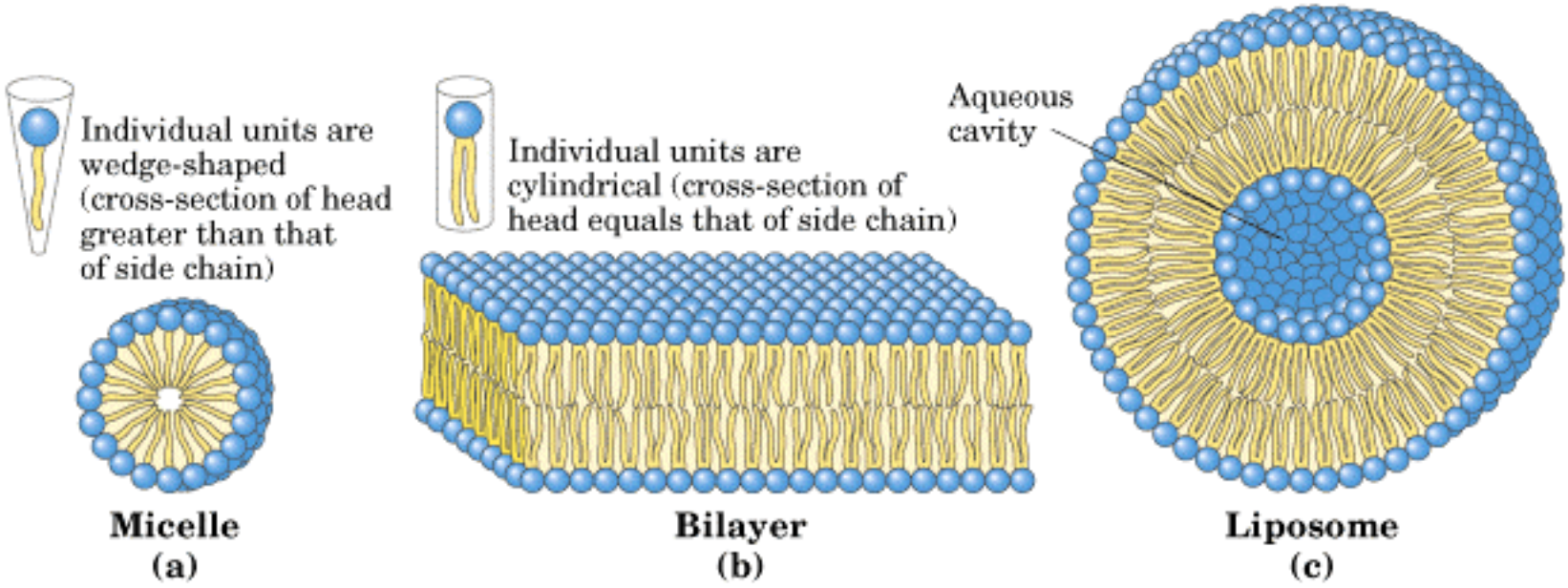

Individual units are wedge-shaped (cross-section of head greater than that of side chain)
Micelle
(a)
Individual units are cylindrical (cross-section of head equals that of side chain)
Bilayer
(b)
Aqueous cavity
Liposome
(c)

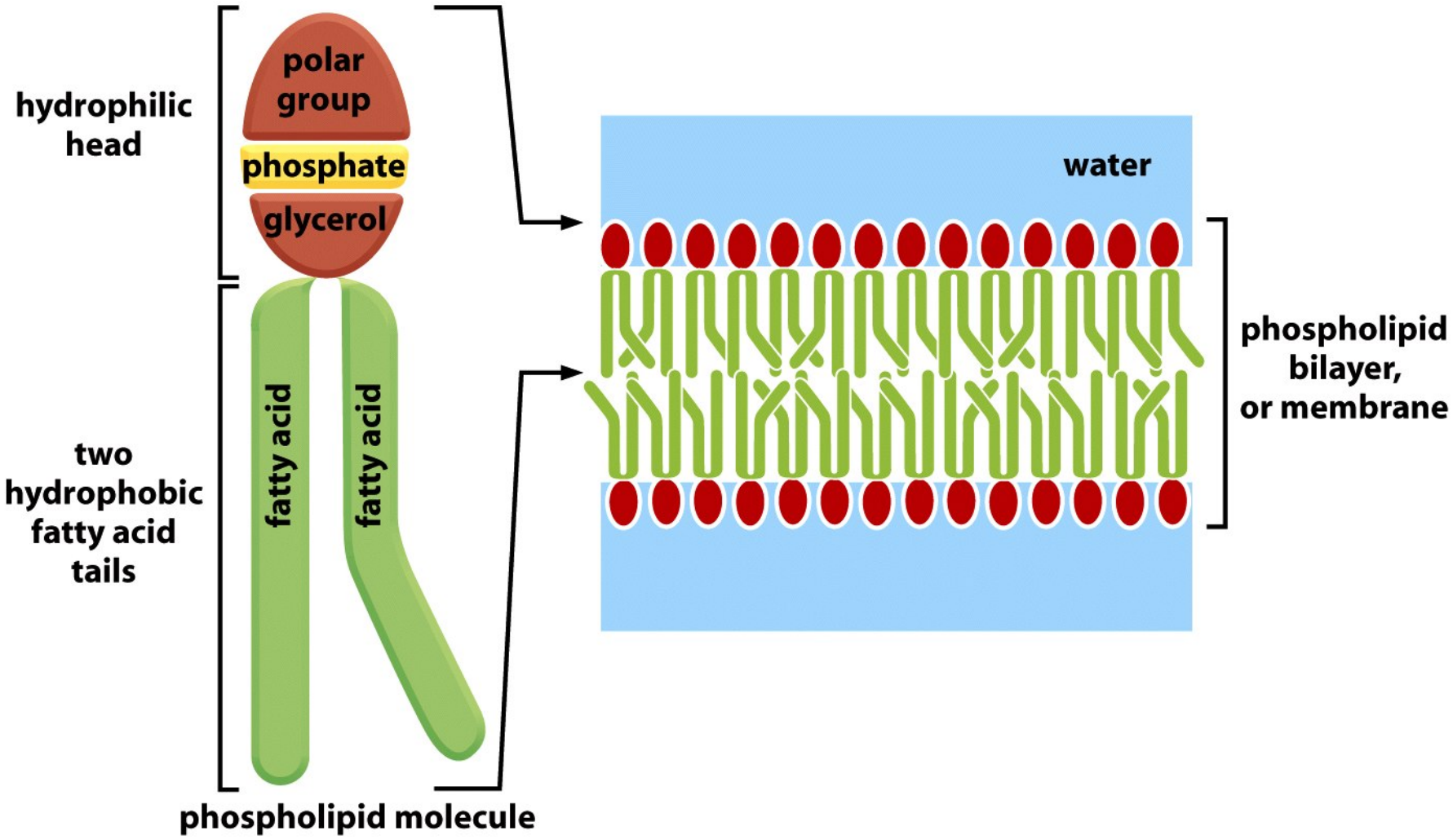


Figure 2-22 *Molecular Biology of the Cell* (© Garland Science 2008)

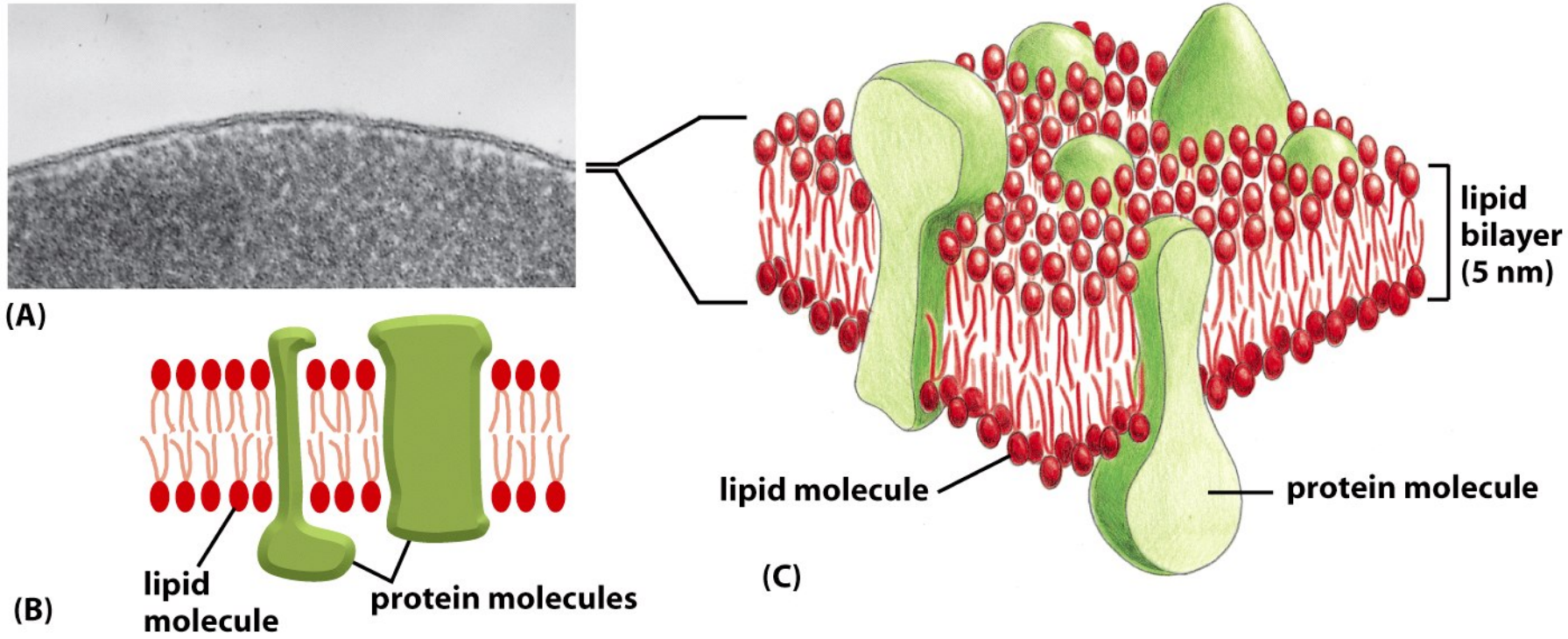


Figure 10-1 *Molecular Biology of the Cell* (© Garland Science 2008)

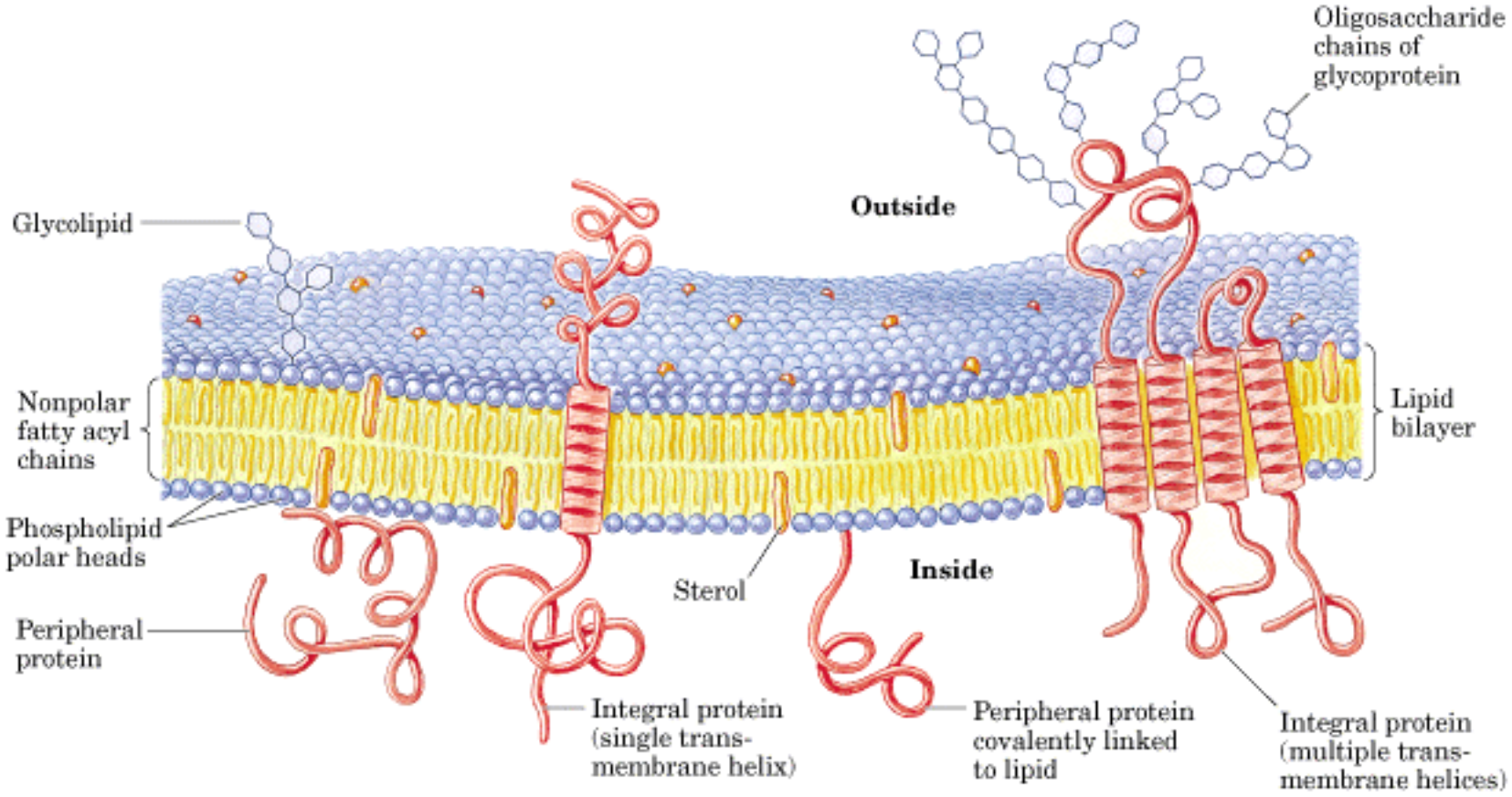
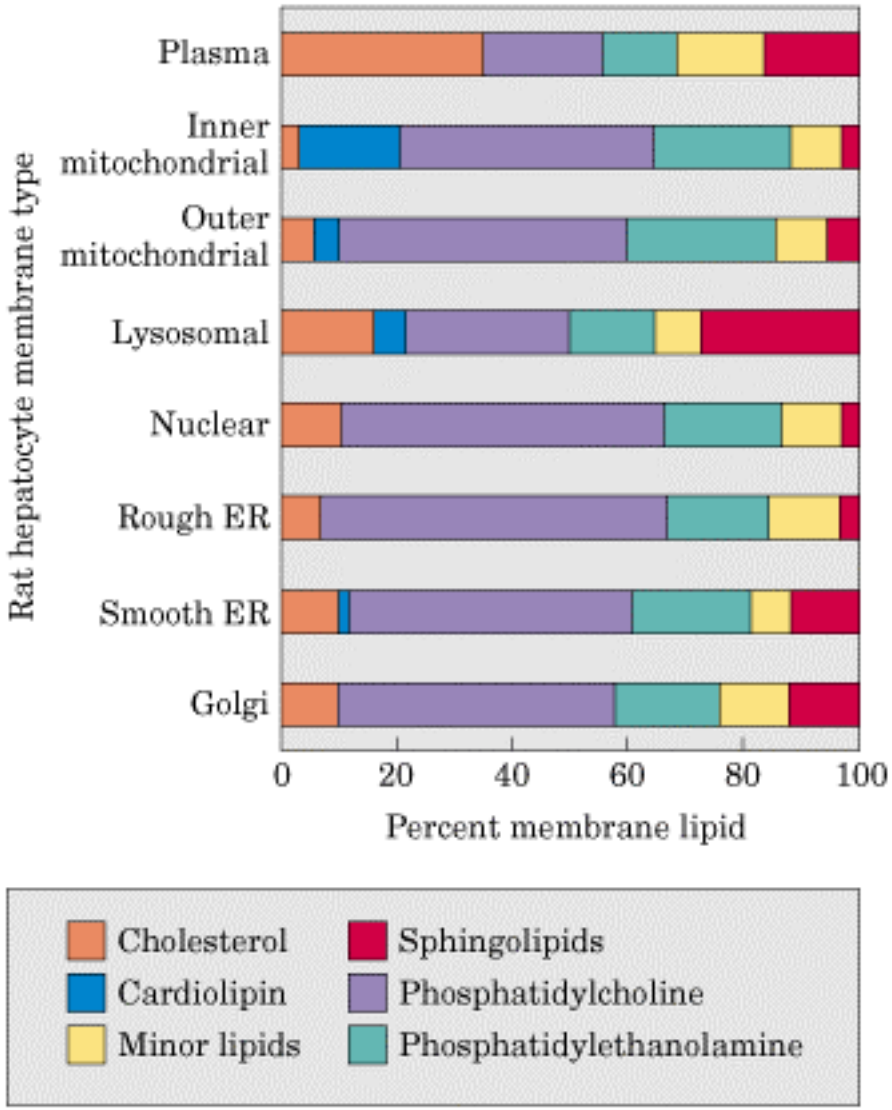

Oligosaccharide chains of glycoprotein
Outside
Glycolipid
Nonpolar fatty acyl chains
Lipid bilayer
Phospholipid polar heads
Sterol
Inside
Peripheral protein
Integral protein (single trans-membrane helix)
Peripheral protein covalently linked to lipid
Integral protein (multiple trans-membrane helices)

table 12–1

Major Components of Plasma Membranes in Various Organisms

	Components (% by weight)				
	Protein	**Phospholipid**	**Sterol**	**Sterol type**	**Other lipids**
Human myelin sheath	30	30	19	Cholesterol	Galactolipids, plasmalogens
Mouse liver	45	27	25	Cholesterol	—
Maize leaf	47	26	7	Sitosterol	Galactolipids
Yeast	52	7	4	Ergosterol	Triacylglycerols, steryl esters
Paramecium (ciliated protist)	56	40	4	Stigmasterol	—
E. coli	75	25	0	—	—


Plasma
Inner mitochondrial
Outer mitochondrial
Lysosomal
Nuclear
Rough ER
Smooth ER
Golgi
Rat hepatocyte membrane type
0
20
40
60
80
100
Percent membrane lipid
Cholesterol
Cardiolipin
Minor lipids
Sphingolipids
Phosphatidylcholine
Phosphatidylethanolamine

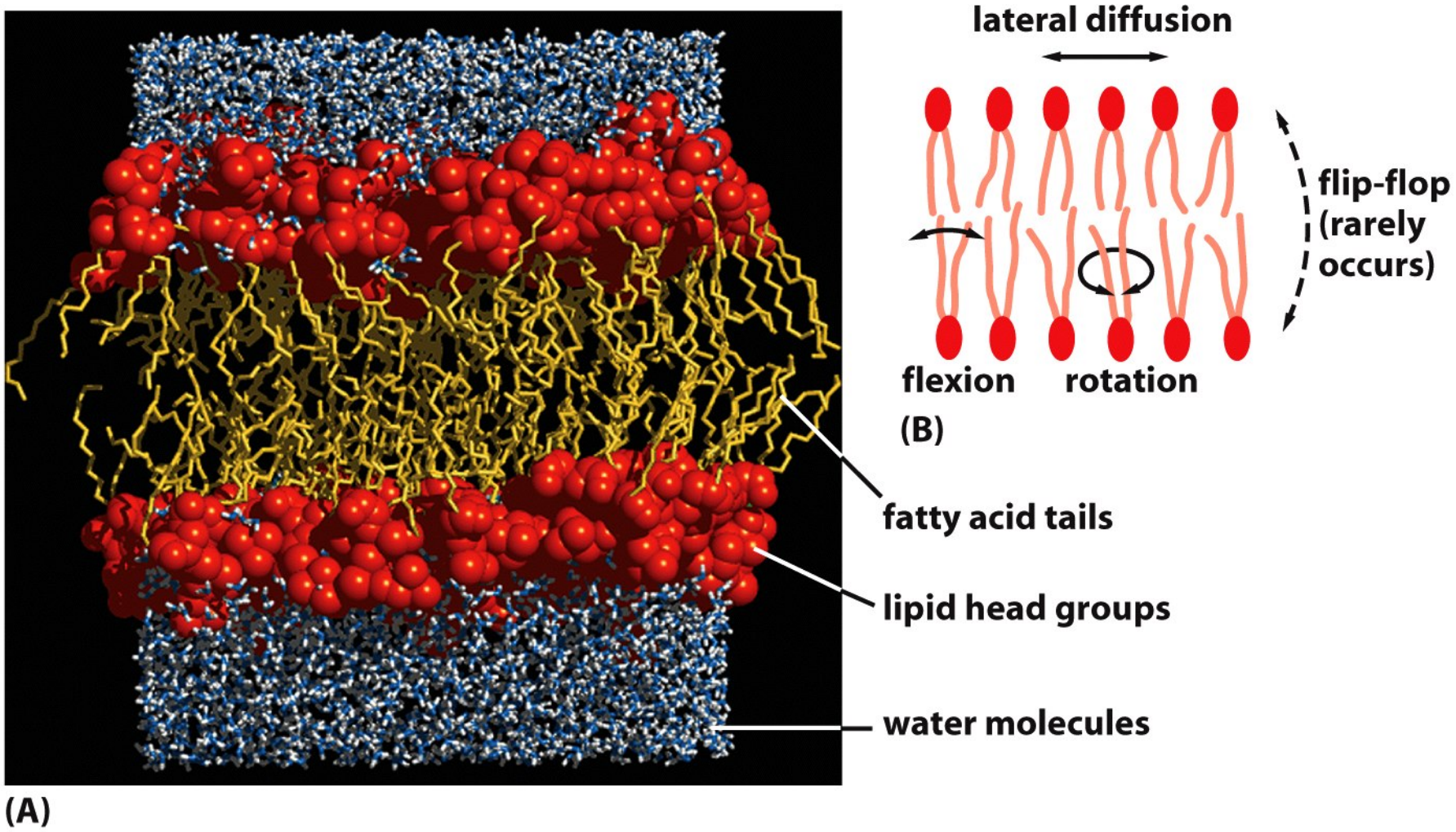


Figure 10-11 *Molecular Biology of the Cell* (© Garland Science 2008)

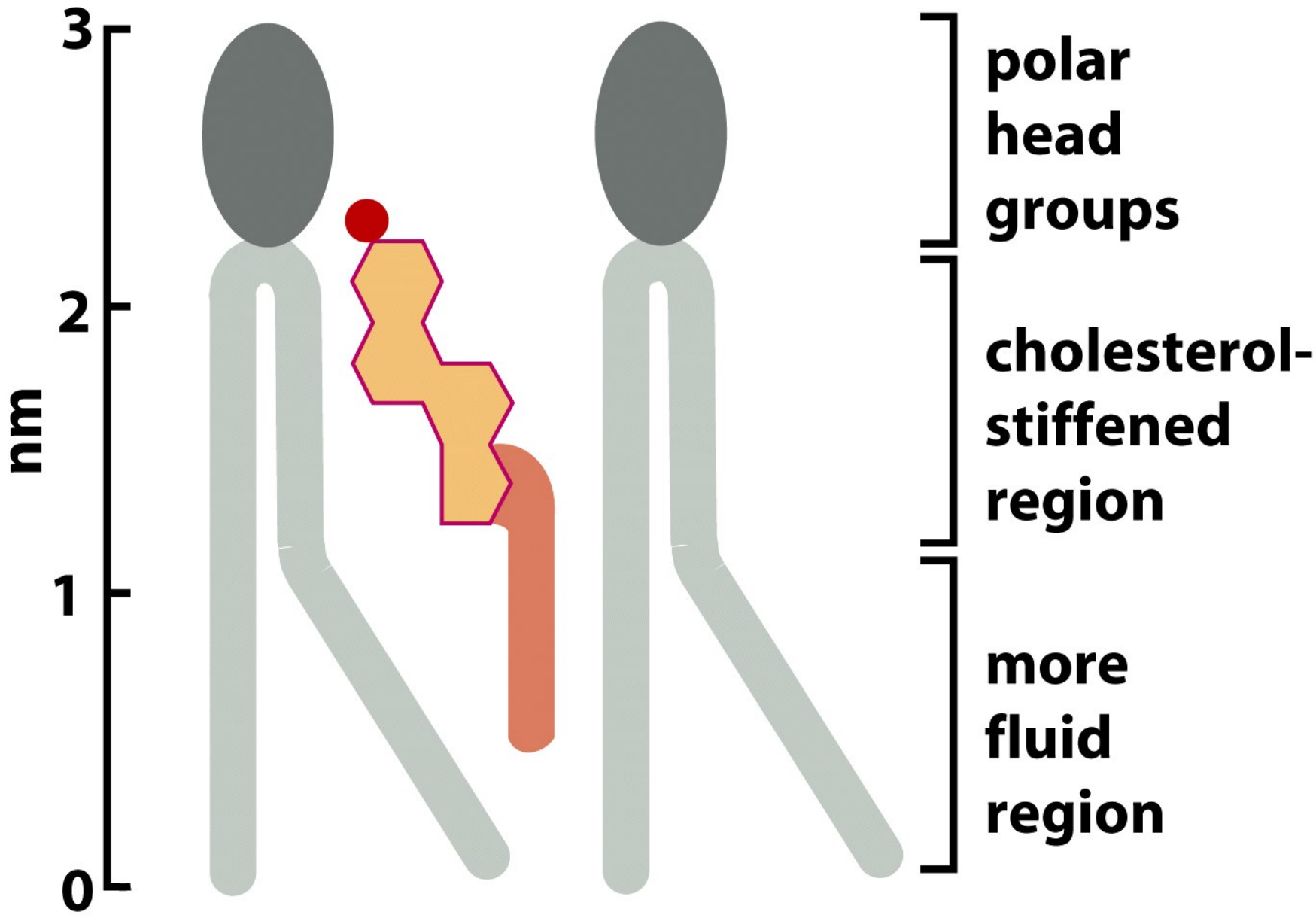


Figure 10-5 *Molecular Biology of the Cell* (© Garland Science 2008)

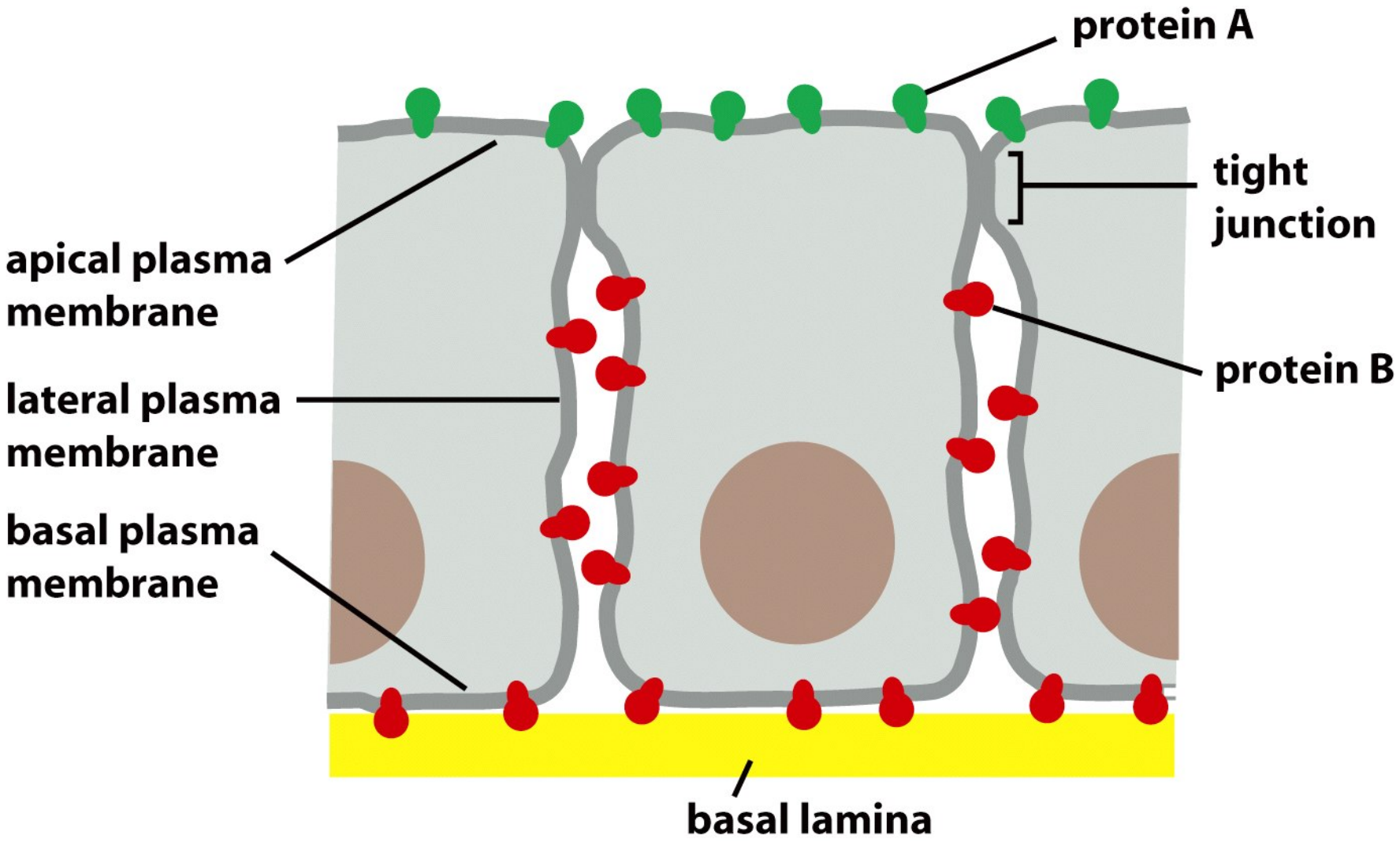


Figure 10-37 *Molecular Biology of the Cell* (© Garland Science 2008)

table 12–2

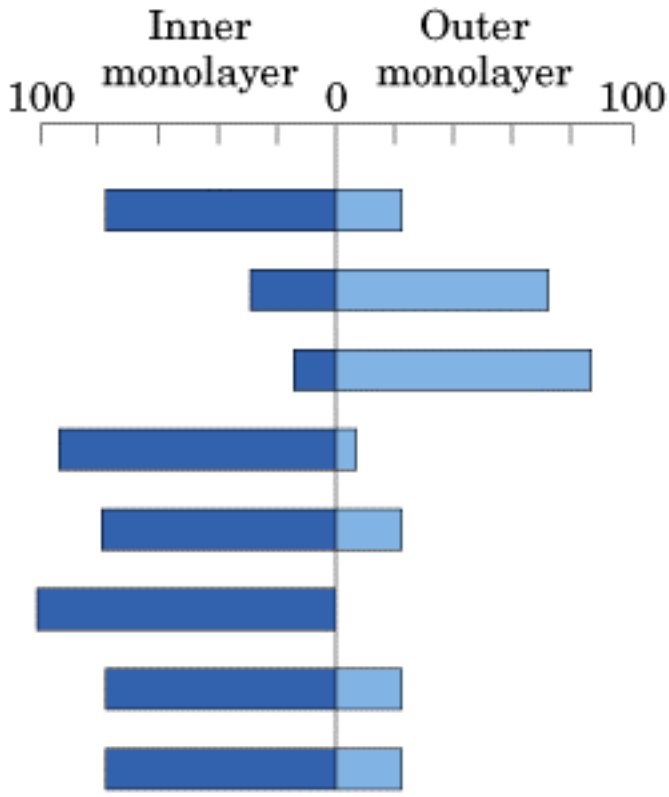
Fatty Acid Composition of *E. coli* Cells Cultured at Different Temperatures

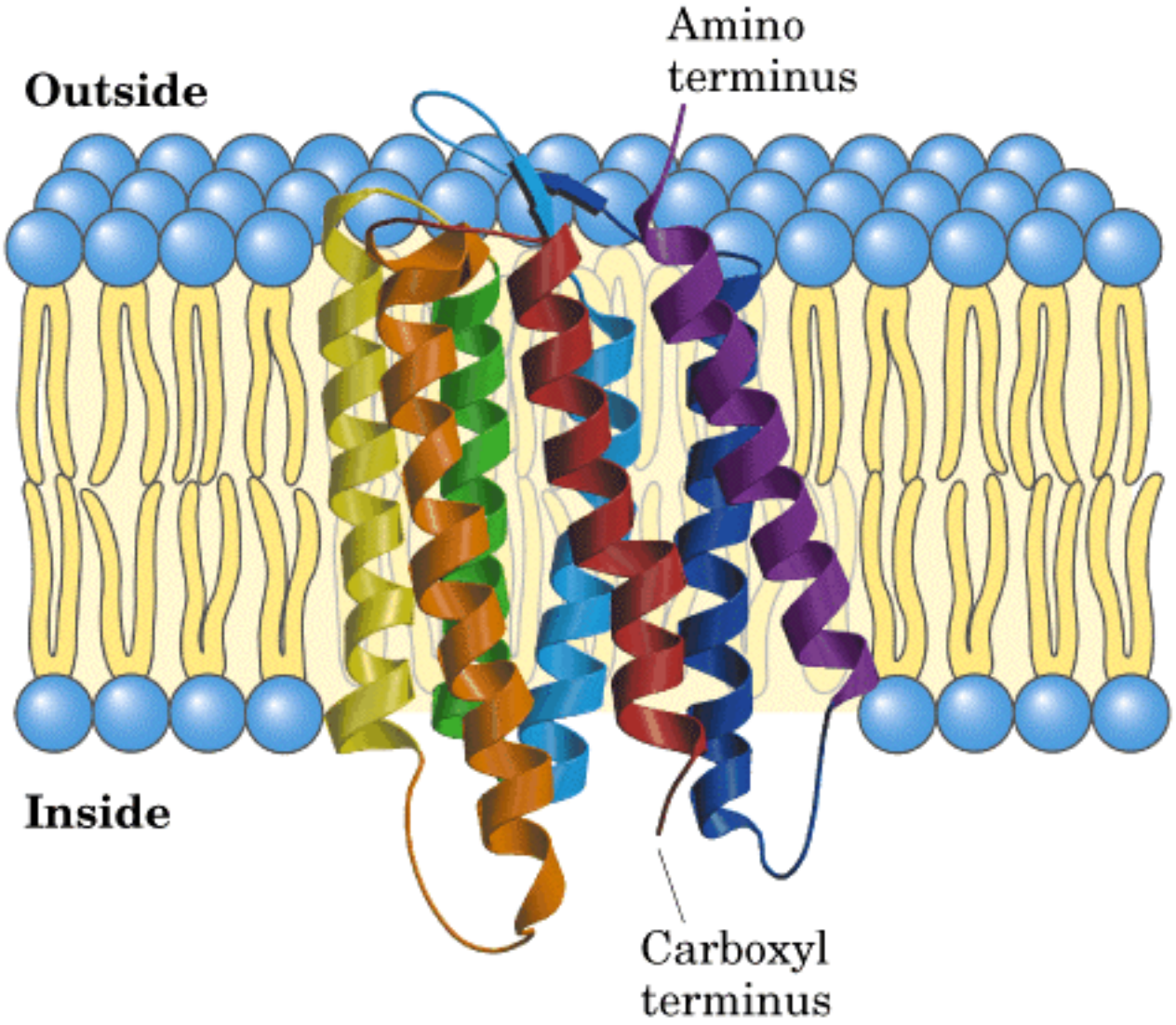
	Percentage of total fatty acids*			
	10 °C	20 °C	30 °C	40 °C
Myristic acid (14:0)	4	4	4	8
Palmitic acid (16:0)	18	25	29	48
Palmitoleic acid (16:1)	26	24	23	9
Oleic acid (18:1)	38	34	30	12
Hydroxymyristic acid	13	10	10	8
Ratio of unsaturated to saturated†	2.9	2.0	1.6	0.38

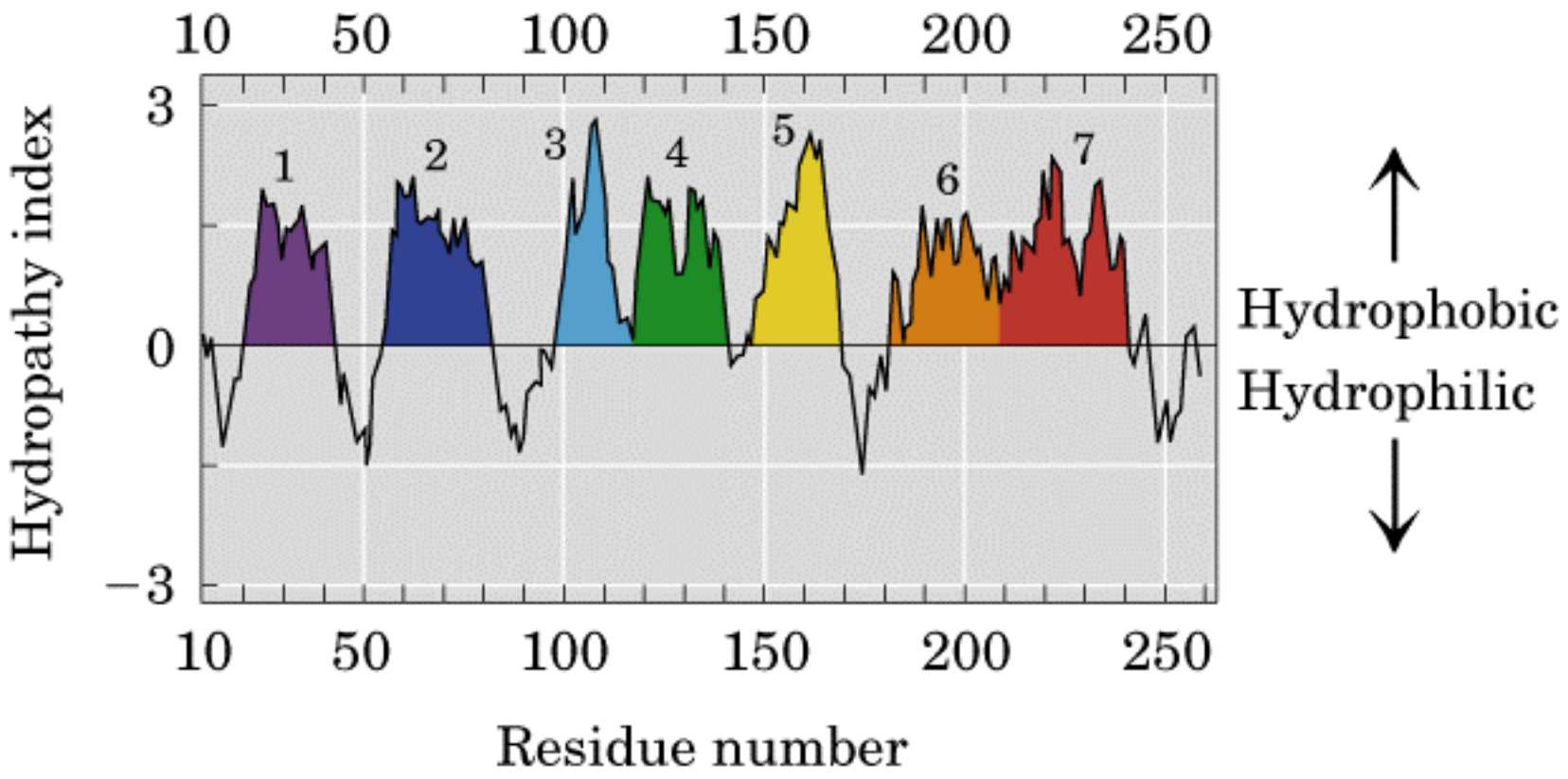
Source: Data from Marr, A.G. & Ingraham, J.L. (1962) Effect of temperature on the composition of fatty acids in *Escherichia coli*. *J. Bacteriol.* **84,** 1260.

*The exact fatty acid composition depends not only on growth temperature but on growth stage and growth medium composition.

†Calculated as the total percentage of 16:1 plus 18:1 divided by the total percentage of 14:0 plus 16:0. Hydroxymyristic acid was omitted from this calculation.

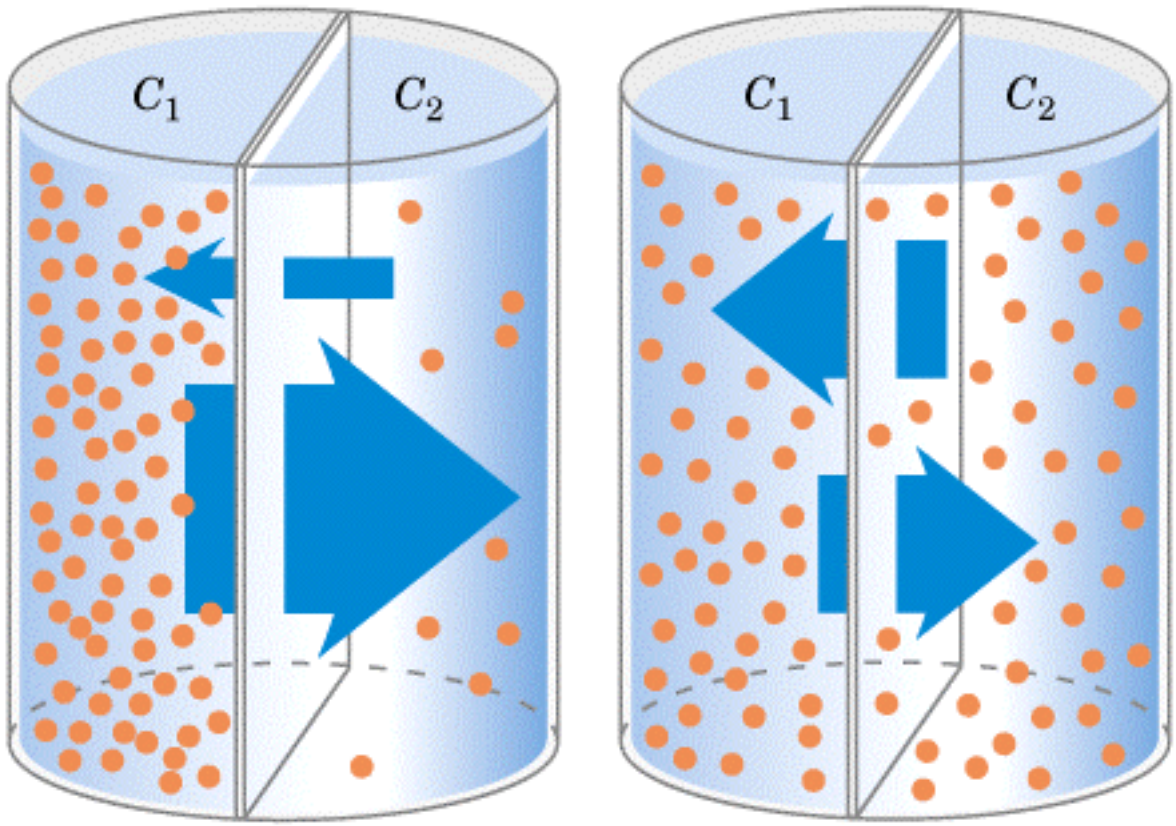
Membrane phospholipid	Percent of total membrane phospholipid	Distribution in membrane
Phosphatidylethanolamine	30	
Phosphatidylcholine	27	
Sphingomyelin	23	
Phosphatidylserine	15	
Phosphatidylinositol	5	
Phosphatidylinositol 4-phosphate		
Phosphatidylinositol 4,5-bisphosphate		
Phosphatidic acid		


Amino
terminus
Outside
Inside
Carboxyl
terminus



Bacteriorhodopsin

(b)


C_1
C_2
C_1
C_2
$C_1 >> C_2$
$C_1 = C_2$
Before equilibrium
Net flux
At equilibrium
No net flux
(a)

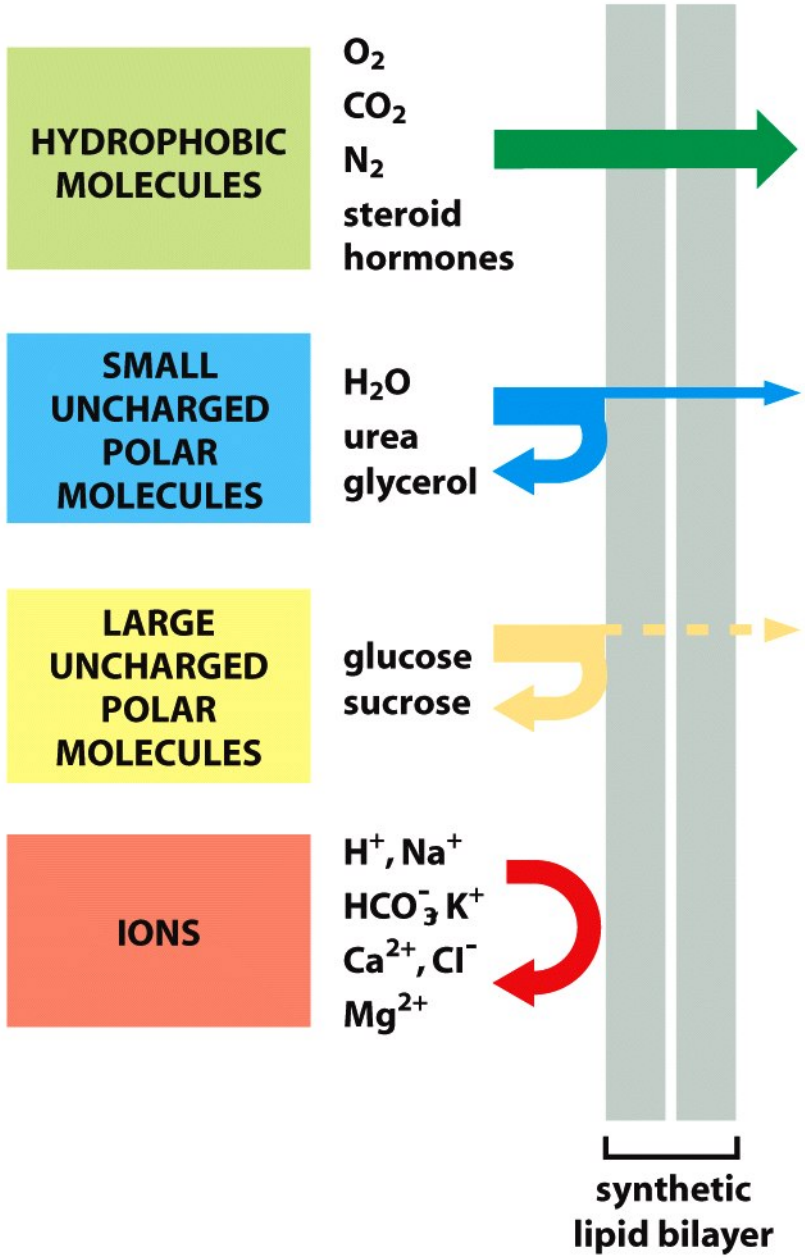


Figure 11-1 *Molecular Biology of the Cell* (© Garland Science 2008)

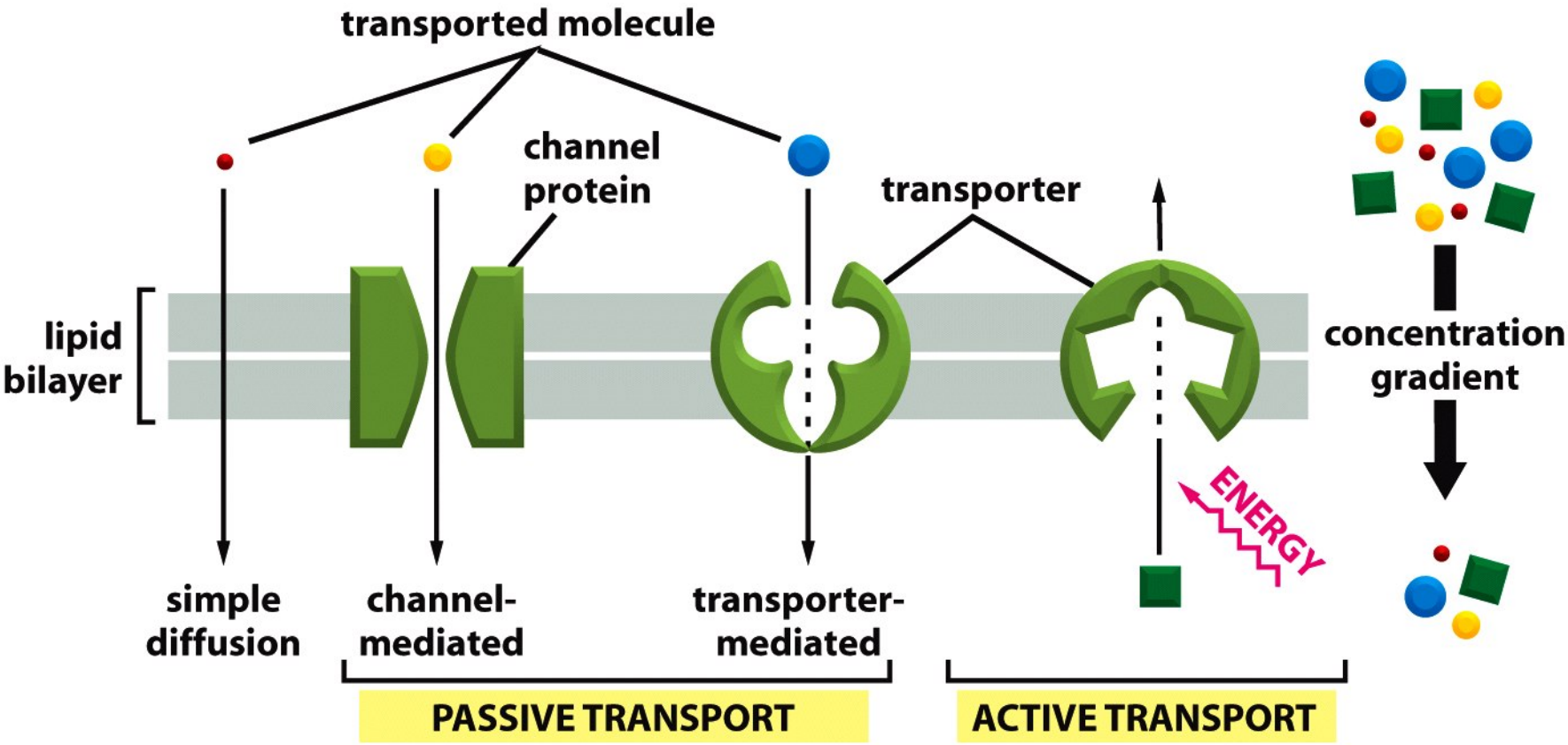


Figure 11-4a *Molecular Biology of the Cell* (© Garland Science 2008)

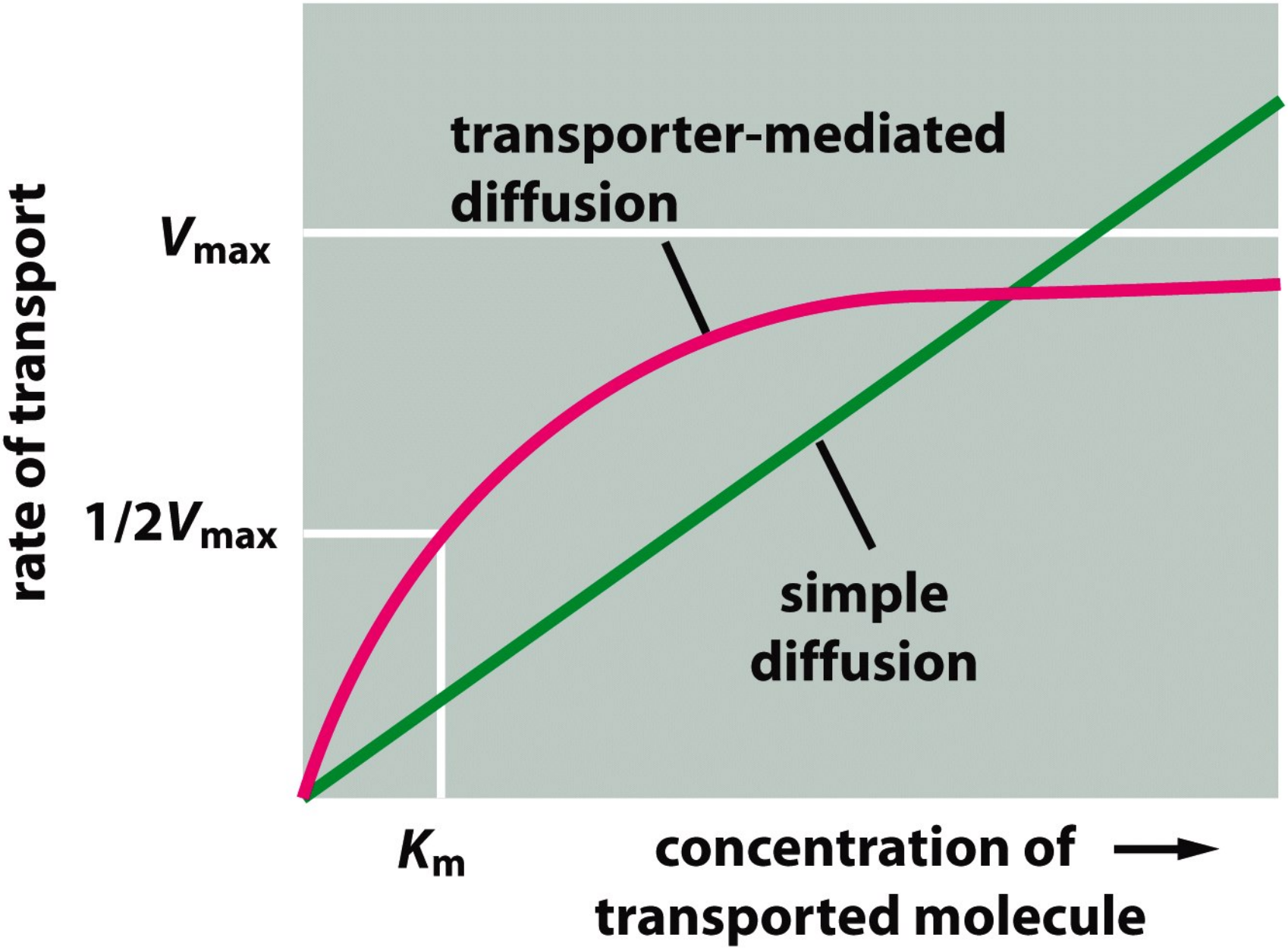
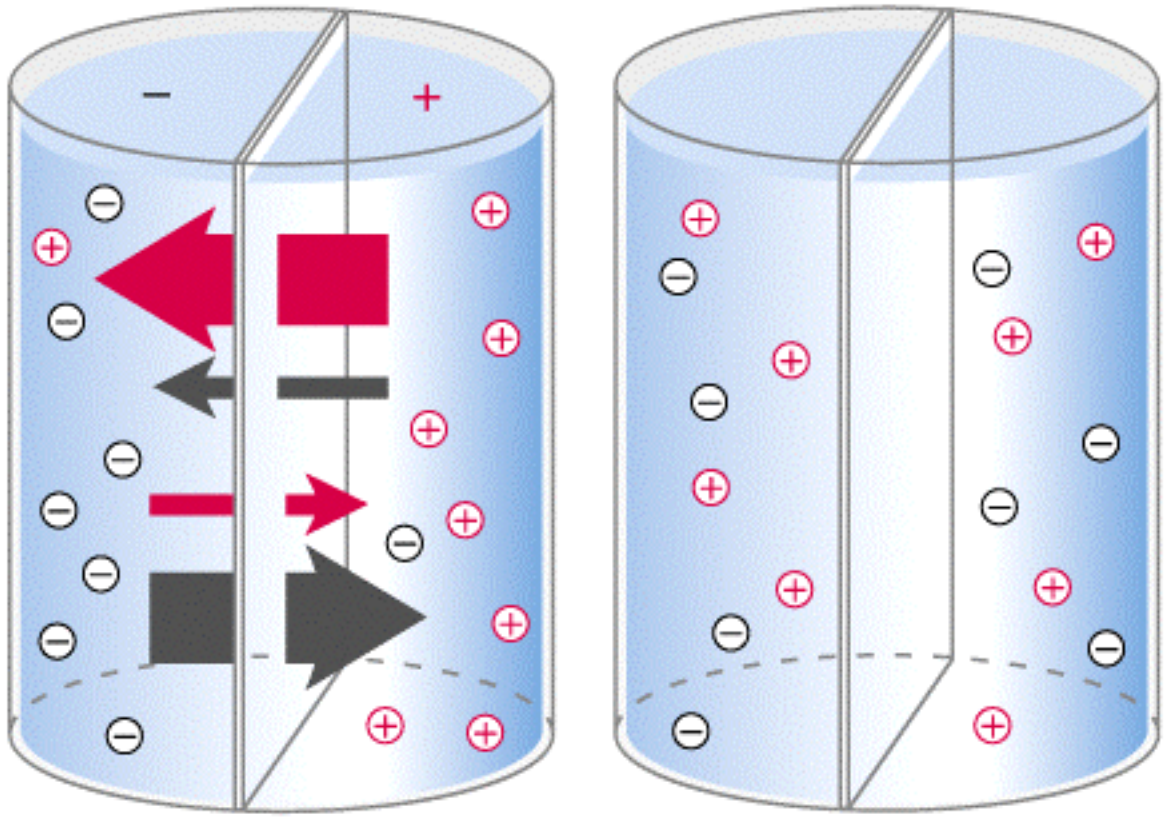


Figure 11-6 *Molecular Biology of the Cell* (© Garland Science 2008)



(b)

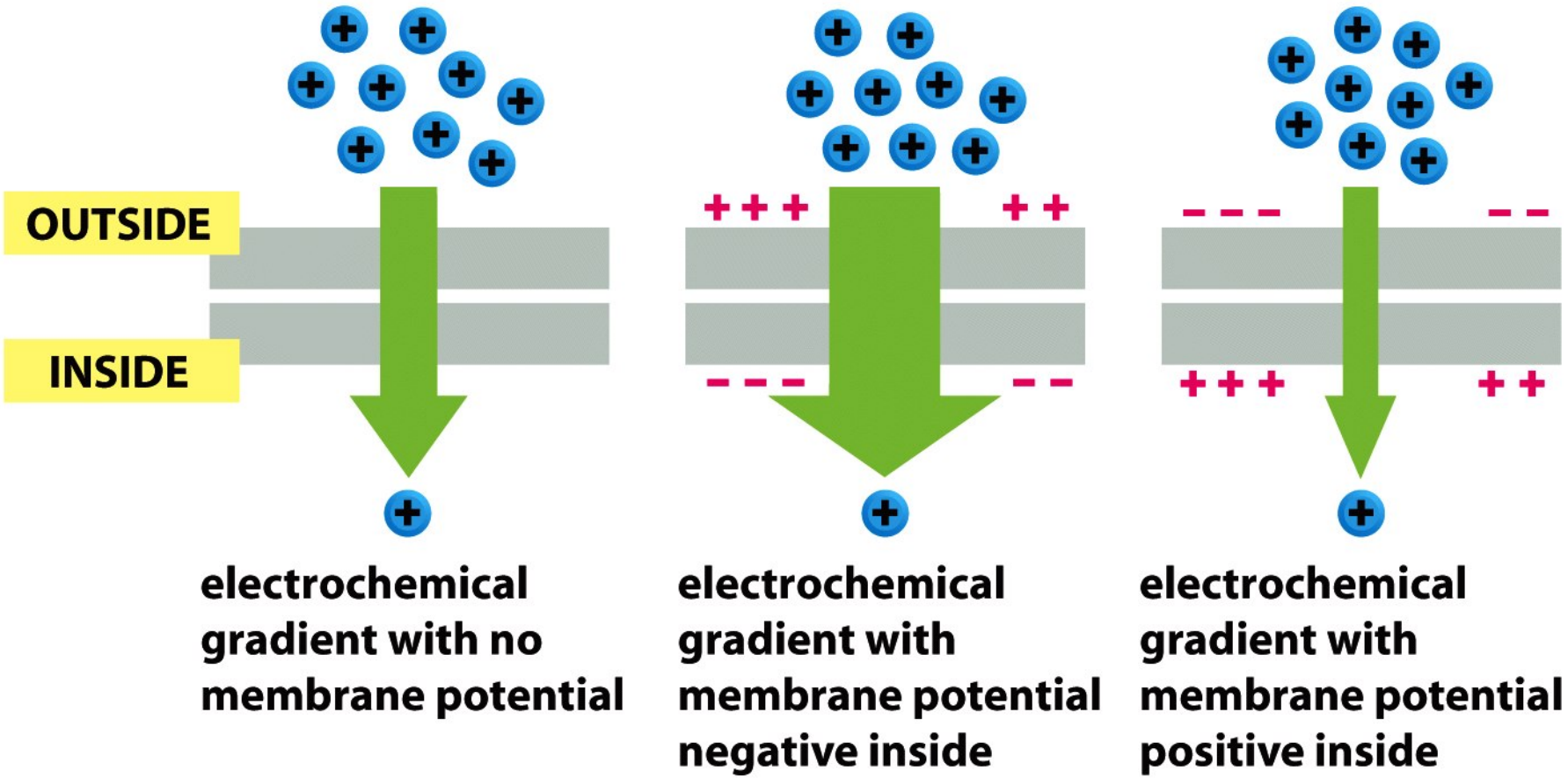


Figure 11-4b *Molecular Biology of the Cell* (© Garland Science 2008)

Table 11–1 A Comparison of Ion Concentrations Inside and Outside a Typical Mammalian Cell

COMPONENT	INTRACELLULAR CONCENTRATION (mM)	EXTRACELLULAR CONCENTRATION (mM)
Cations		
Na^+	5–15	145
K^+	140	5
Mg^{2+}	0.5	1–2
Ca^{2+}	10^{-4}	1–2
H^+	7×10^{-5} ($10^{-7.2}$ M or pH 7.2)	4×10^{-5} ($10^{-7.4}$ M or pH 7.4)
Anions*		
Cl^-	5–15	110

*The cell must contain equal quantities of positive and negative charges (that is, it must be electrically neutral). Thus, in addition to Cl^-, the cell contains many other anions not listed in this table; in fact, most cell constituents are negatively charged (HCO_3^-, PO_4^{3-}, proteins, nucleic acids, metabolites carrying phosphate and carboxyl groups, etc.). The concentrations of Ca^{2+} and Mg^{2+} given are for the free ions. There is a total of about 20 mM Mg^{2+} and 1–2 mM Ca^{2+} in cells, but both are mostly bound to proteins and other substances and, for Ca^{2+}, stored within various organelles.

Table 11-1 *Molecular Biology of the Cell* (© Garland Science 2008)

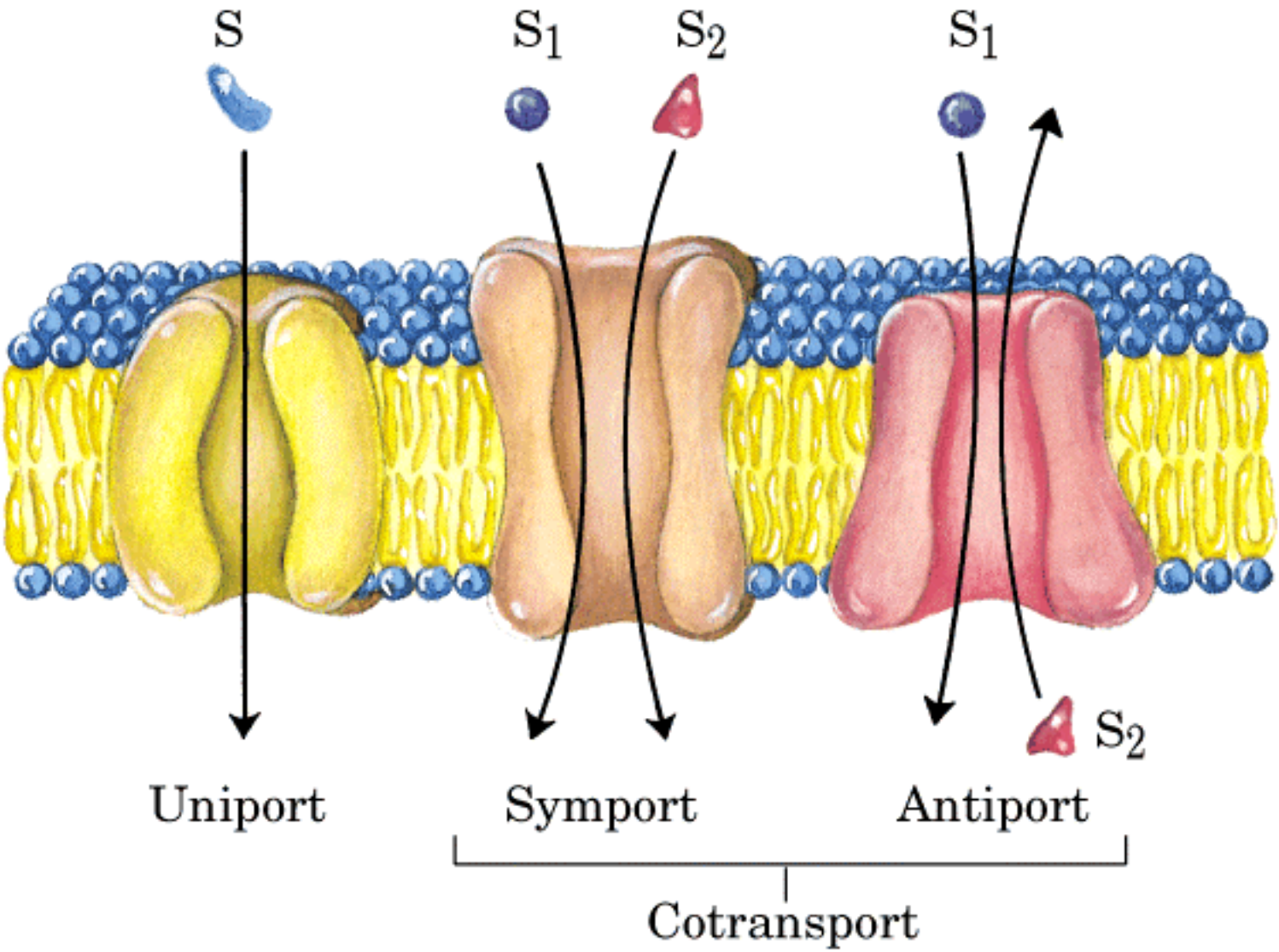
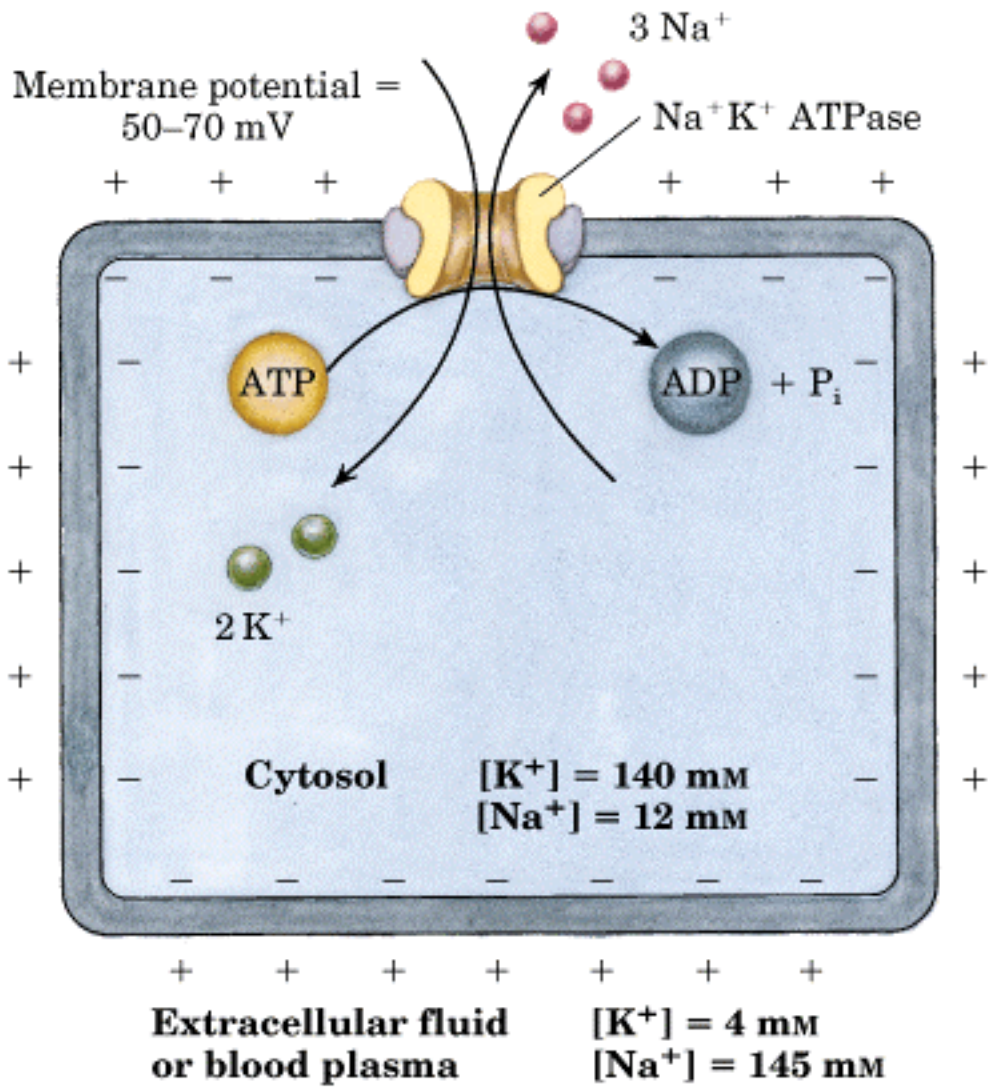

S
S1
S2
S1
S2
Uniport
Symport
Antiport
Cotransport

table 12–5

Cotransport Systems Driven by Gradients of Na^+ or H^+

Organism or tissue	Transported solute (moving against its gradient)	Cotransported solute (moving down its gradient)	Type of transport
E. coli	Lactose	H^+	Symport
	Proline	H^+	Symport
	Dicarboxylic acids	H^+	Symport
Intestine, kidney of vertebrates	Glucose	Na^+	Symport
	Amino acids	Na^+	Symport
Vertebrate cells (many types)	Ca^{2+}	Na^+	Antiport
Higher plants	K^+	H^+	Antiport
Fungi (*Neurospora*)	K^+	H^+	Antiport


3 Na+
Membrane potential = 50–70 mV
Na+K+ ATPase
ATP
ADP + Pi
2 K+
Cytosol
[K+] = 140 mM
[Na+] = 12 mM
Extracellular fluid or blood plasma
[K+] = 4 mM
[Na+] = 145 mM

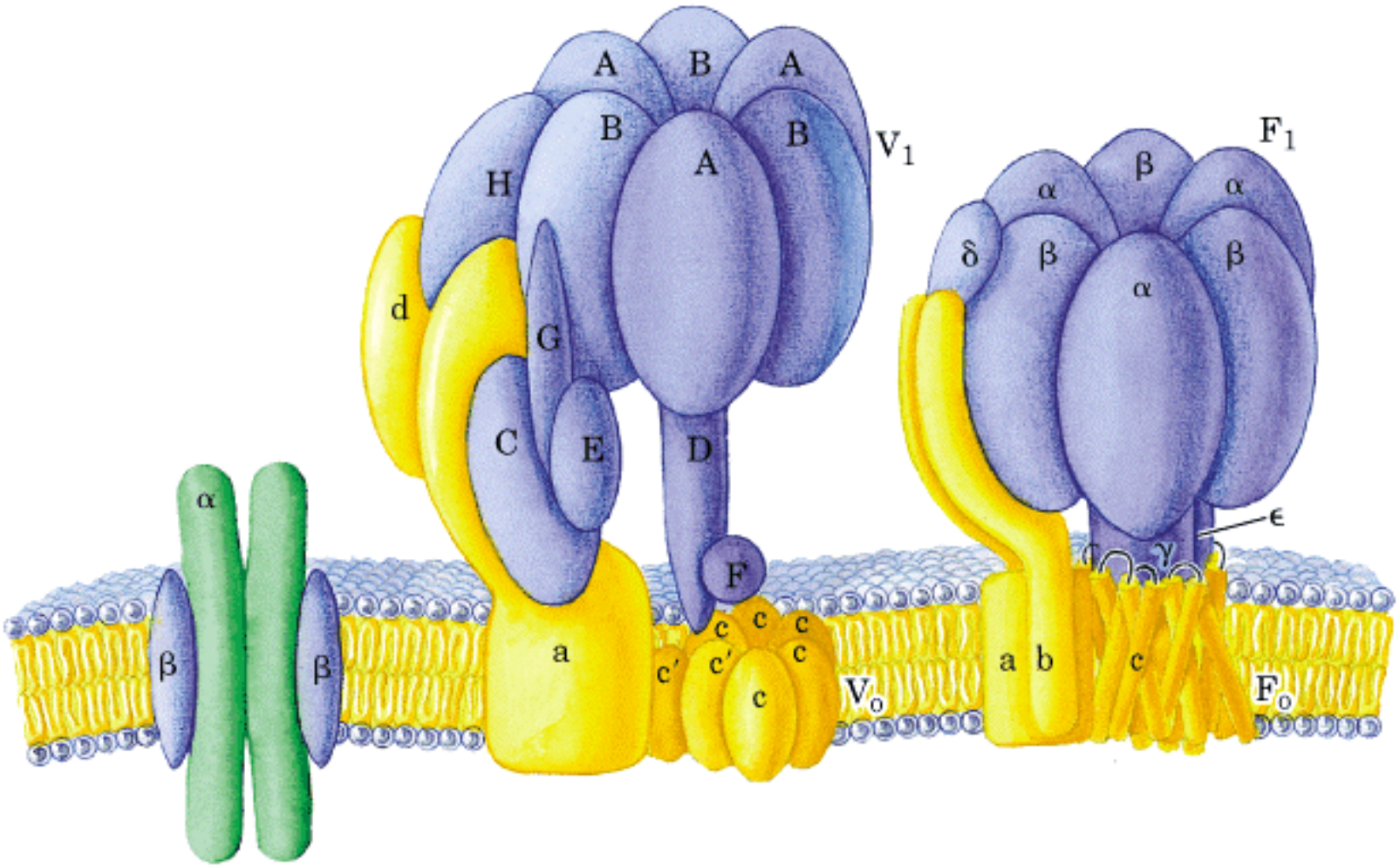
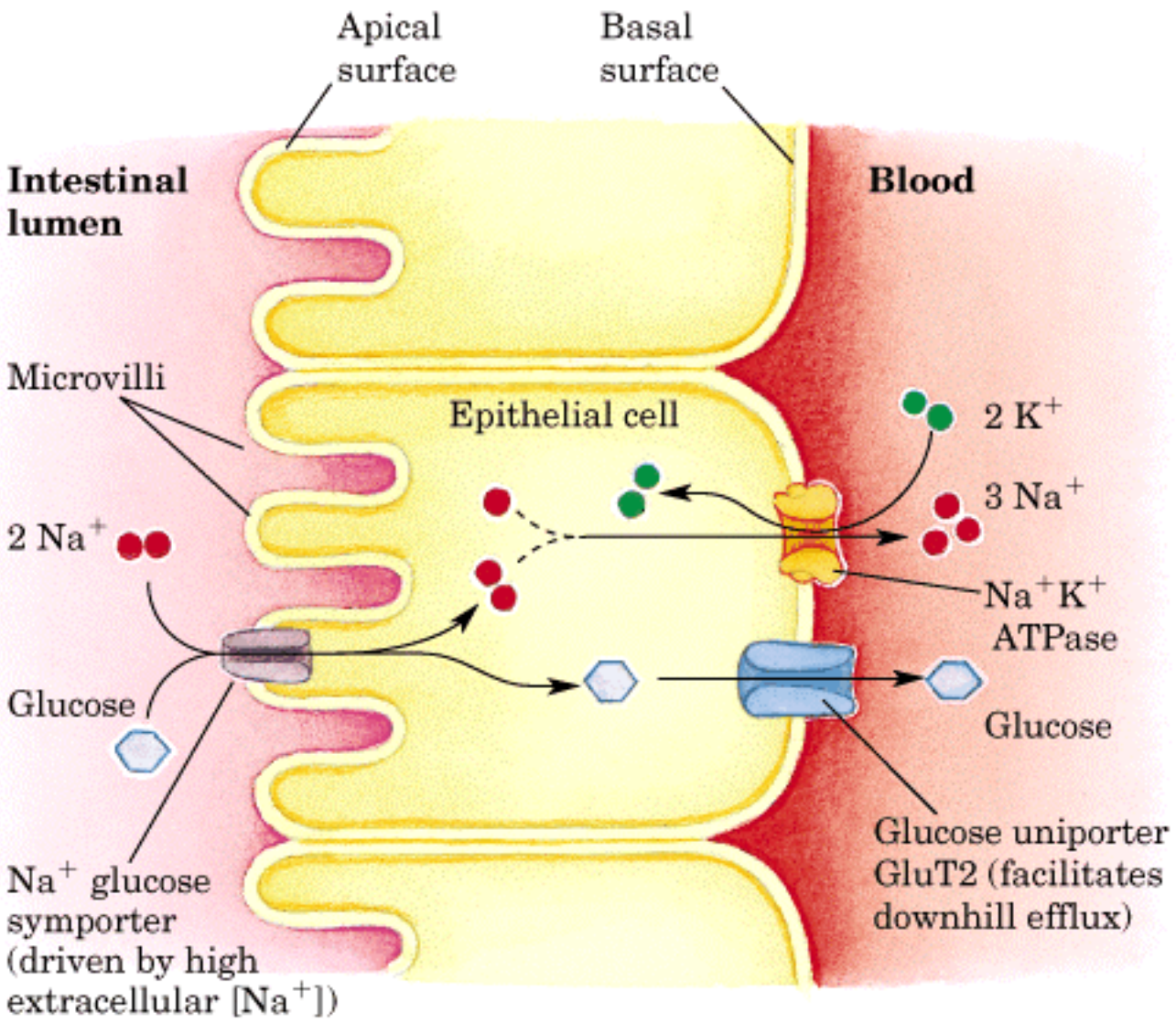
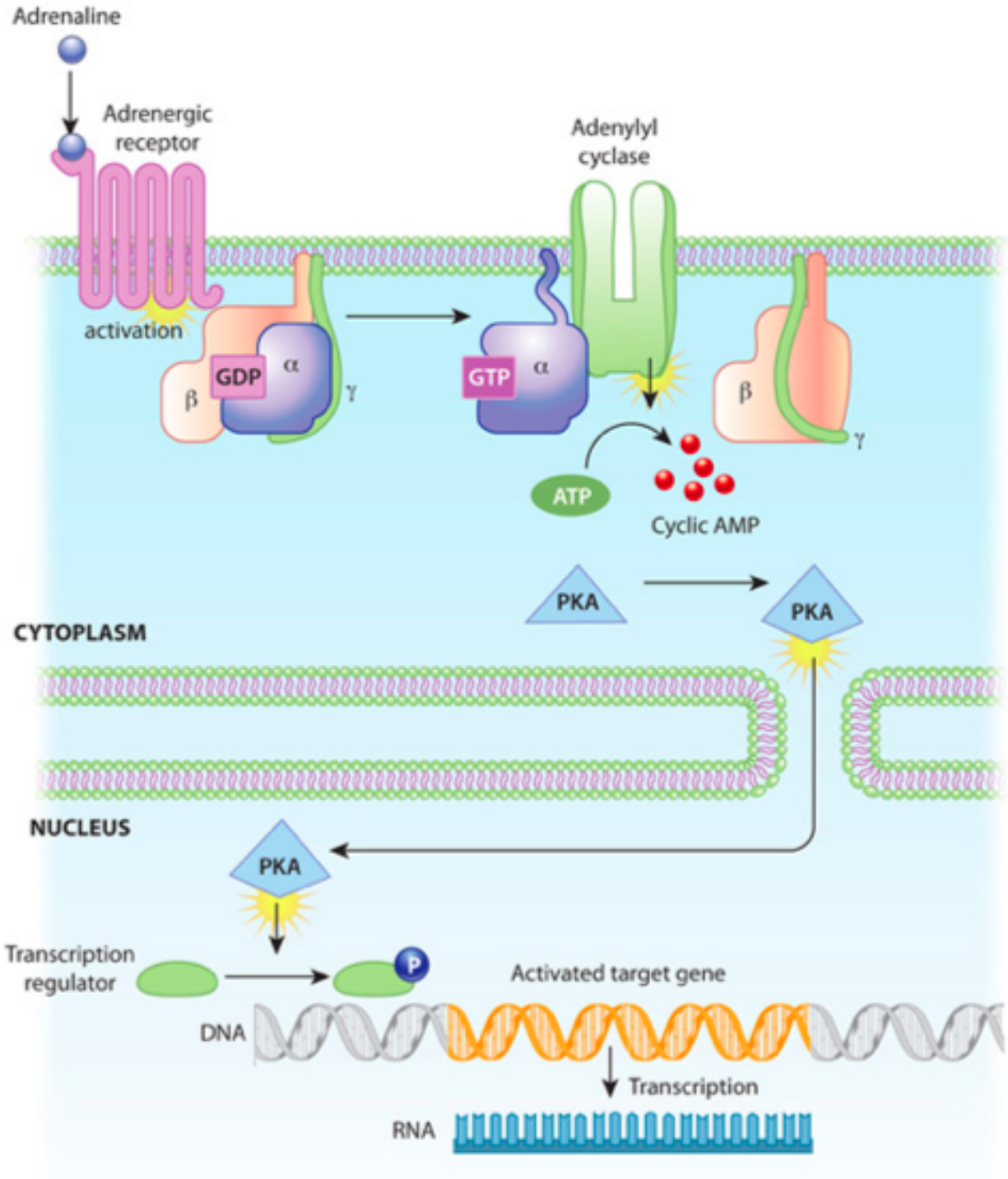

α
β
β
P-type
(a)
A
B
A
B
A
B
H
d
G
C
E
D
F
a
c
c′
V1
Vo
V-type
(b)
F1
α
β
α
δ
β
β
α
ϵ
γ
a
b
c
Fo
F-type
(c)

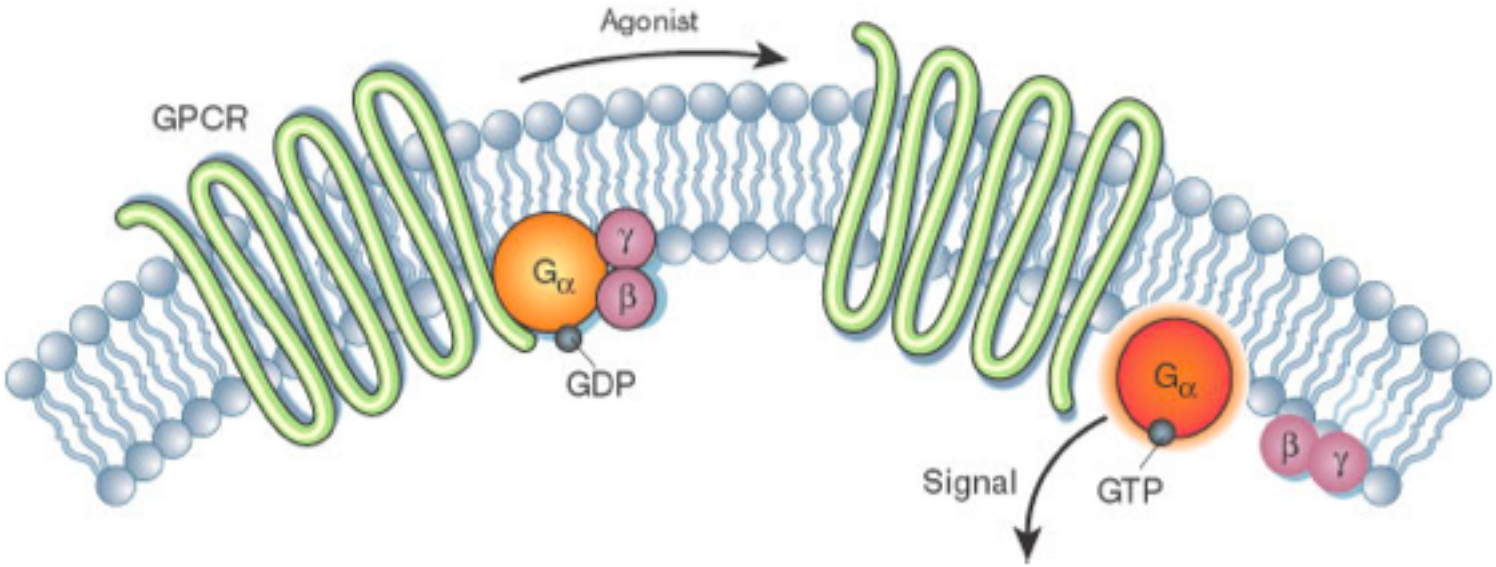
table 12–4

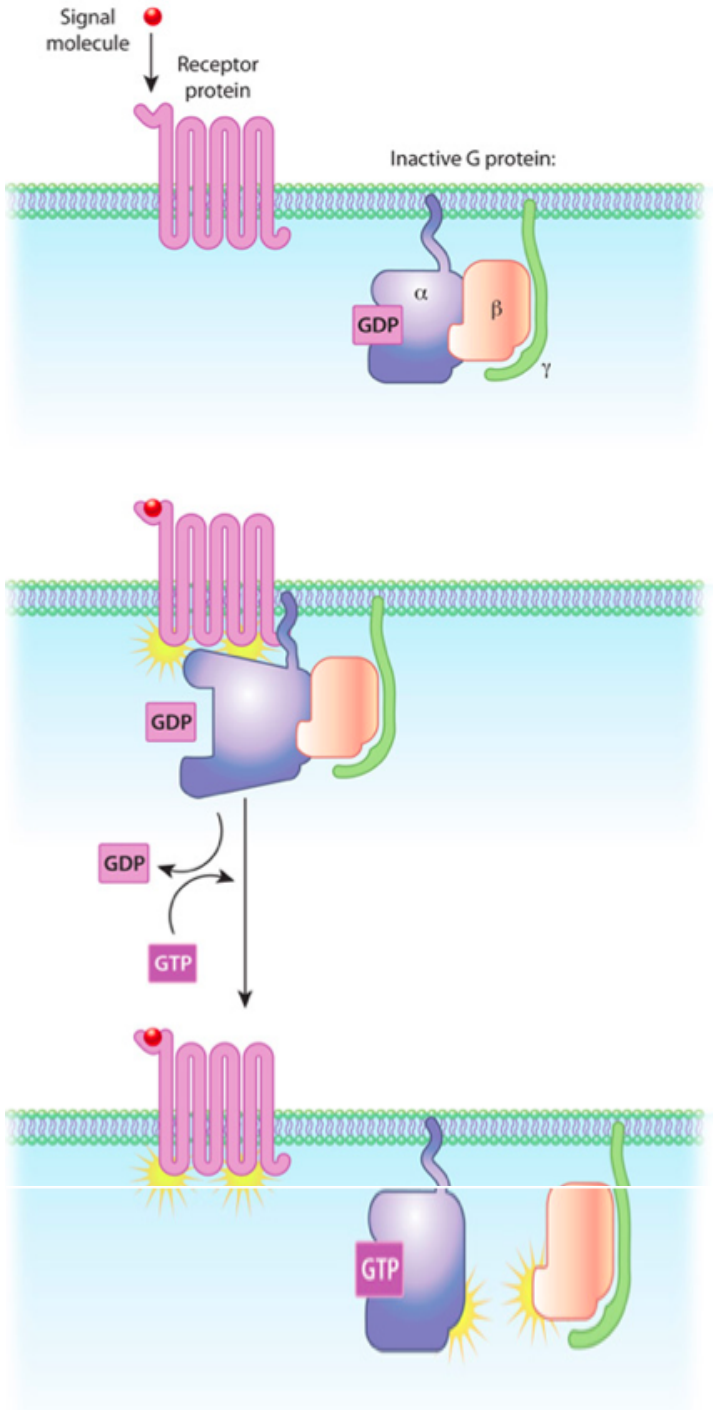
Four Classes of Transport ATPases

	Organism or tissue	Type of membrane	Role of ATPase
P-type ATPases			
Na^+K^+	Animal tissues	Plasma	Maintains low $[Na^+]$, high $[K^+]$ inside cell; creates transmembrane electrical potential
H^+K^+	Acid-secreting (parietal) cells of mammals	Plasma	Acidifies contents of stomach
H^+	Fungi *(Neurospora)*	Plasma	Create H^+ gradient to drive secondary transport of extracellular solutes into cell
H^+	Higher plants	Plasma	
Ca^{2+}	Animal tissues	Plasma	Maintains low $[Ca^{2+}]$ in cytosol
Ca^{2+}	Myocytes of animals	Sarcoplasmic reticulum (endoplasmic reticulum)	Sequesters intracellular Ca^{2+}, keeping cytosolic $[Ca^{2+}]$ low
Cd^{2+}, Hg^{2+}, Cu^{2+}	Bacteria	Plasma	Pumps heavy metal ions out of cell
V-type ATPases			
H^+	Animals	Lysosomal, endosomal, secretory vesicles	Create low pH in compartment, activating proteases and other hydrolytic enzymes
H^+	Higher plants	Vacuolar	
H^+	Fungi	Vacuolar	
F-type ATPases			
H^+	Eukaryotes	Inner mitochondrial	Catalyze formation of ATP from ADP + P_i
H^+	Higher plants	Thylakoid	
H^+	Prokaryotes	Plasma	
Multidrug transporter			
	Animal tumor cells	Plasma	Removes a wide variety of hydrophobic natural products and synthetic drugs from cytosol, including vinblastine, doxorubicin, actinomycin D, mitomycin, taxol, colchicine, and puromycin


Apical surface
Basal surface
Intestinal lumen
Blood
Microvilli
Epithelial cell
2 K+
3 Na+
2 Na+
Na+K+ ATPase
Glucose
Glucose
Glucose uniporter GluT2 (facilitates downhill efflux)
Na+ glucose symporter (driven by high extracellular [Na+])


Adrenaline
Adrenergic receptor
activation
GDP
α
β
γ
Adenylyl cyclase
GTP
α
β
γ
ATP
Cyclic AMP
PKA
PKA
CYTOPLASM
NUCLEUS
PKA
Transcription regulator
P
Activated target gene
DNA
Transcription
RNA


Agonist
GPCR
Gα
γ
β
GDP
Gα
Signal
GTP
β
γ


Signal molecule
Receptor protein
Inactive G protein:
α
β
γ
GDP
GDP
GDP
GTP
GTP

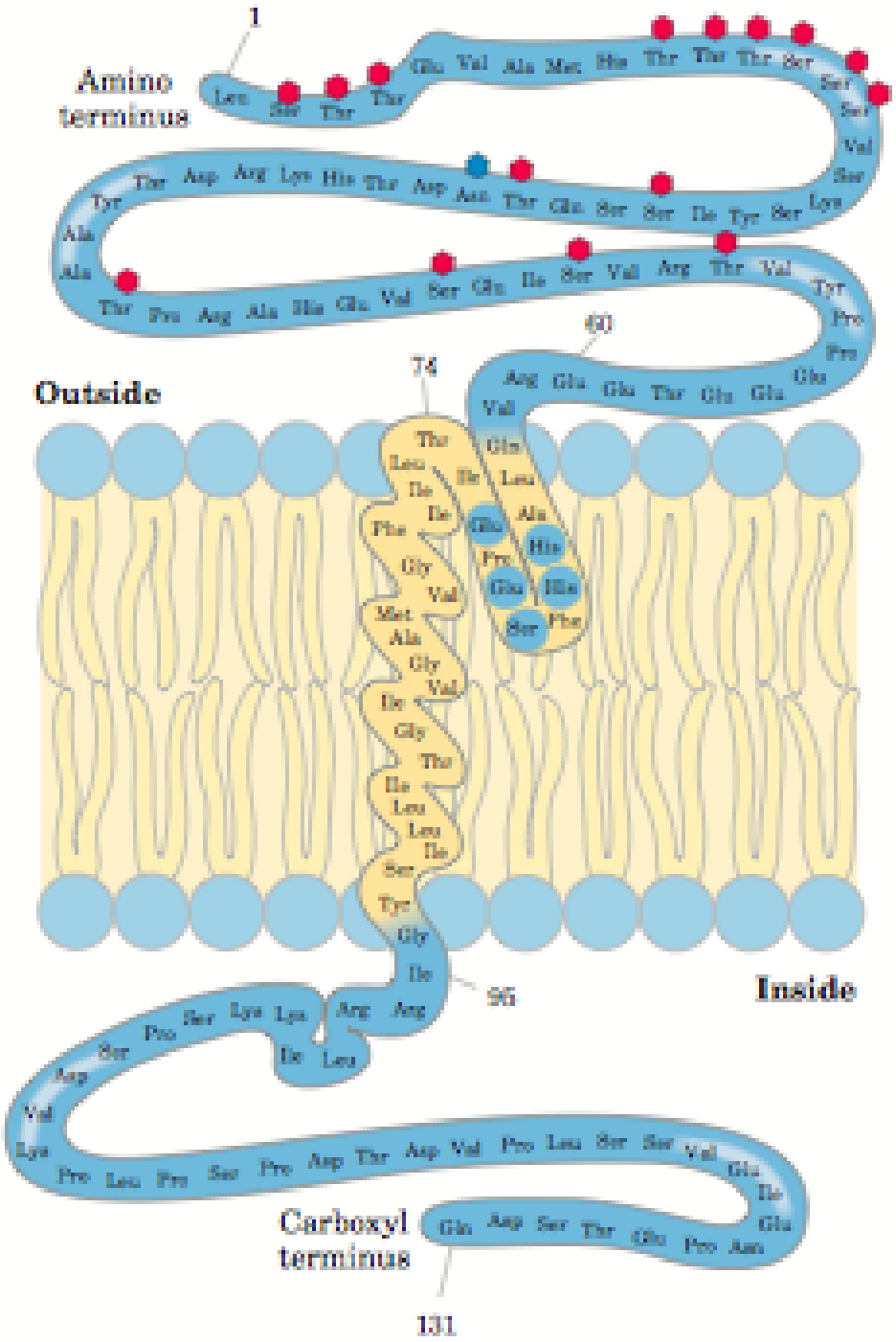
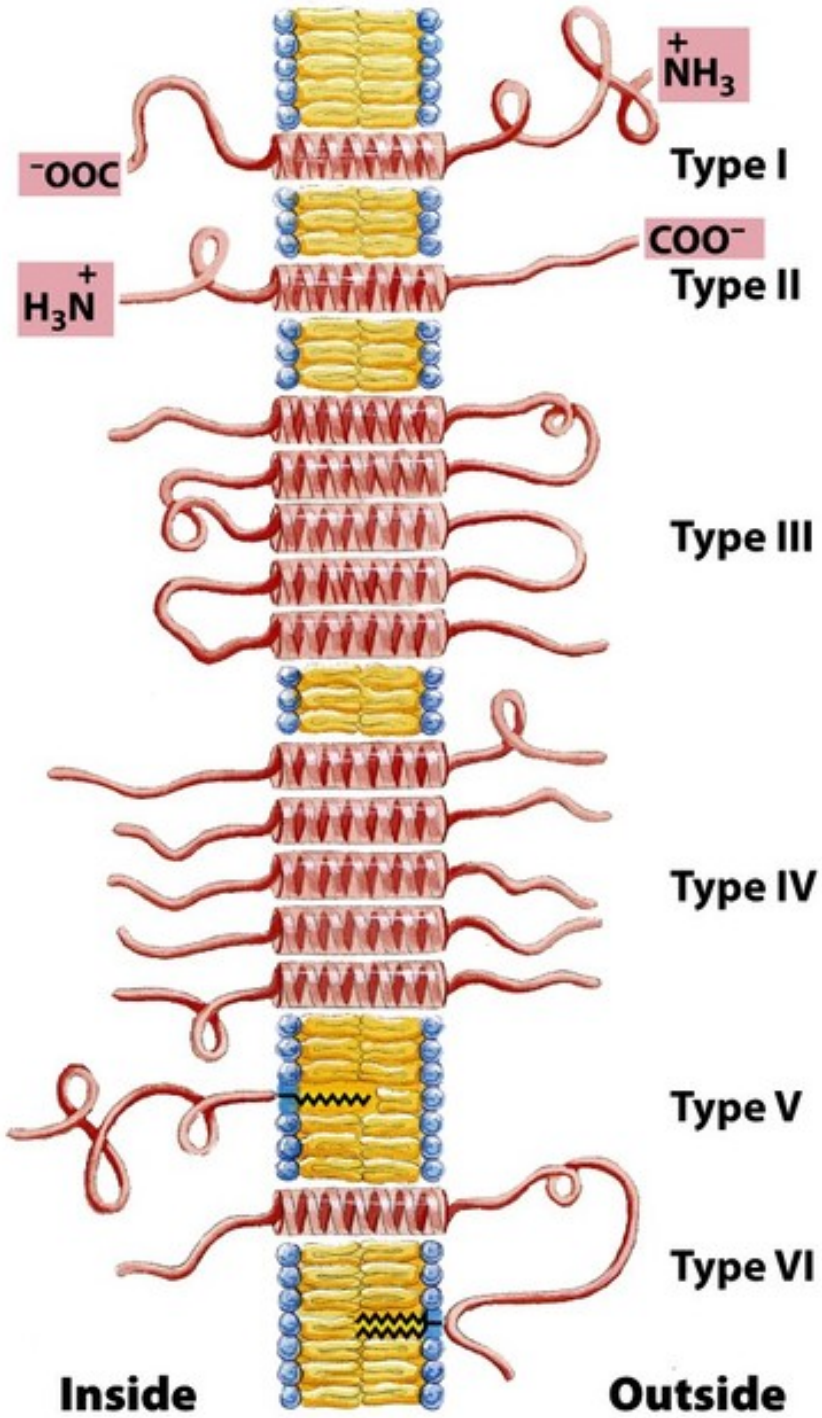


FIGURE 11–7 Transbilayer disposition of glycophorin in an erythrocyte. One hydrophilic domain, containing all the sugar residues, is on the outer surface, and another hydrophilic domain protrudes from the inner face of the membrane. Each red hexagon represents a tetrasaccharide (containing two Neu5Ac (sialic acid), Gal, and GalNAc) *O*-linked to a Ser or Thr residue; the blue hexagon represents an oligosaccharide chain *N*-linked to an Asn residue. The relative size of the oligosaccharide units is larger than shown here. A segment of 19 hydrophobic residues (residues 75 to 93) forms an α helix that traverses the membrane bilayer (see Fig. 11–11a). The segment from residues 64 to 74 has some hydrophobic residues and probably penetrates into the outer face of the lipid bilayer, as shown.



Integral membrane proteins. For known proteins of the plasma membrane, the spatial relationships of protein domains to the lipid bilayer fall into six categories. Types I and II have a single transmembrane helix; the amino-terminal domain is outside the cell in type I proteins and inside in type II. Type III proteins have multiple transmembrane helices in a single polypeptide. In type IV proteins, transmembrane domains of several different polypeptides assemble to form a channel through the membrane. Type V proteins are held to the bilayer primarily by covalently linked lipids (see Fig. 11-14), and type VI proteins have both transmembrane helices and lipid (GPI) anchors.

In this figure, and in figures throughout the book, we represent transmembrane protein segments in their most likely conformations: as α helices of six to seven turns. Sometimes these helices are shown simply as cylinders. As relatively few membrane protein structures have been deduced by x-ray crystallography, our representation of the extramembrane domains is arbitrary and not necessarily to scale.

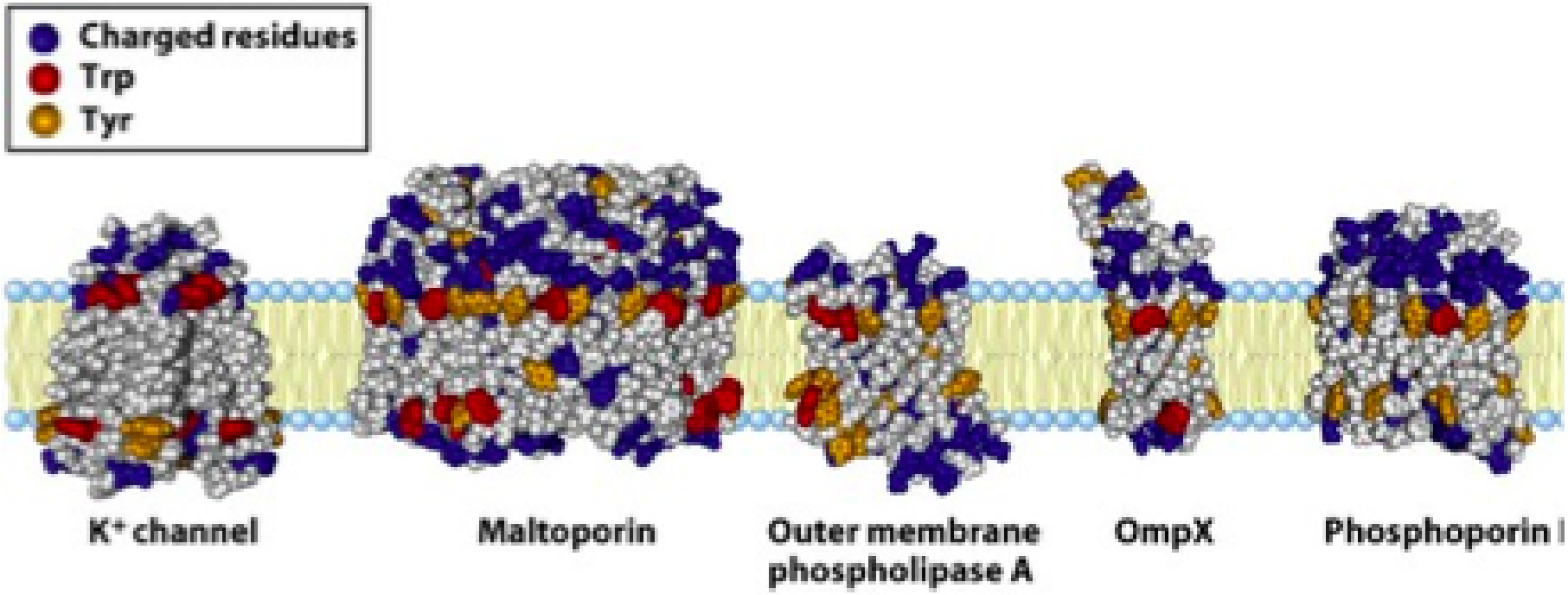


FIGURE 11-12 (3D Jmol representations by PDB ID: 1AF6 1QD5 1QJ9 1PHO) **Tyr and T residues of membrane proteins clustering at the water-lipid interface.** The detailed structures of these five integral membrane proteins are known from crystallographic studies K^+ channel (PDB ID 1BL8) is from the bacterium *Streptomyces lividans* (see Fig. 11-48); maltoporin (PDB ID 1AF6), outer membrane phospholipase A (PDB ID 1QD5), OmpX (PDB ID 1QJ9), and phosphoporin E (PDB ID 1PHO) are proteins of the outer membrane of *E. coli*. Residues of Tyr (orange) and Trp (red) are found predominantly where the nonpolar region of acyl chains meets the polar head group region. Charged residues (Lys, Arg, Glu, Asp; shown blue) are found almost exclusively in the aqueous phases.

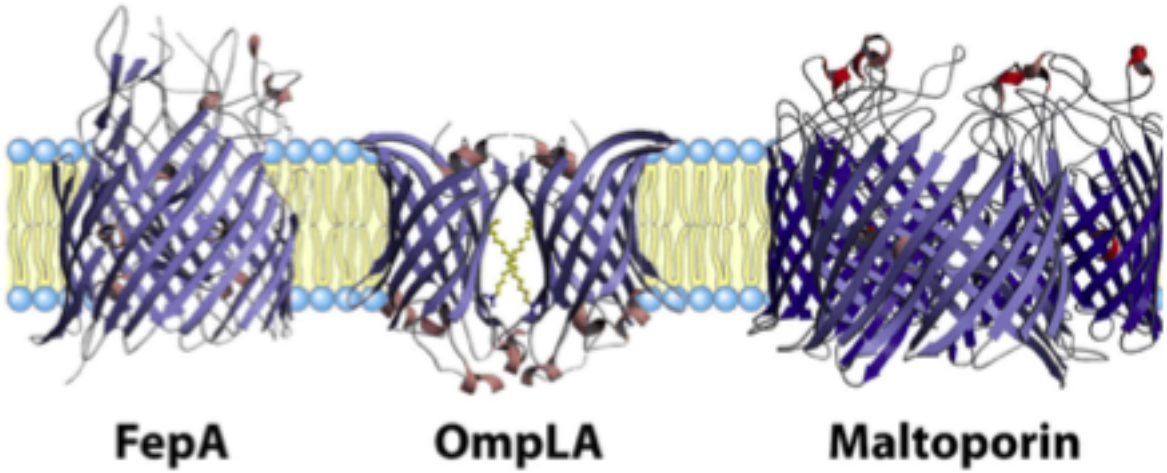


FIGURE 11-13 (3D Jmol representations by PDB ID: **1FEP 1QD5 1MAL**) **Membrane prot with β-barrel structure.** Three proteins of the *E. coli* outer membrane are shown, viewe the plane of the membrane. FepA (PDB ID 1FEP), involved in iron uptake, has 22 membran spanning β strands. OmpLA (derived from PDB ID 1QD5), a phospholipase, is a 12-stranded barrel that exists as a dimer in the membrane. Maltoporin (derived from PDB ID 1MAL), a maltose transporter, is a trimer; each monomer consists of 16 β strands.

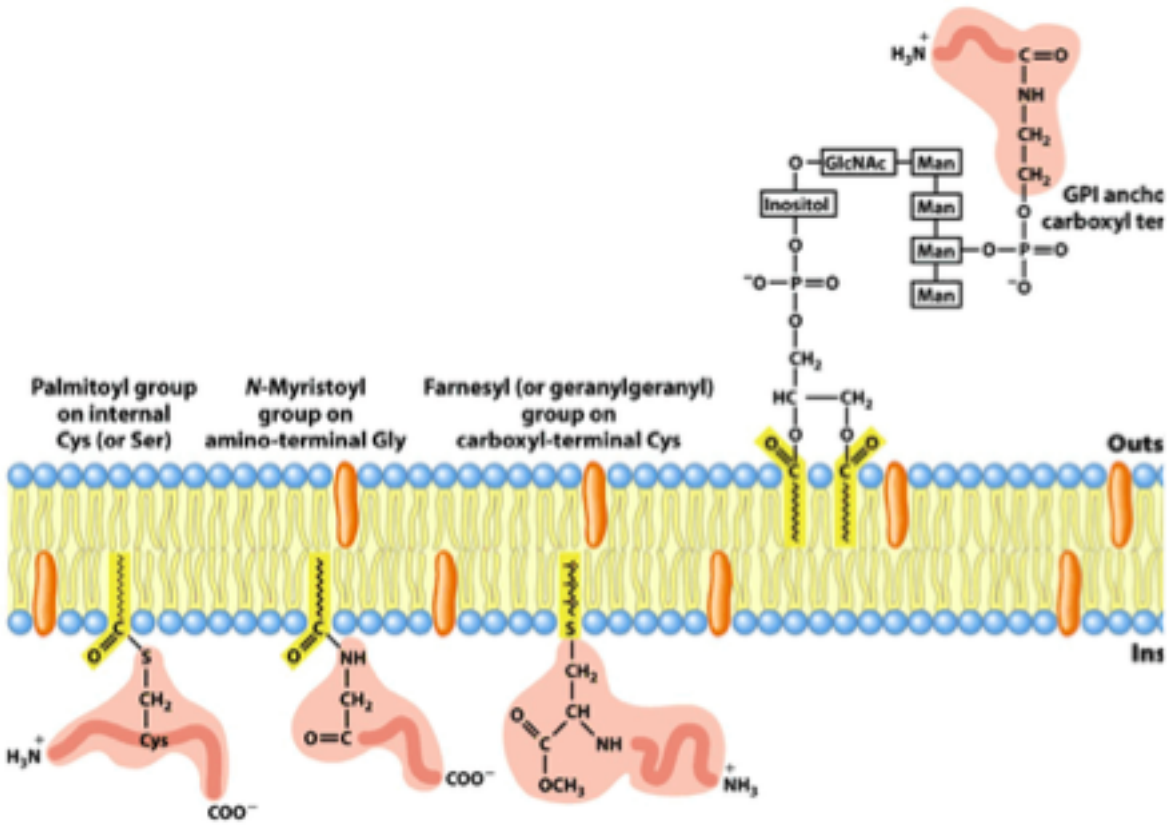
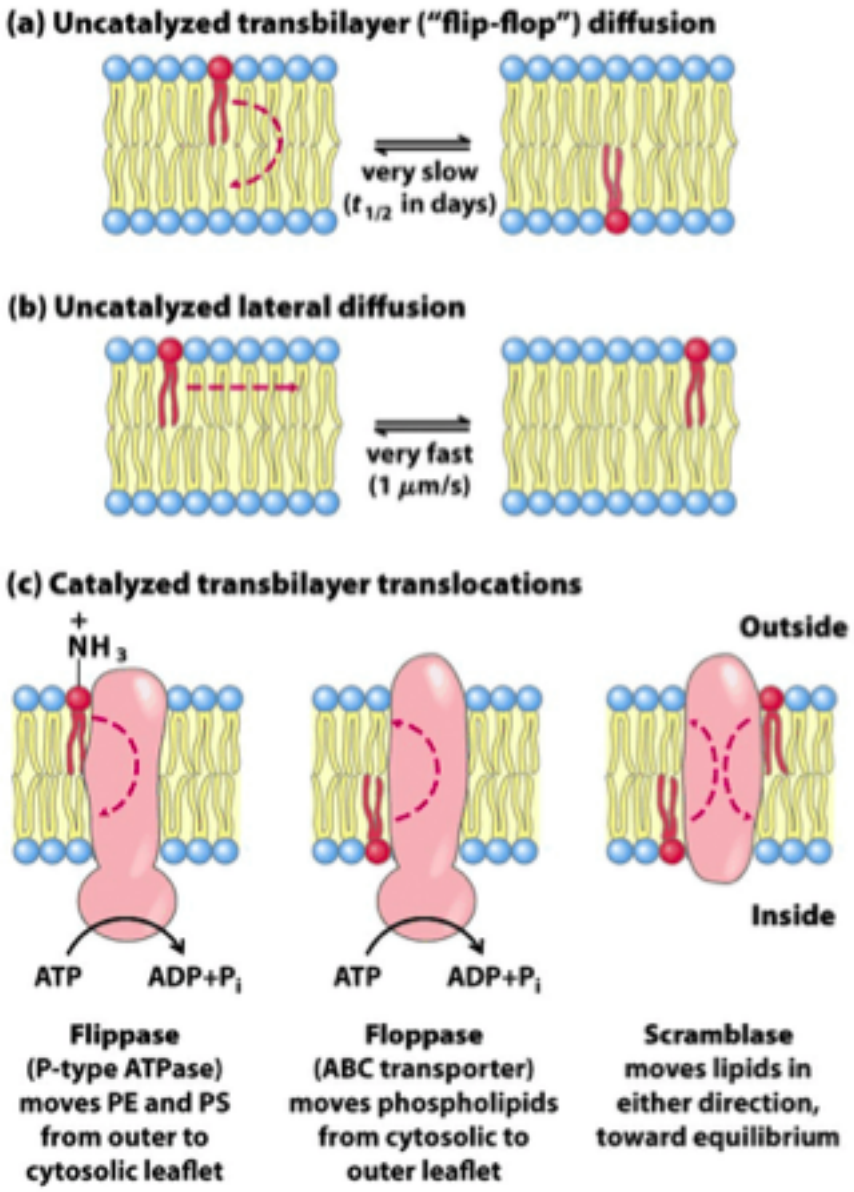


FIGURE 11-14 **Lipid-linked membrane proteins.** Covalently attached lipids anchor membrane proteins to the lipid bilayer. A palmitoyl group is shown attached by thioester linl to a Cys residue; an *N*-myristoyl group is generally attached to an amino-terminal Gly; the farnesyl and geranylgeranyl groups attached to carboxyl-terminal Cys residues are isoprenoi 15 and 20 carbons, respectively. These three lipid-protein assemblies are found only on the face of the plasma membrane. Glycosyl phosphatidylinositol (GPI) anchors are derivatives of phosphatidylinositol in which the inositol bears a short oligosaccharide covalently joined to tl carboxyl-terminal residue of a protein through phosphoethanolamine. GPI-linked proteins ar always on the extracellular face of the plasma membrane.


(a) Uncatalyzed transbilayer ("flip-flop") diffusion
very slow
($t_{1/2}$ in days)
(b) Uncatalyzed lateral diffusion
very fast
(1 μm/s)
(c) Catalyzed transbilayer translocations
+
NH 3
ATP
ADP+Pi
Flippase
(P-type ATPase)
moves PE and PS
from outer to
cytosolic leaflet
ATP
ADP+Pi
Floppase
(ABC transporter)
moves phospholipids
from cytosolic to
outer leaflet
Outside
Inside
Scramblase
moves lipids in
either direction,
toward equilibrium