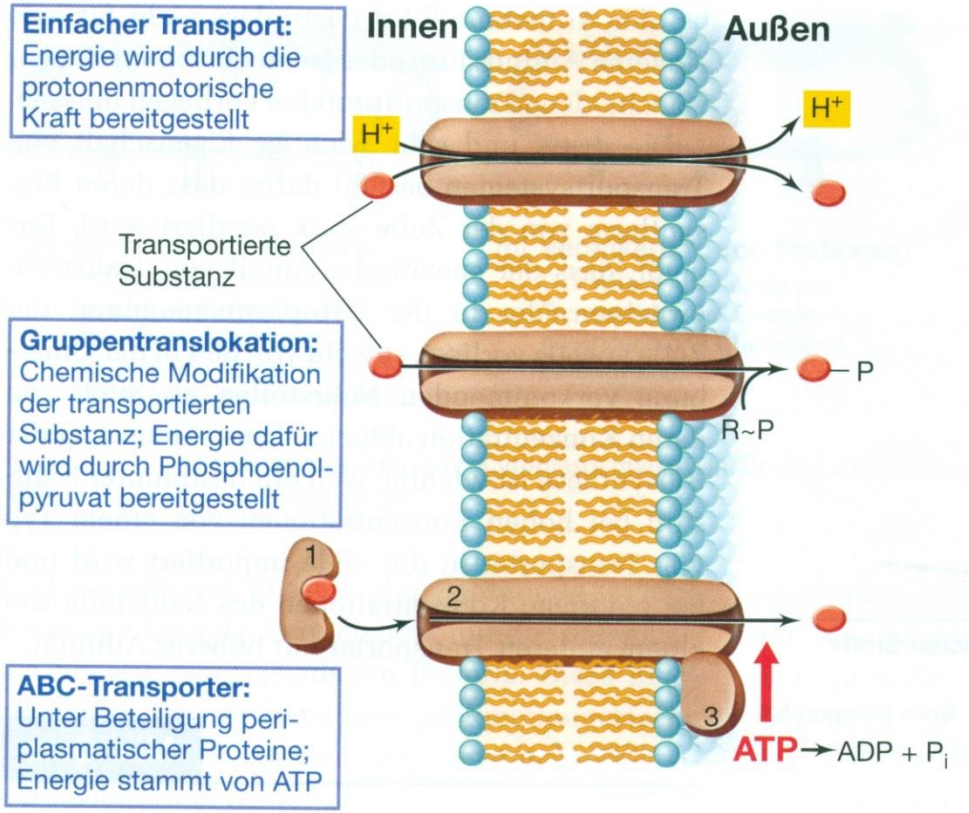
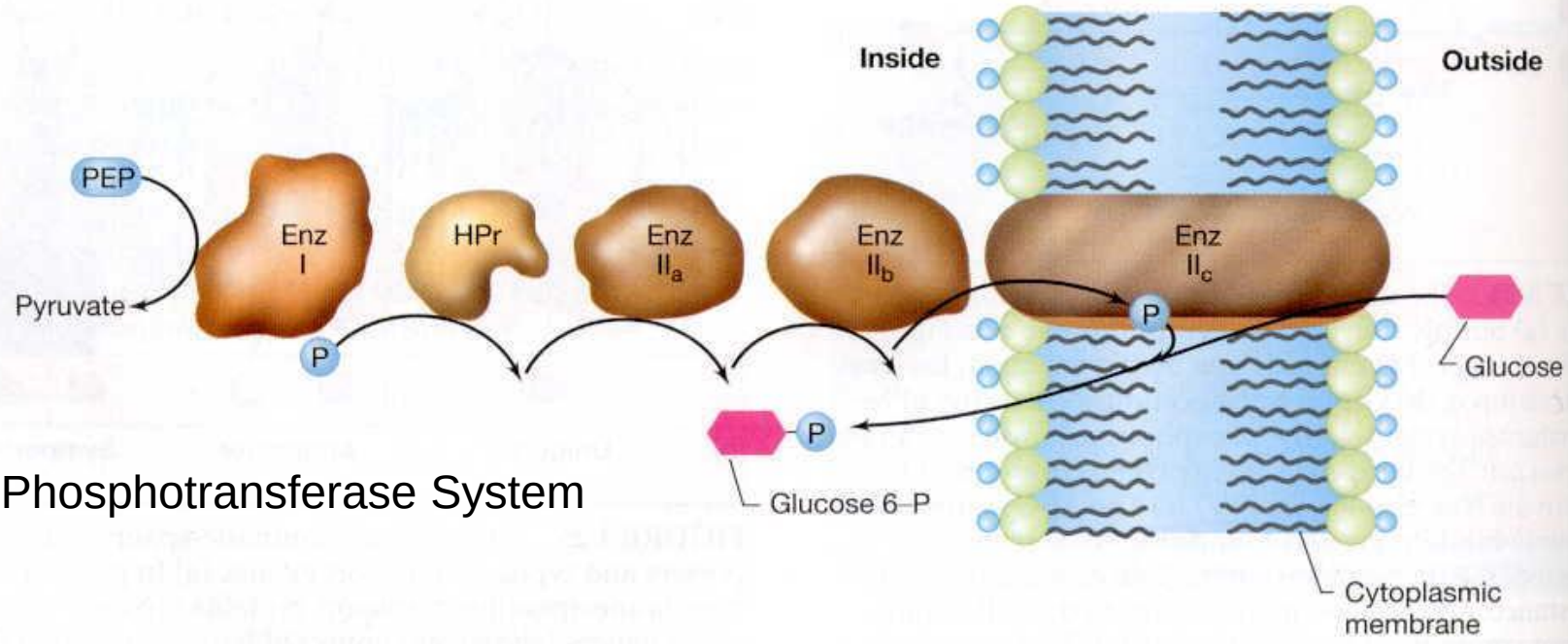


FIGURE 3.26 Function of the Lac permease (a symporter) of *Escherichia coli*, and several other well-characterized simple transporters. Although for simplicity the membrane-spanning proteins are drawn here in globular form, note that their structure is actually as depicted in Figure 3.25*a*. To review the action of transport proteins, see Figure 3.25*b*.



Active Transport of Molecules



Phosphotransferase System

FIGURE 3.27 Mechanism of the phosphotransferase system of *Escherichia coli*. For glucose uptake, the system consists of five proteins: Enzyme (Enz) I; Enzymes II_a, II_b, and II_c; and HPr. Sequential phosphate transfer occurs from phosphoenolpyruvate (PEP) through the proteins shown to Enzyme II_c. The latter actually transports (and phosphorylates) the sugar.

Active Transport of Molecules

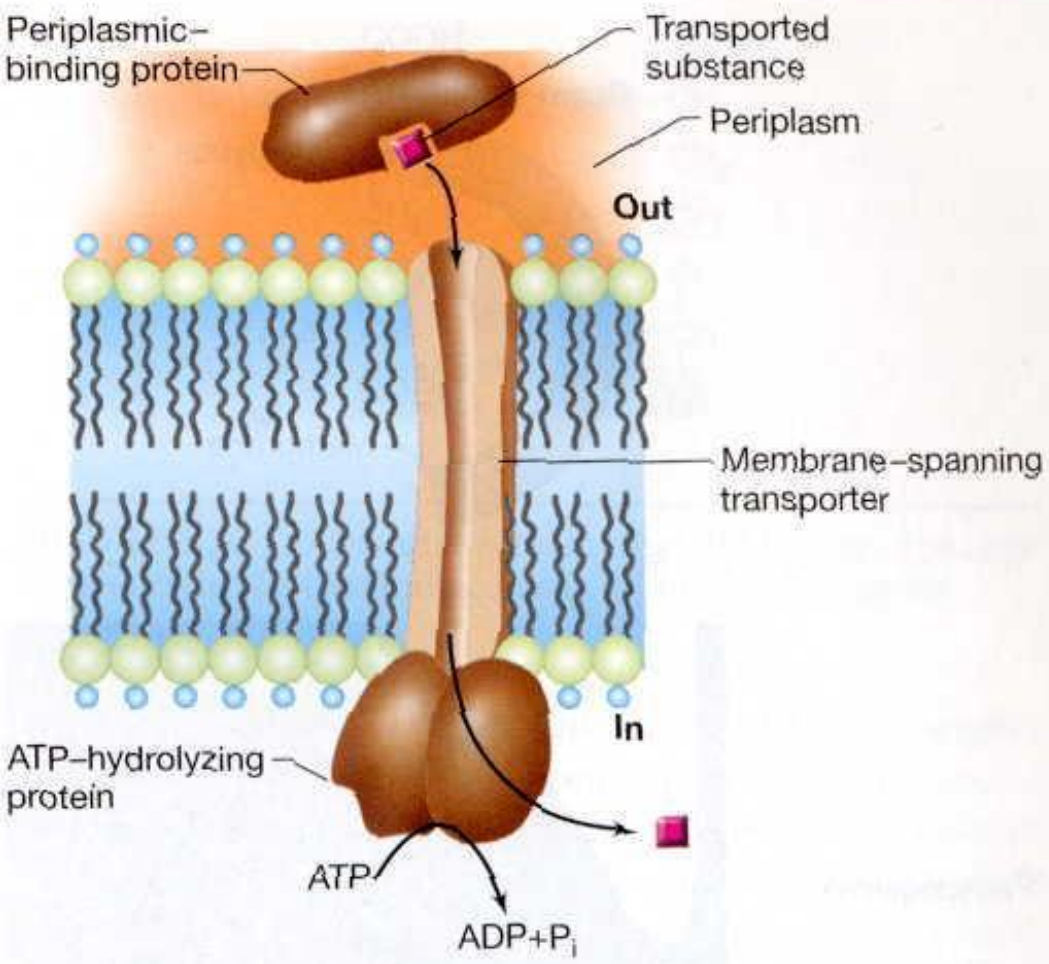


FIGURE 3.28 Mechanism of an Antigen-Binding Cassette (ABC-type) transporter. The periplasmic binding protein has high affinity for substrate, the membrane-spanning protein is the transport channel, and the cytoplasmic ATP-hydrolyzing protein supplies the energy for the transport event. In *Escherichia coli*, the maltose (a disaccharide sugar) transport system is an example of an ABC system.

ABC Transporters

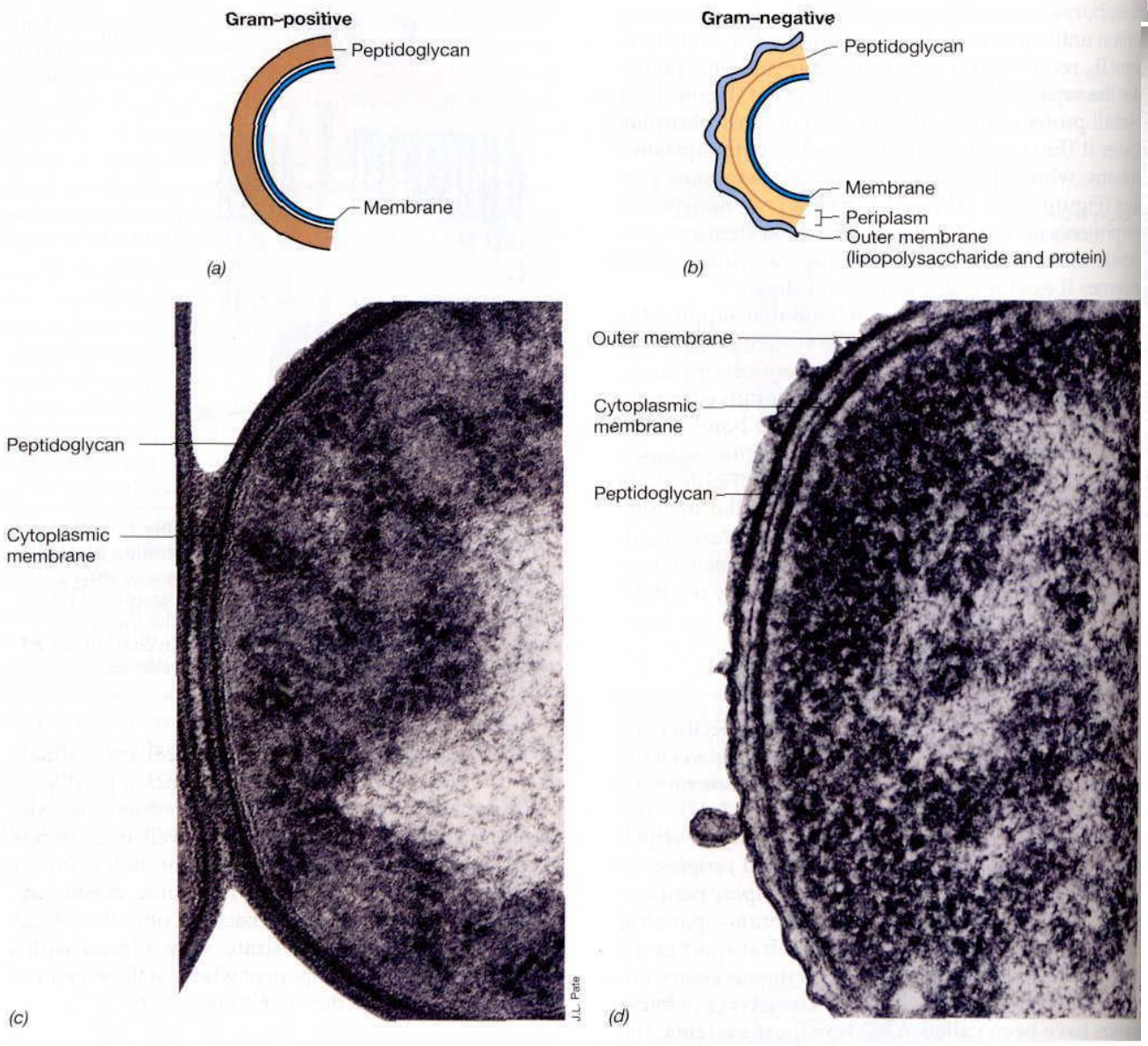


FIGURE 3.29 Cell walls of Bacteria. (a,b) Schematic diagrams of gram-positive and gram-negative cell walls. (c) Electron micrograph showing the cell wall of a gram-positive bacterium, *Arthrobacter crystallopoietes*. (d) Gram-negative bacterium, *Leucothrix mucor*. (e,f) Scanning electron micrographs of gram-positive (*Bacillus subtilis*) and gram-negative (*Escherichia coli*) Bacteria. Note the surface texture in the cells shown in (e) and (f). A single cell of *B. subtilis* or *E. coli* is about 1 μm in diameter.

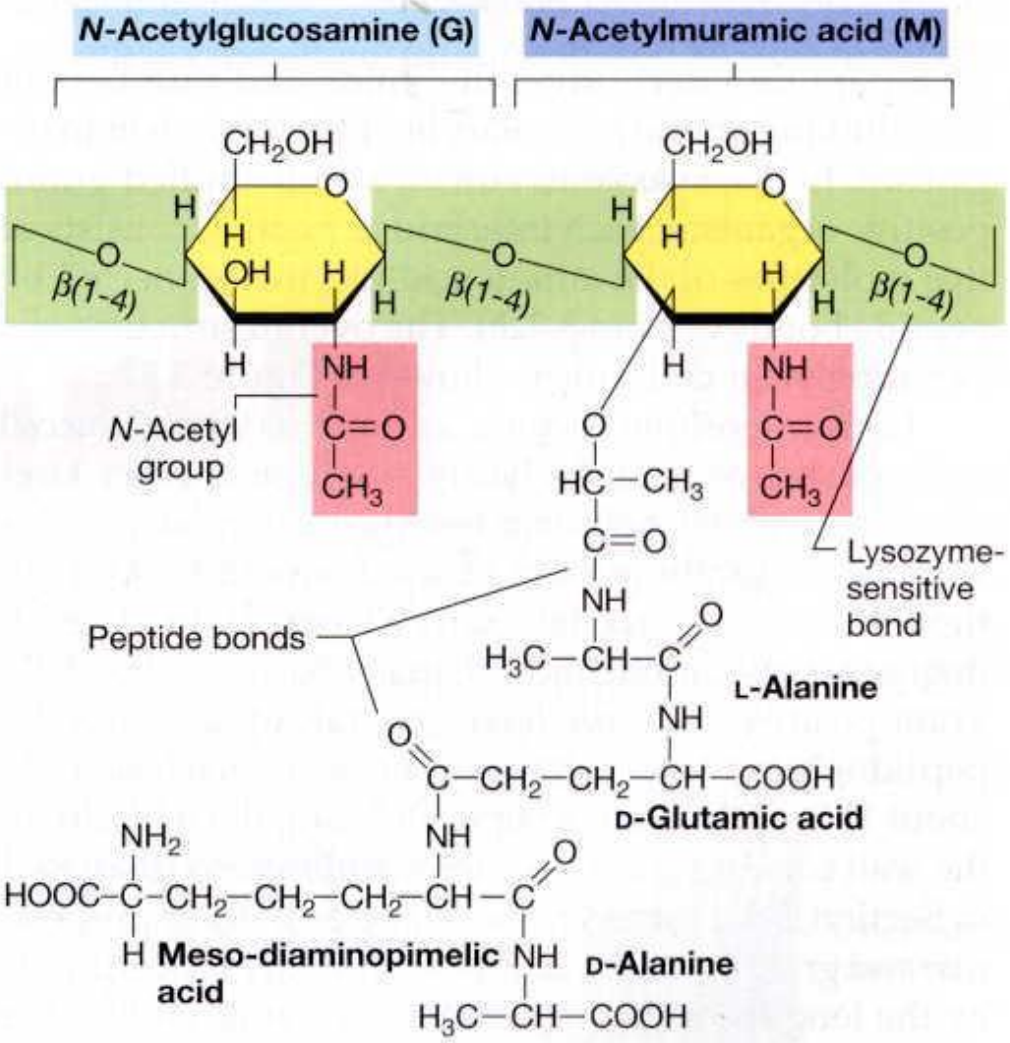


FIGURE 3.31 Structure of one of the repeating units of the peptidoglycan cell wall structure, the glycan tetrapeptide. The structure given is that found in *Escherichia coli* and most other gram-negative Bacteria. In some Bacteria, other amino acids are found.

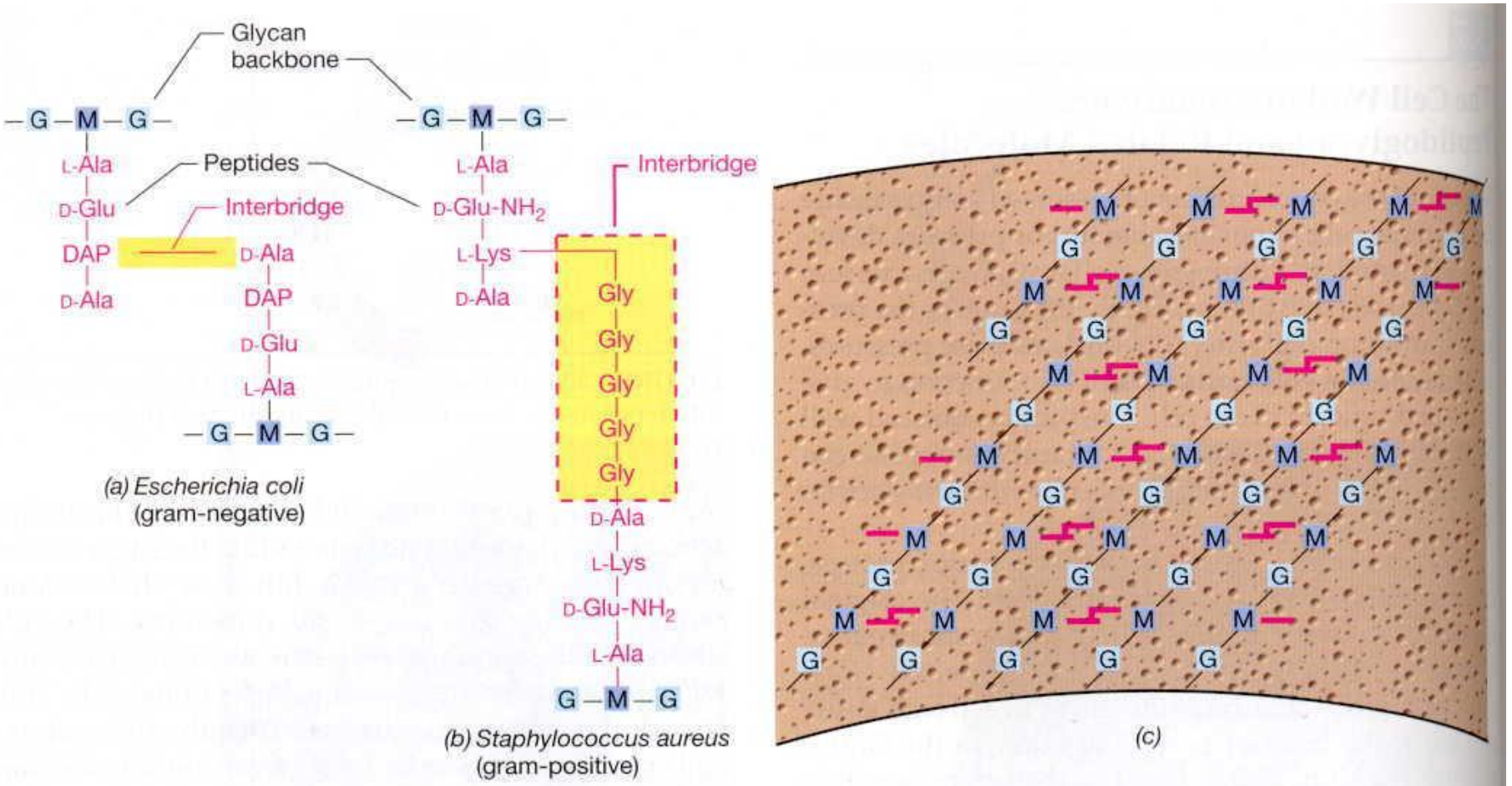


FIGURE 3.32 Manner in which the peptide and glycan units are connected in formation of the peptidoglycan sheet. (a) Direct interbridge in gram-negative Bacteria. (b) Glycine interbridge in *Staphylococcus aureus* (gram-positive). (c) Overall structure of peptidoglycan. The diagram depicts several ribbons of peptidoglycan cross-linked to one another. To visualize an entire single layer of peptidoglycan, imagine these cross-linked ribbons extending around a cylinder or sphere representing the cell as shown. G, *N*-acetylglucosamine; M, *N*-acetylmuramic acid; bold lines in (c) indicate peptide cross-links.

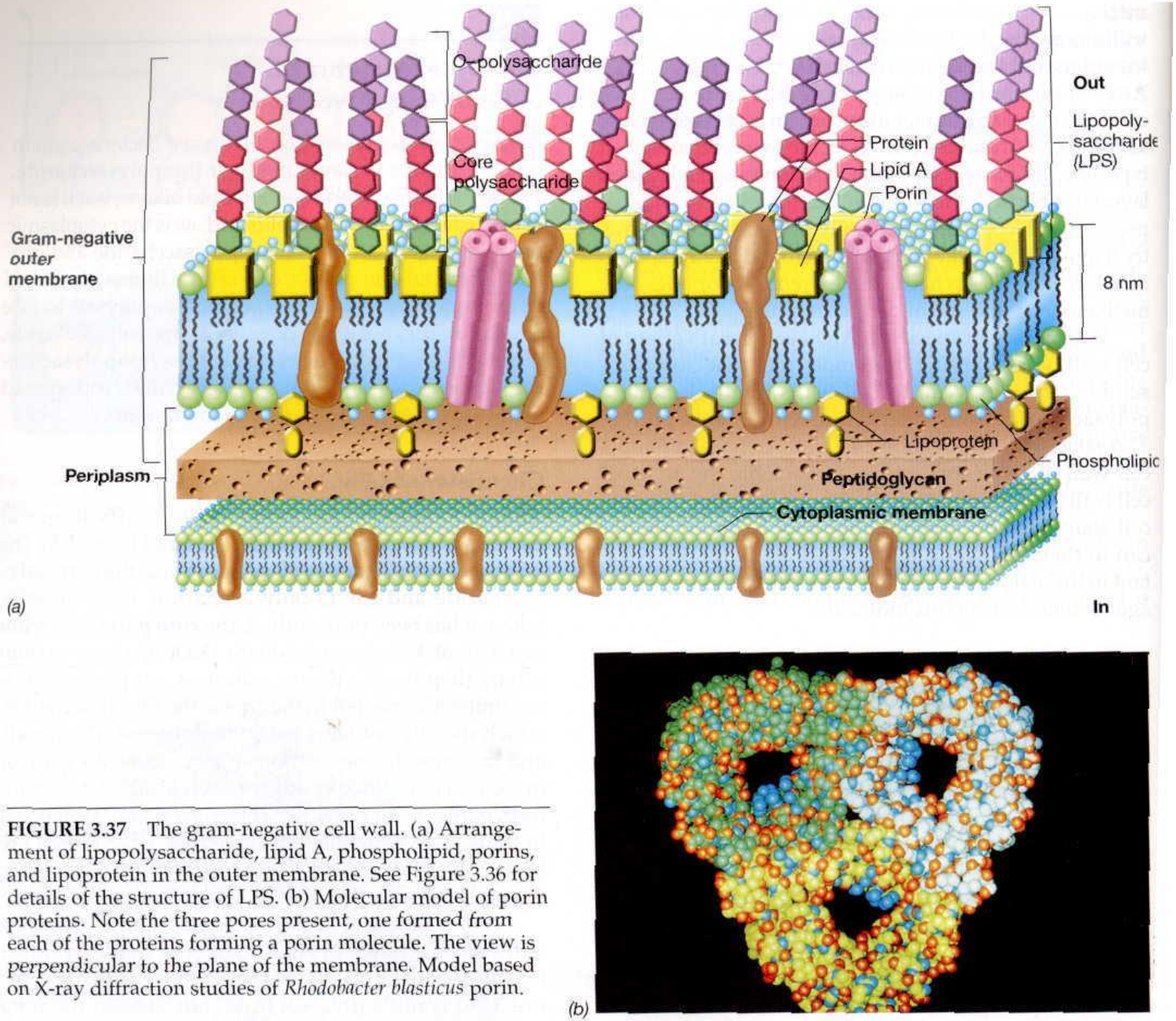


FIGURE 3.37 The gram-negative cell wall. (a) Arrangement of lipopolysaccharide, lipid A, phospholipid, porins, and lipoprotein in the outer membrane. See Figure 3.36 for details of the structure of LPS. (b) Molecular model of porin proteins. Note the three pores present, one formed from each of the proteins forming a porin molecule. The view is perpendicular to the plane of the membrane. Model based on X-ray diffraction studies of *Rhodobacter blasticus* porin.

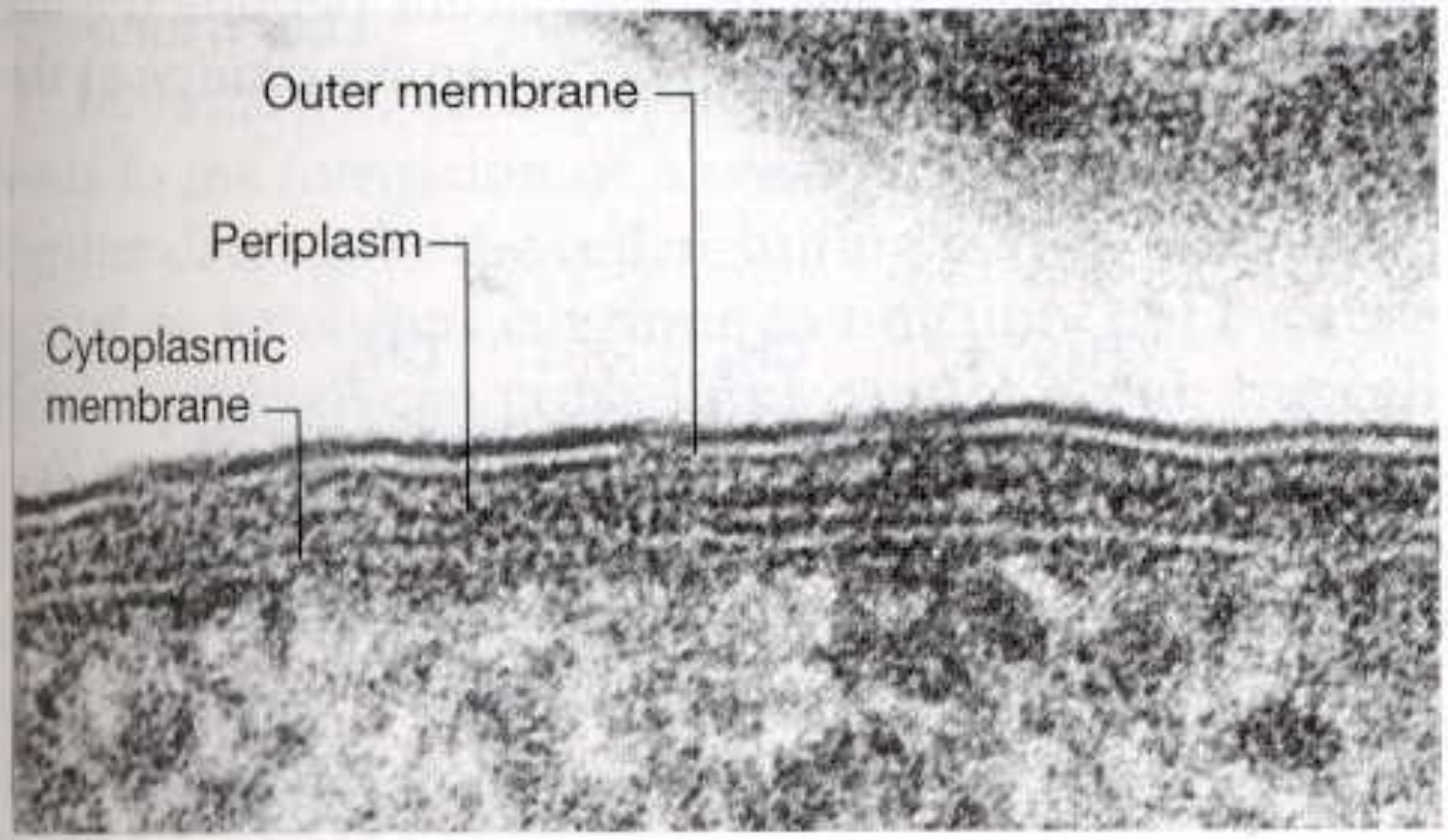


FIGURE 3.38 High magnification thin section of the cell envelope of *Escherichia coli* showing the periplasmic gel bounded by the outer membrane and the cytoplasmic membrane. The large, dark particles in the cytoplasm are ribosomes.

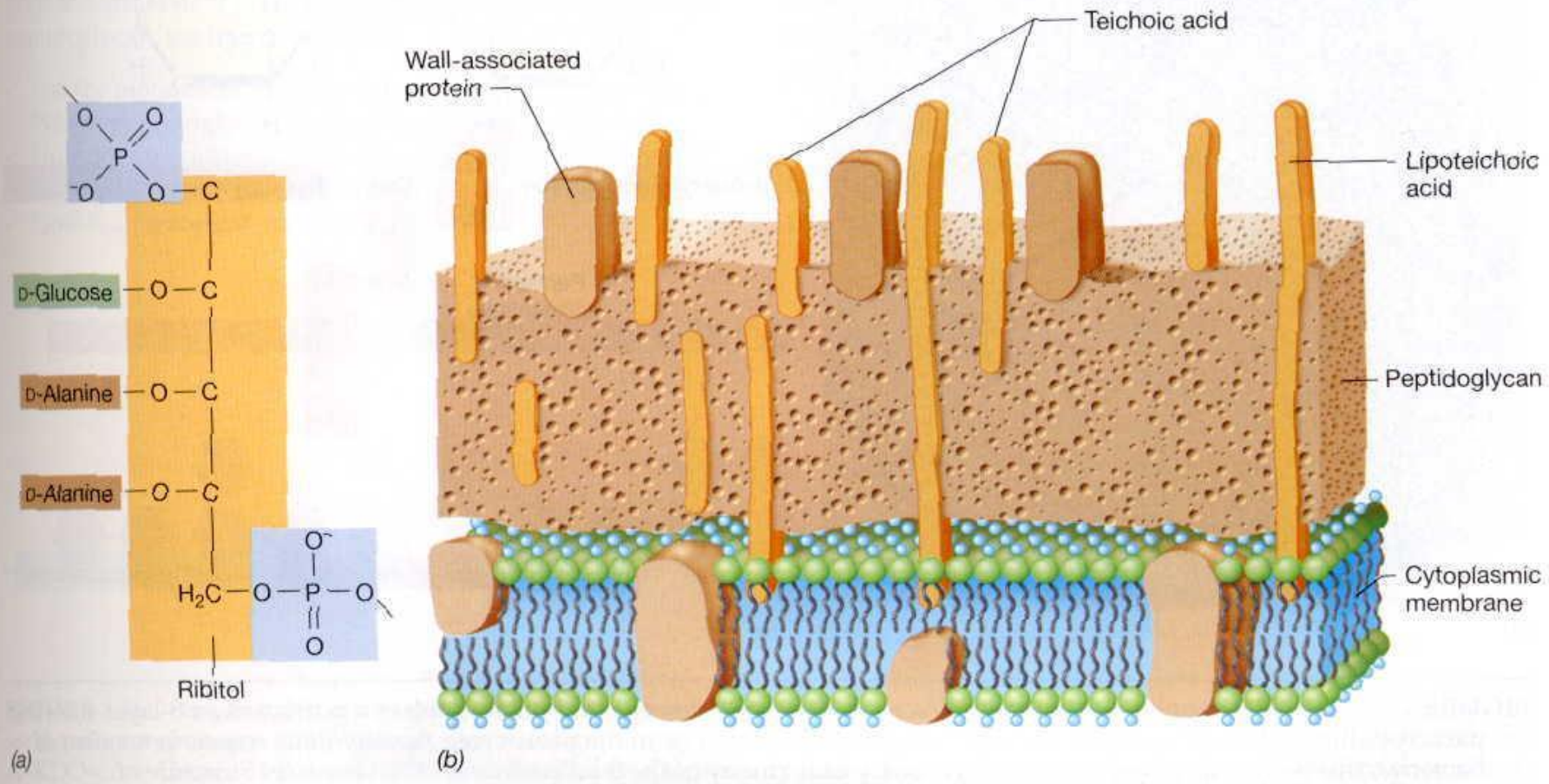
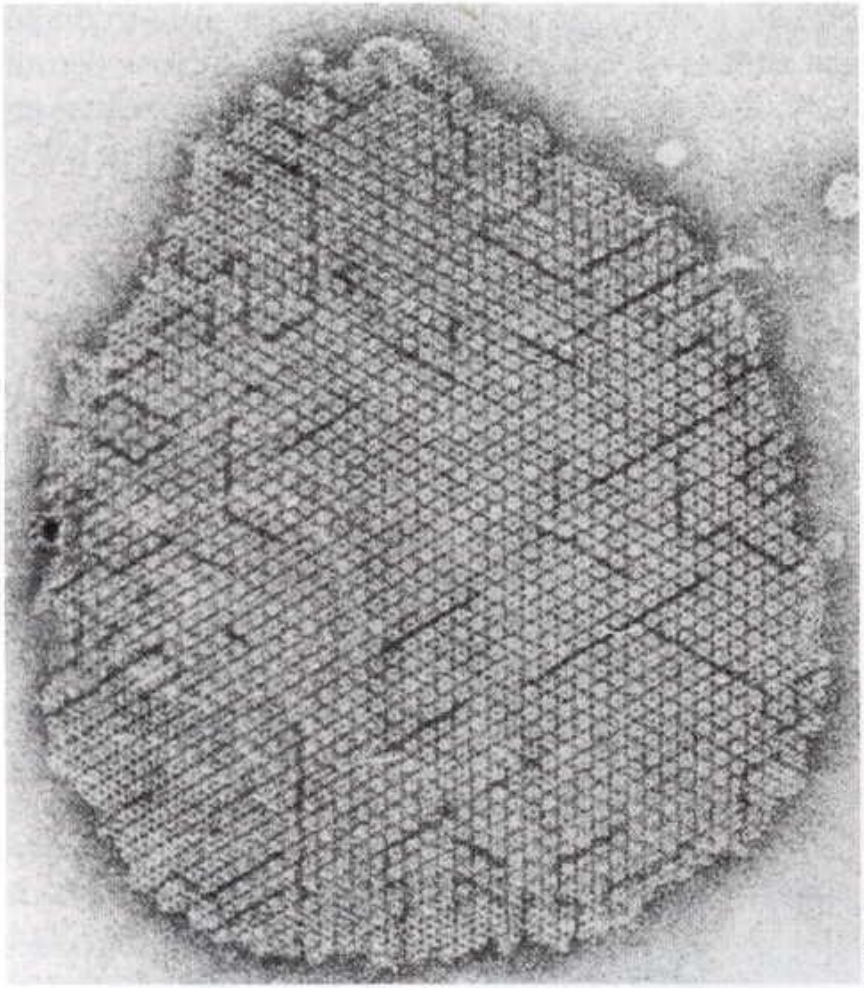
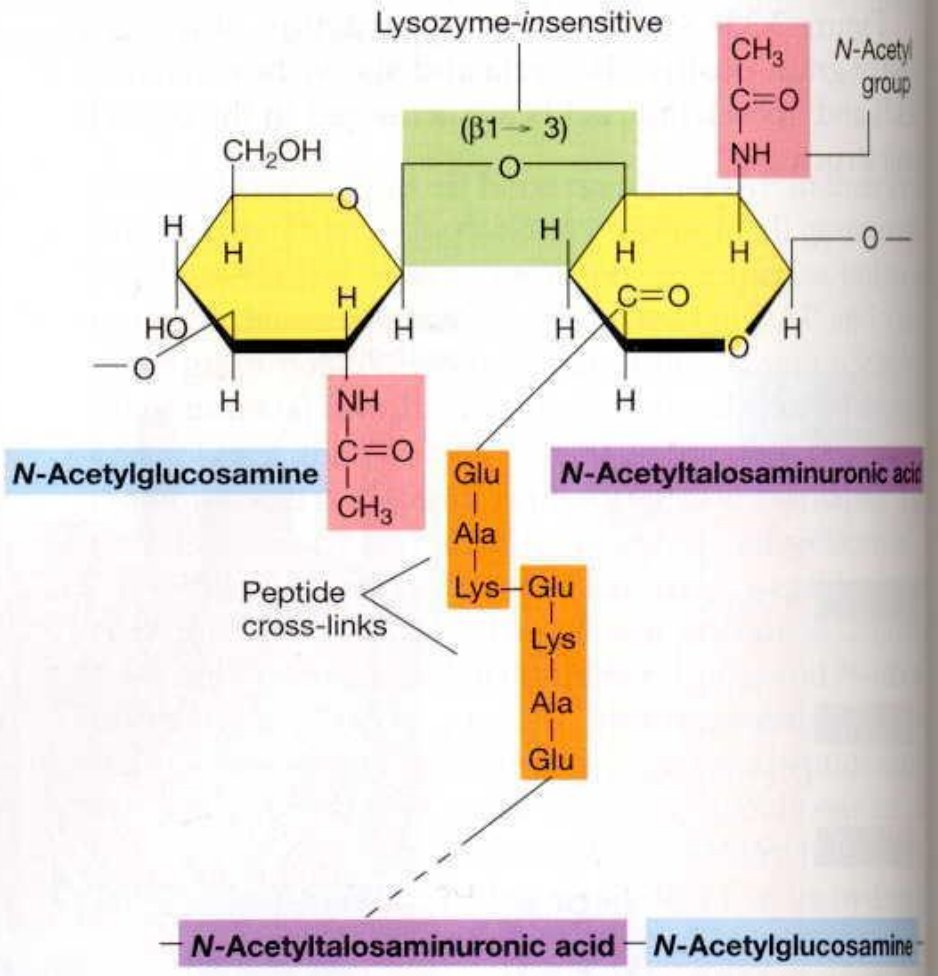


FIGURE 3.33 Teichoic acids and the overall structure of the gram-positive cell wall. (a) Structure of the ribitol teichoic acid of *Bacillus subtilis*. The teichoic acid is a polymer of the repeating ribitol units shown here. (b) Summary diagram of the gram-positive cell wall.



Susan F. Koval

(a)



(b)

FIGURE 3.35 The S-layer and pseudopeptidoglycan. (a) Transmission electron micrograph of a portion of an S-layer showing the paracrystalline nature of this cell wall layer. Shown is the S-layer from the prokaryote *Aquaspirillum serpens* (a member of the Bacteria); this S-layer displays hexagonal symmetry as do many of the S-layers found in Archaea. (b) Structure of pseudopeptidoglycan, the cell wall polymer of *Methanobacterium* species. Note the resemblance to the structure of peptidoglycan shown in Figure 3.31, especially the peptide cross-links, in this case between *N*-acetyltalosaminuronic acid residues instead of muramic acid residues.

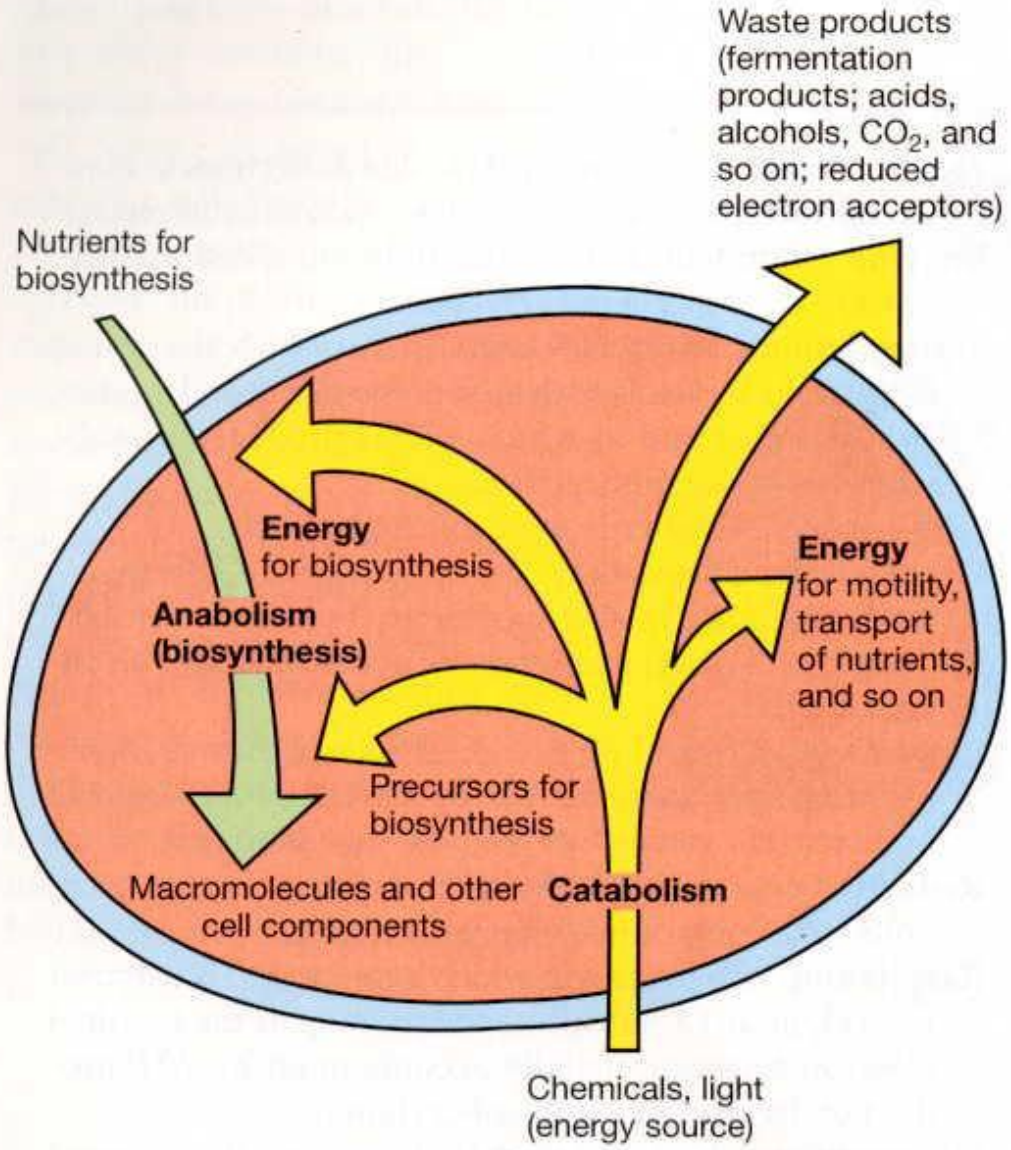


FIGURE 4.1 A simplified view of cell metabolism. Note the coupling between catabolic and anabolic processes.

Makronährstoffe

Grundkomponenten für den Aufbau von biologischen Molekülen

TABLE 4.1 Macronutrients in nature and in culture media

Element	Usual form of nutrient found in the environment	Chemical form supplied in culture media
Carbon (C)	CO_2, organic compounds	Glucose, malate, acetate, pyruvate, hundreds of other compounds, or complex mixtures (yeast extract, peptone, and so on)
Hydrogen (H)	H_2O, organic compounds	H_2O, organic compounds
Oxygen (O)	H_2O, O_2, organic compounds	H_2O, O_2, organic compounds
Nitrogen (N)	NH_3, NO_3^-, N_2, organic nitrogen compounds	*Inorganic:* NH_4Cl, $(NH_4)_2SO_4$, KNO_3, N_2 *Organic:* Amino acids, nitrogen bases of nucleotides, many other N-containing organic compounds
Phosphorus (P)	PO_4^{3-}	KH_2PO_4, Na_2HPO_4
Sulfur (S)	H_2S, SO_4^{2-}, organic S compounds, metal sulfides (FeS, CuS, ZnS, NiS, and so on)	Na_2SO_4, $Na_2S_2O_3$, Na_2S, cysteine, or other organic sulfur compounds
Potassium (K)	K^+ in solution or as various K salts	KCl, KH_2PO_4
Magnesium (Mg)	Mg^{2+} in solution or as various Mg salts	$MgCl_2$, $MgSO_4$
Sodium (Na)	Na^+ in solution or as NaCl or other Na salts	NaCl
Calcium (Ca)	Ca^{2+} in solution or as $CaSO_4$ or other Ca salts	$CaCl_2$
Iron (Fe)	Fe^{2+} or Fe^{3+} in solution or as FeS, $Fe(OH)_3$, or many other Fe salts	$FeCl_3$, $FeSO_4$, various chelated iron solutions (Fe^{3+} EDTA, Fe^{3+} citrate, and so on)

TABLE 4.2 Micronutrients (trace elements) needed by living organisms[a]

Element	Cellular function
Chromium (Cr)	Required by mammals for glucose metabolism; no known microbial requirement
Cobalt (Co)	Vitamin B_{12}; transcarboxylase (propionic acid bacteria)
Copper (Cu)	Certain proteins, notably those involved in respiration, for example, cytochrome *c* oxidase; or in photosynthesis, for example, plastocyanin; some superoxide dismutases
Manganese (Mn)	Activator of many enzymes; present in certain superoxide dismutases and in the water-splitting enzyme of photosystem II in oxygenic phototrophs
Molybdenum (Mo)	Present in various flavin-containing enzymes; also in molybdenum nitrogenase, nitrate reductase, sulfite oxidase, DMSO-TMAO reductases, some formate dehydrogenases, oxotransferases
Nickel (Ni)	Most hydrogenases; coenzyme F_{430} of methanogens; carbon monoxide dehydrogenase; urease
Selenium (Se)	Formate dehydrogenase; some hydrogenases; the amino acid selenocysteine
Tungsten (W)	Some formate dehydrogenases; oxotransferases of hyperthermophiles (for example, aldehyde:ferredoxin oxidoreductase of *Pyrococcus furiosus*)
Vanadium (V)	Vanadium nitrogenase; bromoperoxidase
Zinc (Zn)	Present in the enzymes carbonic anhydrase, alcohol dehydrogenase, RNA and DNA polymerases, and many DNA-binding proteins
Iron (Fe)[b]	Cytochromes, catalases, peroxidases, iron–sulfur proteins (for example, ferredoxin), oxygenases, all nitrogenases

a Not every micronutrient listed is required by all cells; some metals listed are found in enzymes present in only specific microorganisms.

b Needed in greater amounts than other metals—not generally considered a trace element.

Spezifische komplexe Nährstoffkomponenten

Essentielle Aminosäuren
Vitamine
Hormone (Growth hormons)
Wuchsstoffe (Giberelline)

Bedarf je nach Stoffwechseleigenschaften der Organismen

TABLE 4.3 Vitamins and their functions

Vitamin	Function
p-Aminobenzoic acid	Precursor of folic acid
Folic acid	One-carbon metabolism; methyl group transfer
Biotin	Fatty acid biosynthesis; β-decarboxylations; some CO_2 fixation reactions
Cobalamin (B_{12})	Reduction of and transfer of single carbon fragments; synthesis of deoxyribose
Lipoic acid	Transfer of acyl groups in decarboxylation of pyruvate and α-ketoglutarate
Nicotinic acid (niacin)	Precursor of NAD^+; electron transfer in oxidation–reduction reactions
Pantothenic acid	Precursor of coenzyme A; activation of acetyl and other acyl derivatives
Riboflavin	Precursor of FMN, FAD in flavoproteins involved in electron transport
Thiamine (B_1)	α-Decarboxylations; transketolase
Vitamins B_6 (pyridoxal-pyridoxamine group)	Amino acid and keto acid transformations
Vitamin K group; quinones	Electron transport; synthesis of sphingolipids
Hydroxamates	Iron-binding compounds; solubilization of iron and transport into cell

Versorgung von Organismen mit Nährstoffen in Laborkulturen und Bioreaktoren

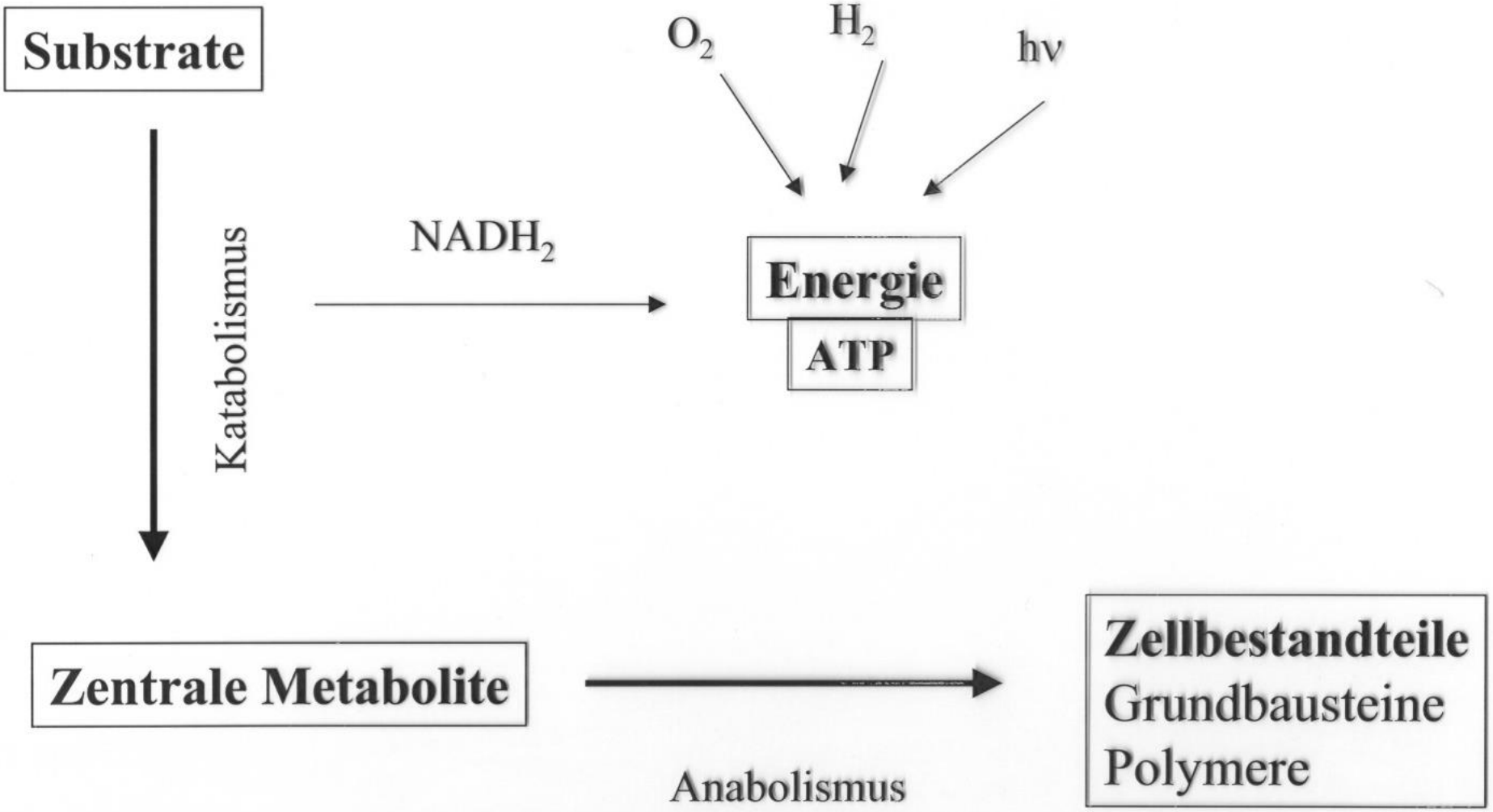
Definierte Medien (Minimalmedien)

→ Zusammensetzung genau bekannt und reproduzierbare Herstellung ist möglich
→ Nur bei Organismen mit geringen Ansprüchen an spezifische komplexe Nährstoffkomponenten (Bakterien, einfache Pilze)
→ Chemische Zusammensetzung der Rohstoffquellen genau definiert (kann bis zu p.A. Qualität gehen

Komplexe Medien

→ Bereitstellung der notwendigen Komponenten in Form von komplexen Gemischen
→ Zusammensetzung oft nicht genau bekannt
→ Schwierig reproduzierbar herzustellen, da Rohstoffquellen nicht konstant sind
→ Beispiele für Komplexe Komponenten: Hefeextrakt, Fleischextrakte, Proteinhydrolysate (Peptone, Tryptone auf Basis tierischer oder pflanzlicher Proteine, Melasse, Stärkehydrolysate etc.)

Stoffwechsel



Strategien der Energiegewinnung

Organotroph
Aerob
Anaerob

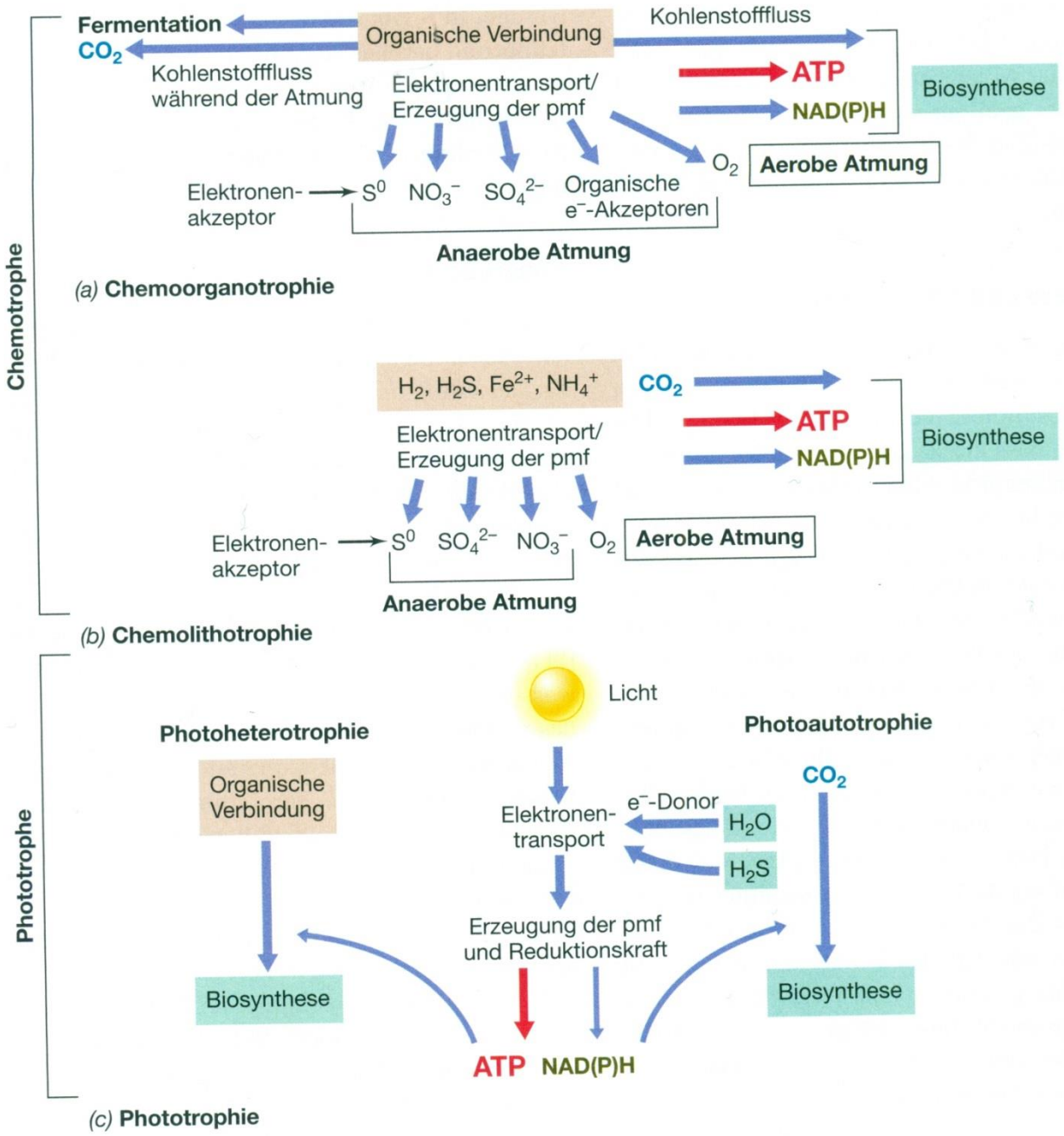
Chemolithotroph
Aerob
Anaerob

Phototroph

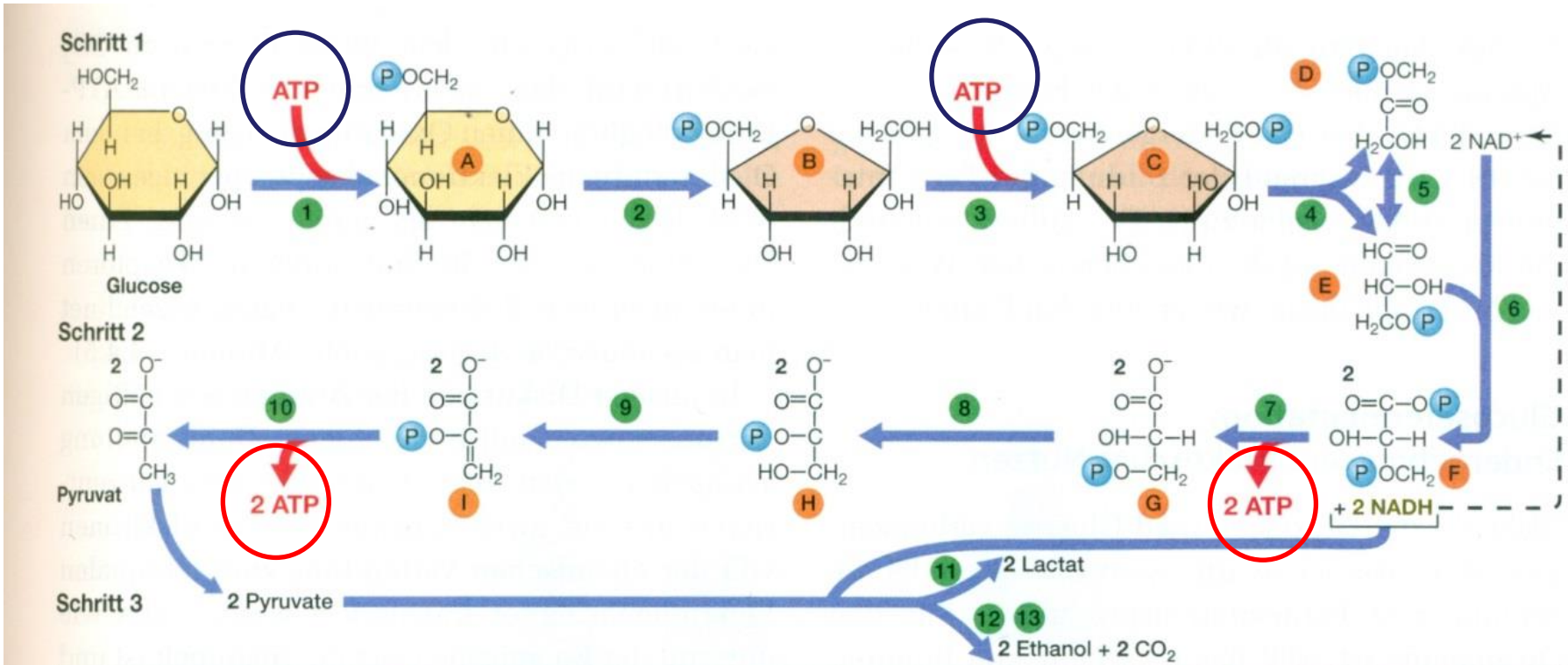
Electron Flow

Proton Motive Force

Carbon Flow



Glycolyse



Zwischenprodukte

- A Glucose-6-P
- B Fructose-6-P
- C Fructose-1,6-P
- D Dihydroxyaceton-P
- E Glycerinaldehyd-3-P
- F 1,3-Bisphosphoglycerat
- G 3-P-Glycerat
- H 2-P-Glycerat
- I Phosphoenolpyruvat

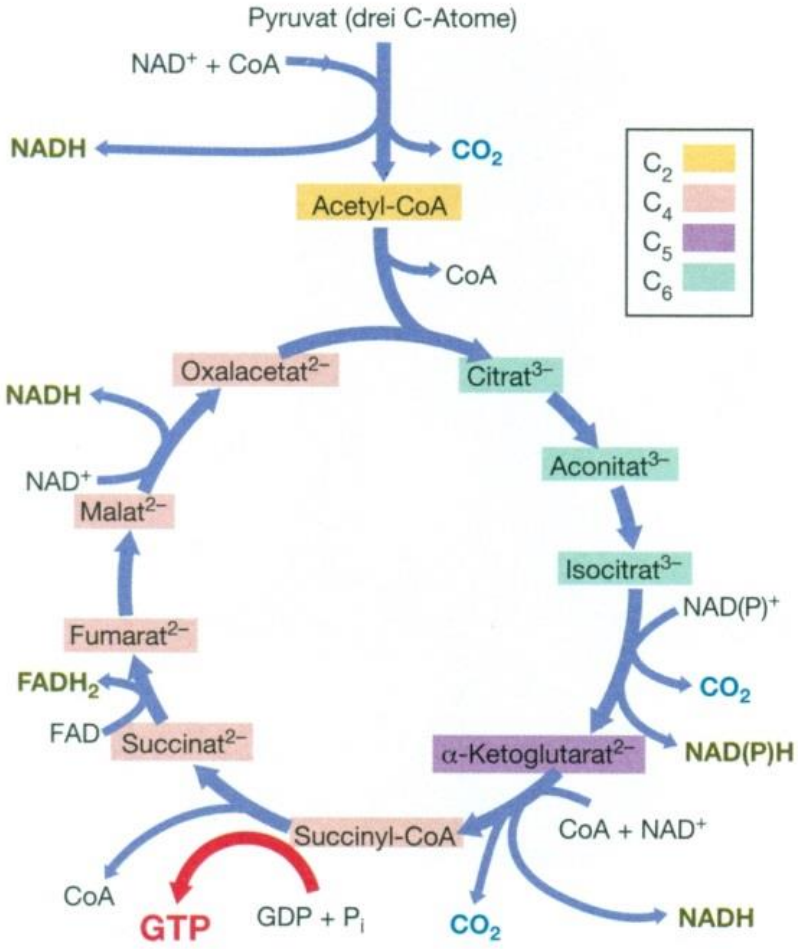
Enzyme

1. Hexokinase
2. Isomerase
3. Phosphofructokinase
4. Aldolase
5. Triosephosphatisomerase
6. Glycerinaldehyd-3-P-Dehydrogenase
7. Phosphoglycerokinase
8. Phosphoglyceromutase
9. Enolase
10. Pyruvatkinase
11. Lactatdehydrogenase
12. Pyruvatdecarboxylase
13. Alkoholdehydrogenase

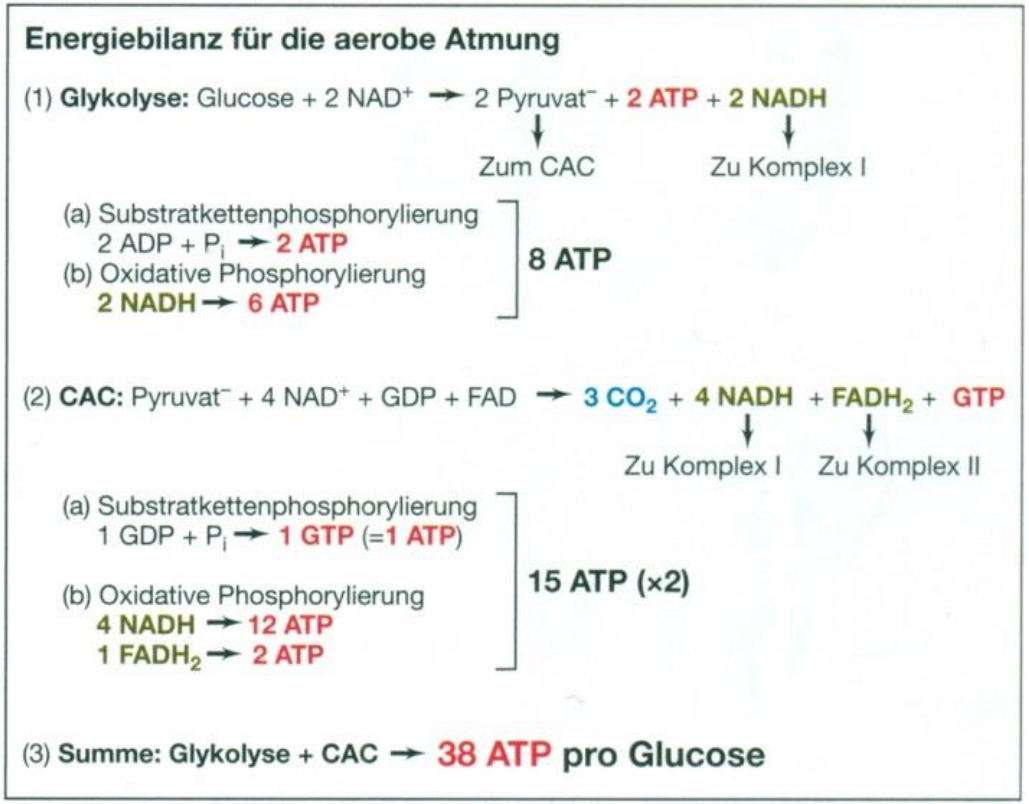
Energetik

Hefe	Glucose → 2 Ethanol + 2 CO_2	−239 kJ
Milchsäurebakterien	Glucose → 2 Lactat	−196 kJ

Citratcyclus



(a)



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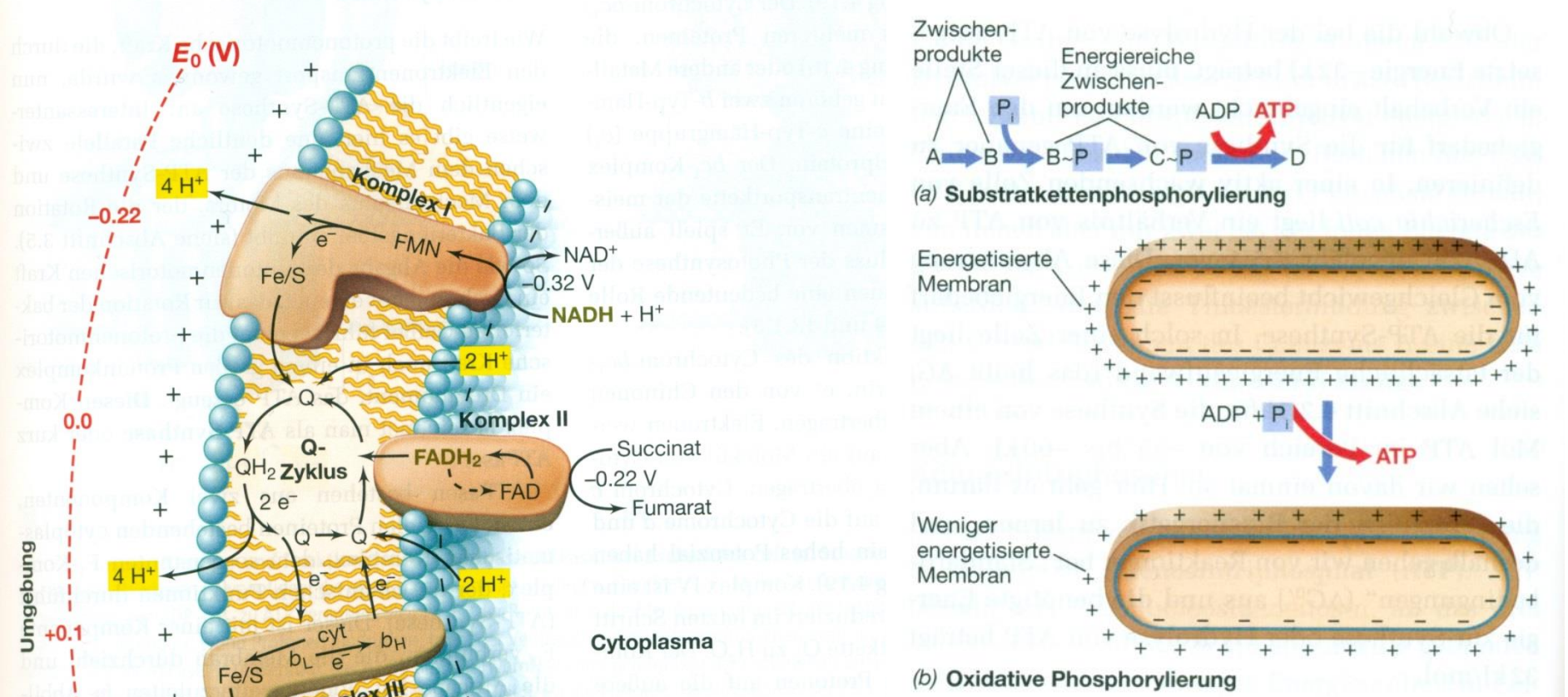
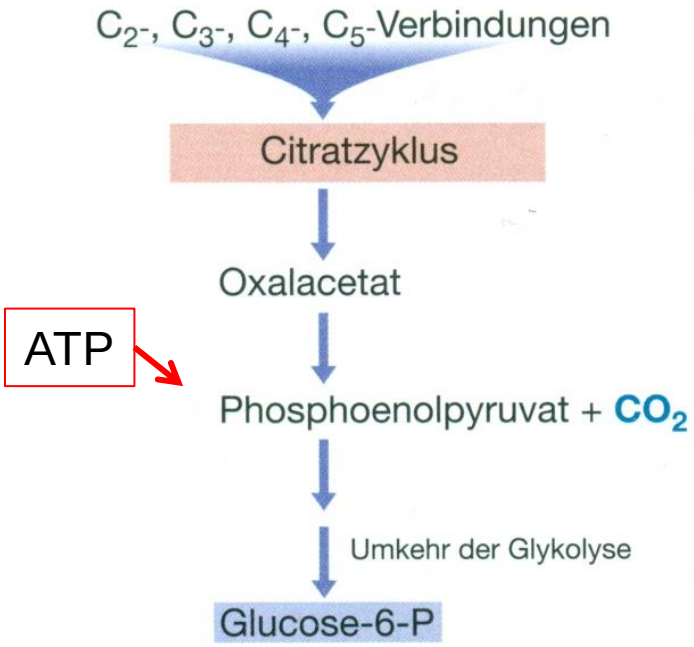


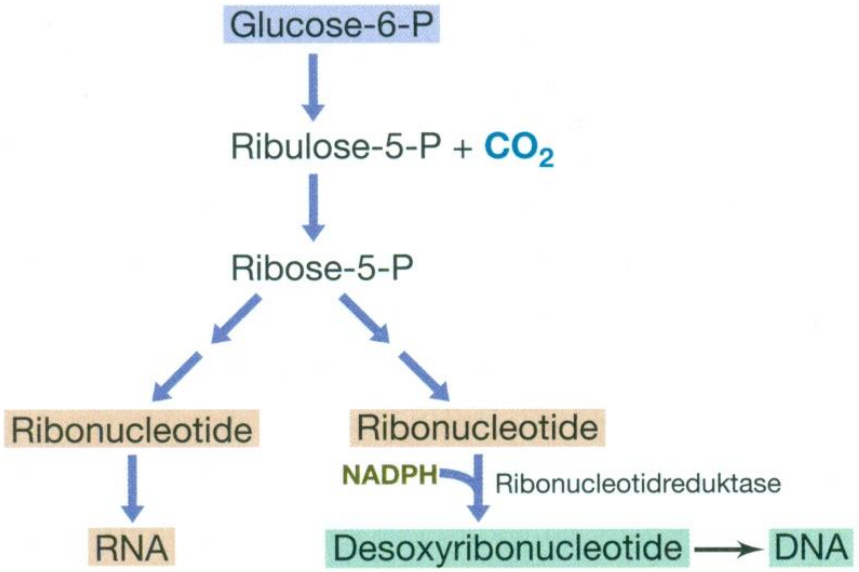
Abbildung 4.19: Die Erzeugung der protonenmotorischen Kraft während der aeroben Atmung. Die Ausrichtung der Elektronenträger in der Membran von *Paracoccus denitrificans*, einem Modellorganismus für die Untersuchung der Atmung. Die +- und —Ladungen an den Seiten der Membran entsprechen jeweils H^+ und OH^-. Es sind die E_0'-Werte der wichtigsten Elektronenüberträger angegeben. Beachten Sie folgendes: wenn ein Wasserstoffatomüberträger (zum Beispiel FMN in Komplex I) einen elektronenakzeptierenden Elektronenüberträger reduziert (zum Beispiel das Fe/S-Protein in Komplex I), dann werden Protonen auf die äußere Oberfläche der Membran ausgeschleust. Die Abkürzungen lauten folgendermaßen: FMN, Flavinmononucleotid; FAD, Flavinadenindinucleotid; Q, Chinon; Fe/S, Eisenschwefelprotein; cyt a, b und c, Cytochrome (b_L und b_H, jeweils Cytochrom vom b-Typ mit niedrigem und hohem Potenzial). An der Chinonstelle findet während des „Q-Zyklus" eine Wiederaufbereitung von Elektronen statt. Das liegt daran, dass Elektronen von QH_2 im bc_1-Komplex (Komplex III) zwischen dem Fe/S-Protein und den Cytochromen vom b-Typ aufgeteilt werden können. Elektronen, die über die Cytochrome laufen, reduzieren Q (in zwei Schritten mit einem Elektron) zurück zu QH_2, wodurch die Anzahl der Protonen, die an der Q-bc_1-Stelle eingeschleust werden, erhöht wird. Elektronen, die über Fe/S laufen, reduzieren Cytochrom c_1, dann Cytochrom c und anschließend Cytochrom vom a-Typ in Komplex IV, schließlich reduzieren sie O_2 zu H_2O (man braucht zwei Elektronen und vier Protonen, um $\frac{1}{2}$ O_2 zu H_2O zu reduzieren und zwei 2 H^+ auszuschleusen, die jeweils von zwei über cyt c übertragenen Elektronen und cytoplasmatischen Protonen stammen). Komplex II, der Succinatdehydrogenase-Komplex, umgeht Komplex I und schleust Elektronen direkt in die Chinonsammelstelle bei einem positiveren E_0'-Wert als NADH ein (siehe Elektronenturm in Abbildung 4.9).

Anabolischer Stoffwechsel

Aufbau von komplexeren Molekülen aus Grundbauteilen
Ausgang: Citratcyclus

Aufbau von Zuckern





Anabolischer Stoffwechsel

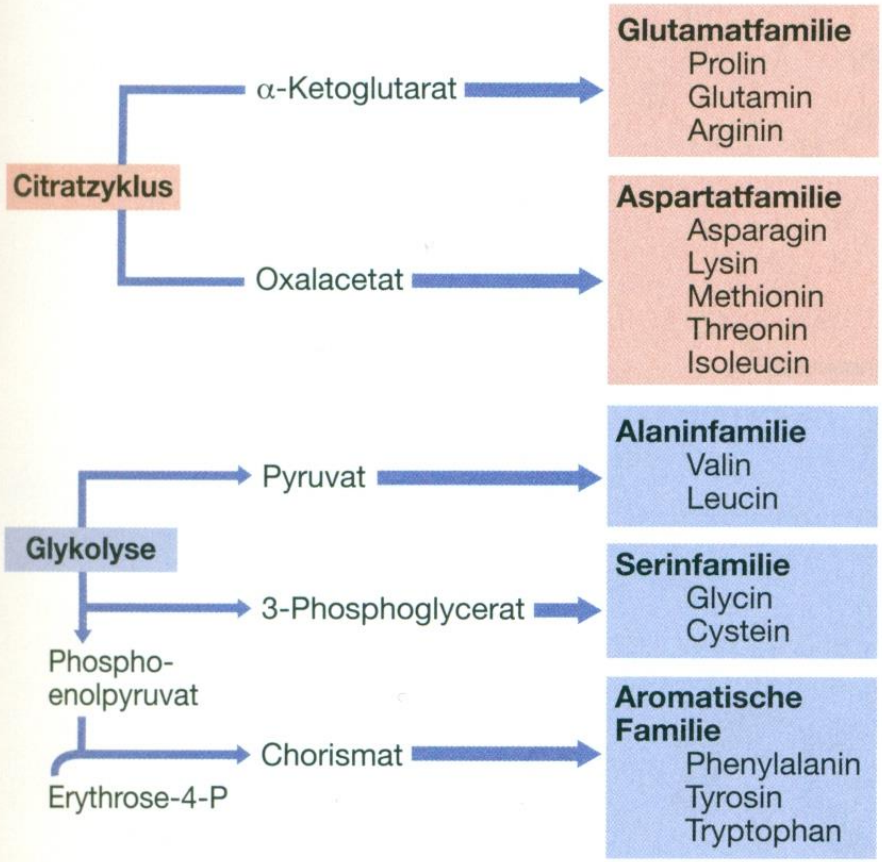


Abbildung 4.24: Aminosäurefamilien. Der Citratzyklus und die Glykolyse liefern die Kohlenstoffskelette für die meisten Aminosäuren. Die Synthese verschiedener Aminosäuren innerhalb einer Familie erfordert häufig viele getrennte Schritte, die mit der Hauptaminosäure beginnen (Fettbuchstaben markieren die jeweilige Familie). In Abschnitt 4.4.1 (siehe Abbildung 4.14) wird die Glykolyse besprochen und in Abschnitt 4.4.4 (siehe Abbildung 4.21) gehen wir auf den Citratzyklus ein.

Aufbau von Aminosäuren

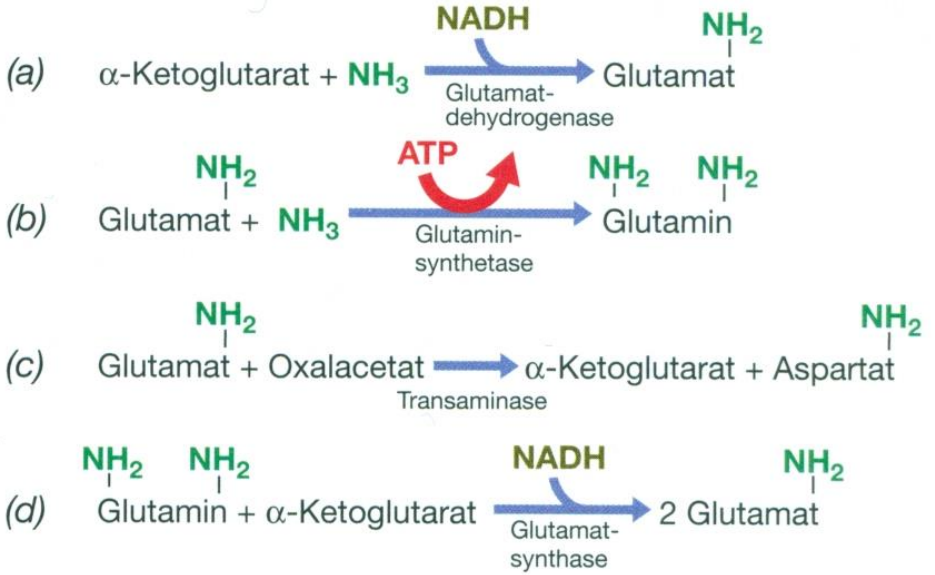


Abbildung 4.25: Die Aufnahme von Ammoniak bei Bakterien. Um den Fluss des Stickstoffs hervorzuheben, sind sowohl der freie Ammoniak (NH_3) als auch die Aminogruppen aller Aminosäuren grün dargestellt. Zwei der Hauptwege für die Assimilierung von NH_3 bei Bakterien werden von den Enzymen (a) Glutamatdehydrogenase und (b) Glutaminsynthetase katalysiert. (c) Transaminasereaktionen übertragen eine Aminogruppe von einer Aminosäure zu einer organischen Säure. (d) Das Enzym Glutamatsynthase bildet aus einem Glutamin und einem α-Ketoglutarat zwei Glutamat.

Relevante Umweltparameter für Bioprozesse

Temperatur

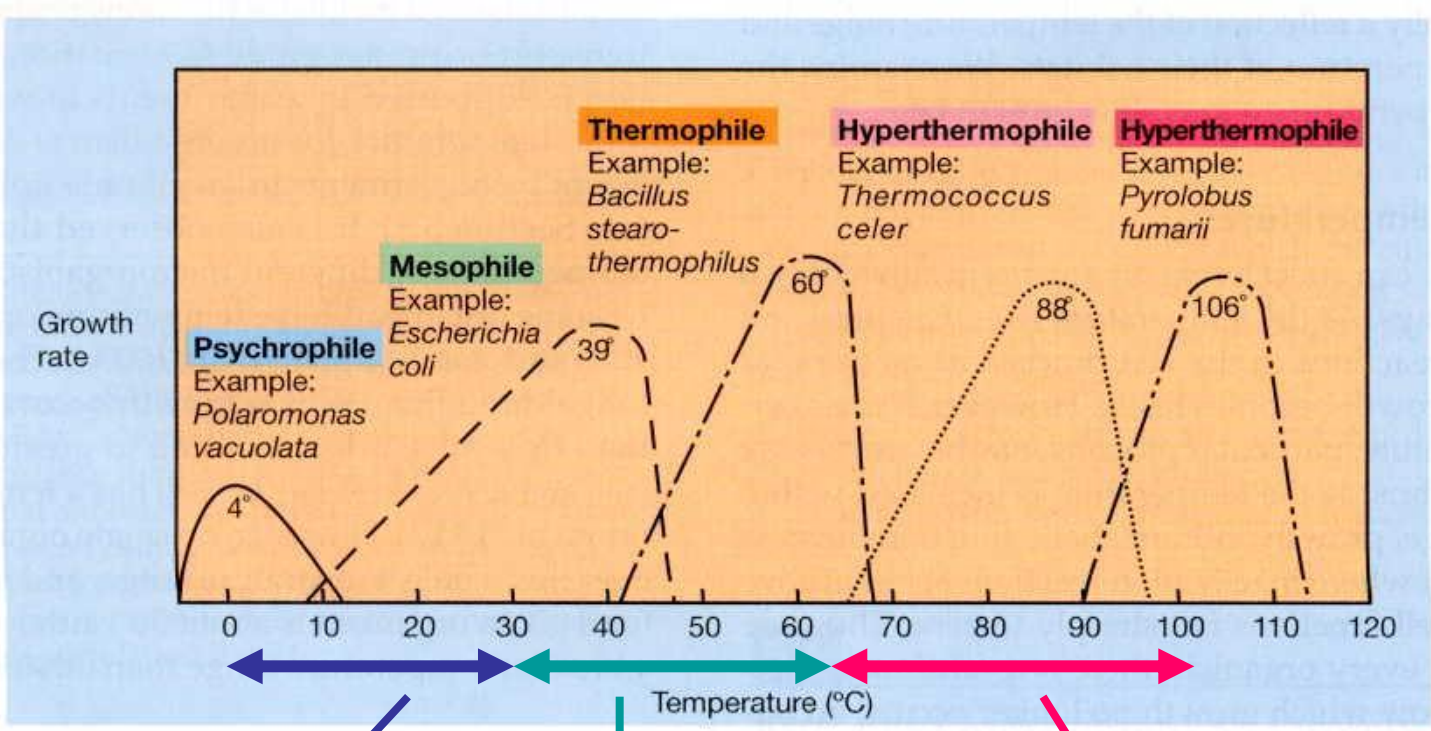


FIGURE 5.13 Relation of temperature to growth rates of a typical psychrophile, a typical mesophile, a typical thermophile, and two different hyperthermophiles. The temperature optima of the example organisms are shown on the graph.

Kühlprobleme

Optimale Prozess-bedingungen

Technische Probleme z.B. Verdunstung

Relevante Umweltparameter für Bioprozesse

TABLE 5.1 **Presently known upper temperature limits for growth of living organisms**

Group	Upper temperature limits (°C)
Animals	
Fish and other aquatic vertebrates[a]	38
Insects	45–50
Ostracods (crustaceans)	49–50
Plants	
Vascular plants	45
Mosses	50
Eukaryotic microorganisms	
Protozoa	56
Algae	55–60
Fungi	60–62
Prokaryotes	
Bacteria	
Cyanobacteria	70–74
Anoxygenic phototrophs	70–73
Chemoorganotrophic/chemolithotrophic Bacteria	95
Archaea	
Chemoorganotrophic/chemolithotrophic Archaea	113

a See a possible exception in Section 16.12 and Figure 16.34.

Relevante Umweltparameter für Bioprozesse

Breiter Arbeitsbereich möglich

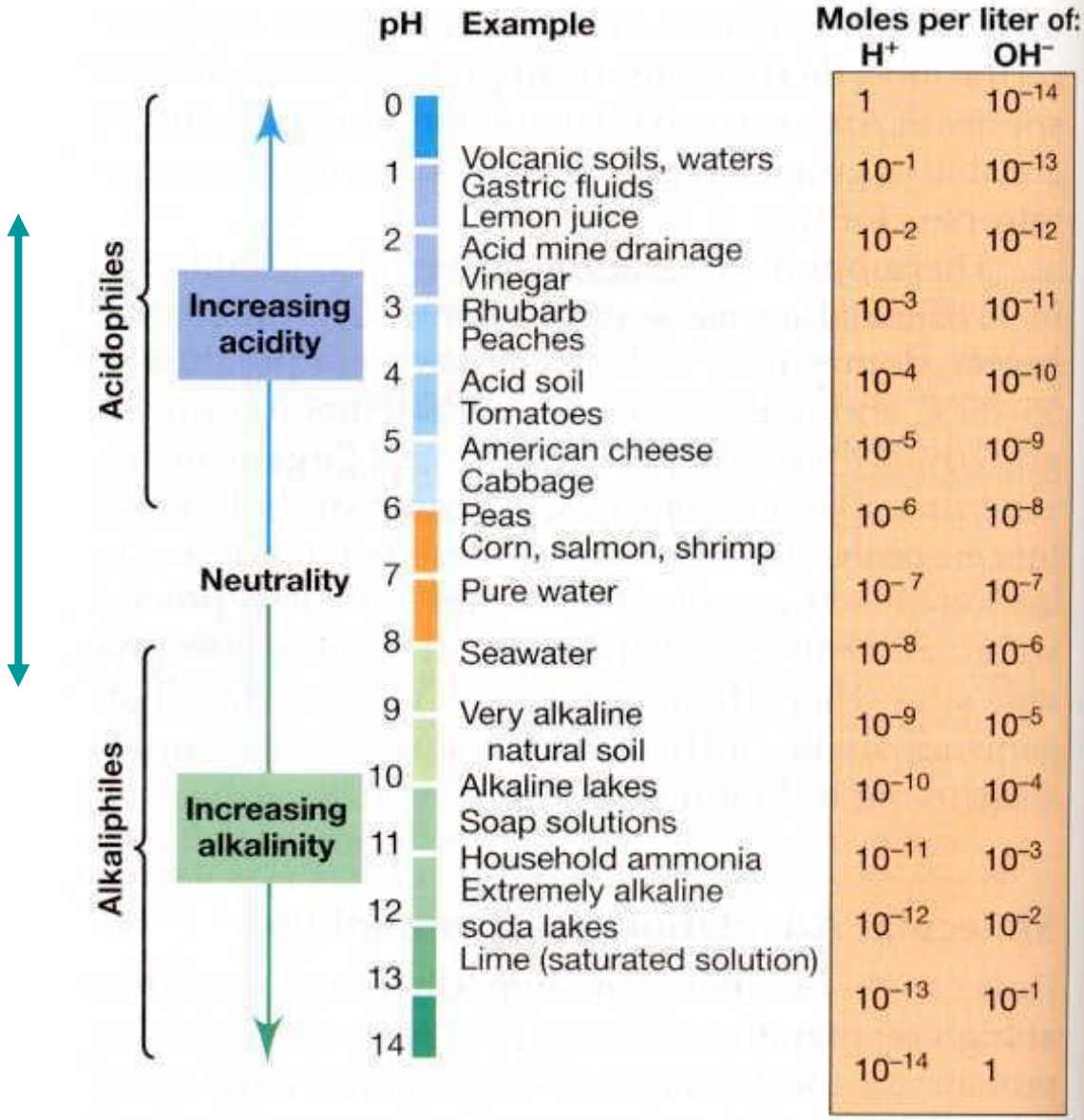


FIGURE 5.18 The pH scale. Note that although some microorganisms can live at very low or very high pH, the cell's internal pH remains near neutrality.

Relevante Umweltparameter für Bioprozesse

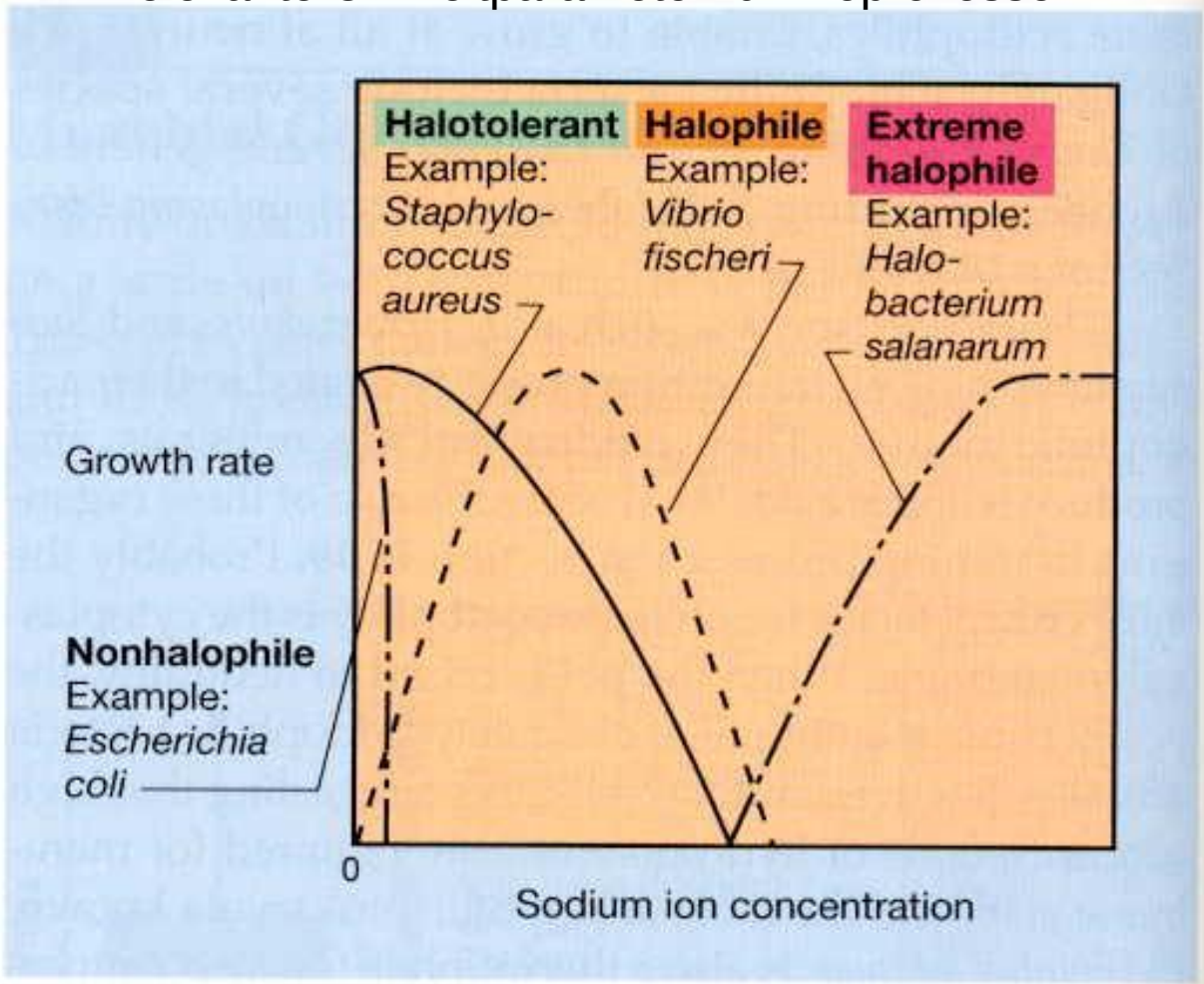


FIGURE 5.19 Effect of sodium ion concentration on growth of microorganisms of different salt tolerances. The optimum NaCl concentration for marine microorganisms such as *V. fischeri* is about 3%; for extreme halophiles, it is between 15 and 30%, depending on the organism.

Relevante Umweltparameter für Bioprozesse

Wasseraktivität

TABLE 5.2 Water activity of several substances

Water activity, a_w	Material	Examples of organisms growing at stated water activity
1.000	Pure water	*Caulobacter, Spirillum*
0.995	Human blood	*Streptococcus, Escherichia*
0.980	Seawater	*Pseudomonas, Vibrio*
0.950	Bread	Most gram-positive rods
0.900	Maple syrup, ham	Gram-positive cocci such as *Staphylococcus*
0.850	Salami	*Saccharomyces rouxii* (yeast)
0.800	Fruit cake, jams	*Saccharomyces bailii, Penicillium* (fungus)
0.750	Salt lakes, salted fish	*Halobacterium, Halococcus*
0.700	Cereals, candy, dried fruit	*Xeromyces bisporus* and other xerophilic fungi

Die meisten Bioprozesse werden bei Wasseraktivitäten nahe 1 durchgeführt

In Spezialfällen ist niedrigere Wasseraktivität zu beachten (Feststofffermentation)

Relevante Umweltparameter für Bioprozesse

Sauerstoff

TABLE 5.4 Oxygen relationships of microorganisms

Group	Relationship to O_2	Type of metabolism	Example	Habitat[a]
Aerobes				
Obligate	Required	Aerobic respiration	*Micrococcus luteus*	Skin, dust
Facultative	Not required, but growth better with O_2	Aerobic, anaerobic respiration, fermentation	*Escherichia coli*	Mammalian large intestine
Microaerophilic	Required but at levels lower than atmospheric	Aerobic respiration	*Spirillum volutans*	Lake water
Anaerobes				
Aerotolerant	Not required, and growth no better when O_2 present	Fermentation	*Streptococcus pyogenes*	Upper respiratory tract
Obligate	Harmful or lethal	Fermentation or anaerobic respiration	*Methanobacterium formicicum*	Sewage sludge digestors, anoxic lake sediments

[a] Listed are typical habitats of the example organism.

Breiter Bereich realisierbar

Probleme: Limitierung bei O_2 Eintragskapazität von Bioreaktoren