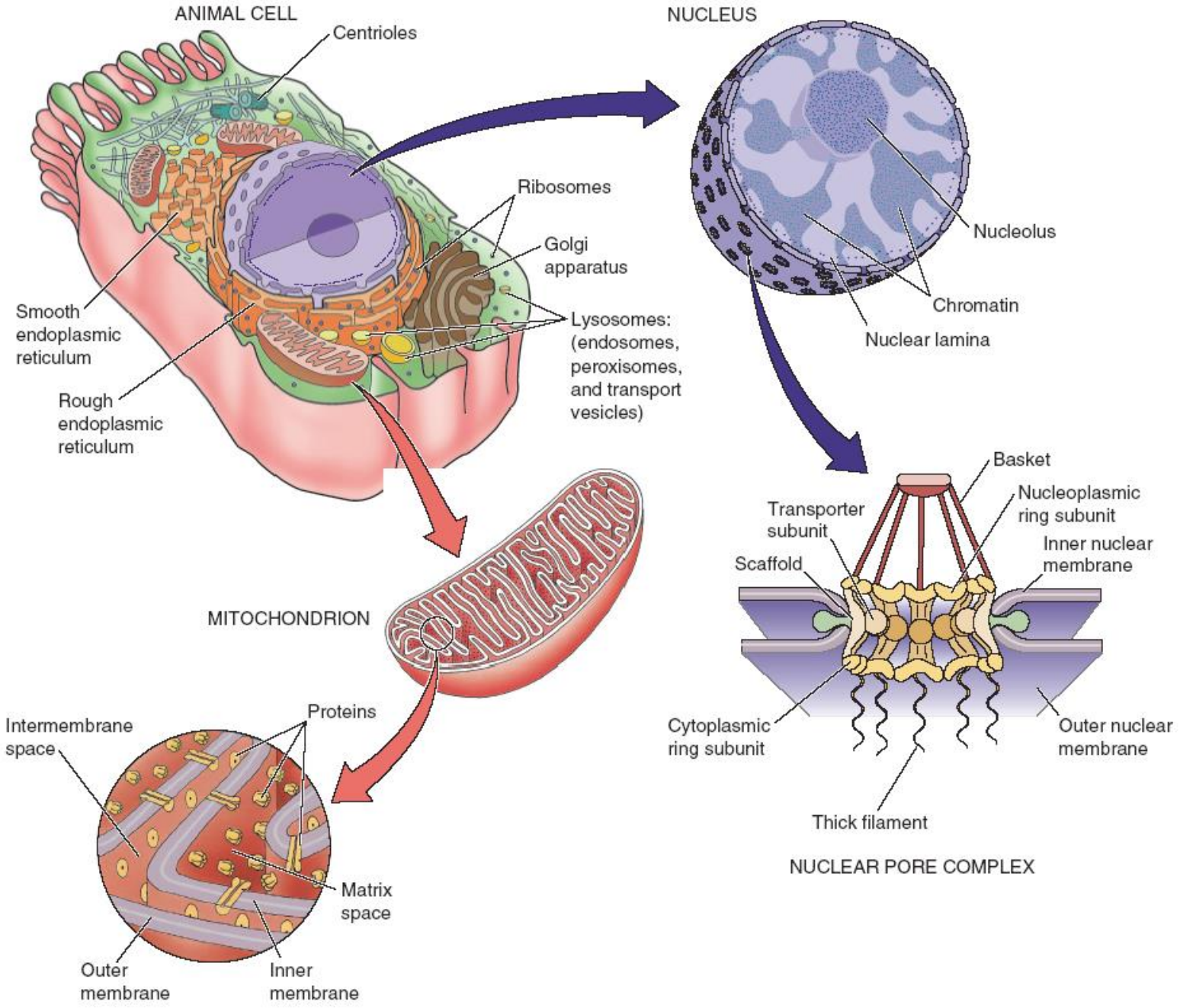
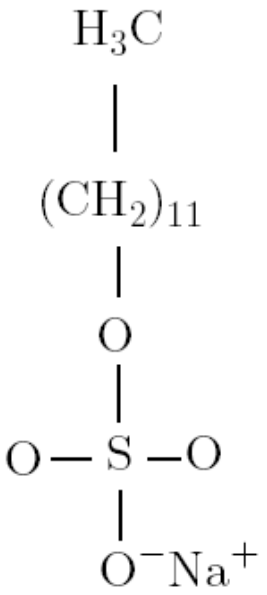
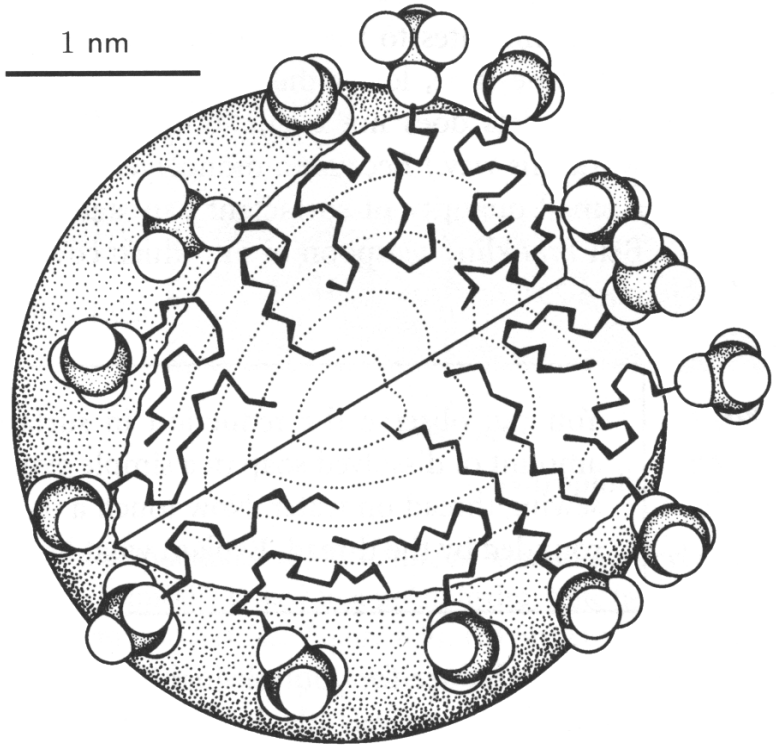
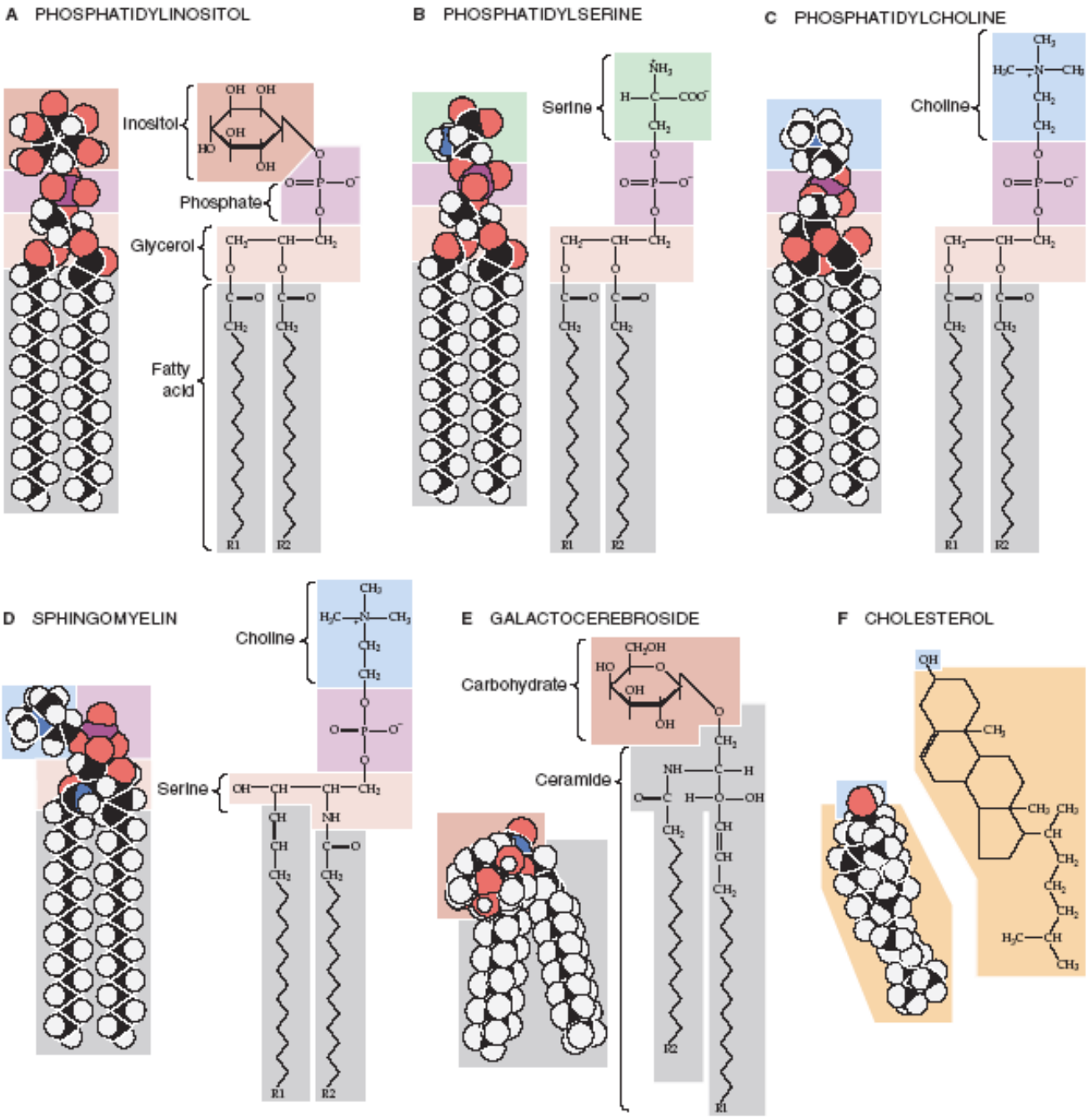

ANIMAL CELL
Centrioles
Ribosomes
Golgi apparatus
Smooth endoplasmic reticulum
Lysosomes: (endosomes, peroxisomes, and transport vesicles)
Rough endoplasmic reticulum
NUCLEUS
Nucleolus
Chromatin
Nuclear lamina
MITOCHONDRION
Intermembrane space
Proteins
Matrix space
Outer membrane
Inner membrane
Basket
Transporter subunit
Nucleoplasmic ring subunit
Scaffold
Inner nuclear membrane
Cytoplasmic ring subunit
Outer nuclear membrane
Thick filament
NUCLEAR PORE COMPLEX

Ion	concentration (mM)	
	interstitial space	cell (“typical”)
Na^+	145	15
K^+	4.5	120
Ca^{2+}	1.2	1×10^{-7}
Mg^{2+}	.55	1
Cl^-	116	20
HCO_3^-	25	15
glucose	5.9	low

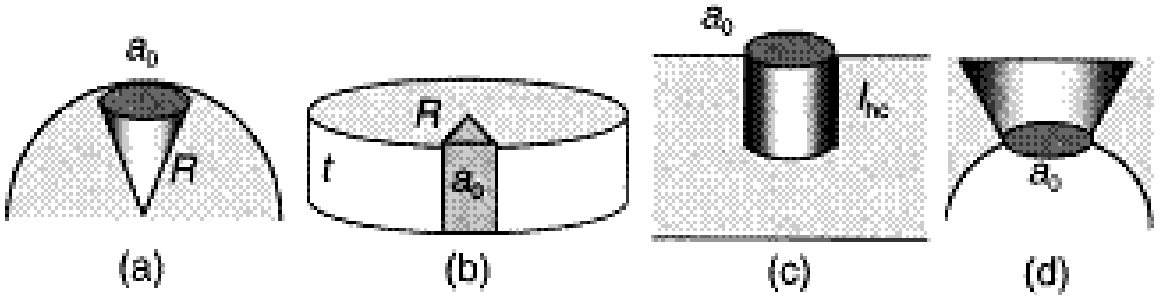
Amphiphiles






A PHOSPHATIDYLINOSITOL
Inositol
Phosphate
Glycerol
Fatty acid
R1
R2
B PHOSPHATIDYLSERINE
Serine
C PHOSPHATIDYLCHOLINE
Choline
D SPHINGOMYELIN
Choline
Serine
E GALACTOCEREBROSIDE
Carbohydrate
Ceramide
F CHOLESTEROL

geometry



$$\text{shape factor} = \frac{v_{hc}}{a_0 l_{hc}}, \text{ where}$$

v_{hc} = volume of hydrocarbon region

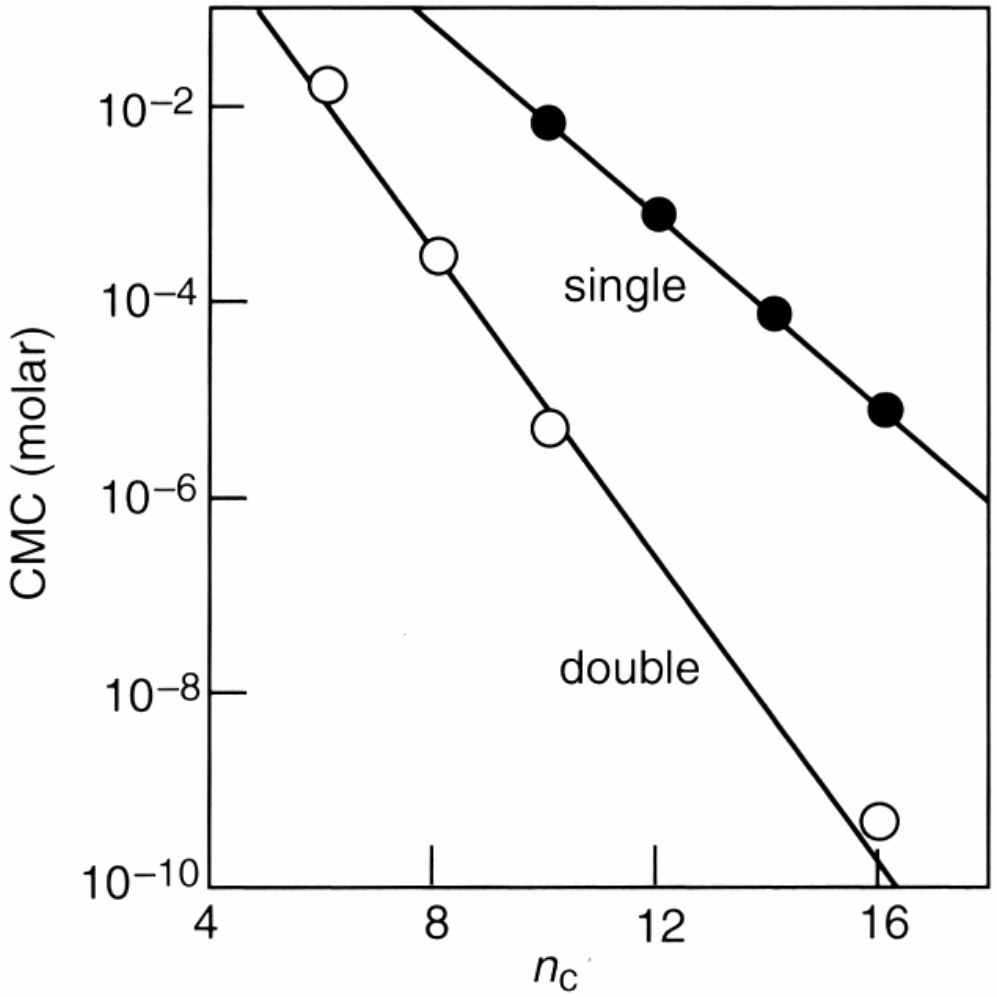
a_0 = surface area of hydrophilic region

l_{hc} = length of hydrocarbon region, also R

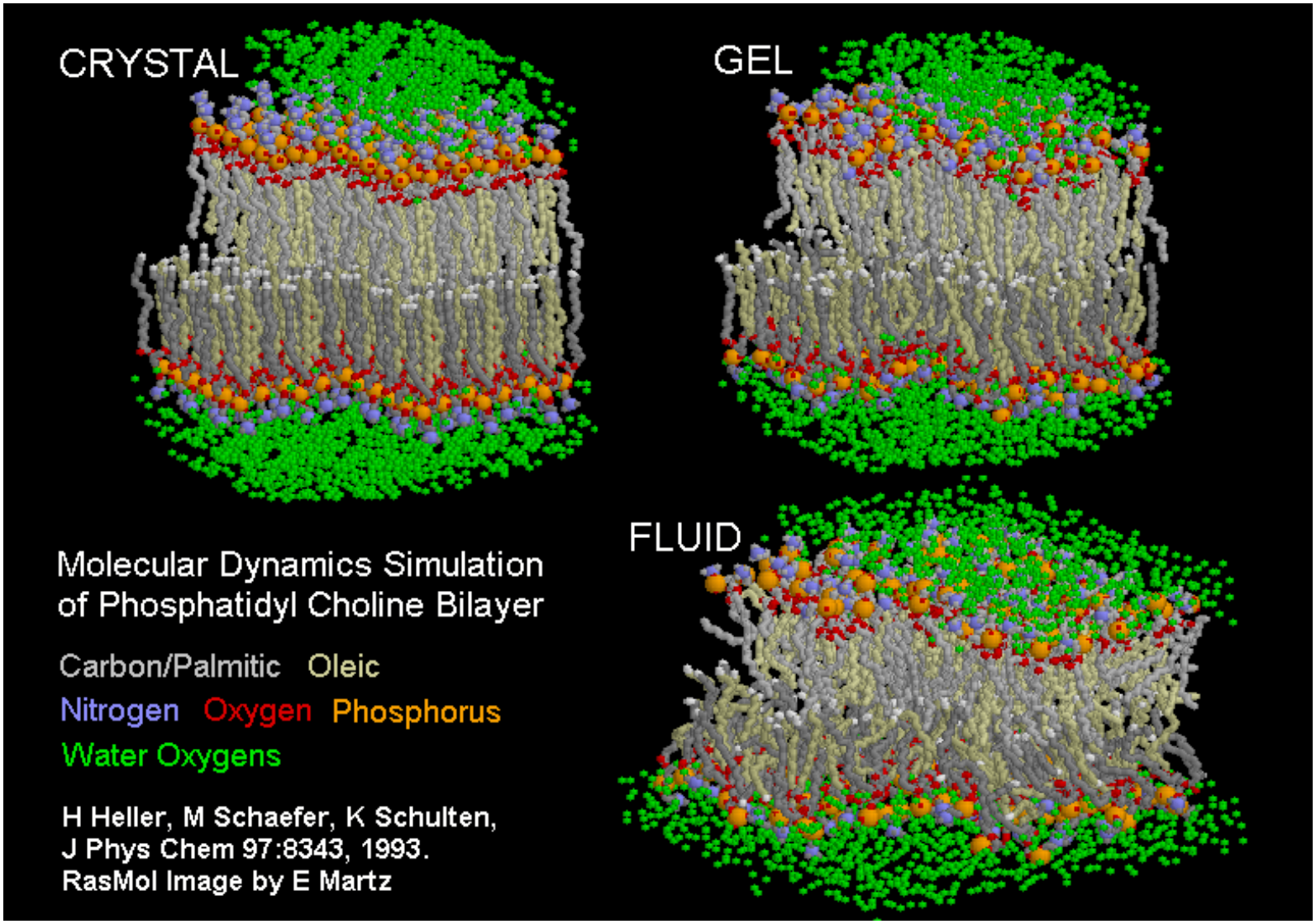
range of shape factor	form
< 1/3	micelles (a)
1/3 to 1/2	cylindrical micelles (b)
1/2 to 1	bilayers (c)
>1	inverted micelles (d)

Critical Micellar Concentration

- At low concentration, amphiphiles exist as individual, solvated molecules
- As concentration of amphiphiles increases above a certain point, amphiphiles organize into aggregates – bilayers, micelle, *etc.*
- This concentration of the critical micellar concentration (CMC)
- Balance of self-assembly (hydrophobic effects) against entropy
- Two tails increases hydrophobic effect, lowering CMC



Transition temperature

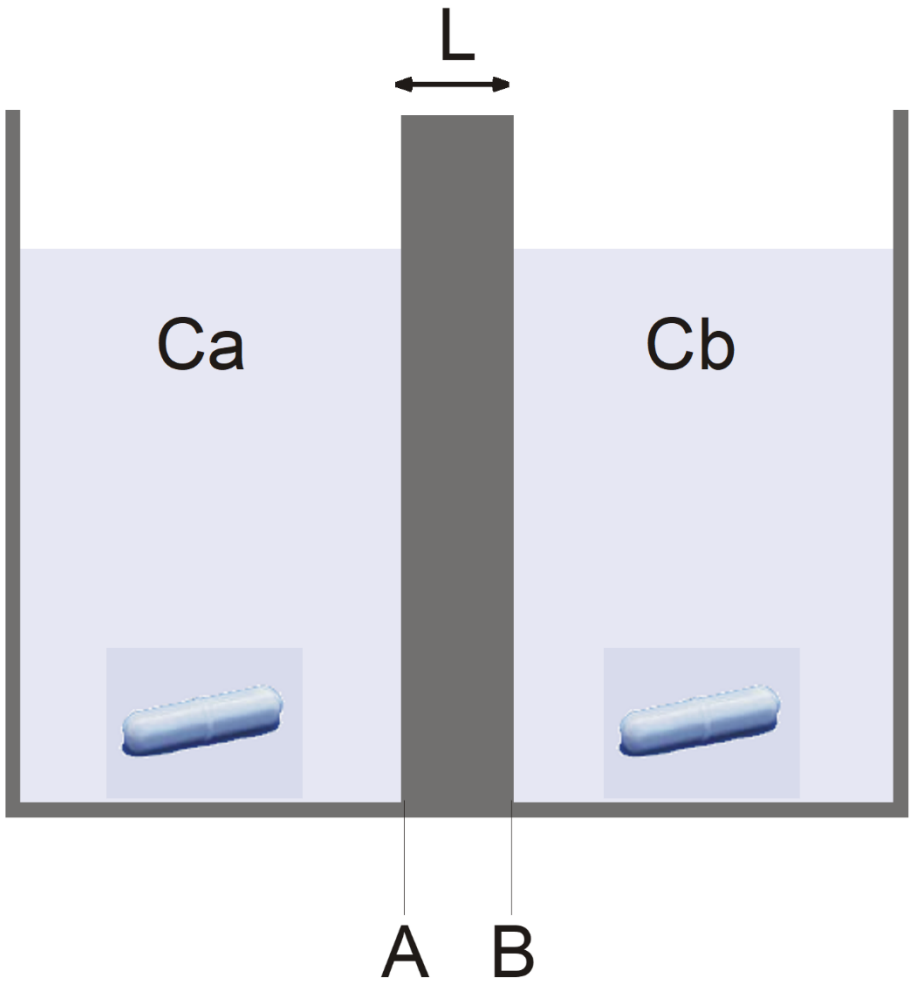


Transition temperature

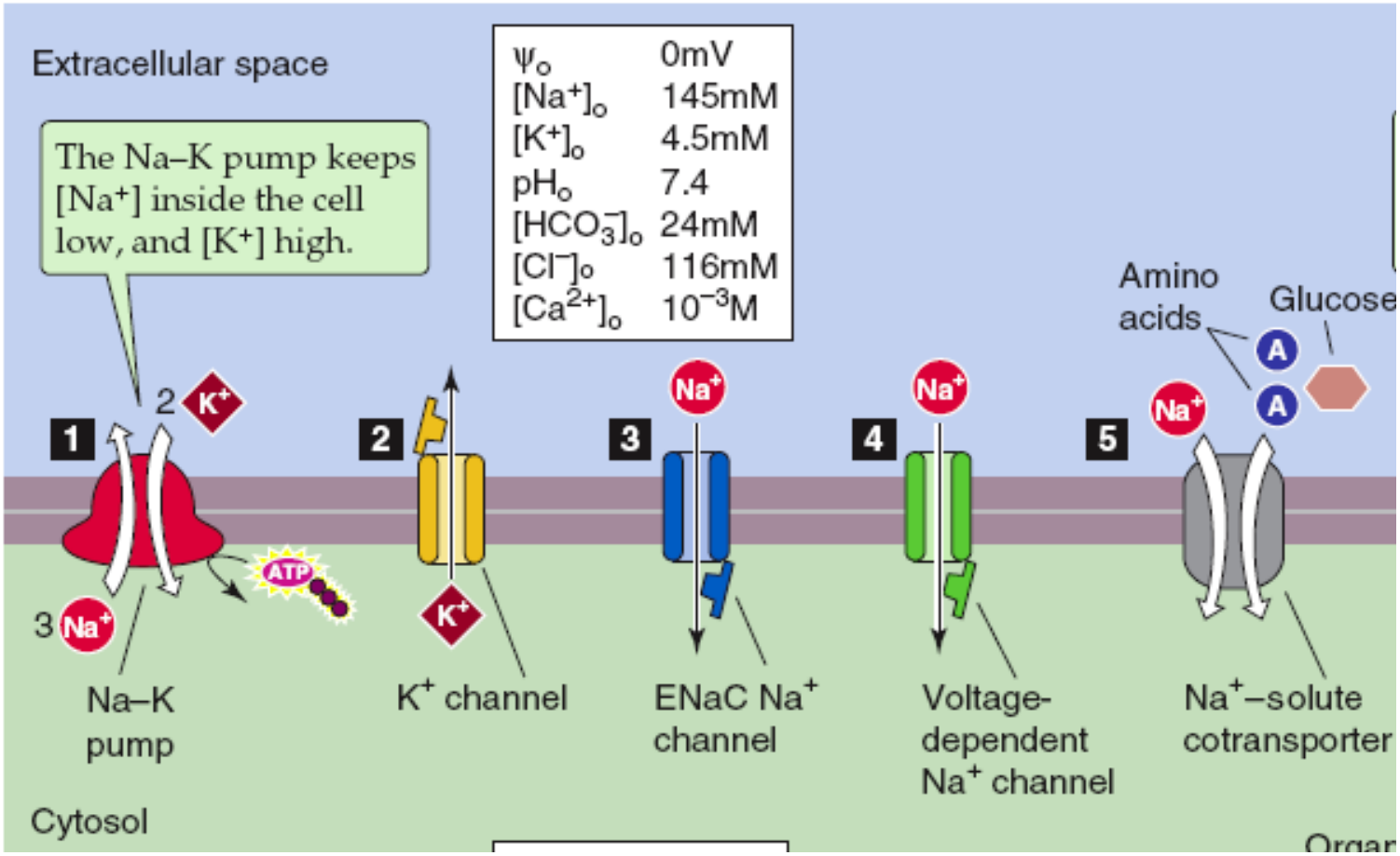
chain length	Tm (°C)
12	-1
13	14
14	23
16	41
18:1 c9 unsat.	-20
16:0-18:1	-1

- Saturation of chains (presence of double bonds) lowers transition temperature
- Headgroup chemistry also modulated transition temperature

Simple diffusion

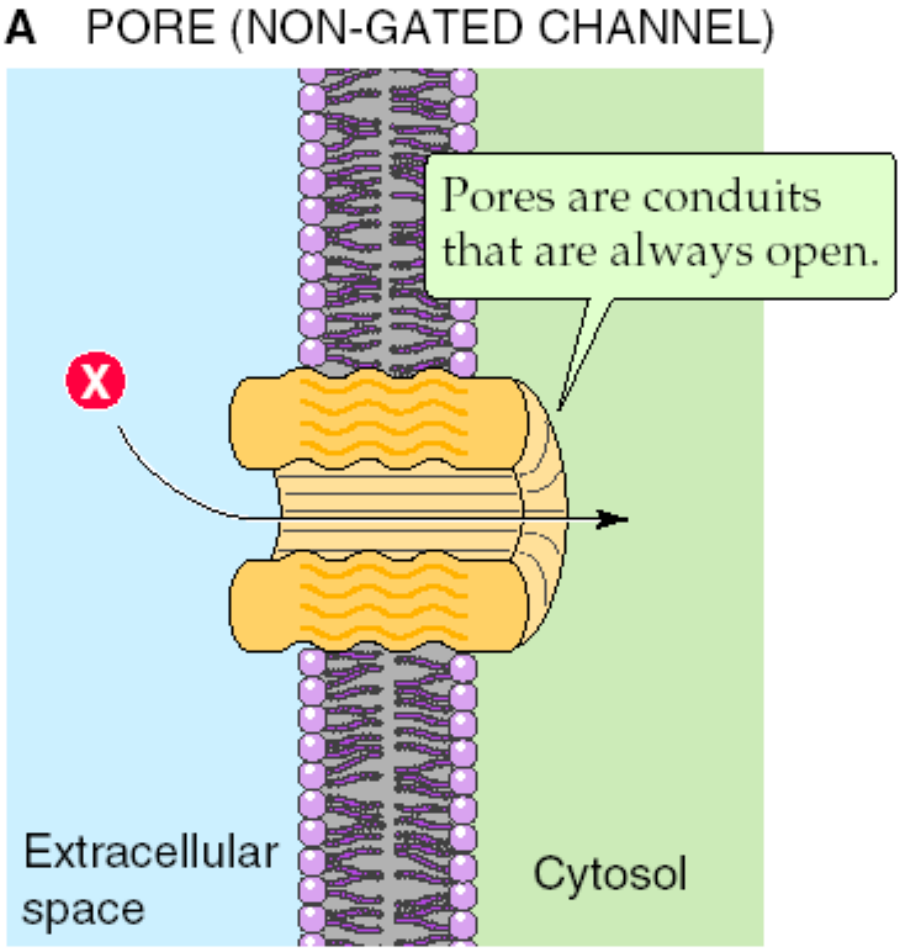


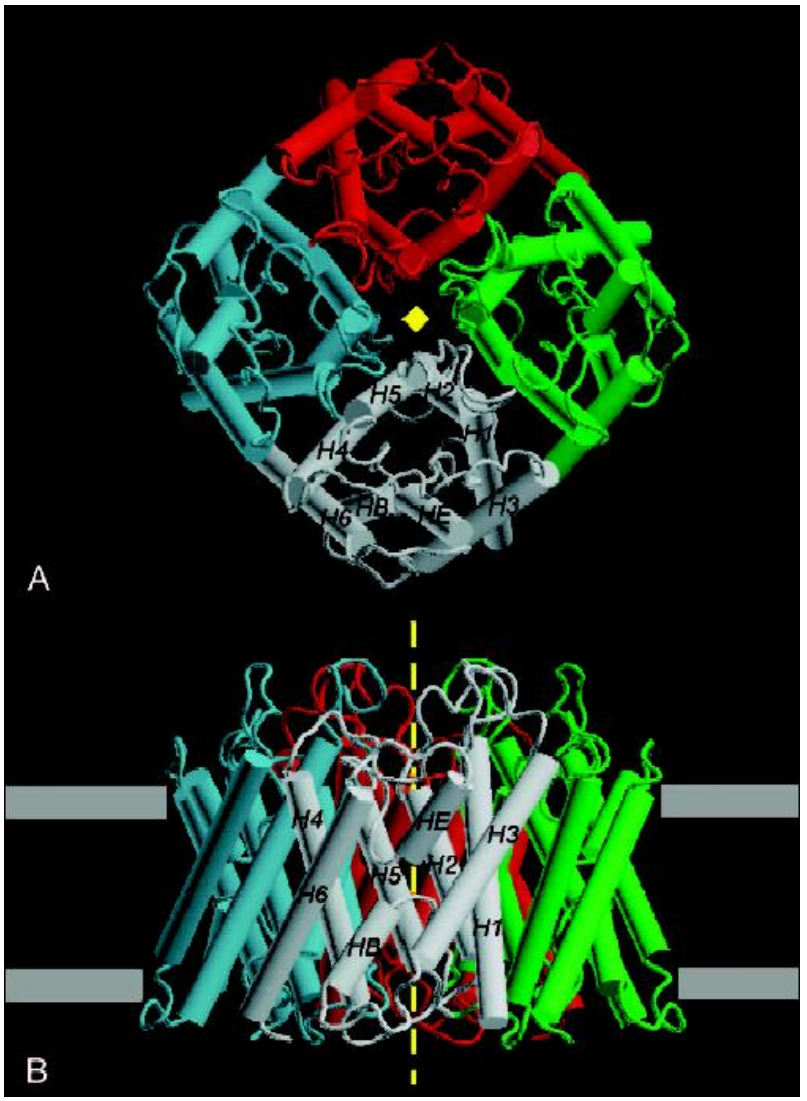
$$j = \beta \frac{D}{L} \Delta C$$



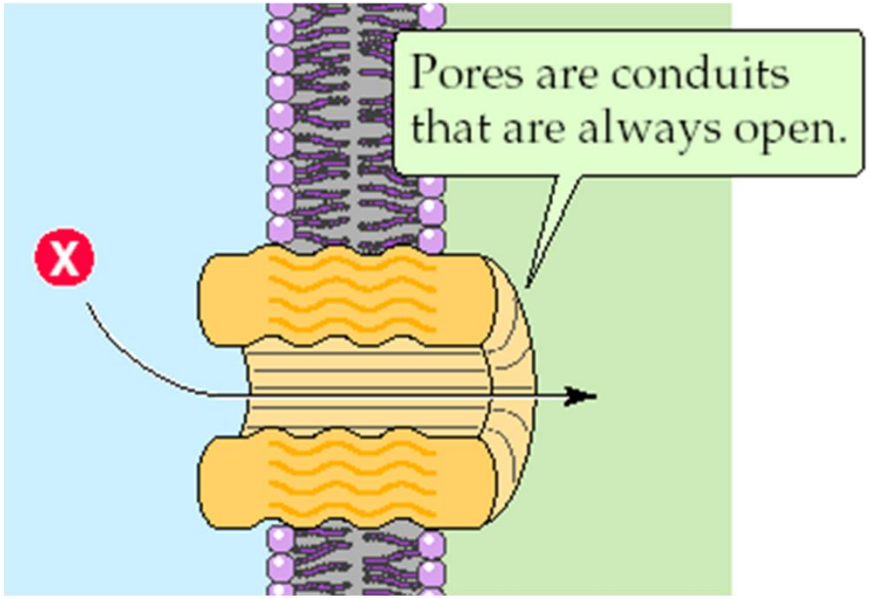
- Transport across membrane mediated by:
  - diffusion
  - transmembrane proteins
  - coupling of energetic sources

Pores and channels

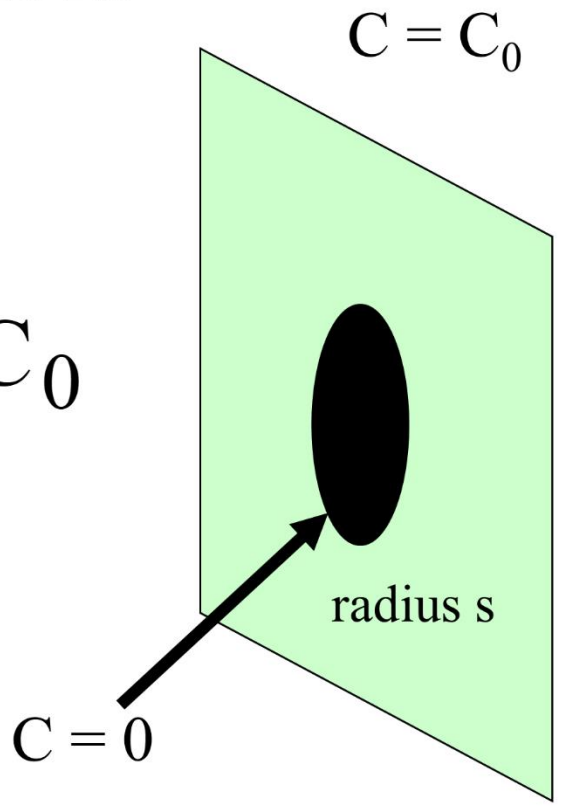


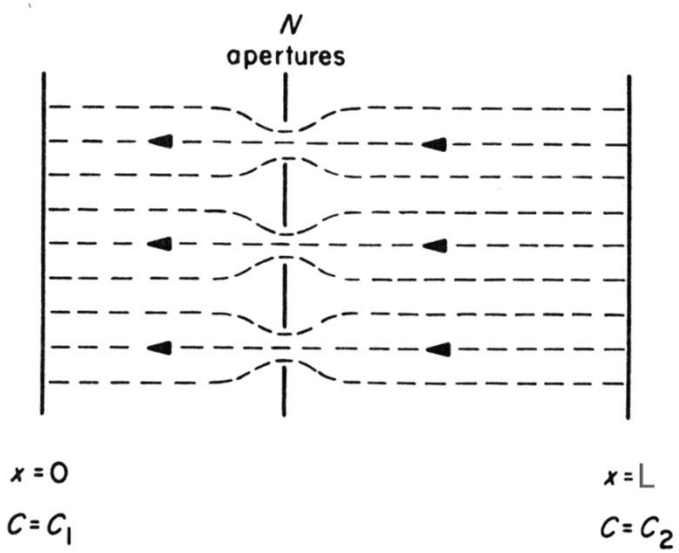


Pores and channels



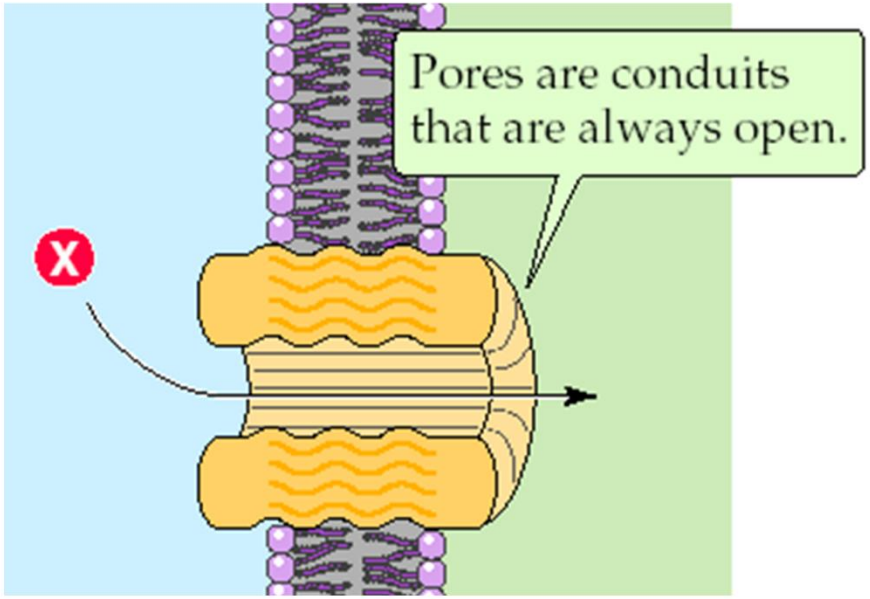
$$J = 4DsC_0$$





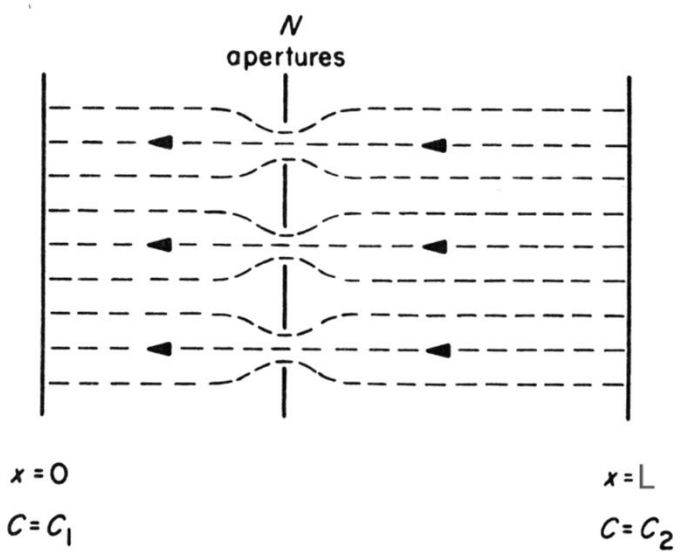
L = distance between planes
n = number of aperatures/area
s = pore radius
H.C. Berg, Random Walks in Biology

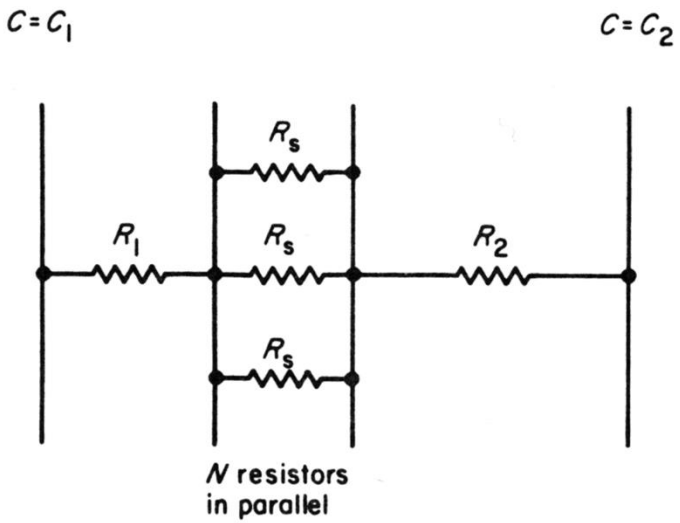
Pores and channels



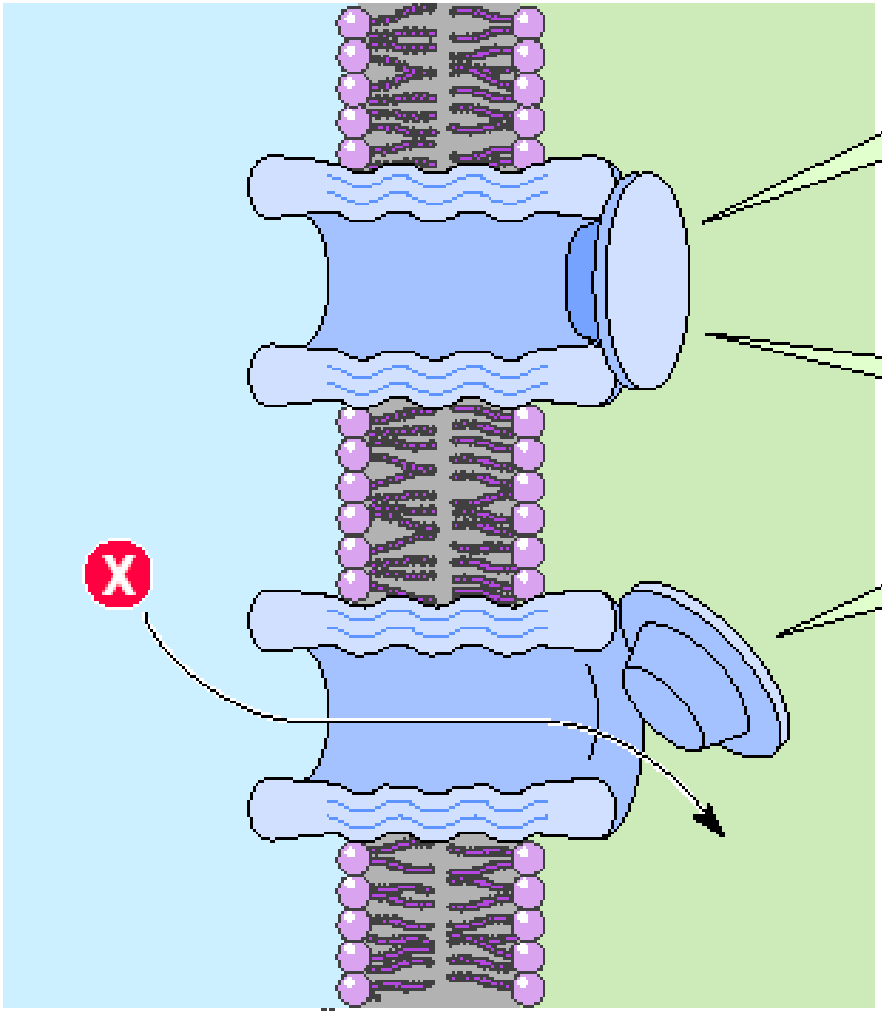
$$J = J_0 \frac{1}{\frac{1}{2Lns} + 1}; J_0 = \frac{DA}{L}\Delta C$$

L = distance between planes
n = number of aperatures/area
s = pore radius
H.C. Berg, Random Walks in Biology





B CHANNEL (GATED PORE)

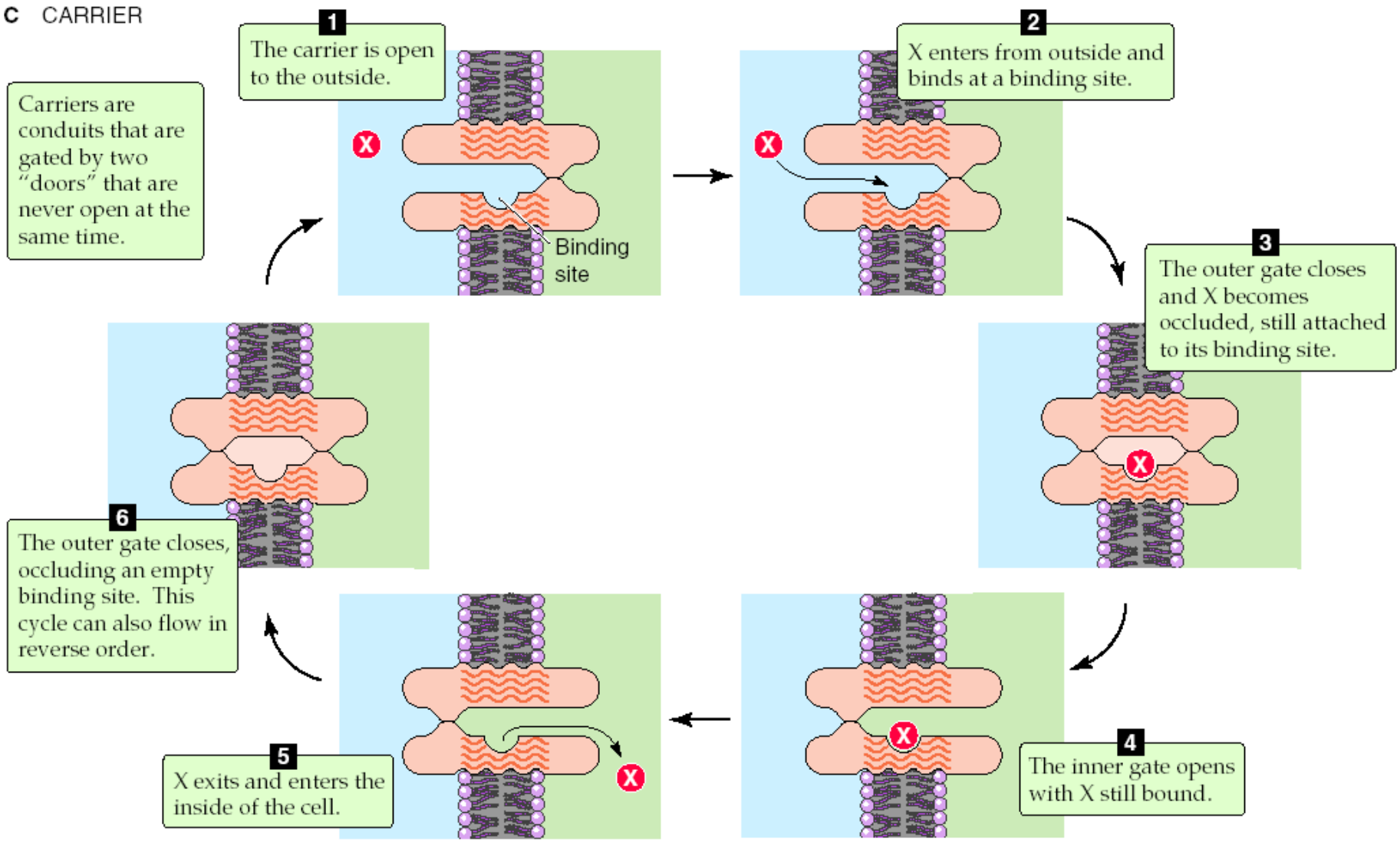


Channels are conduits that are gated by a "door."

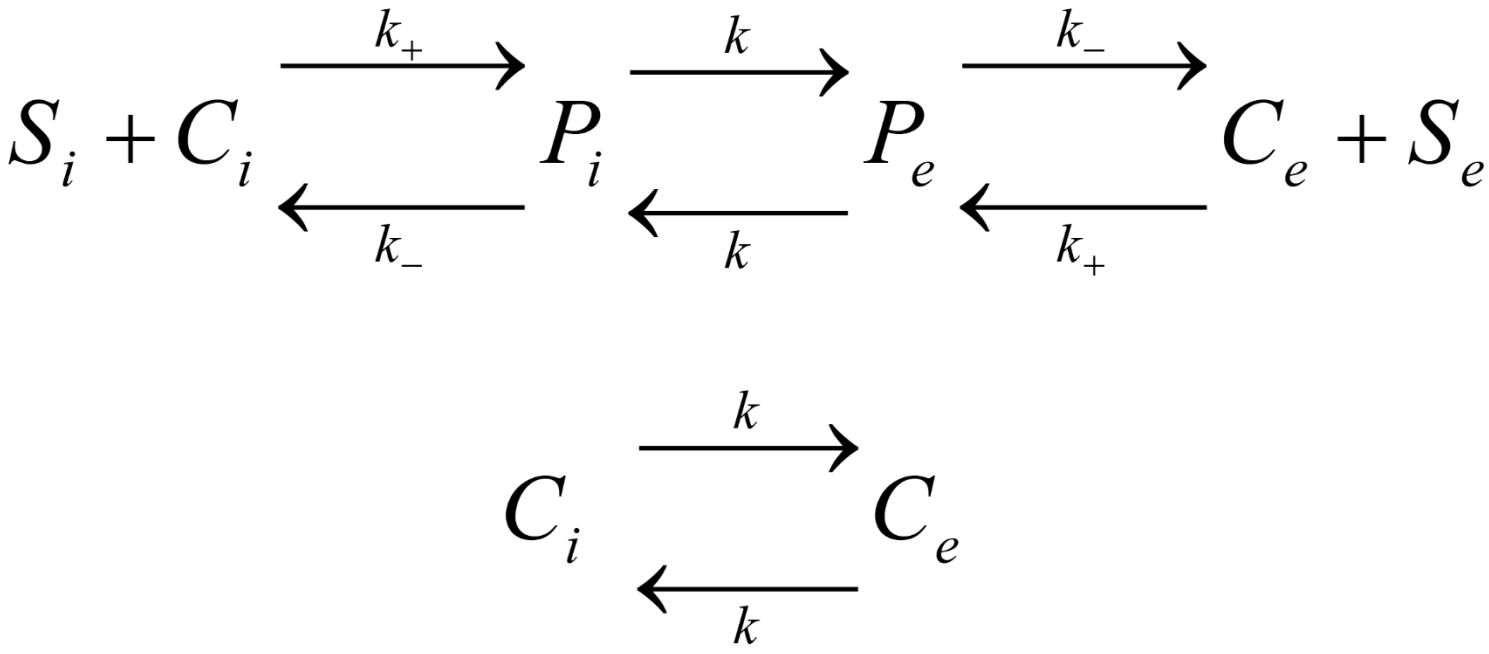
Channel is closed.

Channel is open.

Carriers – passive transport



Model of glucose transport (K&S)



Total glucose remains constant: $s_i+s_e+p_i+p_e$=constant

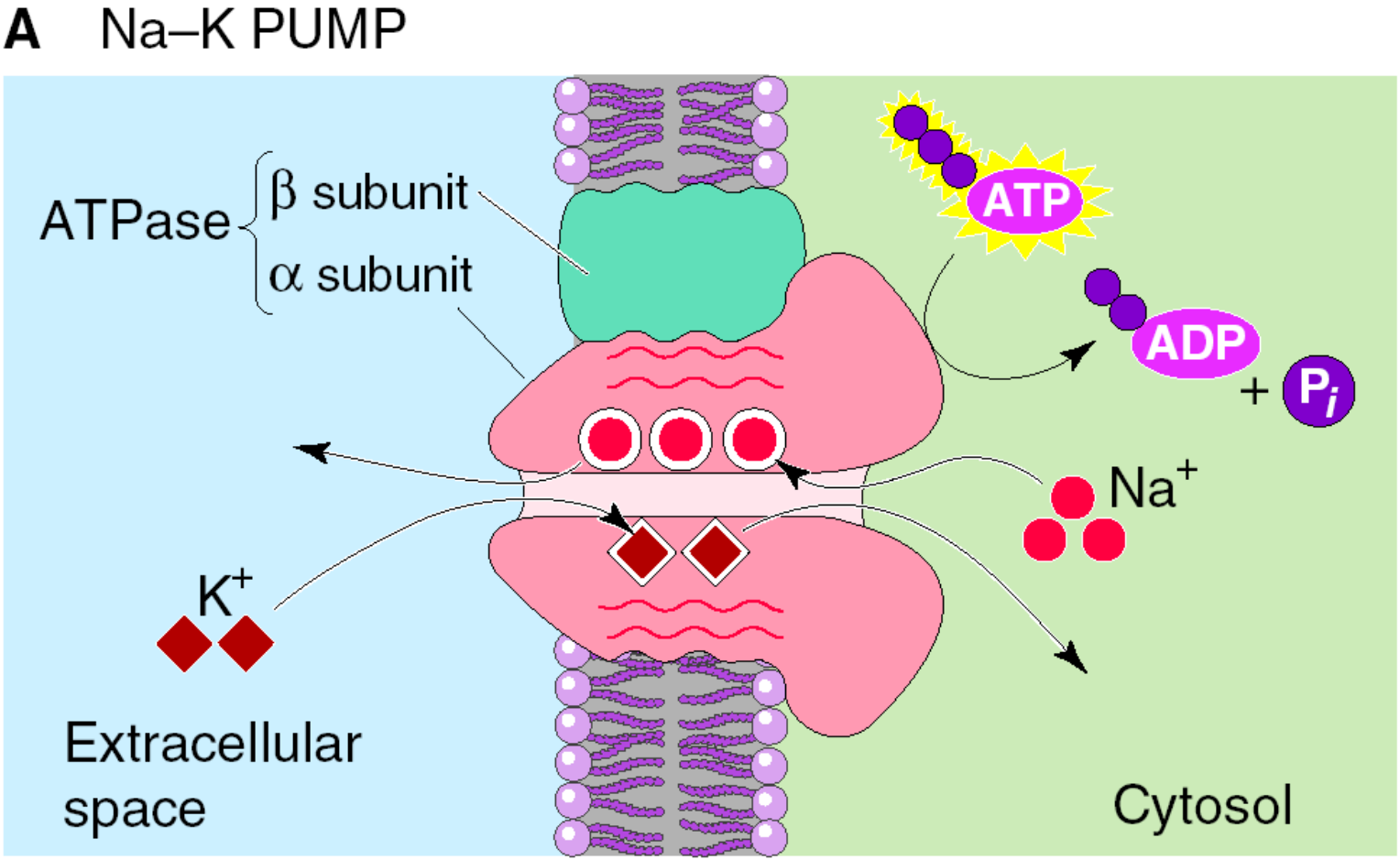
Total receptors remain constant: $p_i+p_e+c_i+c_e=c_0$

$$J = \frac{1}{2} K_d K k_+ C_0 \frac{s_e - s_i}{(s_i + K + K_d)(s_e + K + K_d) - K_d^2}$$

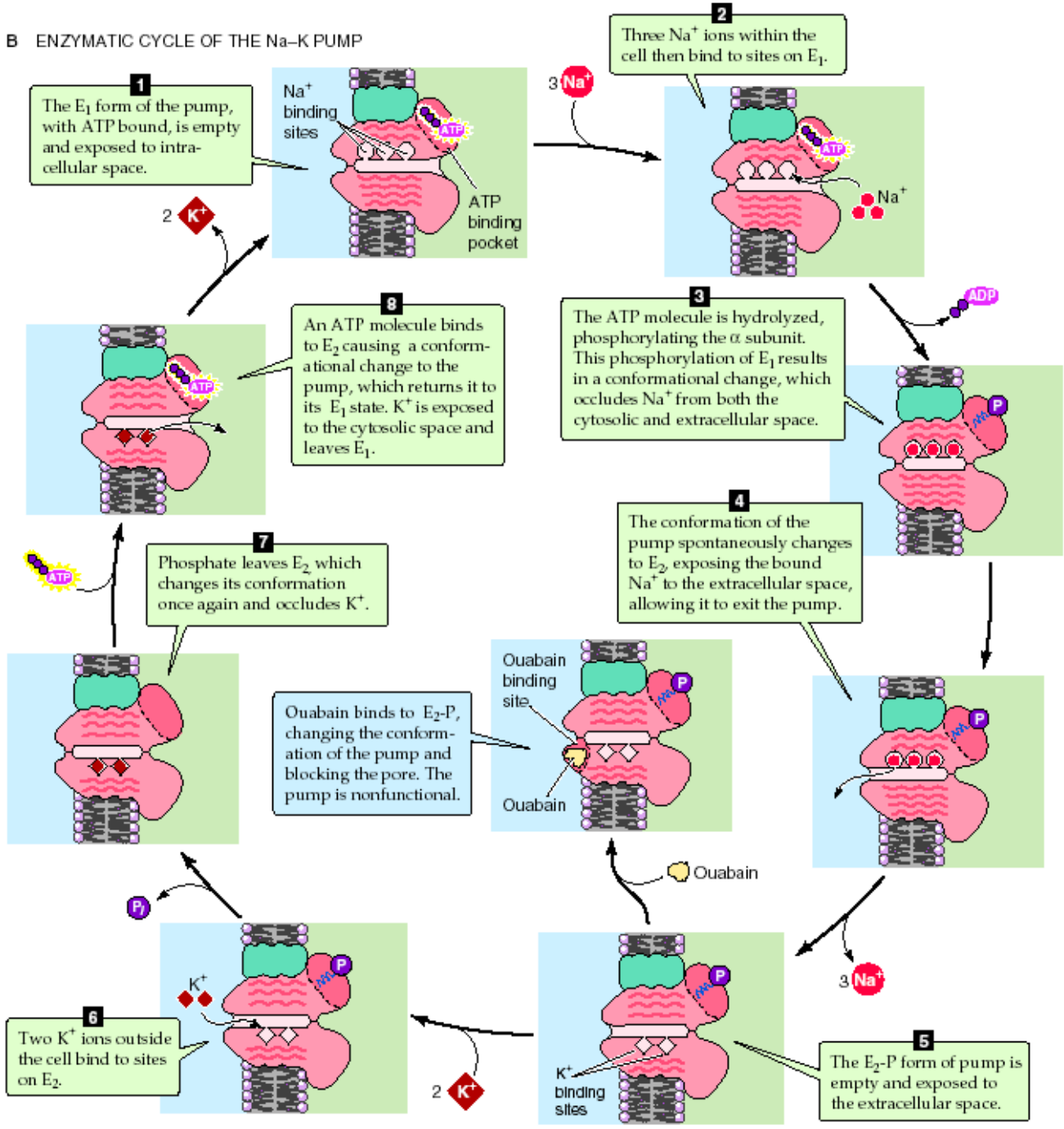
$$K = \frac{k_-}{k_+}; K_d = \frac{k}{k_+}$$

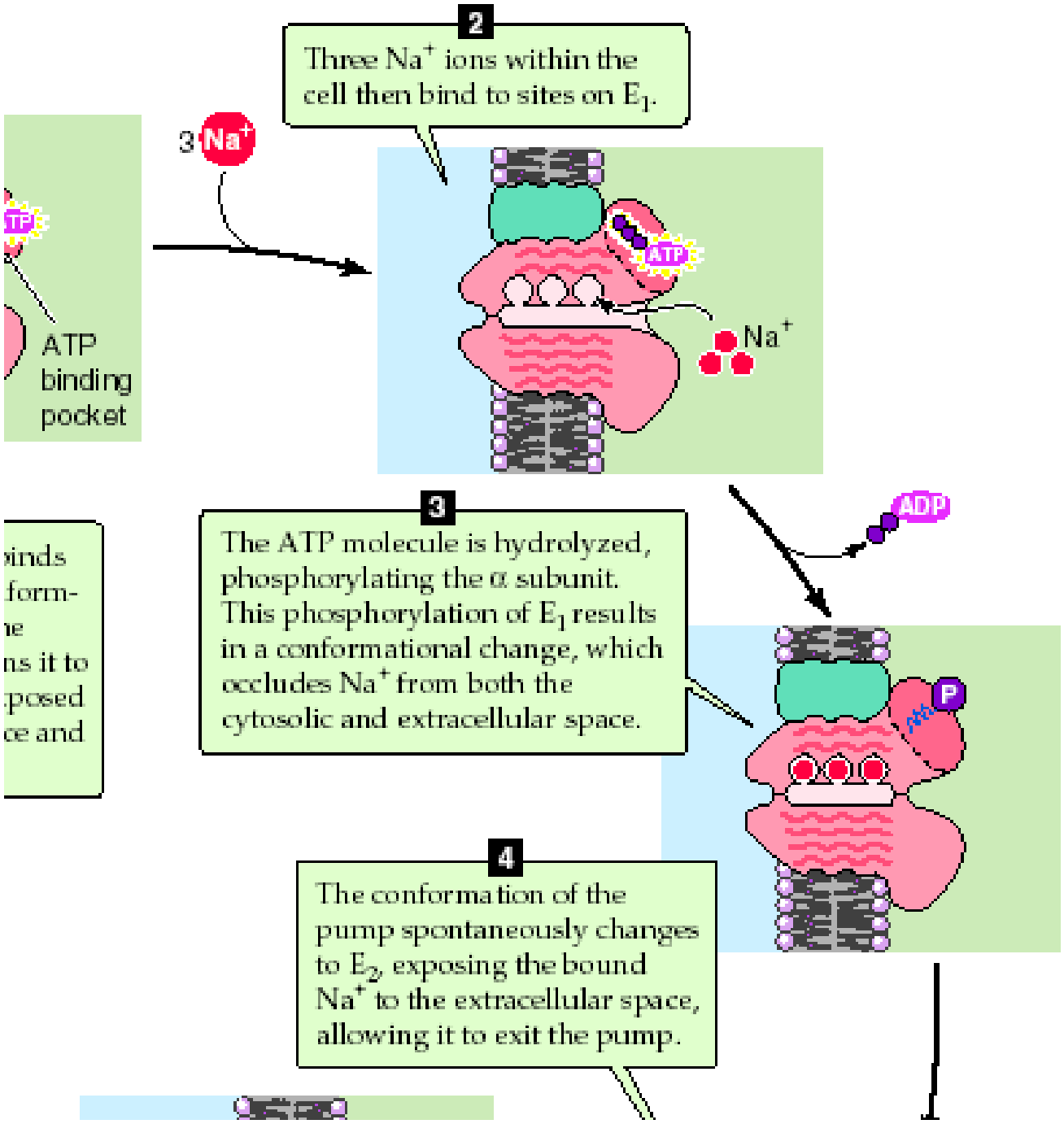
- Symmetric in S_e and S_i
- Consider flow from external to internal.
  - Flow increases with greater difference between concentrations.
  - For constant S_i, it exhibits Michaelis-Menten kinetics as S_e increases, but with an increase in K_m
  - For constant S_e-S_i, increasing S_i and S_e increases K_m.

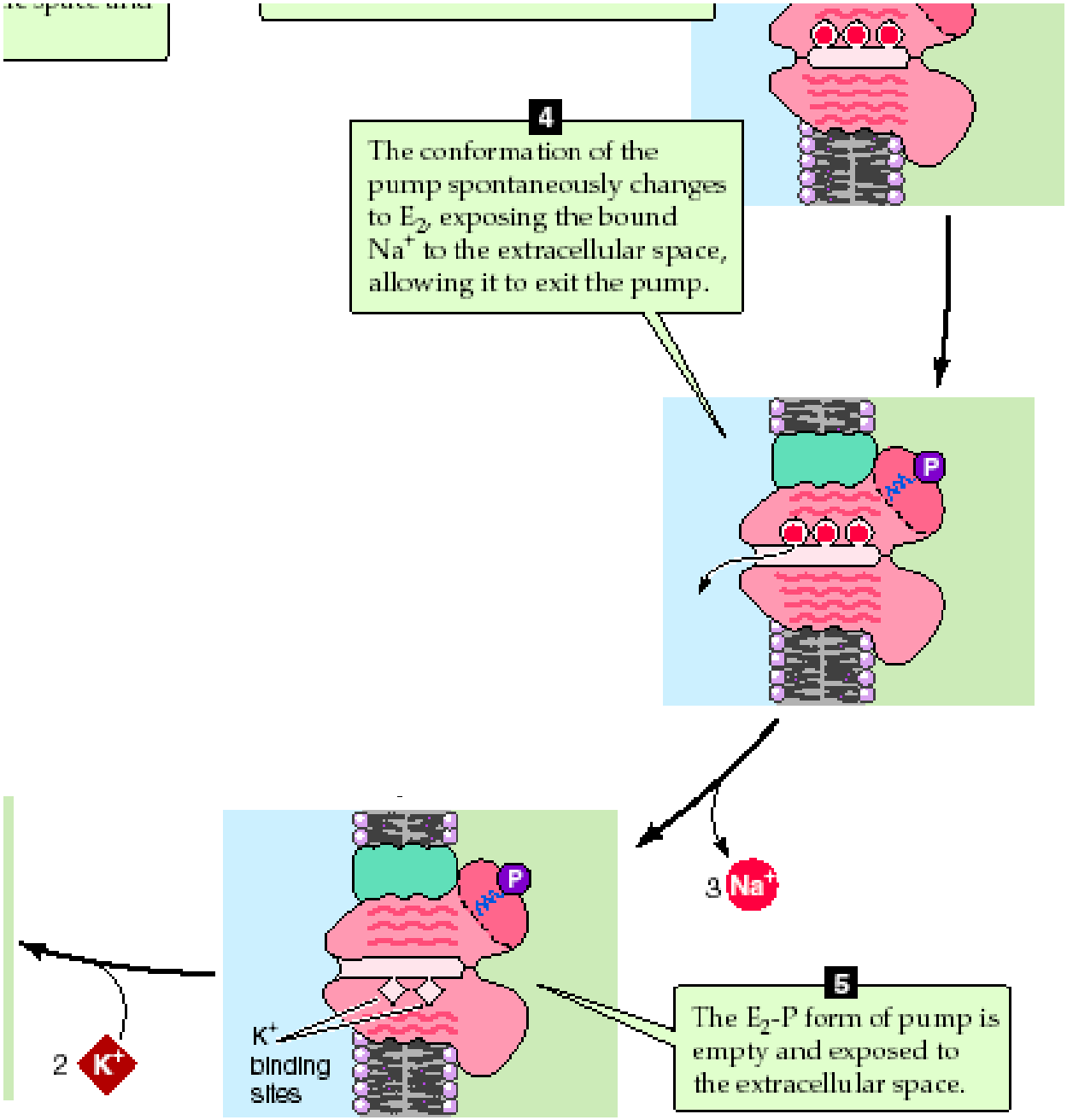
Carriers – Active transport

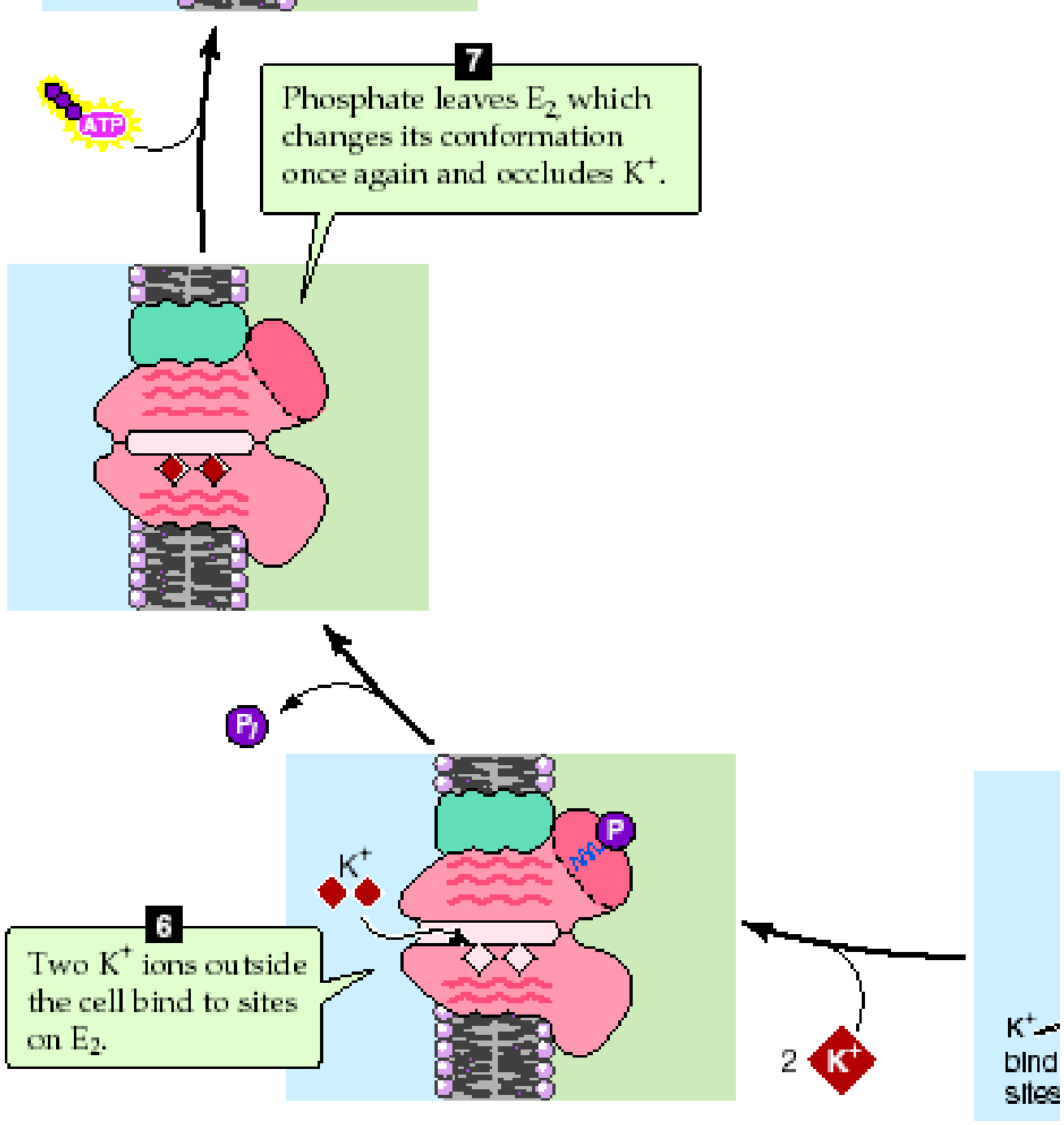


$$ATP+3Na^{+}_{i}+2K^{+}_{e}->ADP+P_{i}+3Na^{+}_{e}+2K^{+}_{I}$$

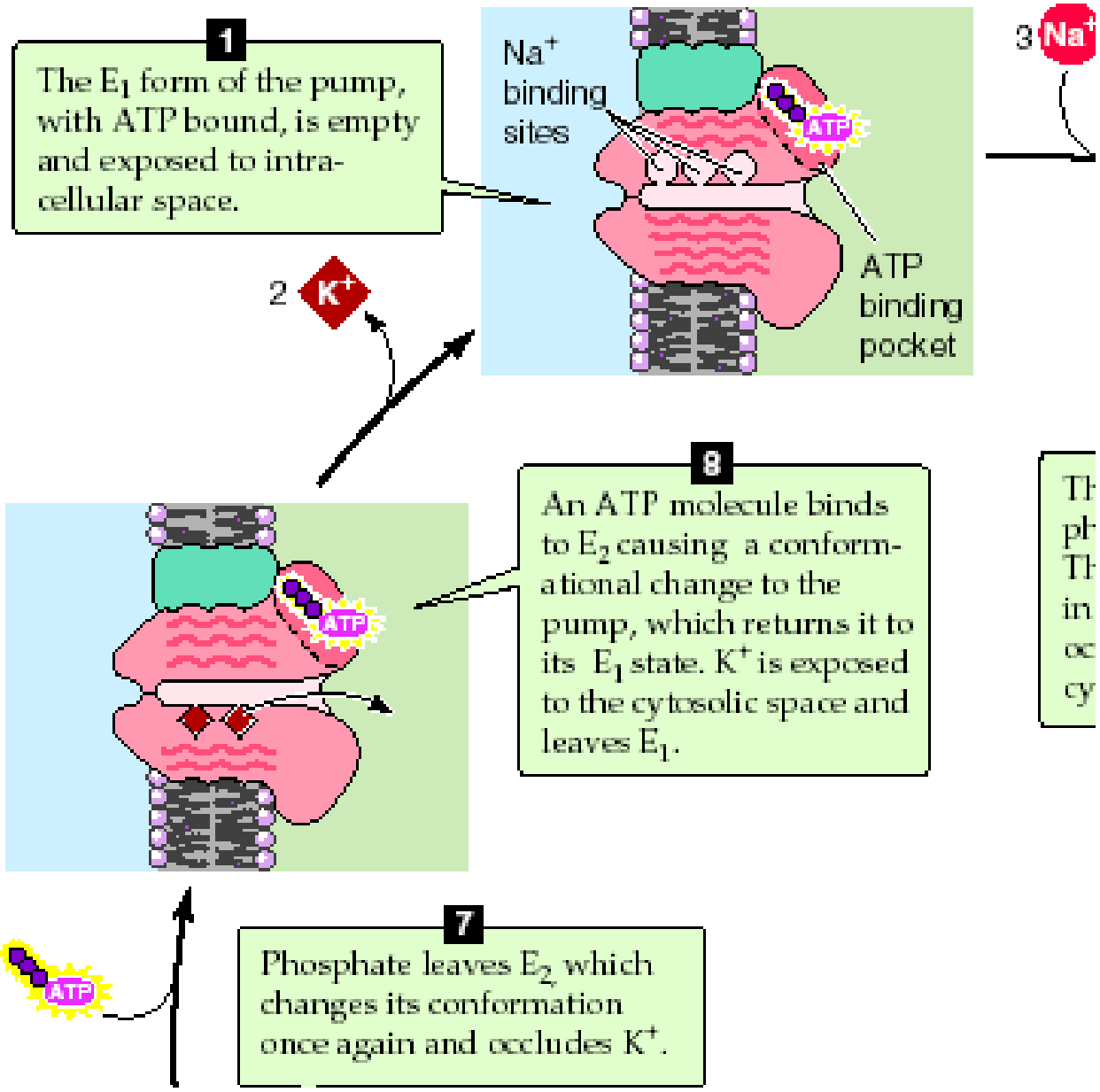

B ENZYMATIC CYCLE OF THE Na–K PUMP
1
The E_1 form of the pump, with ATP bound, is empty and exposed to intracellular space.
Na^+ binding sites
ATP
ATP binding pocket
2 K^+
2
Three Na^+ ions within the cell then bind to sites on E_1.
3 Na^+
Na^+
3
The ATP molecule is hydrolyzed, phosphorylating the α subunit. This phosphorylation of E_1 results in a conformational change, which occludes Na^+ from both the cytosolic and extracellular space.
ADP
P
4
The conformation of the pump spontaneously changes to E_2, exposing the bound Na^+ to the extracellular space, allowing it to exit the pump.
3 Na^+
5
The E_2-P form of pump is empty and exposed to the extracellular space.
K^+ binding sites
2 K^+
6
Two K^+ ions outside the cell bind to sites on E_2.
K^+
P_i
7
Phosphate leaves E_2 which changes its conformation once again and occludes K^+.
ATP
8
An ATP molecule binds to E_2 causing a conformational change to the pump, which returns it to its E_1 state. K^+ is exposed to the cytosolic space and leaves E_1.
Ouabain binding site
Ouabain
Ouabain binds to E_2-P, changing the conformation of the pump and blocking the pore. The pump is nonfunctional.
Ouabain


2
Three Na^+ ions within the cell then bind to sites on E_1.
3 Na^+
ATP
ATP binding pocket
Na^+
3
The ATP molecule is hydrolyzed, phosphorylating the α subunit. This phosphorylation of E_1 results in a conformational change, which occludes Na^+ from both the cytosolic and extracellular space.
ADP
P
4
The conformation of the pump spontaneously changes to E_2, exposing the bound Na^+ to the extracellular space, allowing it to exit the pump.

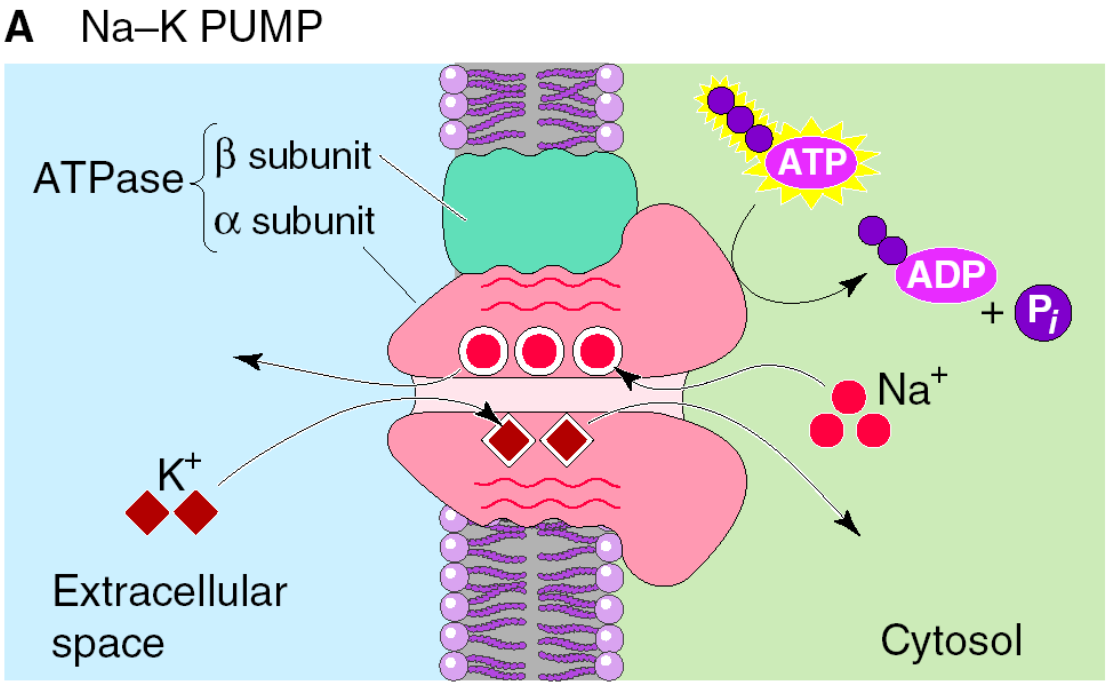

4
The conformation of the pump spontaneously changes to E_2, exposing the bound Na^+ to the extracellular space, allowing it to exit the pump.
P
3 Na^+
5
The E_2-P form of pump is empty and exposed to the extracellular space.
K^+ binding sites
2 K^+


ATP
7
Phosphate leaves E_2 which changes its conformation once again and occludes K^+.
P_i
P
K^+
6
Two K^+ ions outside the cell bind to sites on E_2.
2 K^+
K^+
bind
sites

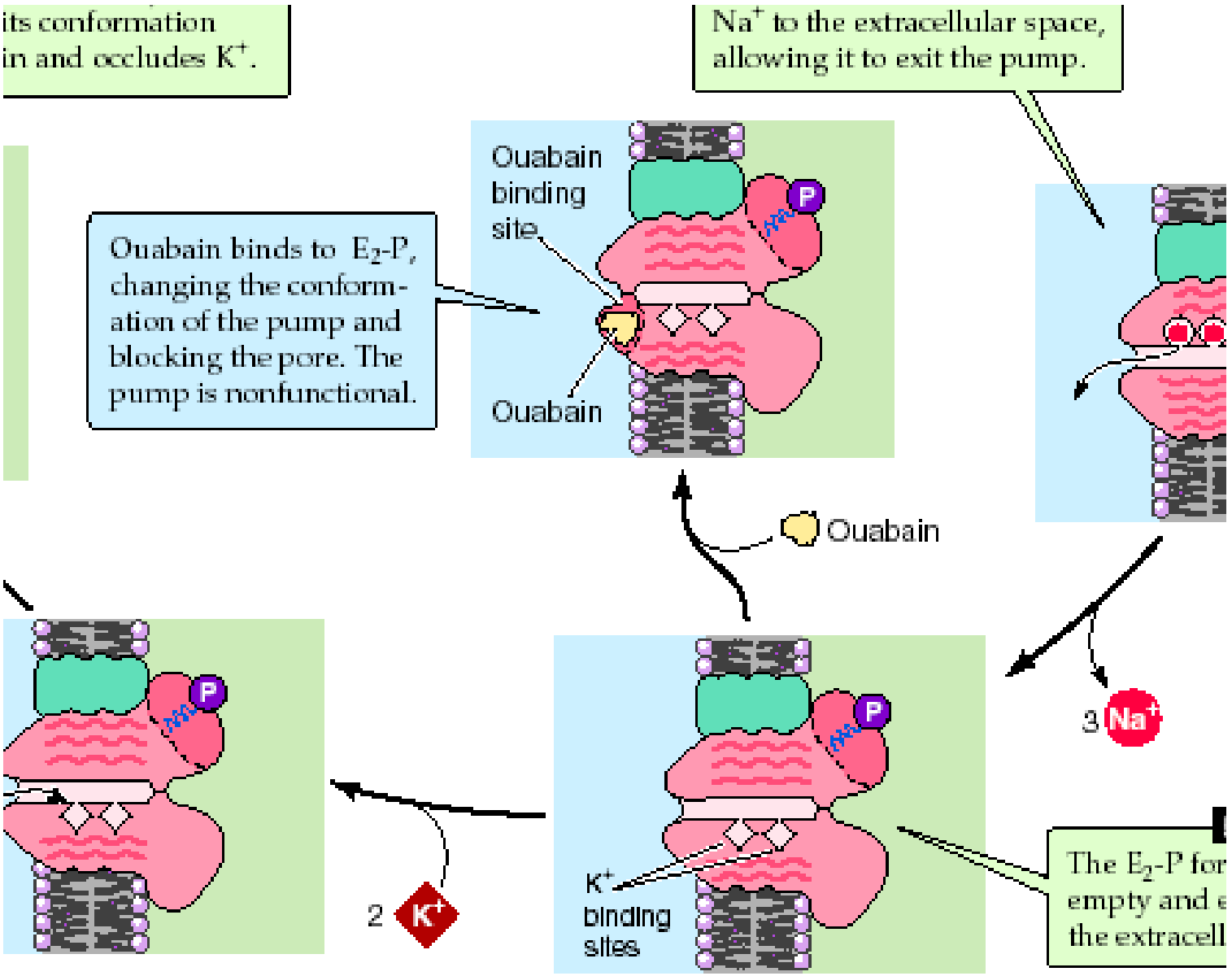
B ENZYMATIC CYCLE OF THE Na–K PUMP



Carriers – Active transport



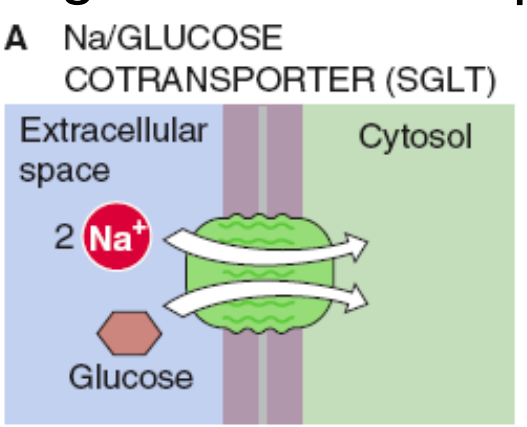
Ion	Affinity (K_D, mM)	
	Inside	Outside
Na^+	1.3	32
K^+	12	0.14

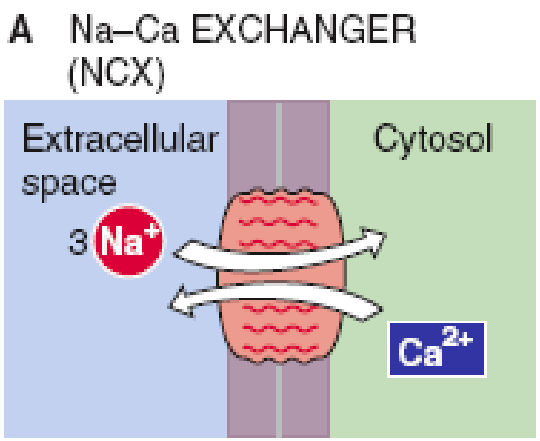

its conformation
in and occludes K^+.
Na^+ to the extracellular space,
allowing it to exit the pump.
Ouabain binds to E_2-P, changing the conformation of the pump and blocking the pore. The pump is nonfunctional.
Ouabain binding site
Ouabain
P
Ouabain
3 Na^+
2 K^+
K^+ binding sites
The E_2-P for
empty and
the extracell

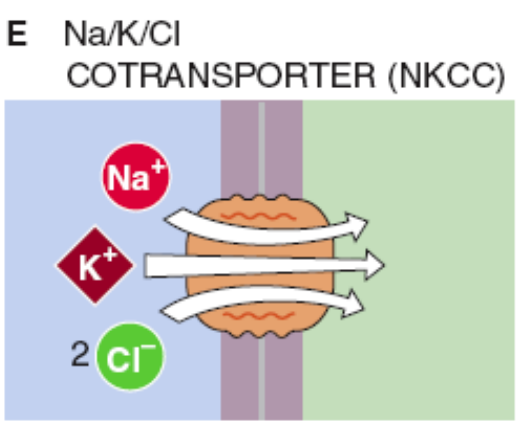
Variations

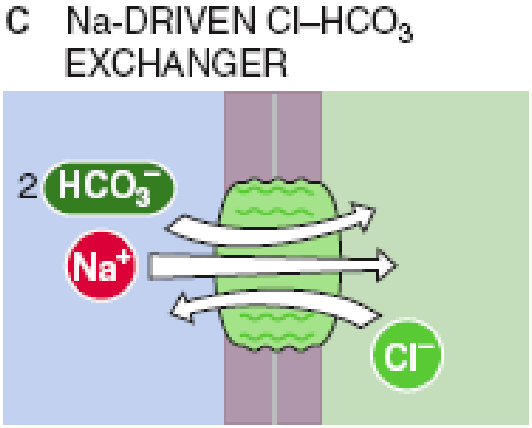
Myriad ways of moving single or multiple types of molecules

- kinetics: pores, channels, gated channels, pumps
- direction: exchanger, cotransport
- driving force: active / passive









Variations

- Next, bioelectric potentials, and how this affects transport of ions across membranes
- Volume regulation of cells
- Electrically excitable membranes