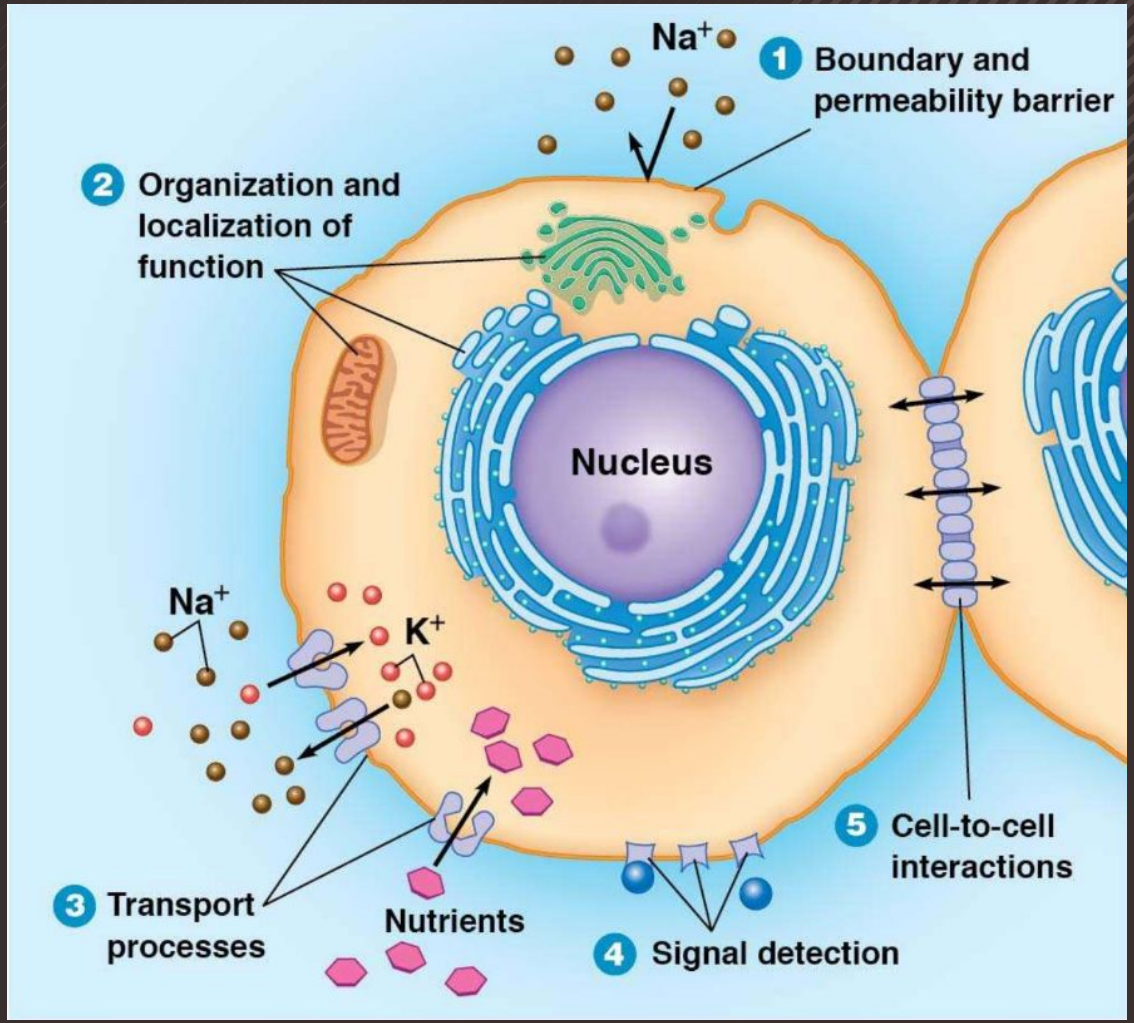
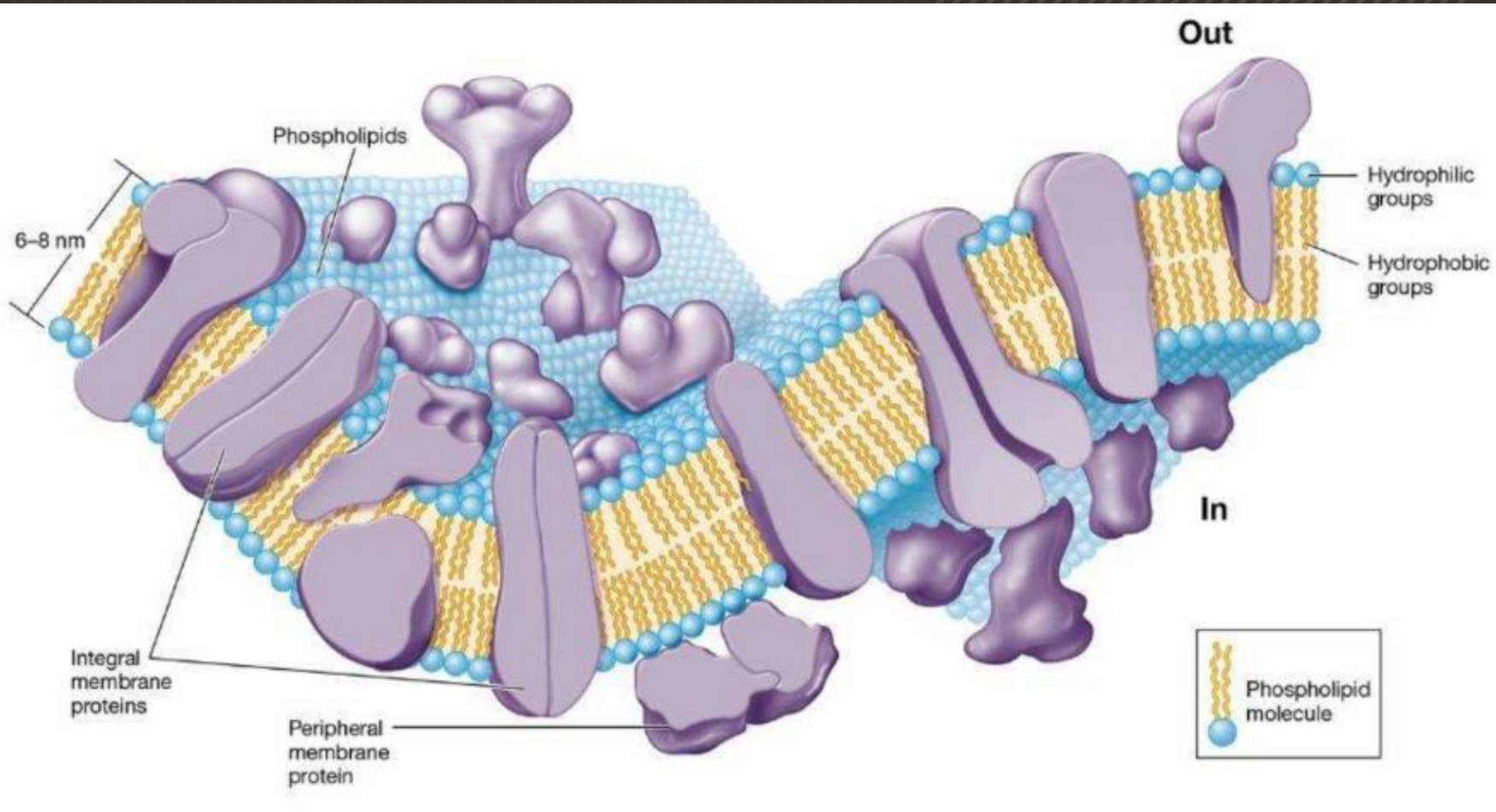
CELLENS TRANSPORTSYSTEM

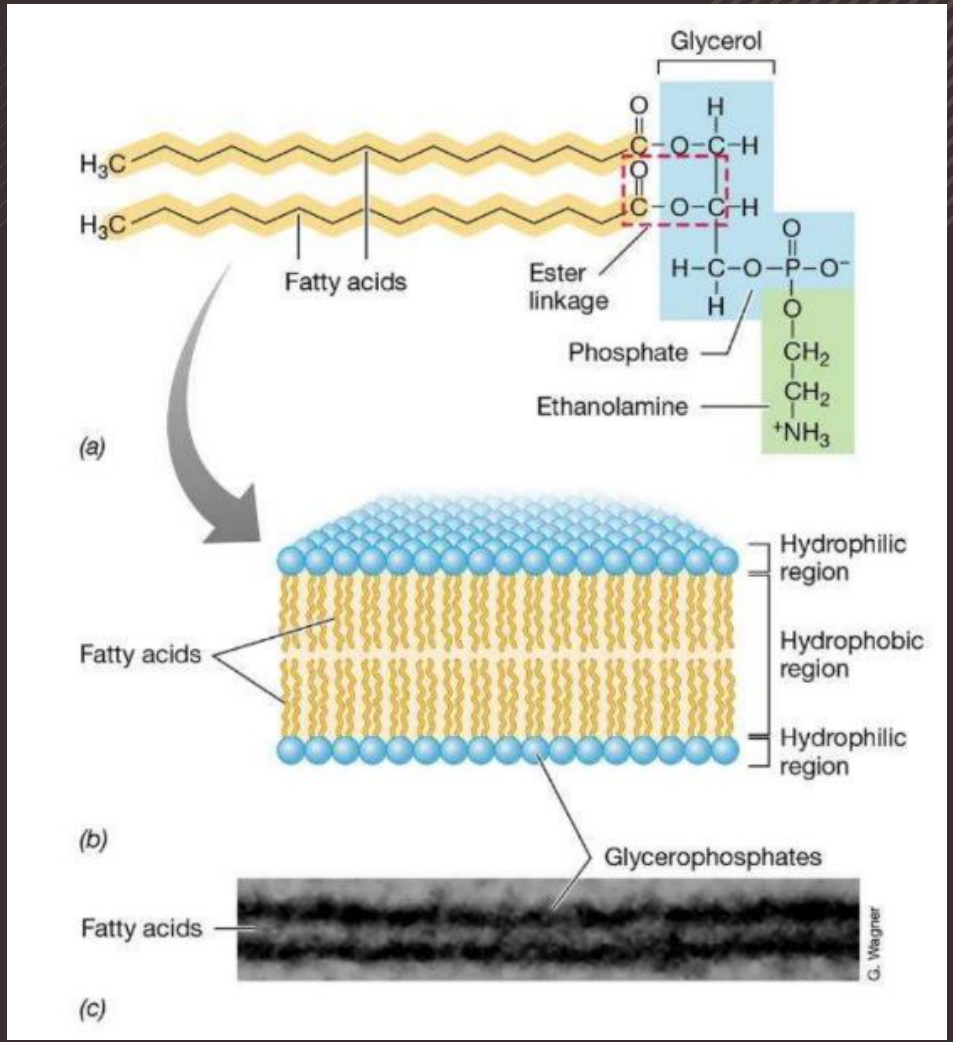
Bio2 2024
KL

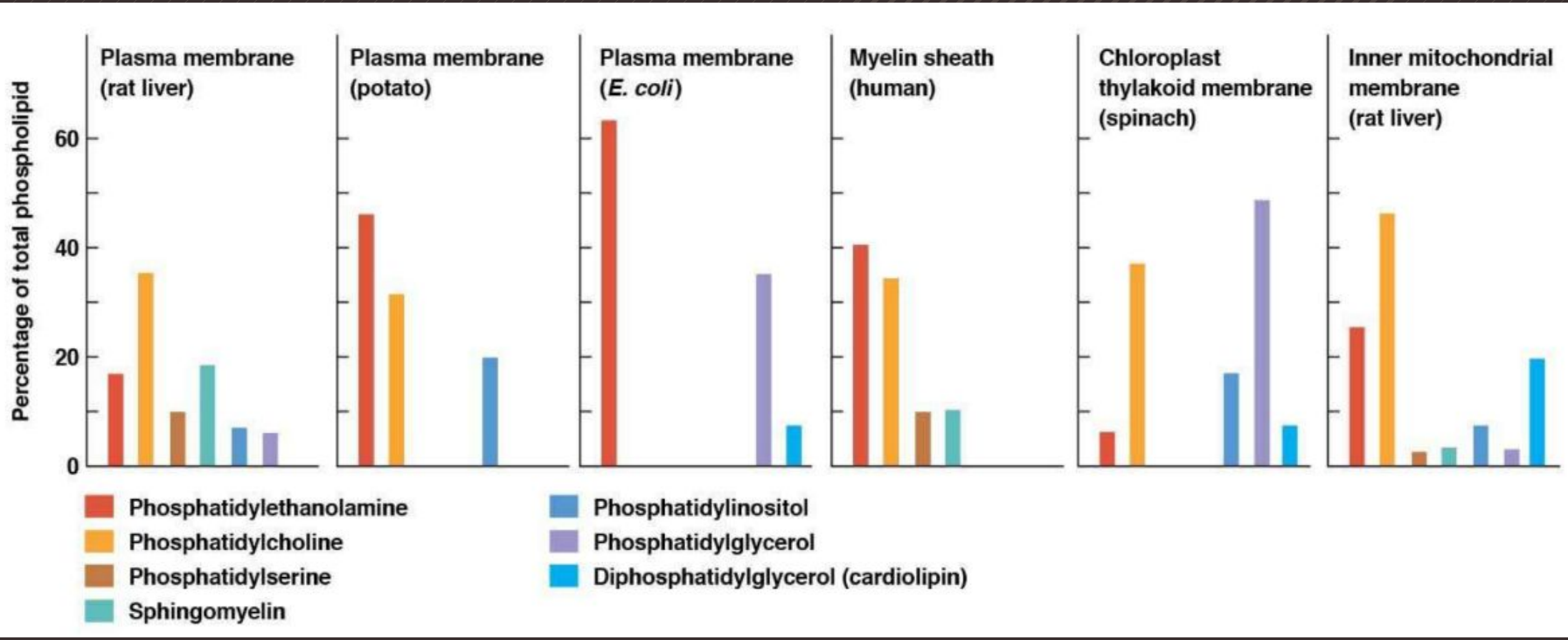
PUNKTER SOM BEHANDLAS

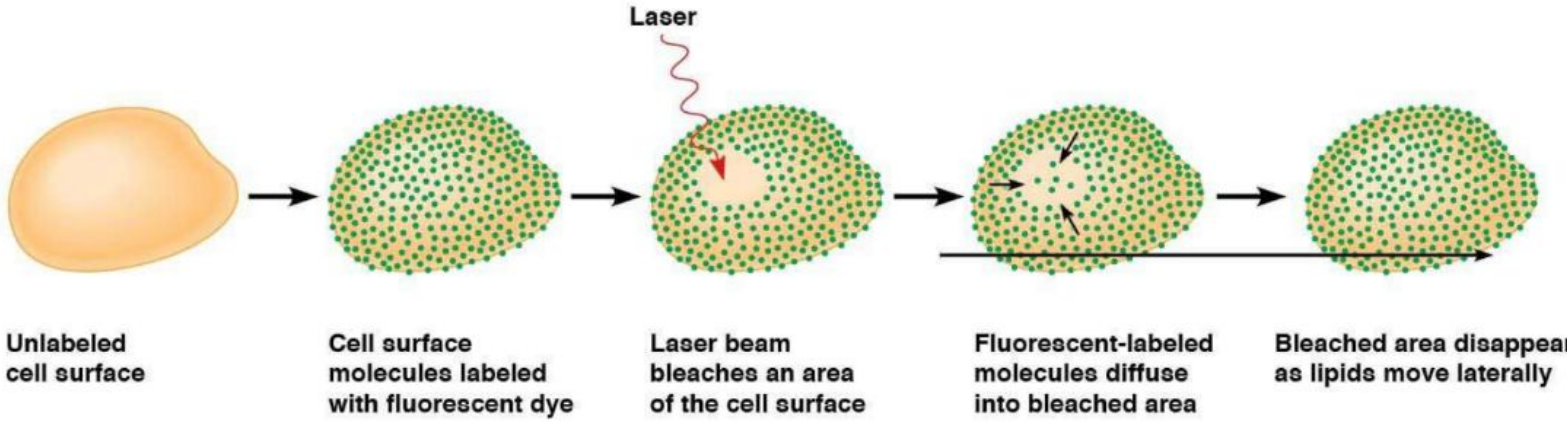
- Cellen och cellmembranet
  - (Struktur och funktion)
- Diffusion
  - (Osmos och passiv transport)
- Membrantransport
  - (Exocytos och endocytos, Aktiv och passiv transport)
- Transport Intracellulärt
  - (Vesiklar, Golgi och ER)
- Cellskelettet
  - (Motorproteiner med mera)


Na+
1 Boundary and permeability barrier
2 Organization and localization of function
Nucleus
Na+
K+
3 Transport processes
Nutrients
4 Signal detection
5 Cell-to-cell interactions

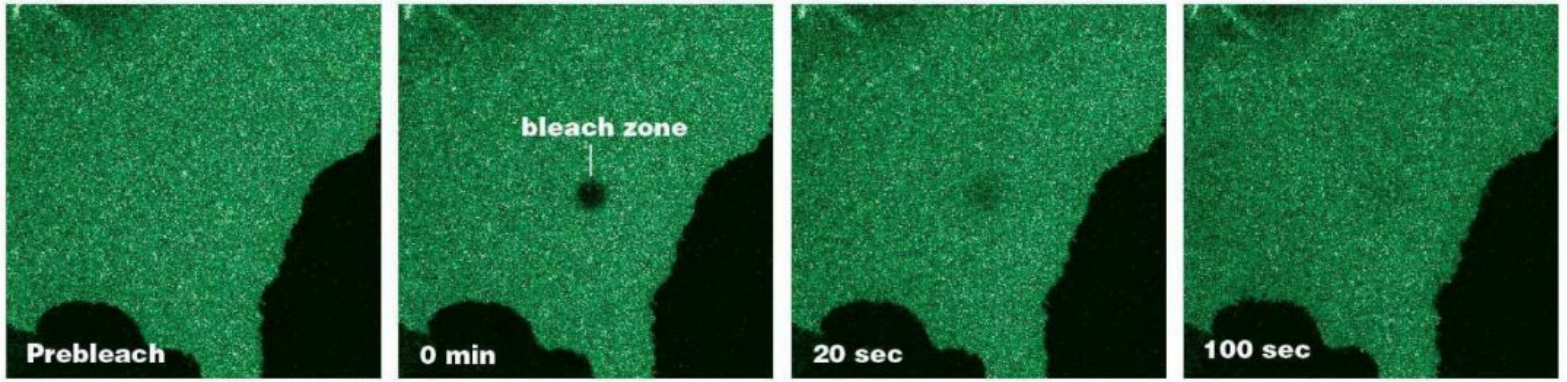

Out
Phospholipids
6–8 nm
Hydrophilic groups
Hydrophobic groups
In
Integral membrane proteins
Peripheral membrane protein
Phospholipid molecule


Glycerol
H_3C
H_3C
Fatty acids
Ester linkage
Phosphate
Ethanolamine
(a)
Hydrophilic region
Hydrophobic region
Hydrophilic region
Fatty acids
(b)
Glycerophosphates
Fatty acids
G. Wagner
(c)

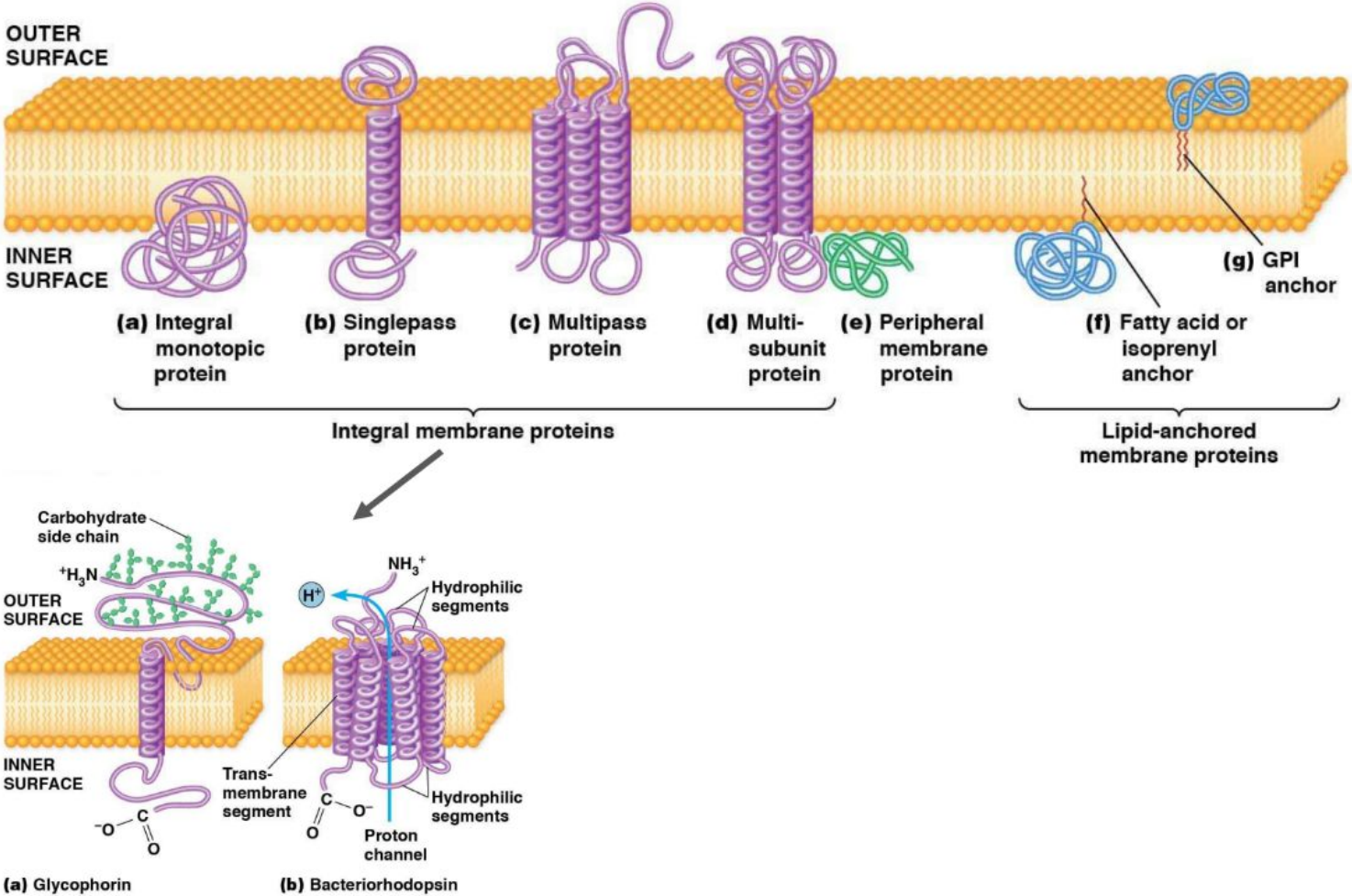

Plasma membrane (rat liver)
Plasma membrane (potato)
Plasma membrane (E. coli)
Myelin sheath (human)
Chloroplast thylakoid membrane (spinach)
Inner mitochondrial membrane (rat liver)
Percentage of total phospholipid
0
20
40
60
Phosphatidylethanolamine
Phosphatidylcholine
Phosphatidylserine
Sphingomyelin
Phosphatidylinositol
Phosphatidylglycerol
Diphosphatidylglycerol (cardiolipin)

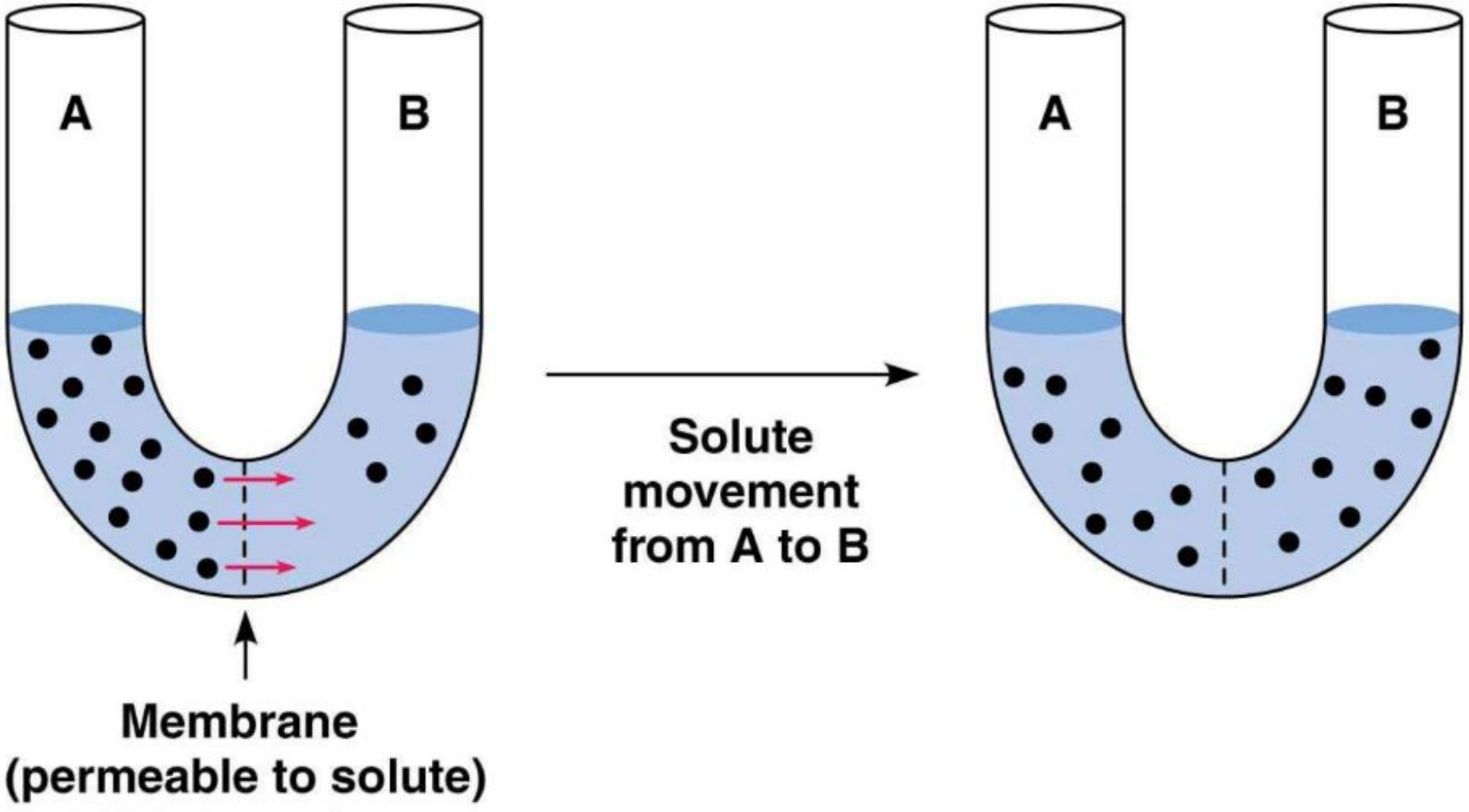


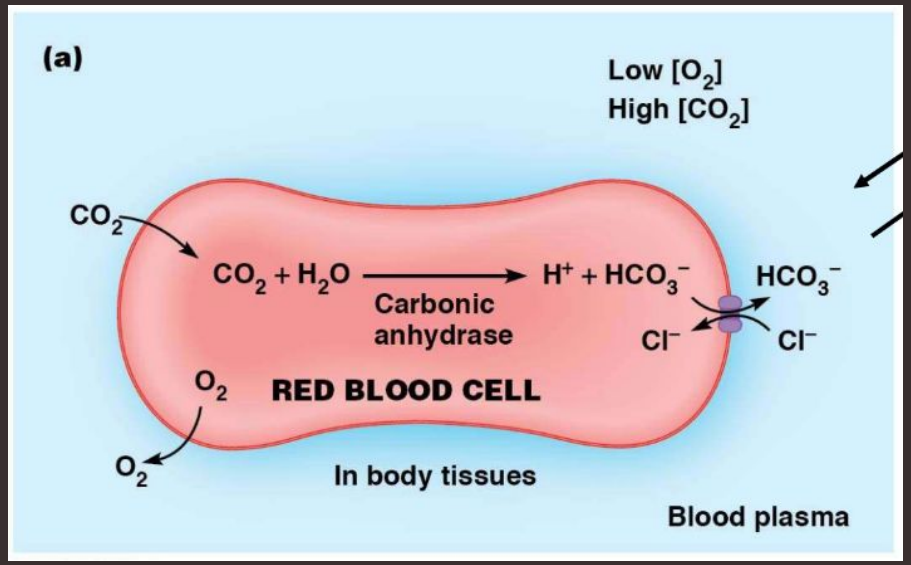
(a) Fluorescence recovery after photobleaching (FRAP)

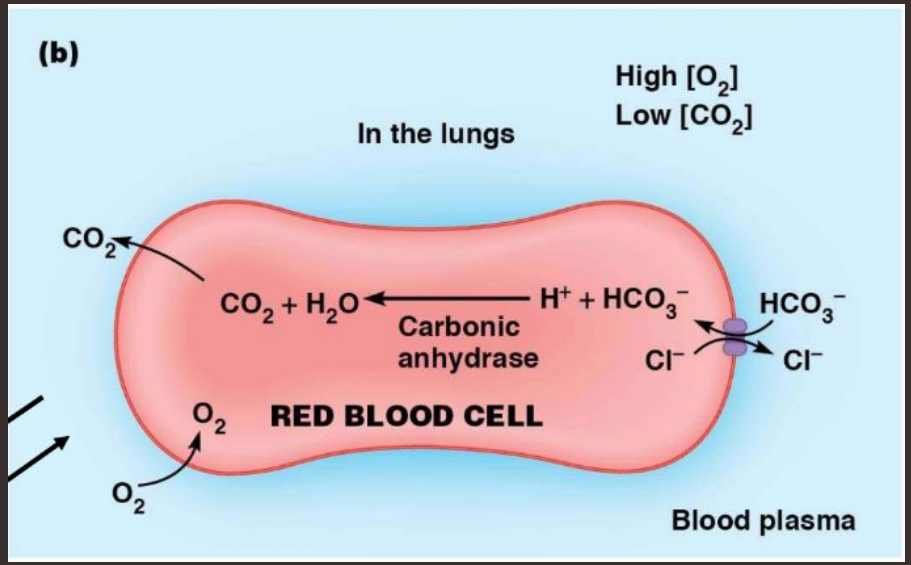


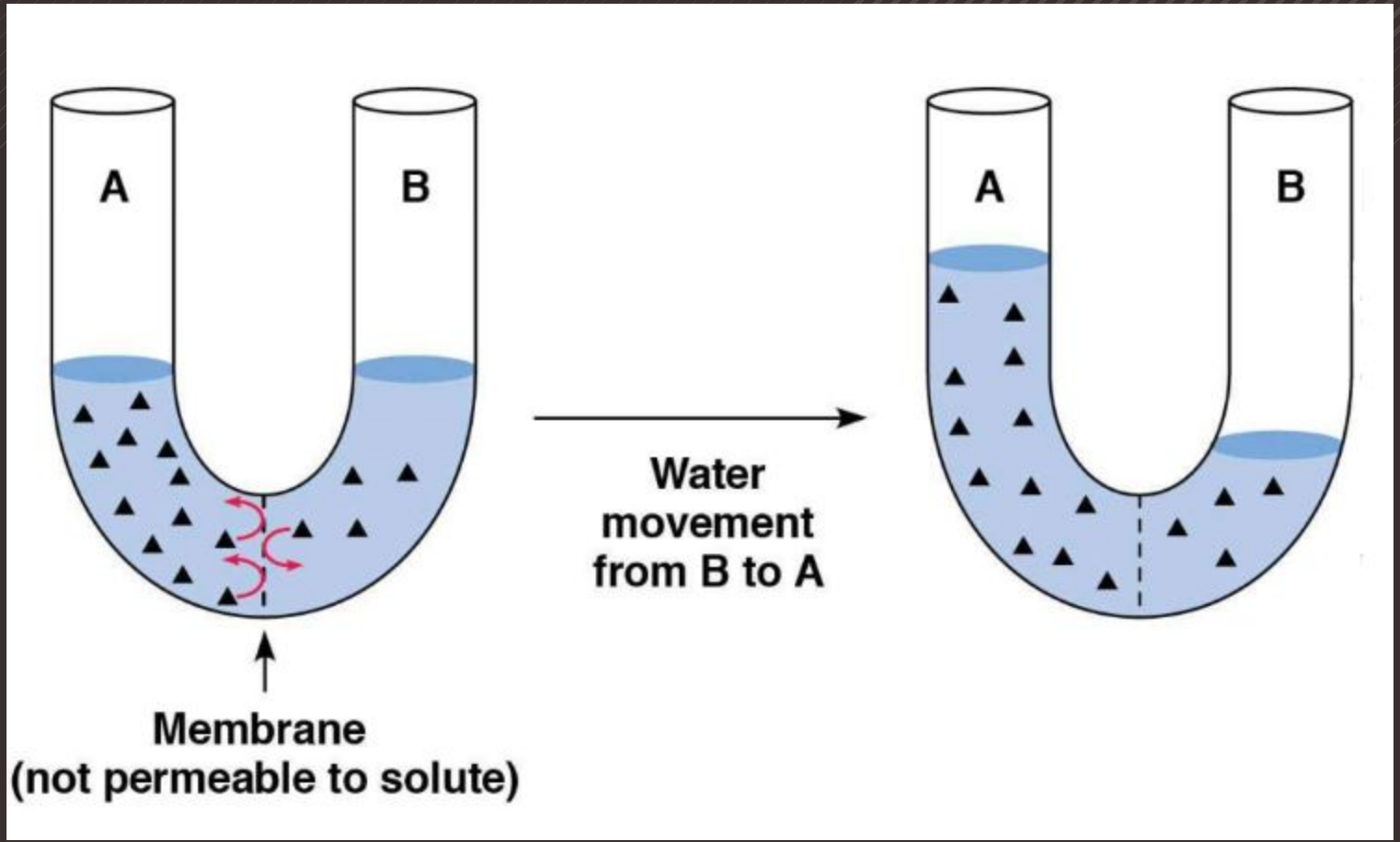
(b) FRAP of labeled protein in the ER membrane

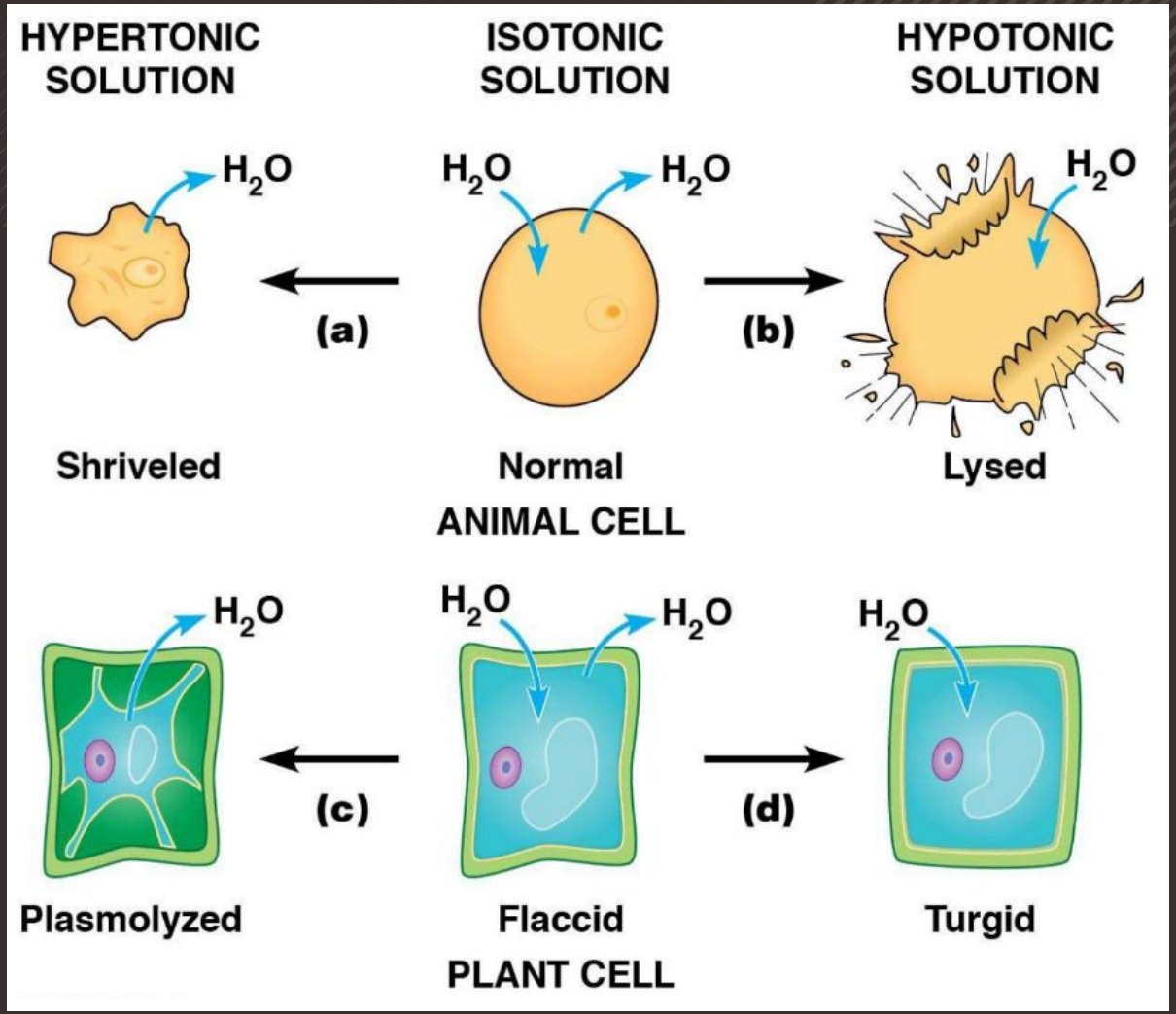

OUTER SURFACE
INNER SURFACE
(a) Integral monotopic protein
(b) Singlepass protein
(c) Multipass protein
(d) Multi-subunit protein
(e) Peripheral membrane protein
(f) Fatty acid or isoprenyl anchor
(g) GPI anchor
Integral membrane proteins
Lipid-anchored membrane proteins
Carbohydrate side chain
$^{+}H_3N$
OUTER SURFACE
INNER SURFACE
^{-}O C O
NH_3^+
H^+
Hydrophilic segments
Trans-membrane segment
C O^- O
Hydrophilic segments
Proton channel
(a) Glycophorin
(b) Bacteriorhodopsin

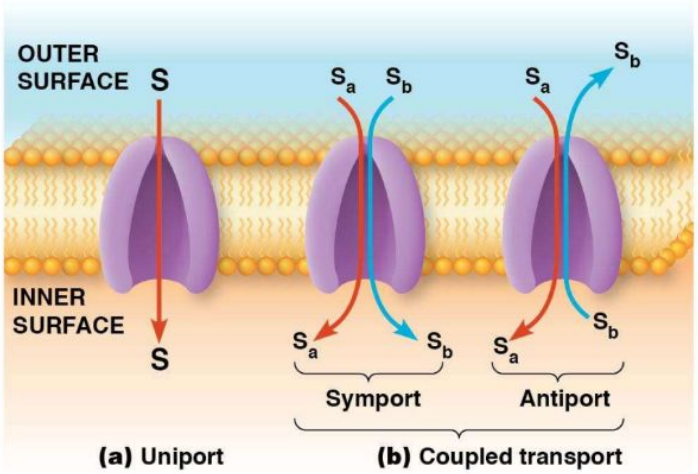

A
B
A
B
Solute
movement
from A to B
Membrane
(permeable to solute)


(a)
Low [O_2]
High [CO_2]
CO_2
$CO_2 + H_2O$
Carbonic anhydrase
$H^+ + HCO_3^-$
HCO_3^-
Cl^-
Cl^-
O_2
RED BLOOD CELL
O_2
In body tissues
Blood plasma

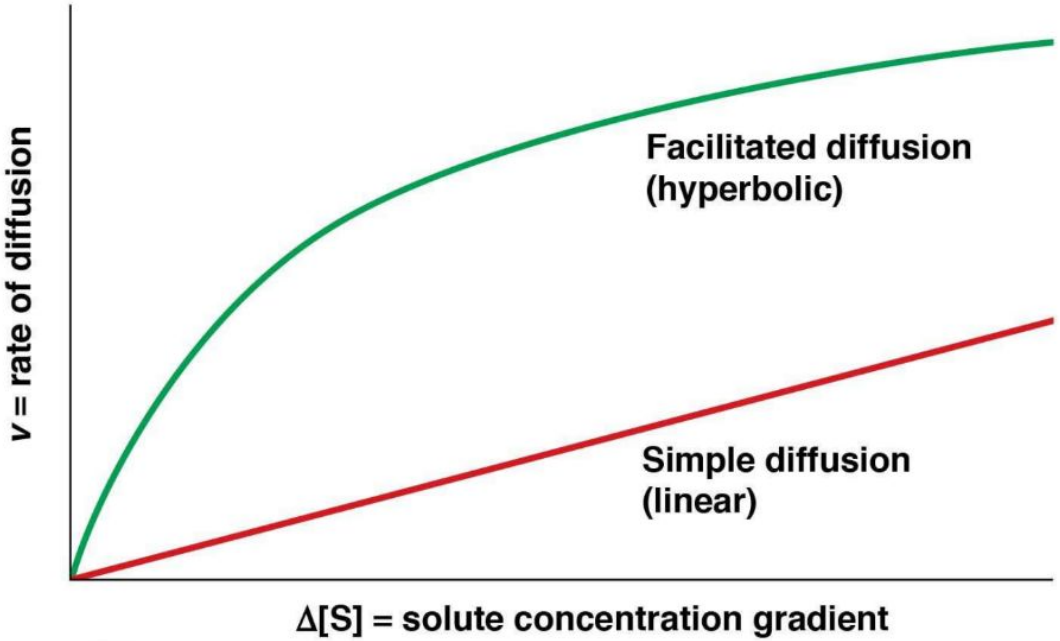

(b)
High [O_2]
Low [CO_2]
In the lungs
CO_2
$CO_2 + H_2O$
Carbonic anhydrase
$H^+ + HCO_3^-$
HCO_3^-
Cl^-
Cl^-
O_2
RED BLOOD CELL
O_2
Blood plasma

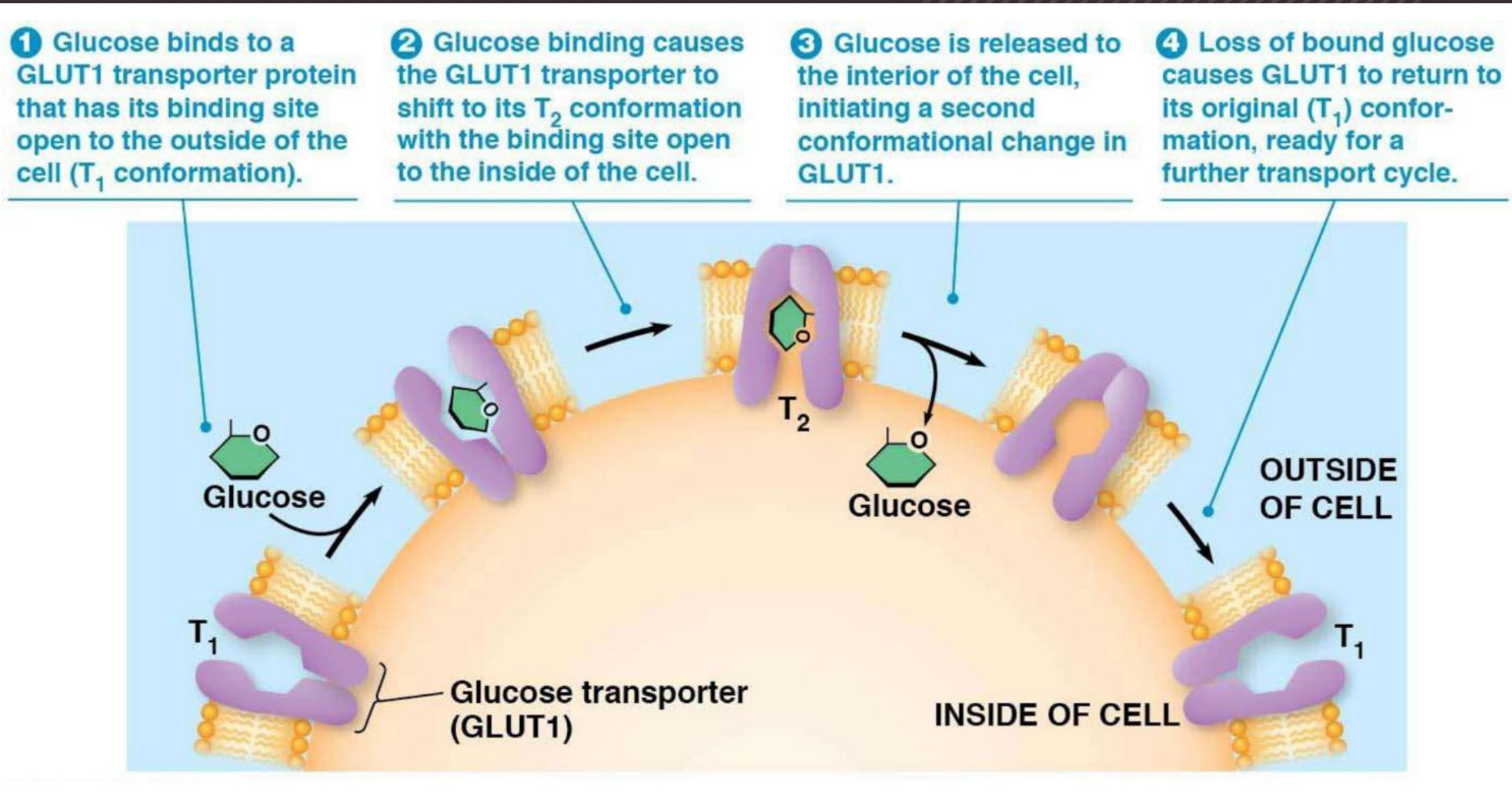

A
B
A
B
Water
movement
from B to A
Membrane
(not permeable to solute)

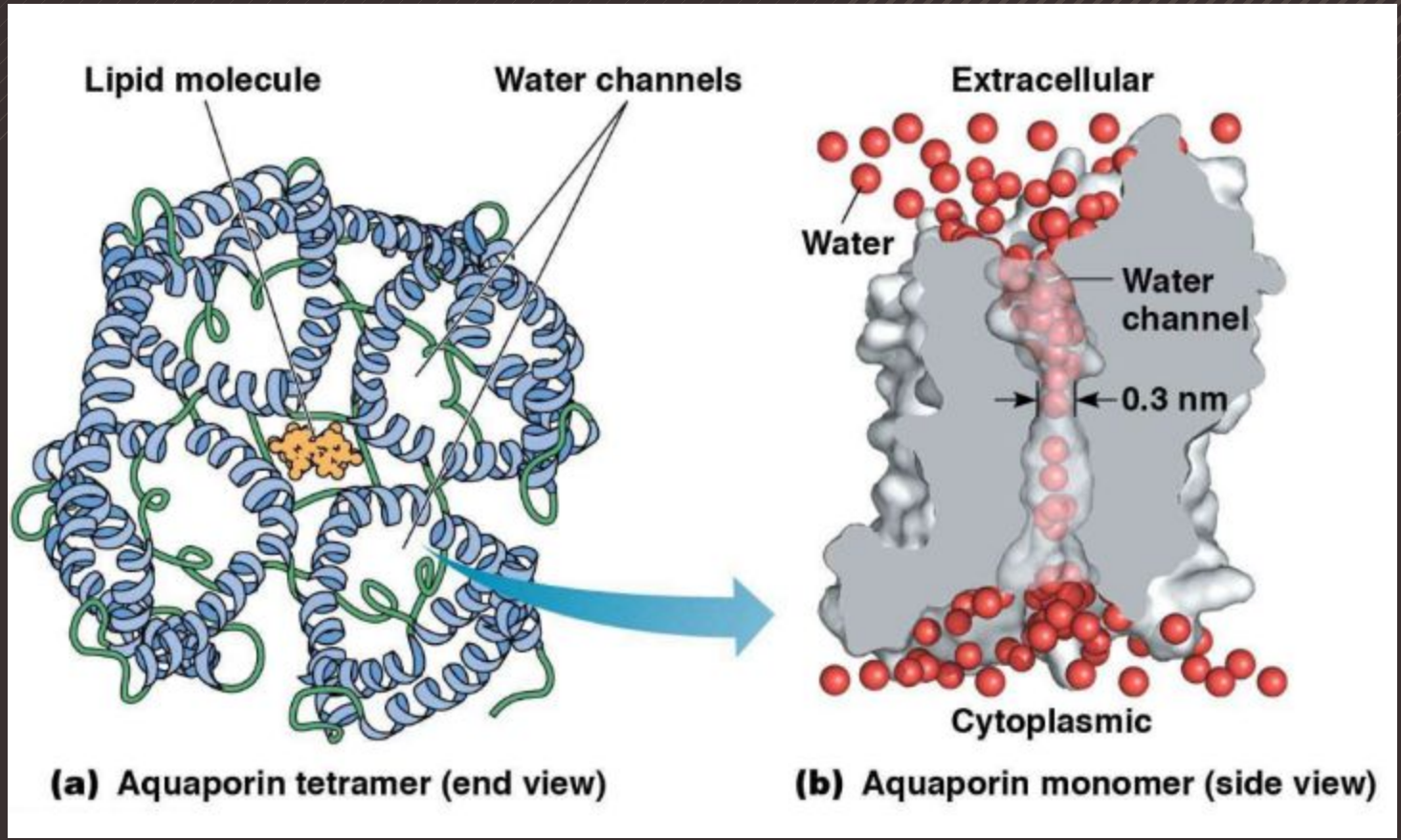

HYPERTONIC SOLUTION
ISOTONIC SOLUTION
HYPOTONIC SOLUTION
H_2O
H_2O
H_2O
H_2O
H_2O
(a)
(b)
Shriveled
Normal
Lysed
ANIMAL CELL
H_2O
H_2O
H_2O
H_2O
H_2O
(c)
(d)
Plasmolyzed
Flaccid
Turgid
PLANT CELL

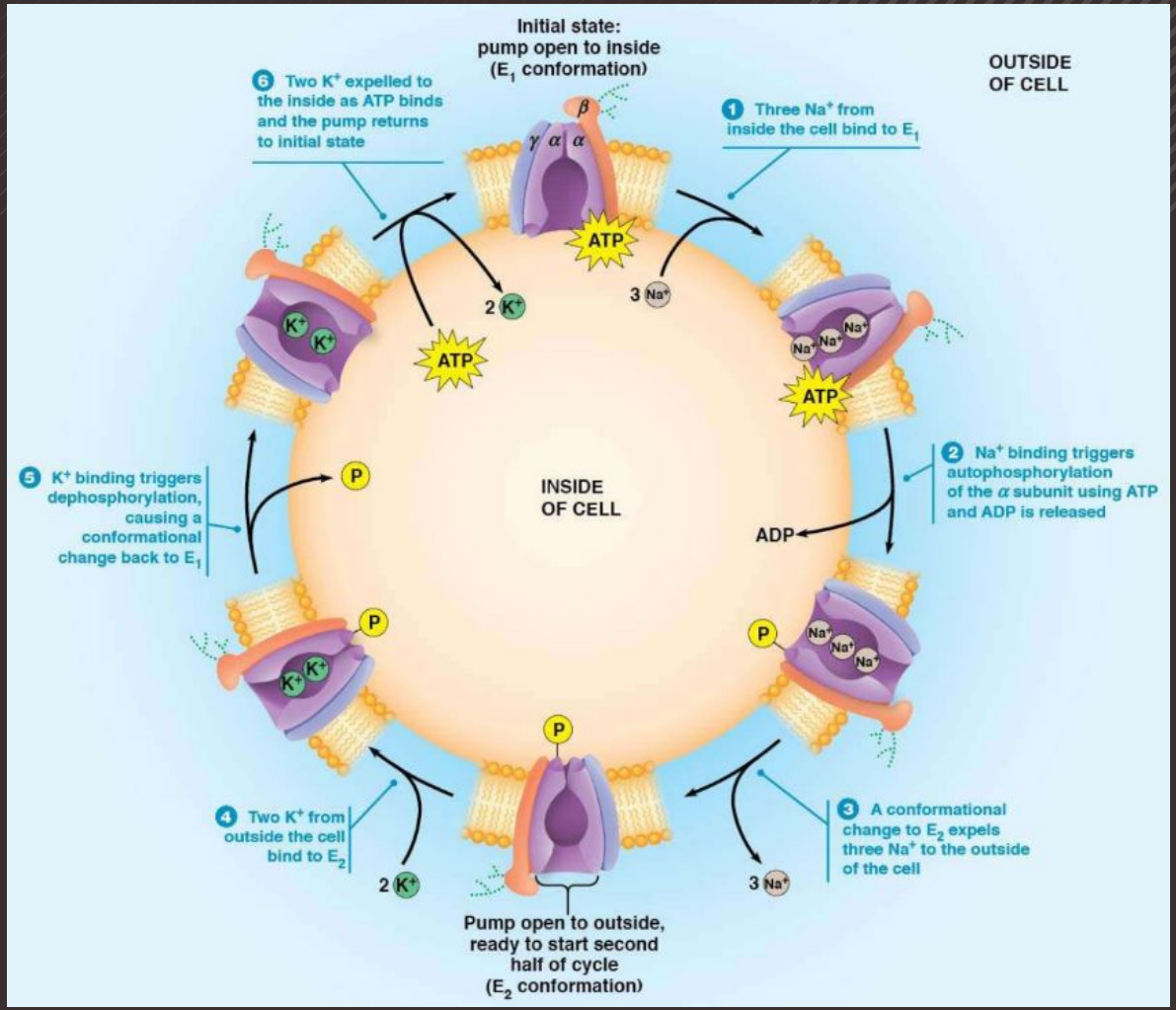


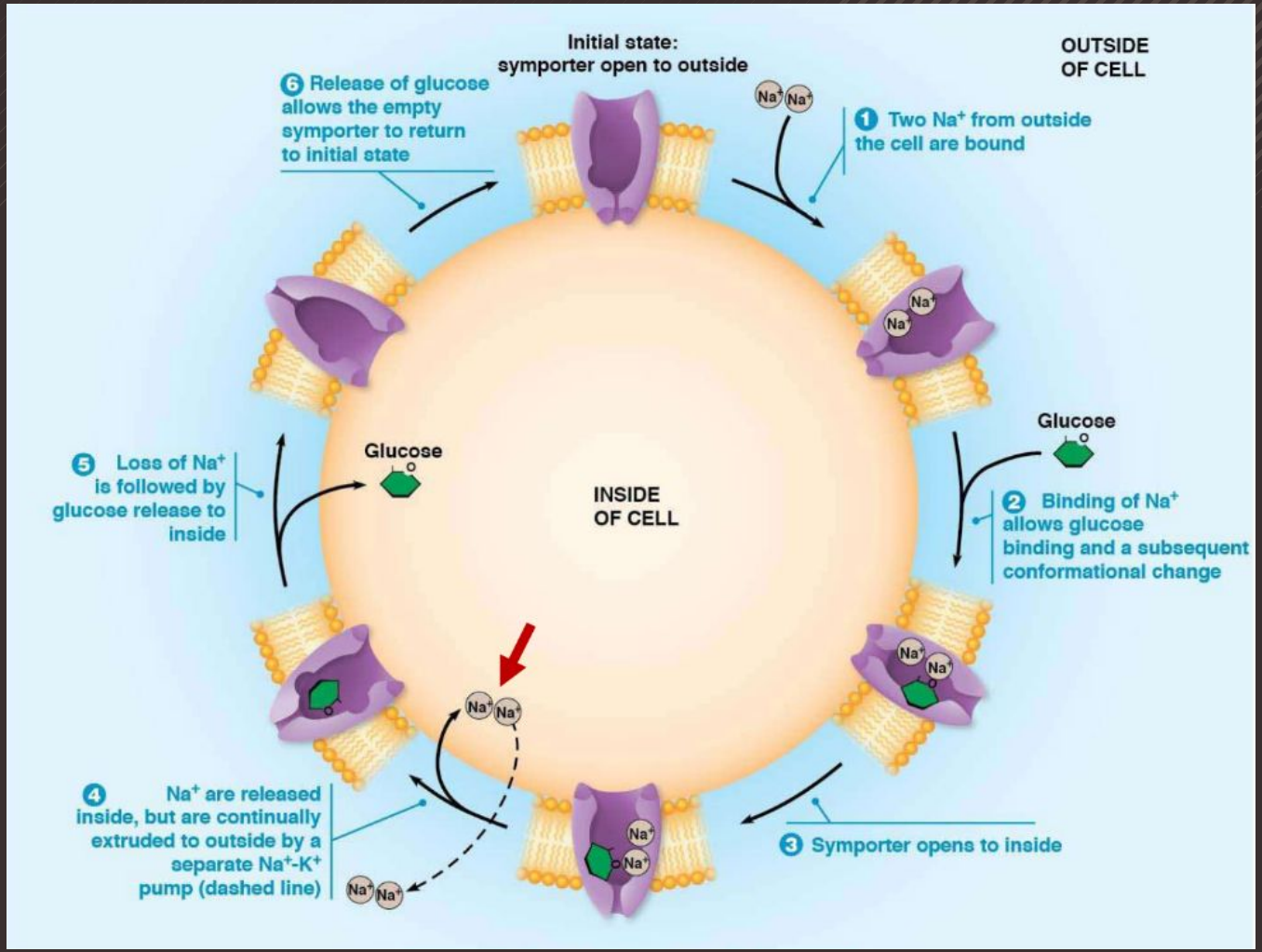
Faciliterad (underlättad) diffusion

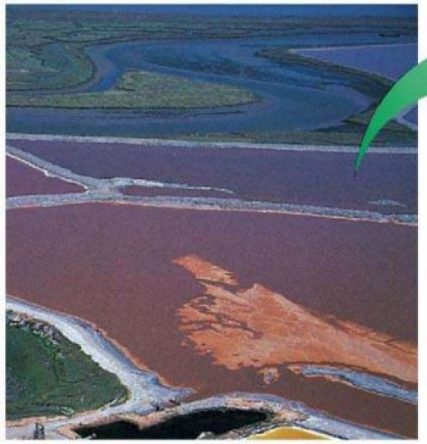



1 Glucose binds to a GLUT1 transporter protein that has its binding site open to the outside of the cell (T_1 conformation).
2 Glucose binding causes the GLUT1 transporter to shift to its T_2 conformation with the binding site open to the inside of the cell.
3 Glucose is released to the interior of the cell, initiating a second conformational change in GLUT1.
4 Loss of bound glucose causes GLUT1 to return to its original (T_1) conformation, ready for a further transport cycle.
Glucose
T_1
Glucose transporter (GLUT1)
T_2
Glucose
OUTSIDE OF CELL
T_1
INSIDE OF CELL

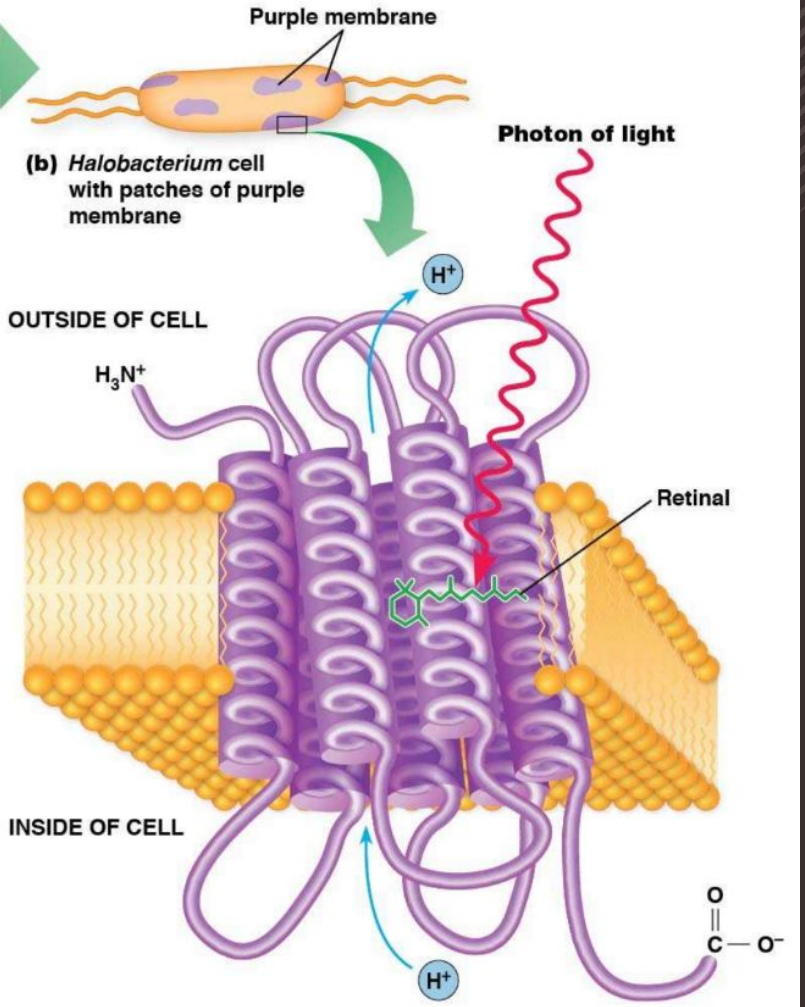

Lipid molecule
Water channels
Extracellular
Water
Water channel
0.3 nm
Cytoplasmic
(a) Aquaporin tetramer (end view)
(b) Aquaporin monomer (side view)

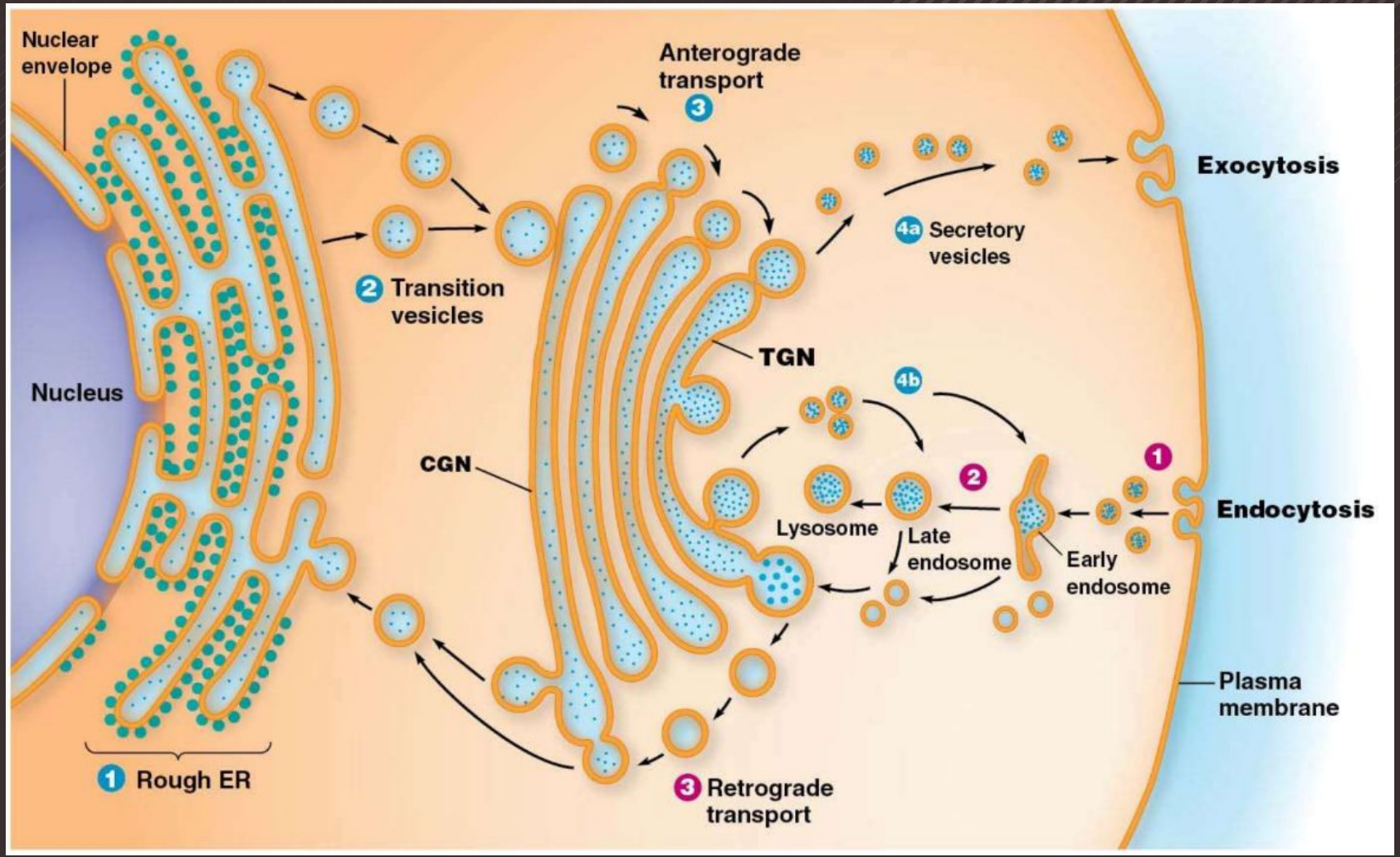

Initial state:
pump open to inside
(E_1 conformation)
OUTSIDE
OF CELL
1 Three Na^+ from inside the cell bind to E_1
2 Na^+ binding triggers autophosphorylation of the α subunit using ATP and ADP is released
3 A conformational change to E_2 expels three Na^+ to the outside of the cell
4 Two K^+ from outside the cell bind to E_2
5 K^+ binding triggers dephosphorylation, causing a conformational change back to E_1
6 Two K^+ expelled to the inside as ATP binds and the pump returns to initial state
INSIDE
OF CELL
ATP
ADP
P
β
γ α α
K^+
Na^+
Pump open to outside,
ready to start second
half of cycle
(E_2 conformation)

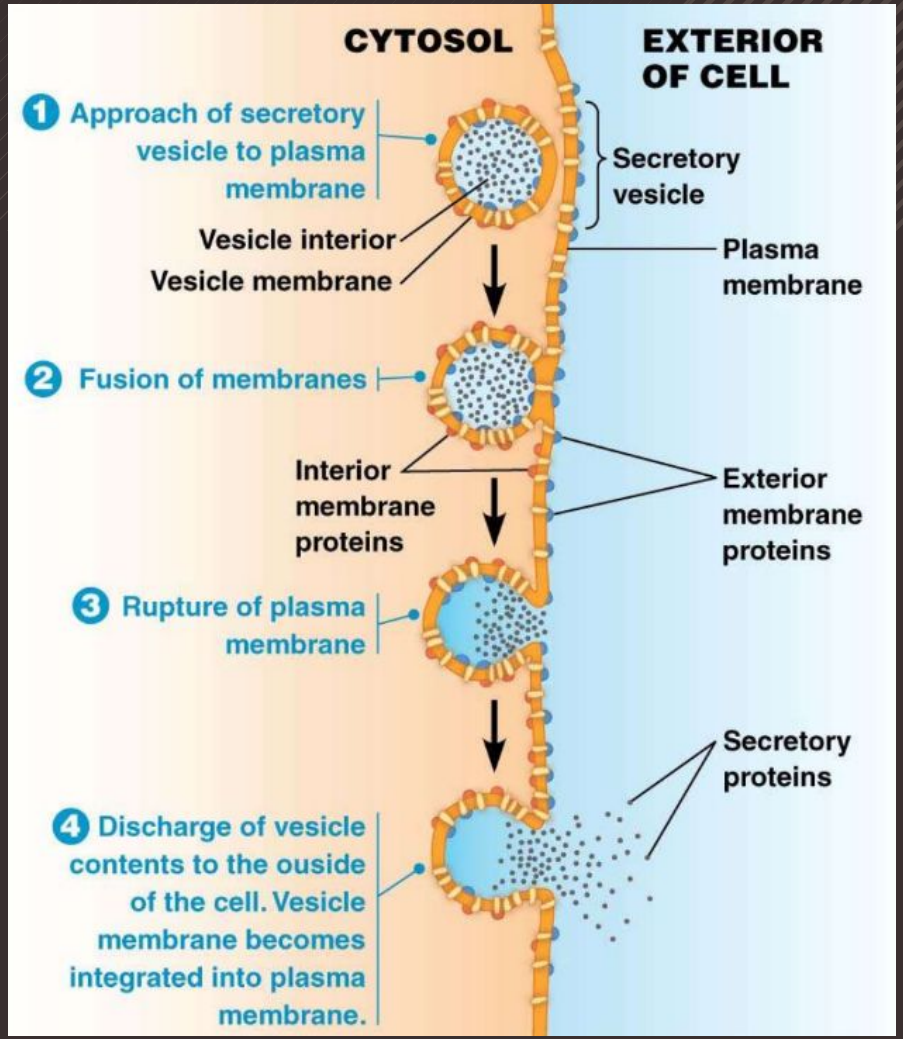

Initial state:
symporter open to outside
OUTSIDE
OF CELL
6 Release of glucose allows the empty symporter to return to initial state
Na+ Na+
1 Two Na+ from outside the cell are bound
Na+
Na+
Glucose
5 Loss of Na+ is followed by glucose release to inside
Glucose
INSIDE
OF CELL
2 Binding of Na+ allows glucose binding and a subsequent conformational change
Na+
Na+
Na+ Na+
4 Na+ are released inside, but are continually extruded to outside by a separate Na+-K+ pump (dashed line)
Na+
Na+
Na+ Na+
3 Symporter opens to inside

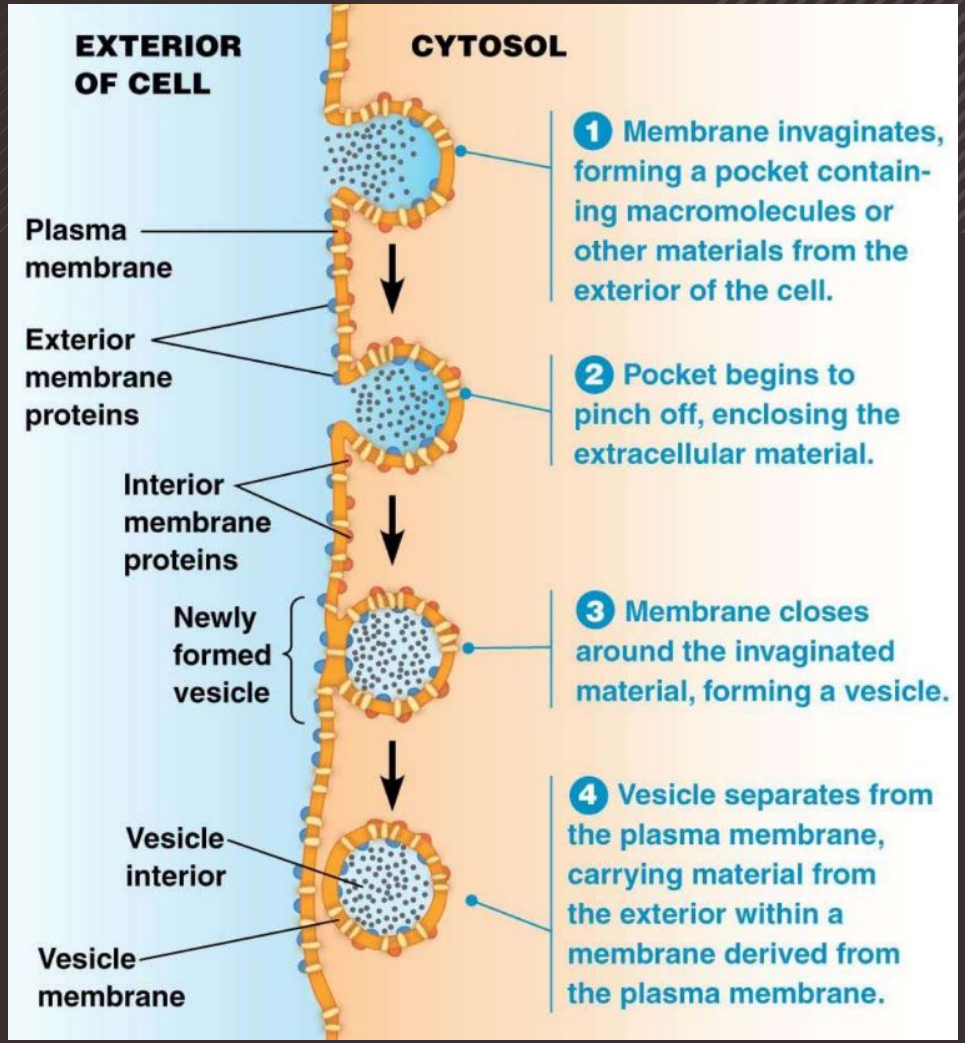


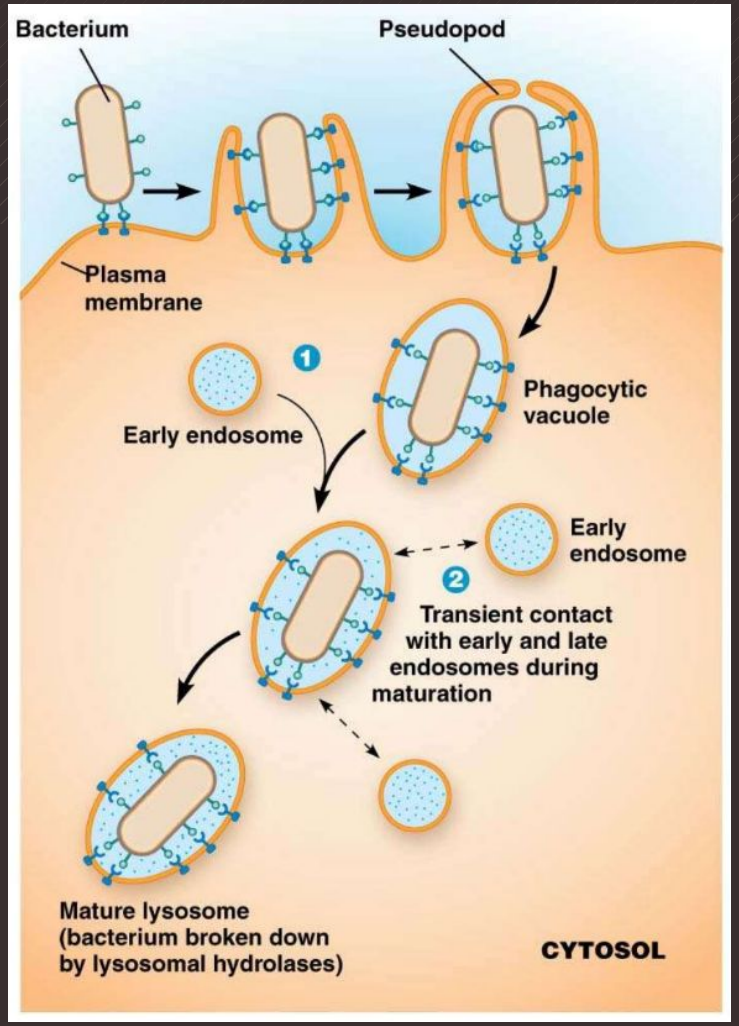
(a) *Halobacterium* (purple color) grows in the high-salt concentration of solar evaporation ponds used for manufacturing salt around San Francisco Bay

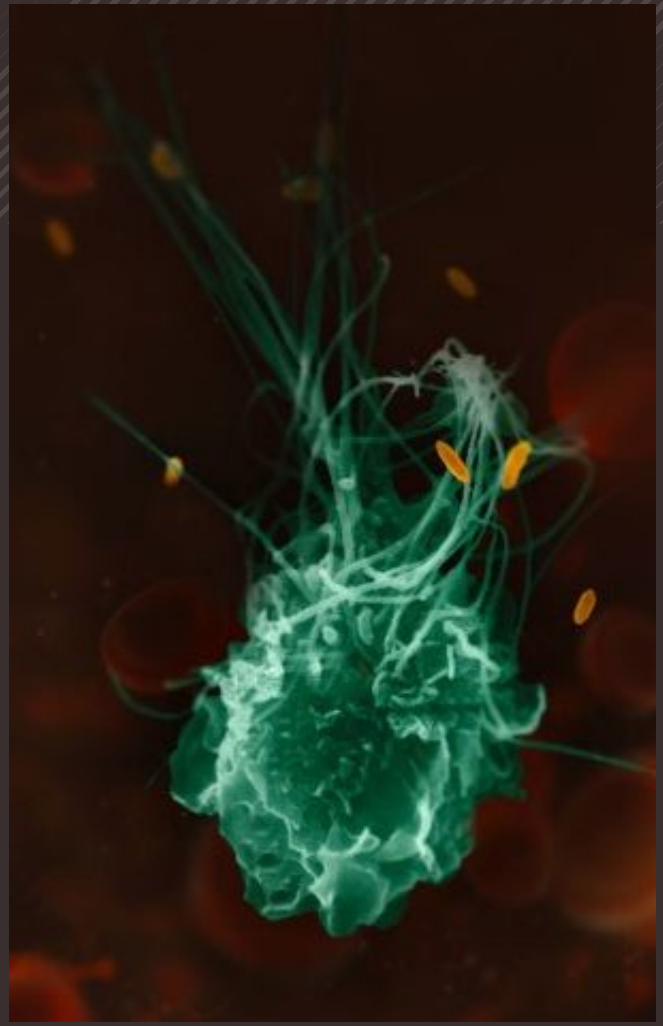



Nuclear envelope
Anterograde transport
3
Exocytosis
4a Secretory vesicles
2 Transition vesicles
TGN
Nucleus
4b
CGN
1
2
Endocytosis
Lysosome
Late endosome
Early endosome
Plasma membrane
1 Rough ER
3 Retrograde transport


CYTOSOL
EXTERIOR OF CELL
1 Approach of secretory vesicle to plasma membrane
Secretory vesicle
Vesicle interior
Vesicle membrane
Plasma membrane
2 Fusion of membranes
Interior membrane proteins
Exterior membrane proteins
3 Rupture of plasma membrane
Secretory proteins
4 Discharge of vesicle contents to the ouside of the cell. Vesicle membrane becomes integrated into plasma membrane.


EXTERIOR OF CELL
CYTOSOL
Plasma membrane
Exterior membrane proteins
Interior membrane proteins
Newly formed vesicle
Vesicle interior
Vesicle membrane
1 Membrane invaginates, forming a pocket containing macromolecules or other materials from the exterior of the cell.
2 Pocket begins to pinch off, enclosing the extracellular material.
3 Membrane closes around the invaginated material, forming a vesicle.
4 Vesicle separates from the plasma membrane, carrying material from the exterior within a membrane derived from the plasma membrane.


Bacterium
Pseudopod
Plasma membrane
1
Early endosome
Phagocytic vacuole
Early endosome
2
Transient contact with early and late endosomes during maturation
Mature lysosome (bacterium broken down by lysosomal hydrolases)
CYTOSOL



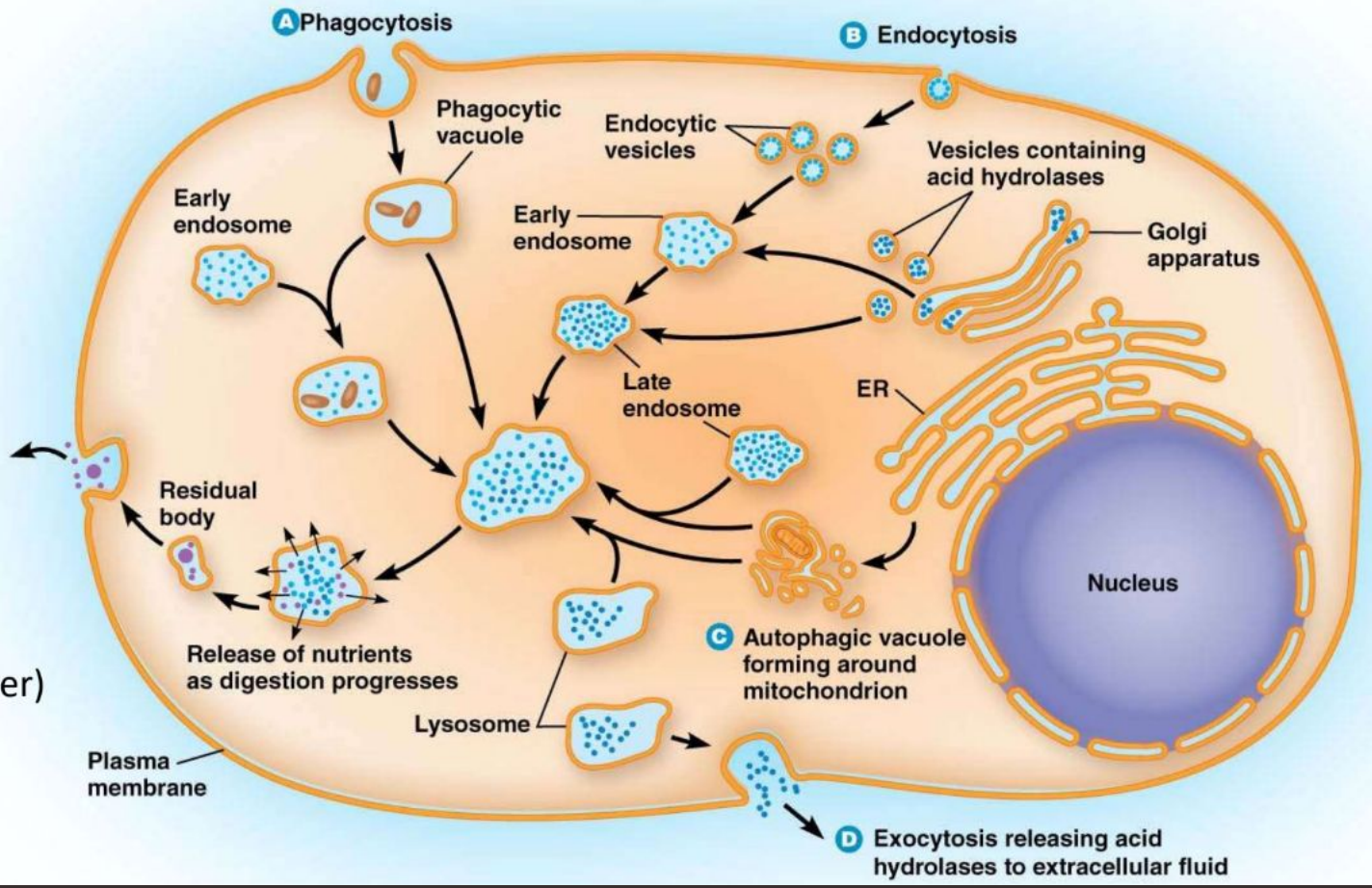
A Fagocytos

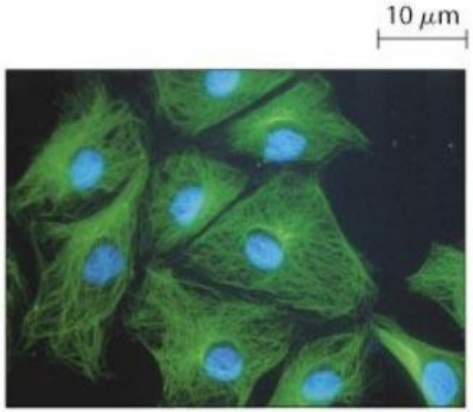
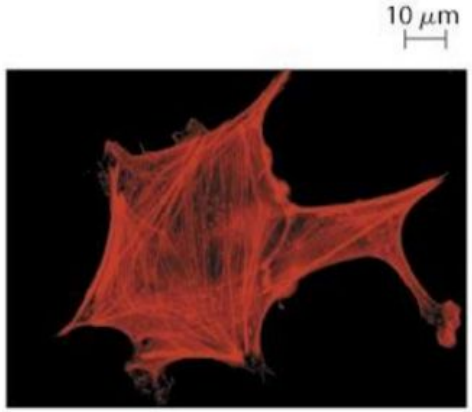
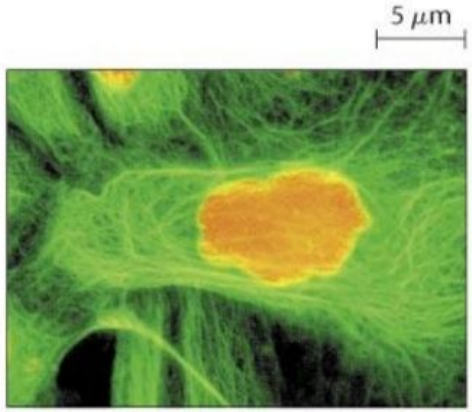
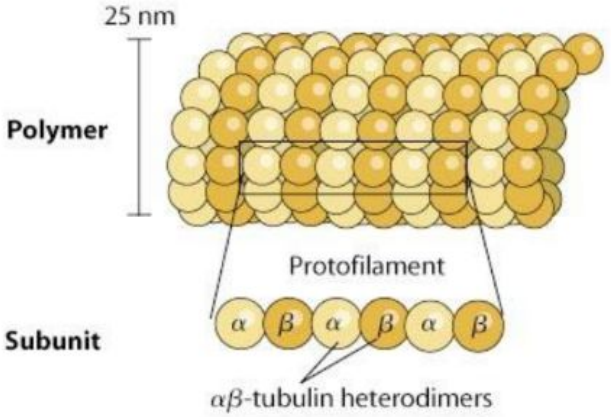
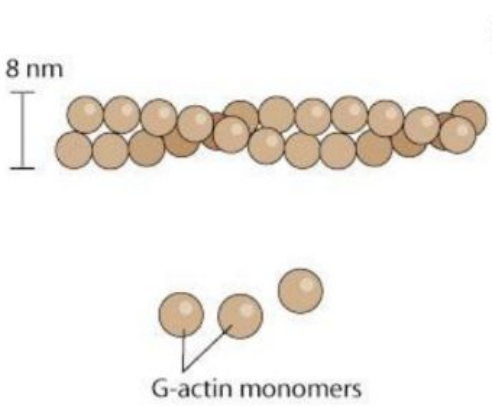
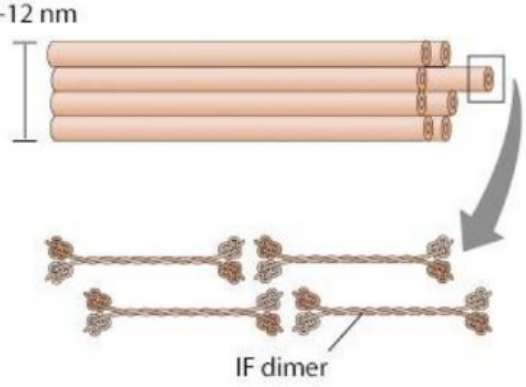
B Endocytos

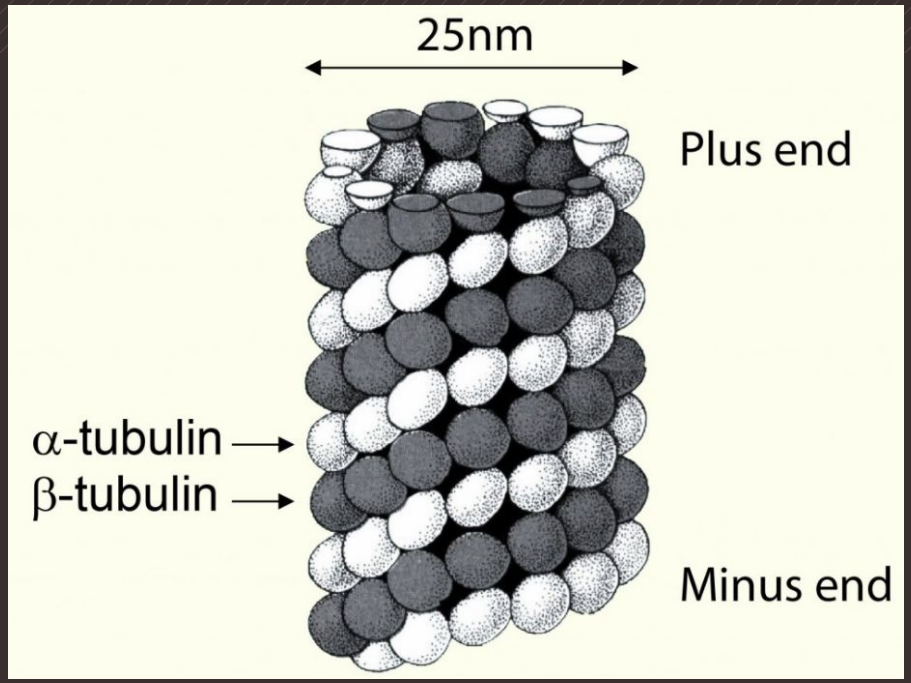
C Autofagi

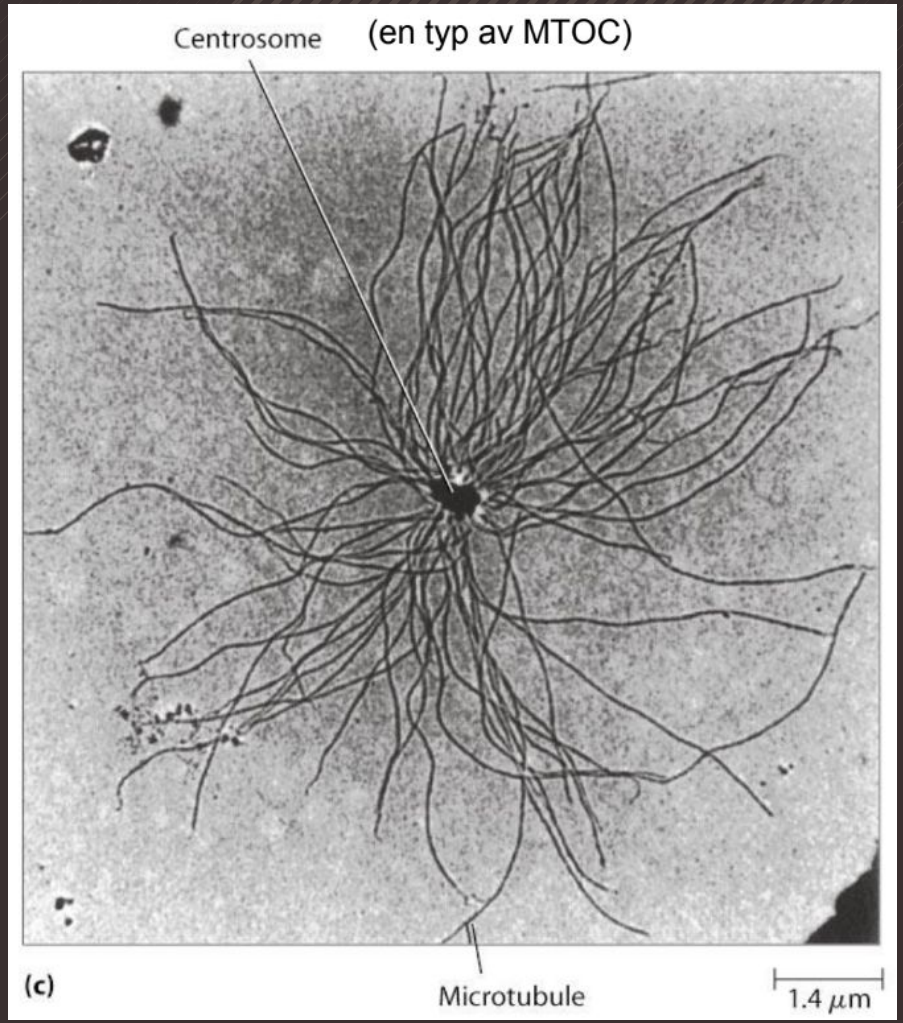
D Exocytos

Lågt pH (aktiva ATPaser) i lysosmen aktiverar sura hydrolaser

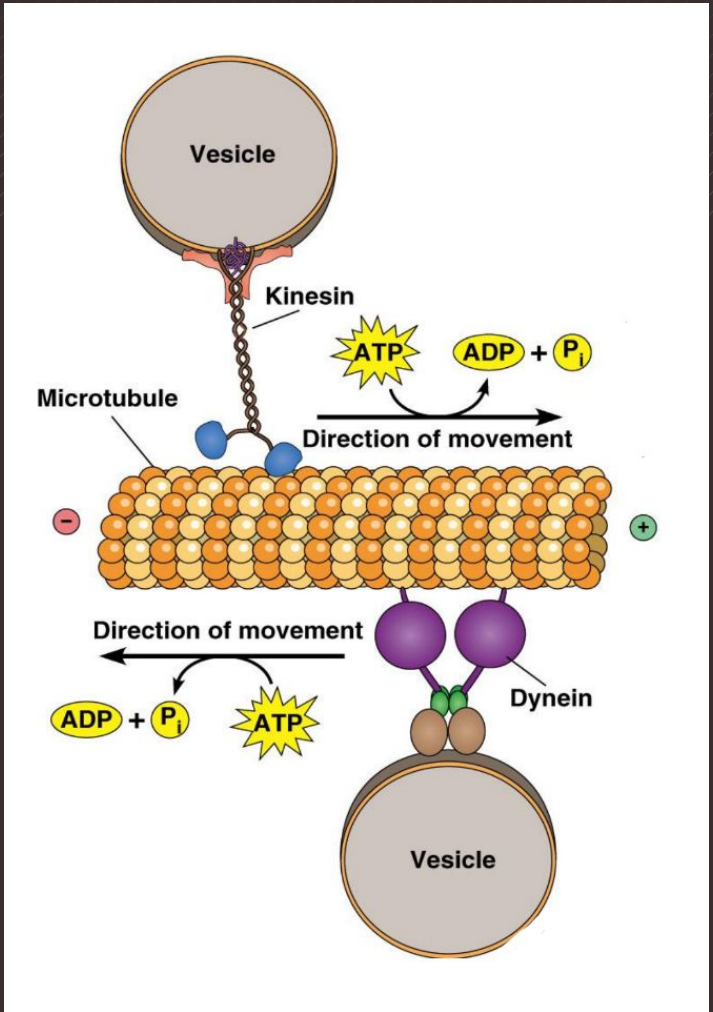


	Microtubules	Microfilaments	Intermediate Filaments
			
			
Structure	Hollow tube with a wall consisting of 13 protofilaments	Two intertwined chains of F-actin	Eight protofilaments joined end to end with staggered overlaps


25nm
Plus end
α-tubulin
β-tubulin
Minus end


Centrosome
(en typ av MTOC)
(c)
Microtubule
1.4 μm

Motorproteiner

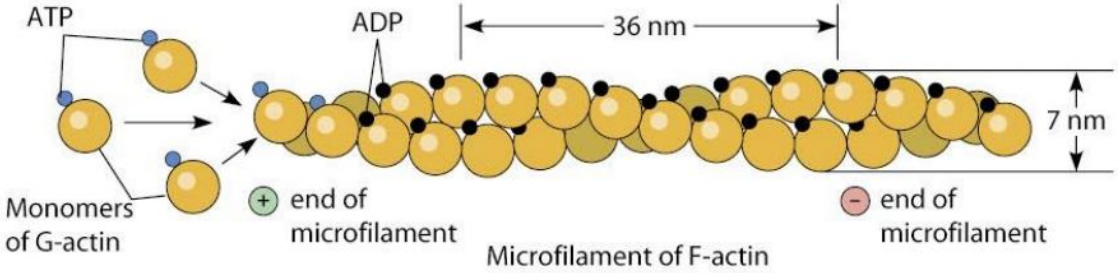


Två familjer motorproteiner:

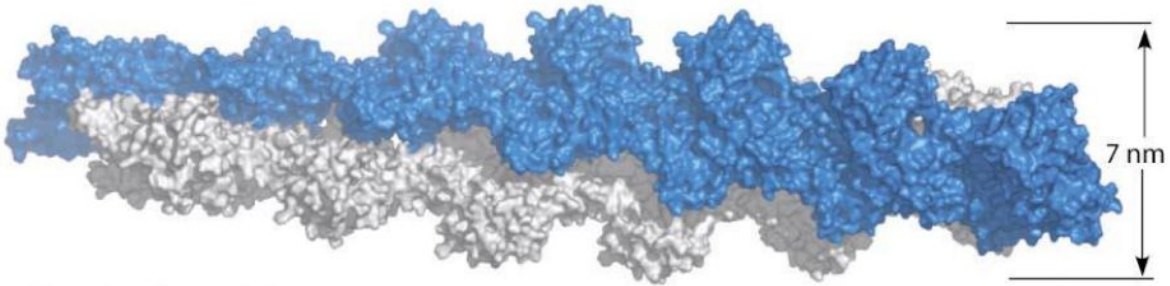
Dynein (Rör sig mot minusänden (oftast in i cellen) av mikrotubulinet)

Kinesin (Rör sig mot plusänden (oftast ut ifrån cellen) av mikrotubulinet)

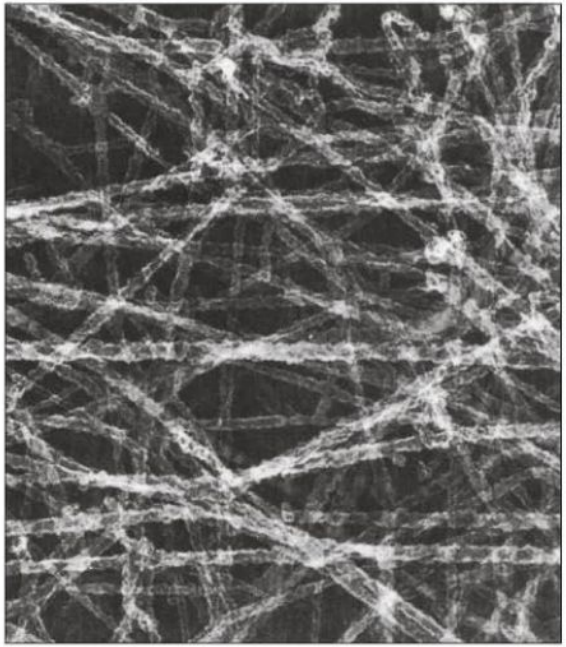
Kinesin protein walking on microtubule



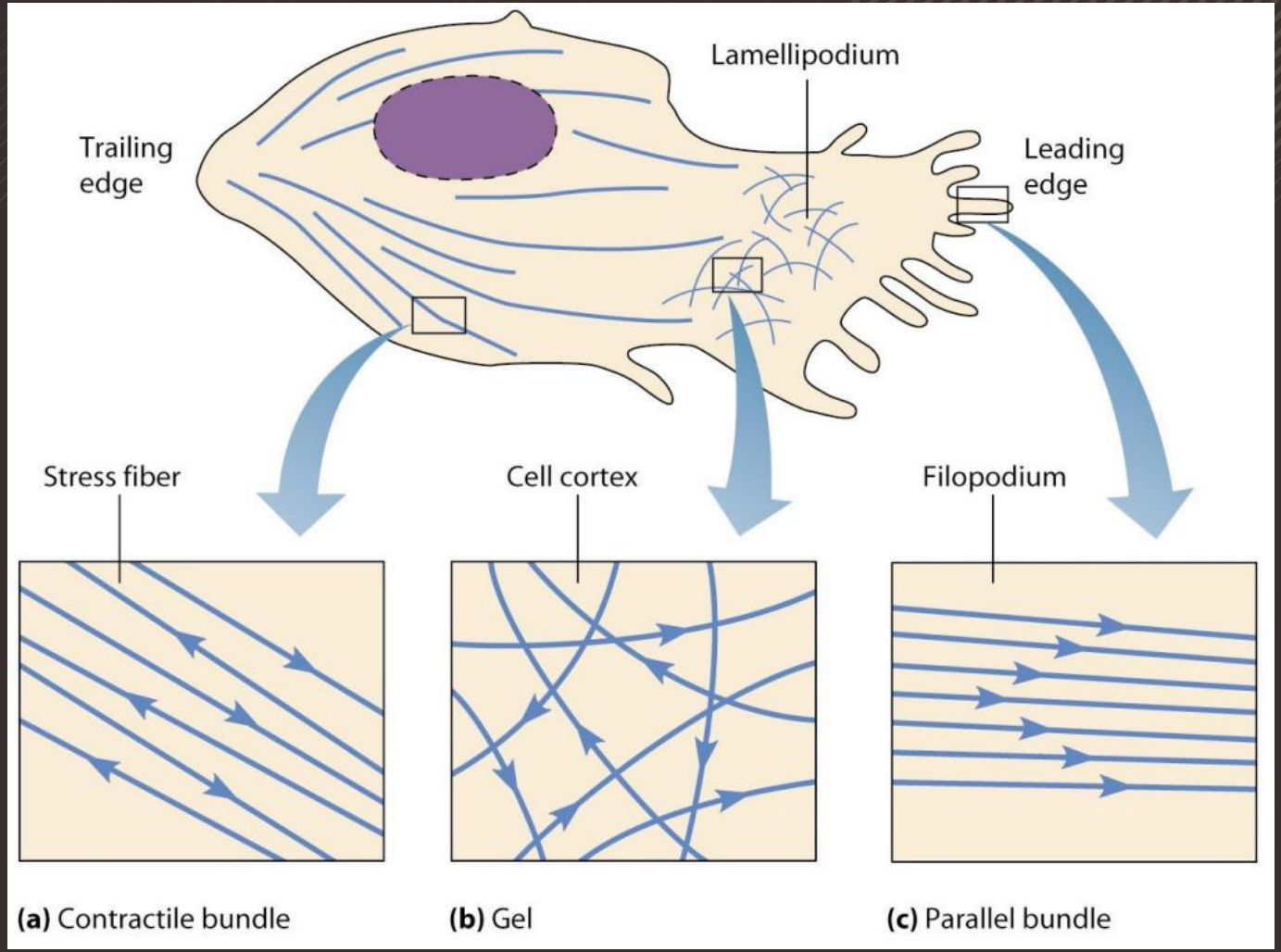
(a) MF assembly

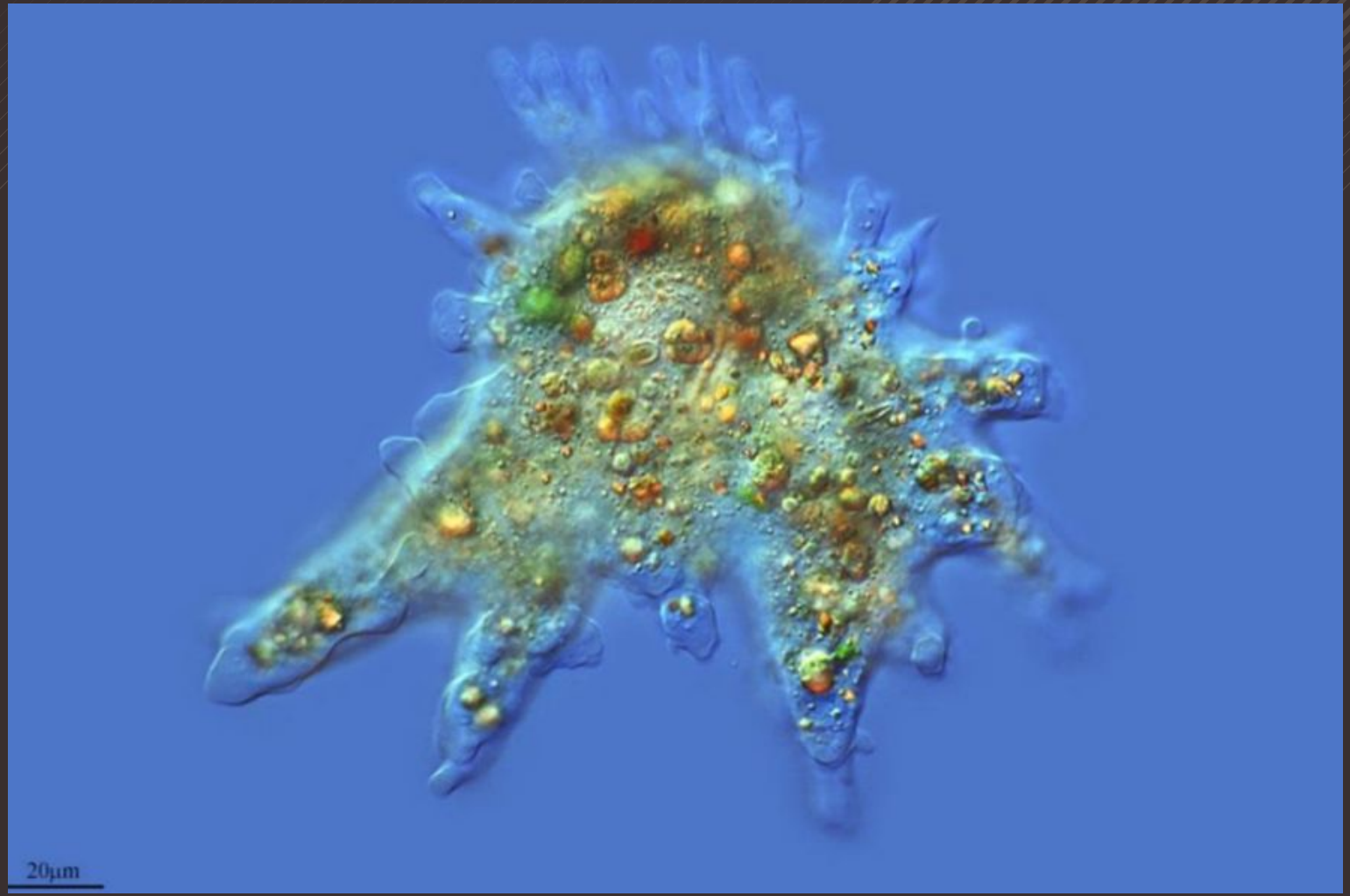


(b) Molecular model



(c) Purified F-actin


Lamellipodium
Trailing edge
Leading edge
Stress fiber
Cell cortex
Filopodium
(a) Contractile bundle
(b) Gel
(c) Parallel bundle


20µm

Property	Intermediate Filaments
Structure	Fibrous proteins supercoiled into thicker cables
Diameter	8–12 nm
Protein subunits	One of several different proteins of the keratin family
Main functions	Maintenance of cell shape Anchorage of nucleus and certain other organelles Formation of nuclear lamina