

Membranes and membrane transport

Marek Vecka

Membranes

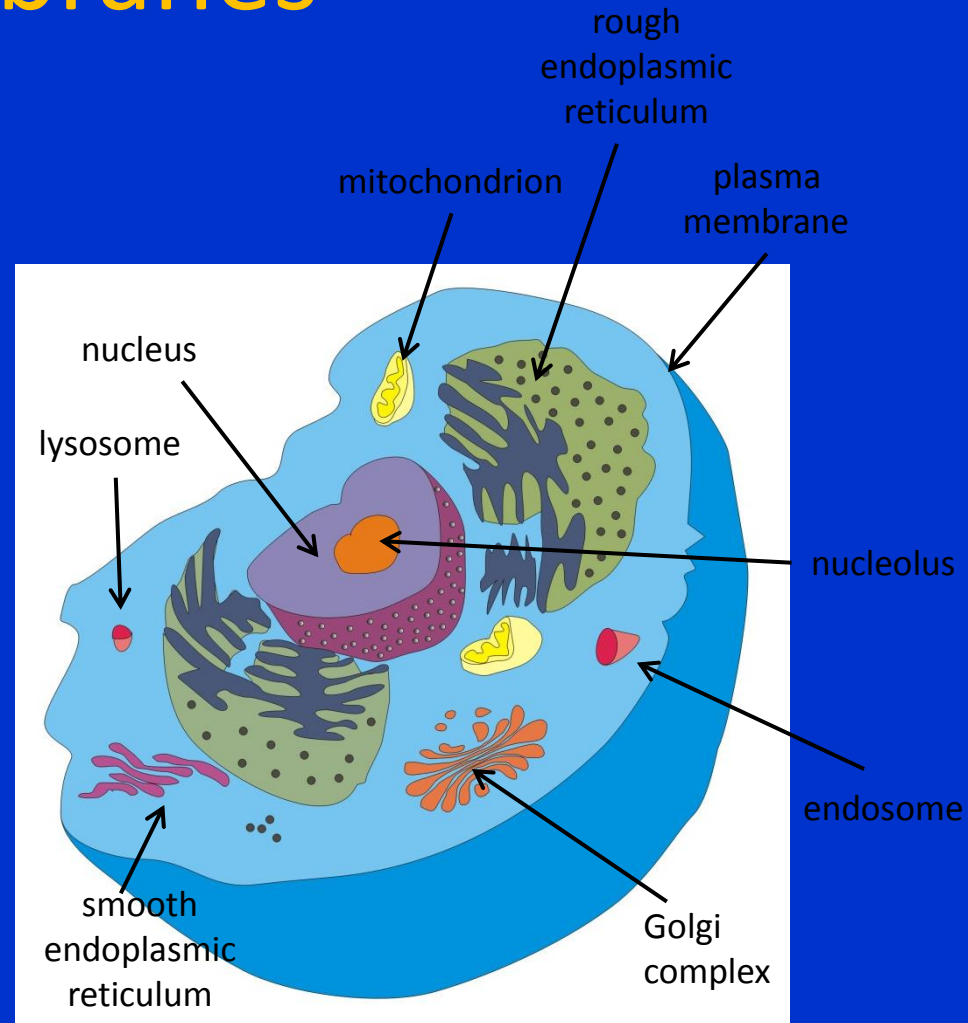
Human body – more than 10 000 mld cells

Surface area of membranes

~ km²

Functions:

- compartmentalization (mt, ER, nucleus...)
- barrier (protection)
- regulation of transport (in and out)
- medium for membrane proteins
 - information transfer
 - enzymatical processes
 - connections to other cells
- cell shape formation
- cytoskeleton anchoring



Compartmentation

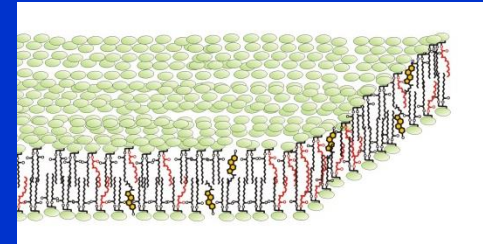
- Intracellular fluid (ICF)
 - 2/3 of total body water
 - 1. production, storage, and consumption of E in the cell
 - 2. environment for cell repair
 - 3. cell replication medium
 - 4. special functions
- Extracellular fluid (ECF)
 - plasma + interstitium
 - 1. mainly transport

compound	ECF	ICF
Na ⁺	140 mmol/l	10 mmol/l
K ⁺	4 mmol/l	140 mmol/l
free Ca ²⁺	2.5 mmol/l	0.1 mmol/l
Cl ⁻	100 mmol/l	4 mmol/l
HCO ₃ ⁻	27 mmol/l	10 mmol/l
PO ₄ ³⁻	2 mmol/l	60 mmol/l
glucose	5.5 mmol/l	up to 1 mmol/l

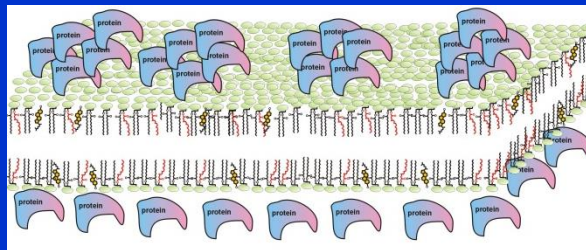
Structure of membranes I

- membranes contain lipids:

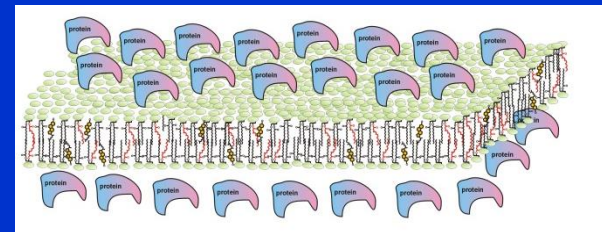
1925: Gortel and Grendel



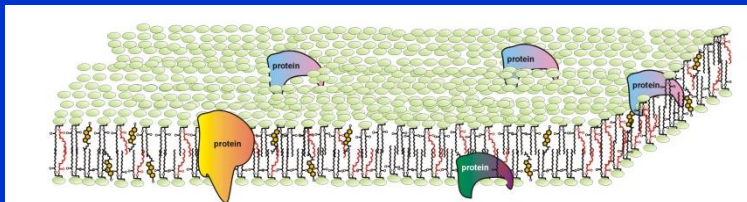
- and proteins: 1935: Danielli and Dawson



1966: Robertson

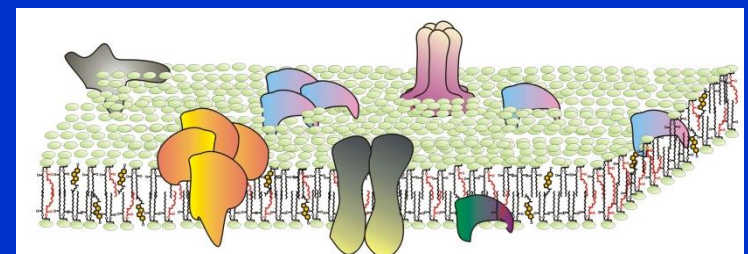


- are fluid: 1972: Singer and Nicolson

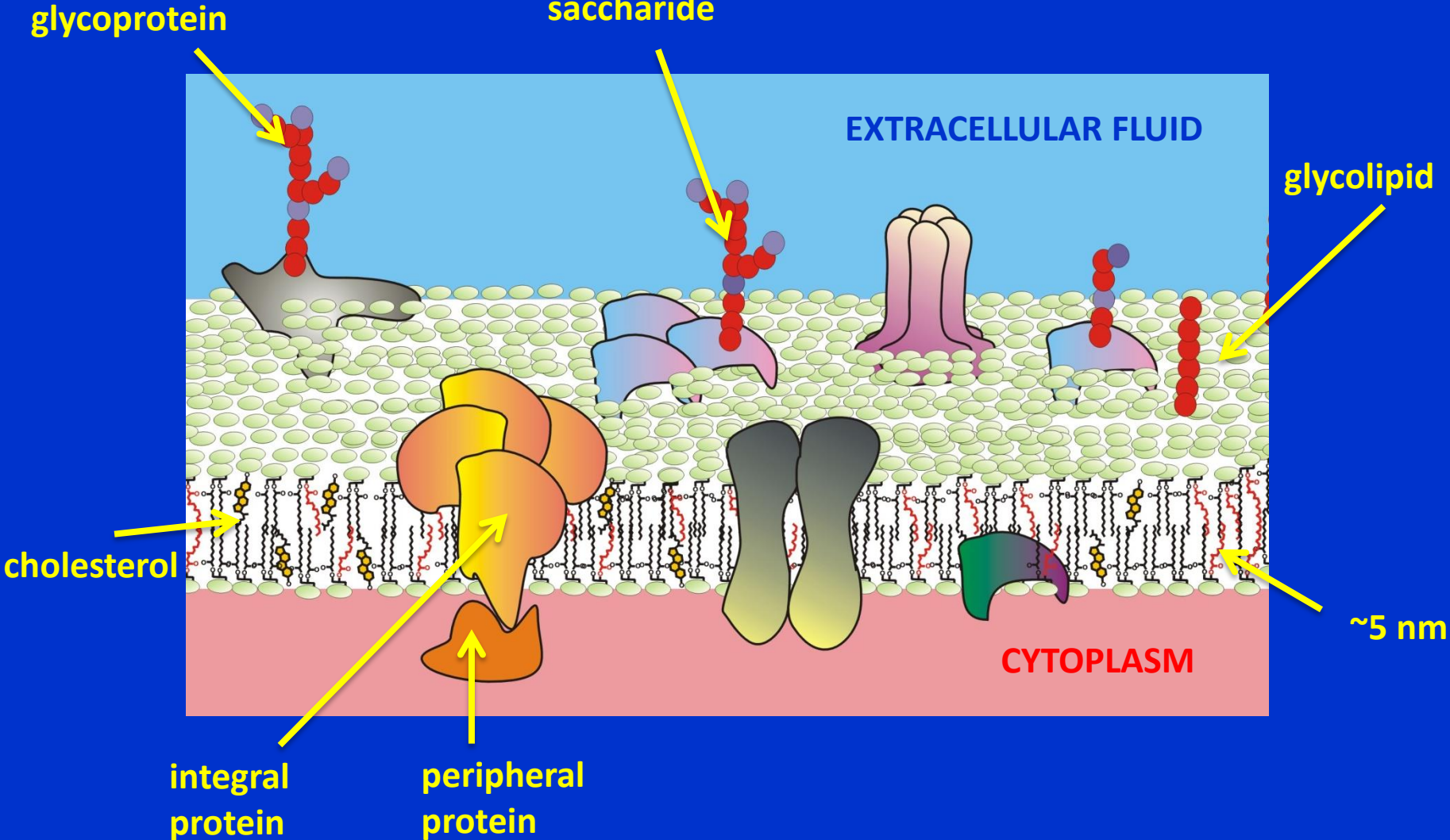


mosaical:

2005: Engelman



Structure of membranes II



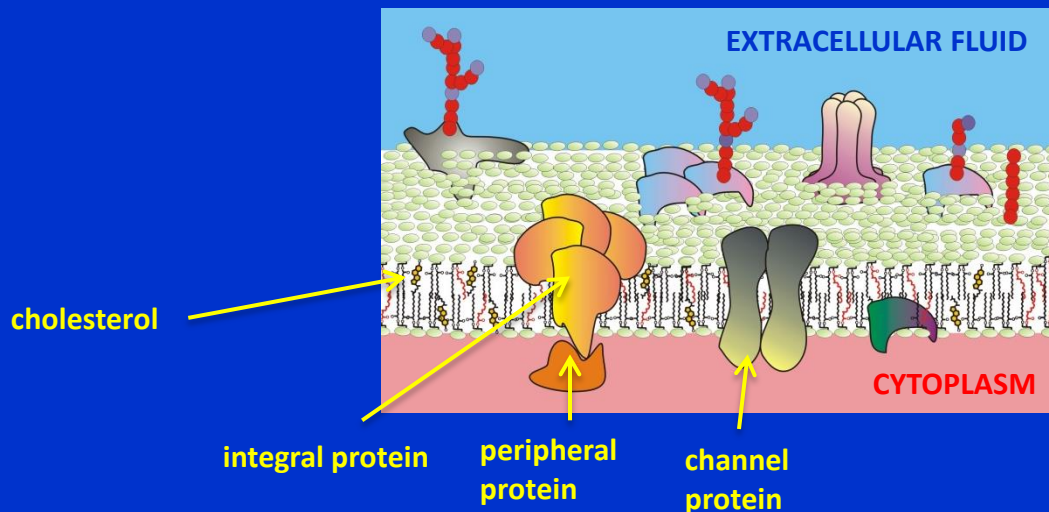
Membrane component function

Lipids

- amphipathic molecules – formation of membrane structure
- cholesterol – keeps membrane fluidity (T, composition)
- DPG (CL) – in mt important for H⁺ gradient transfer

Proteins

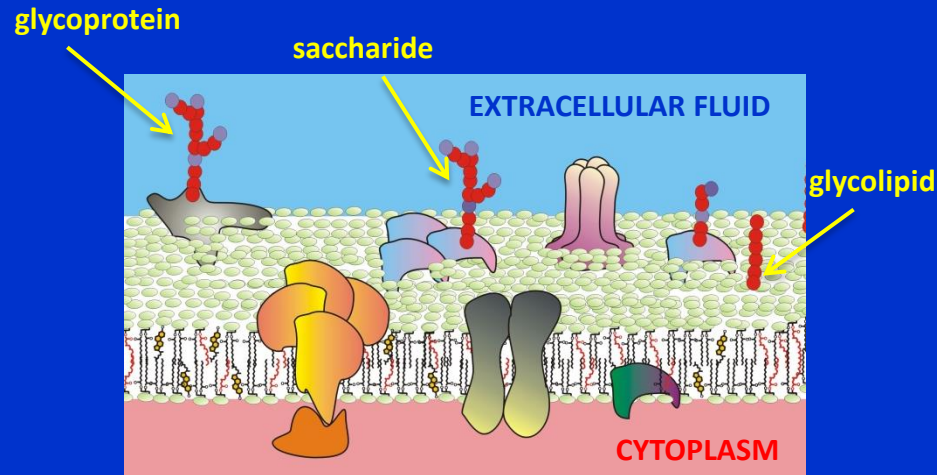
- integral proteins – enzymes, pumps (active transport)
- peripheral proteins - glycoproteins – chemical receptors
- channel proteins – transfer molecules across membranes



Membrane component function

Saccharides

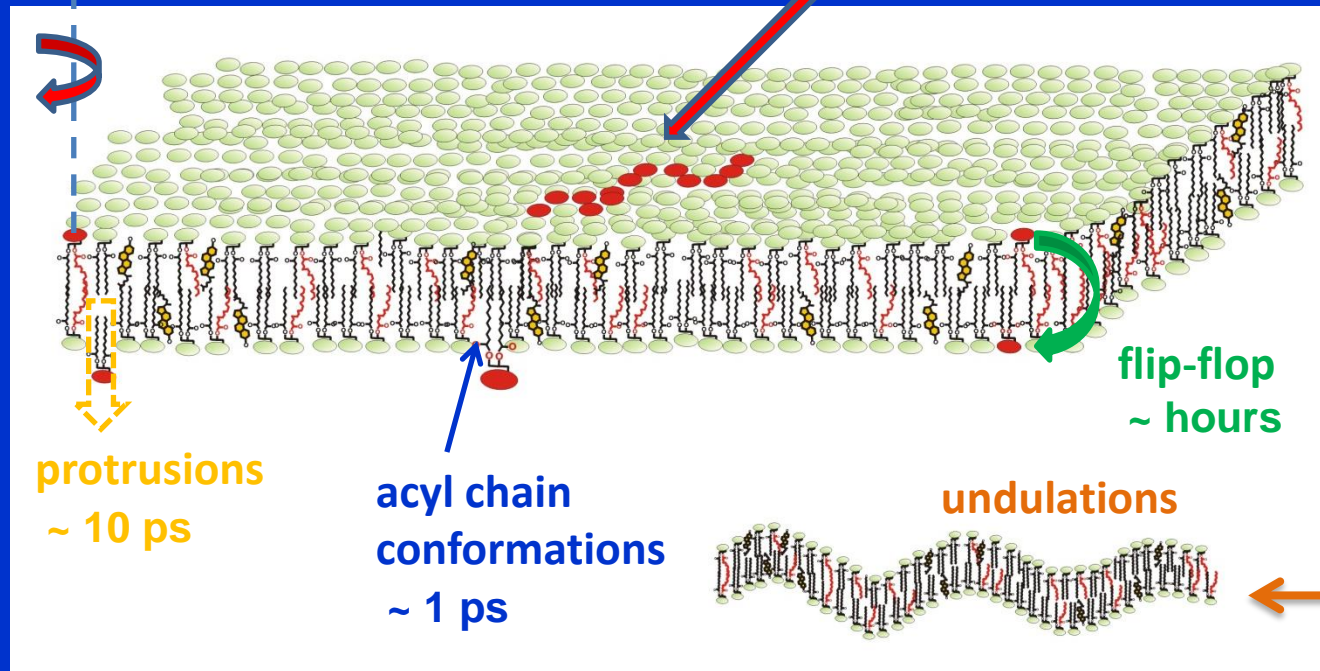
- structural parts of glycolipids or glycoproteins
- saccharide moiety always oriented exofacially



Membrane structure – lipids

rotational
diffusion
~ 1 ns

lateral diffusion
~ 10 ns



flip-flop
~ hours

protrusions
~ 10 ps

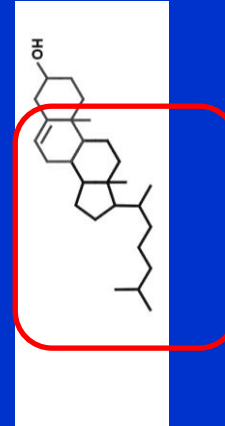
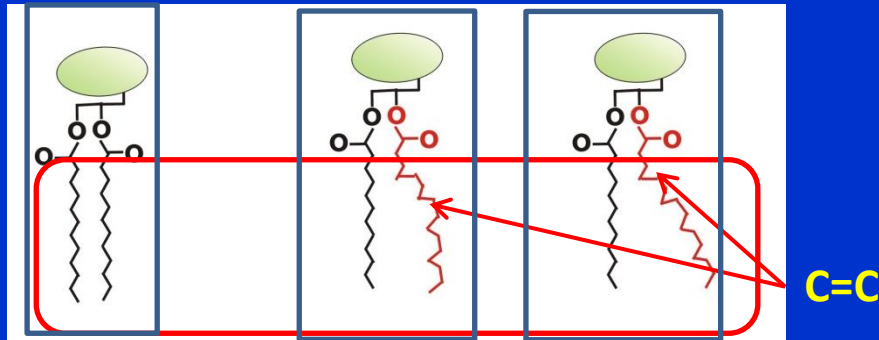
acyl chain
conformations
~ 1 ps

undulations

composition
specific

Lipid structure of biological membranes

- nonpolar part: fatty acid/sterane skeletons



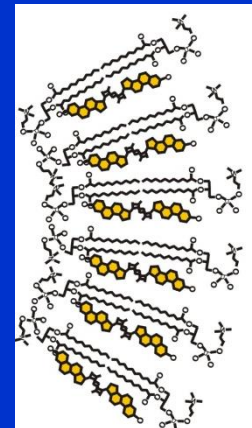
- polar part: phosphate/bases(saccharides) sphingosine/base (saccharide)

glycerolipids

glycerophospholipids

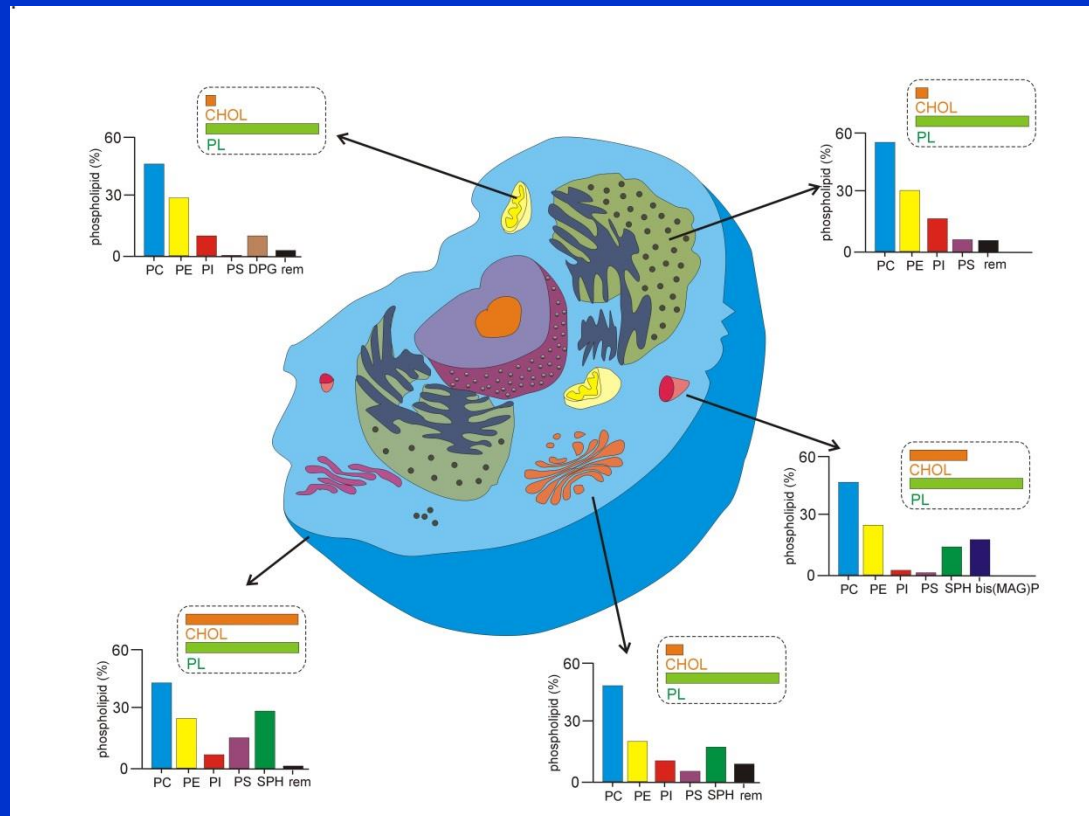
sphingolipids

sterol lipids



Membrane composition - lipids

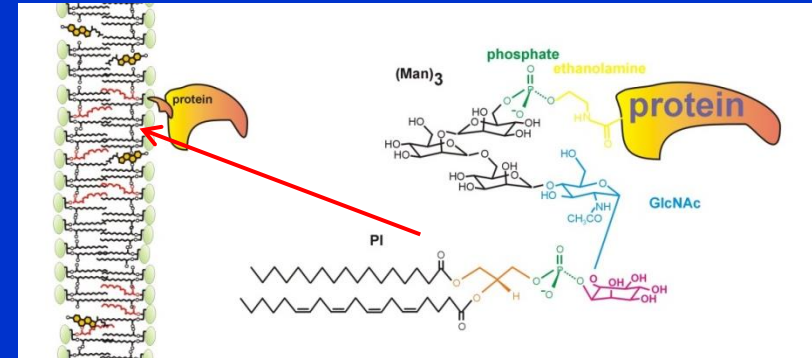
- membrane lipid composition of individual membranes of subcellular structures is different



Lipid – protein bonds

A. GPI-anchored proteins – on outer face bonded via short oligosaccharide to glycosphosphatidylinositol (GPI)

various receptors
enzymes
adhesive proteins



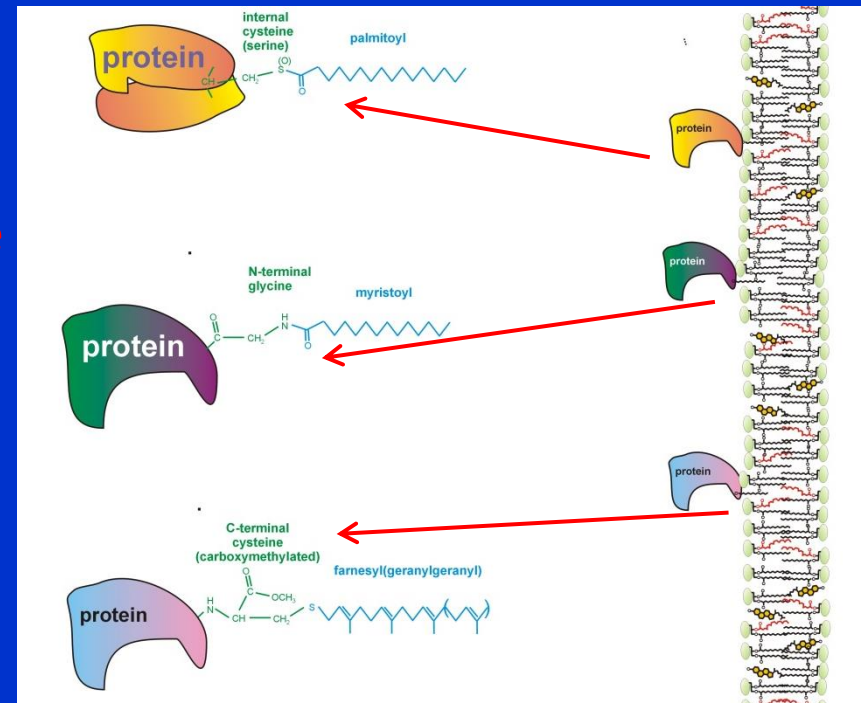
B. other anchoring: on cytoplasmatic face bonded via long hydrocarbon chain

proteins Src & Ras

- normal to malignant transformation

G γ subunits, rhodopsin kinase

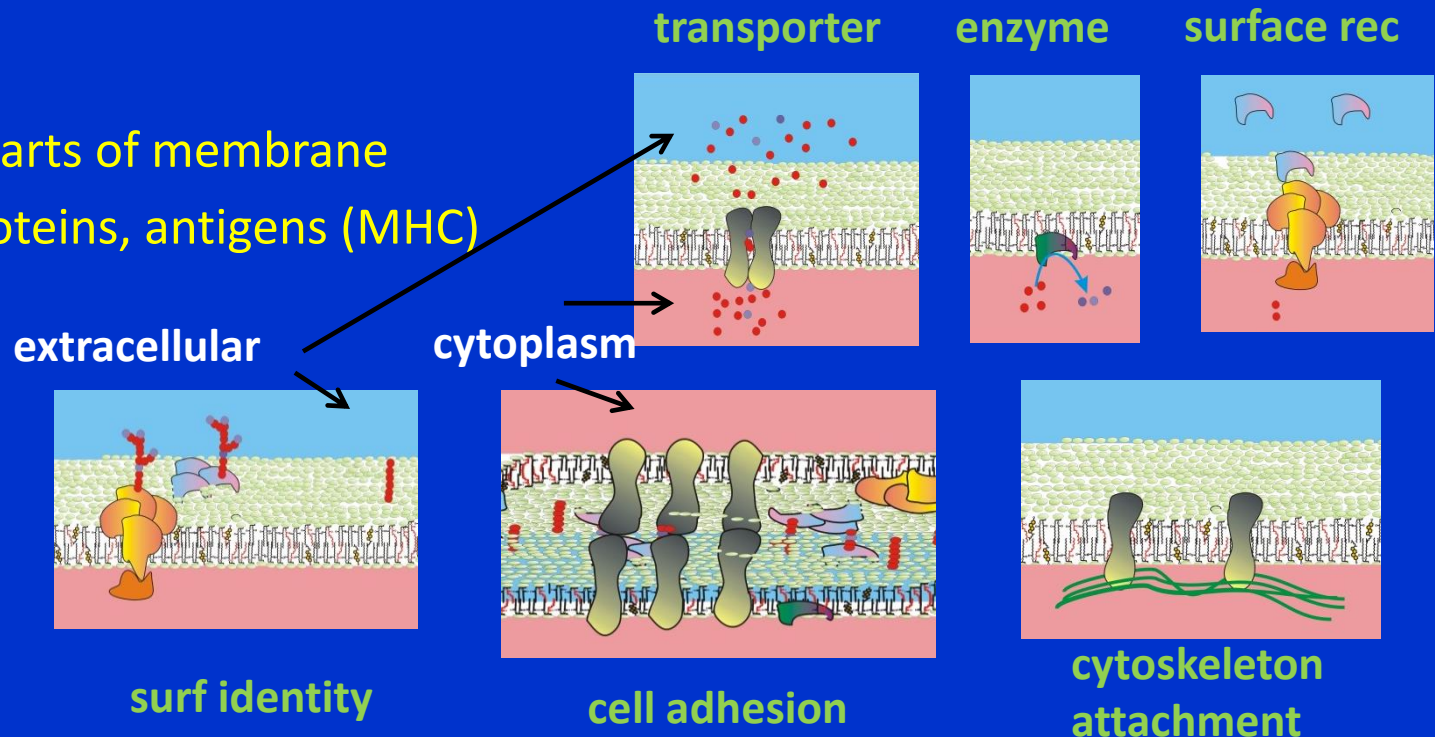
centromeric proteins, nuclear lamins



Membrane proteins

5539 human genes encode membrane proteins, which is approximately 26 % of human protein encoding genes) (Fagerberg 2010)

- receptor dependent channels/transporting molecules
- receptors
- enzymes
- structural parts of membrane
- bonding proteins, antigens (MHC)



Membrane composition - proteins

- protein composition of individual membranes of subcellular structures is different
- protein/lipid ratios also variable: plasma membranes of hepatocyte (0.85), erythrocyte (1.1), myeline (0.23), mitochondrial membranes – inner (3.2) and outer (1.1)
- some typical proteins can be used as markers of isolated membranes

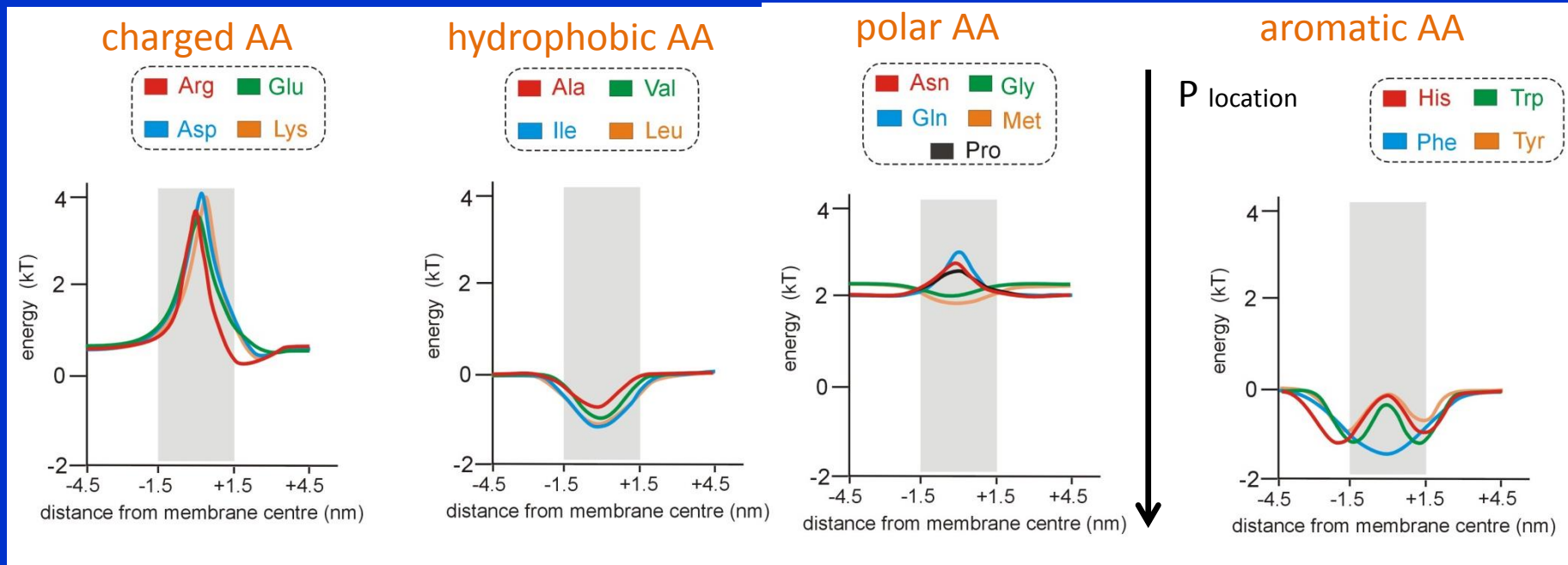
structure	protein (enzyme)
plasma membrane	adenylyl cyclase, Na ⁺ /K ⁺ ATPase
endoplasmatic reticulum	glucose-6-phosphatase
Golgi apparatus	
<i>cis</i>	GlcNAc transferase I
<i>medium</i>	Golgi mannosidase II
<i>trans</i>	galactosyl transferase
mitochondrial membrane (inner)	ATPase

Protein structure of biological membranes

hydrophobic AA - prefer inner membrane space

hydrophilic AA – prefer outer membrane space

low probability of AA location



high probability of AA location

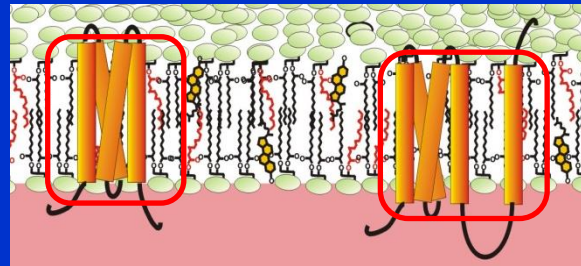
Protein structure of biological membranes

α -helix

minimalization of hydrophilicity of peptide bonds



transmembrane
part of protein
(~20 AA)

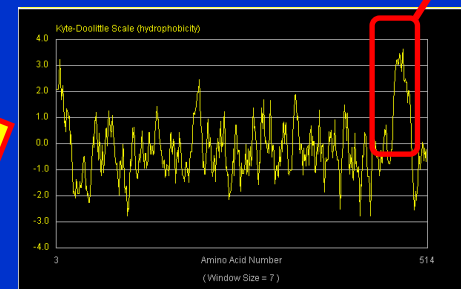


hydropathic index

calculations for consecutive
sequences of 20 AA in peptide

```
1 MLSTLALAVSPLGNEFPQHTTGDWKRVPHEYNICPTACKNSHGTOGRVELT  
91 MPKQLTHQVEGRMCHALVMTTGDPRWYGNVYTHSHHEPTDCLLAKSYKQDVS  
121 FNPGFPPQSCYQVTDAAEAVTVYTHSKVDEYTGWDVDFGRCCKGGICETVHNS  
181 TKWFTSDGSEVCSQFLVGGVFFSCGSEETSMGLPETGRSNVFPYSEGCAMPFC  
241 RWQDVKLKLHFGMMPDLDKTRDLPHAKDCLSSSTPFSHATDLSLQVGRLE  
301 VALQNTWKESEGPFTPVLSYLPNPGVGPVFTINGSLHYFTSKYLRVLESPV  
361 PRMEKAVAGTRVRLVQDQVFFFEVEIGPNDLAKTKQDQKFFLHIGTGEVDSQMR  
421 VAVHVPHEAGTFLAKDQDTEALYIGDTGVKMPHELVGQVPSQVRSMLQVLAH  
481 GFVLMFLKLGVLSSLFRPRRPTKSDVEMAHFR
```

hydrophobic region =
transmembrane domain



Membrane proteins

Integral proteins

majority of membrane proteins
strong interactions with membrane PL – detergent
globular and amphiphatic

two hydrophilic ends with hydrophobic part
inserted into or span through membrane
can span membrane once or more times
(= transmembrane proteins)

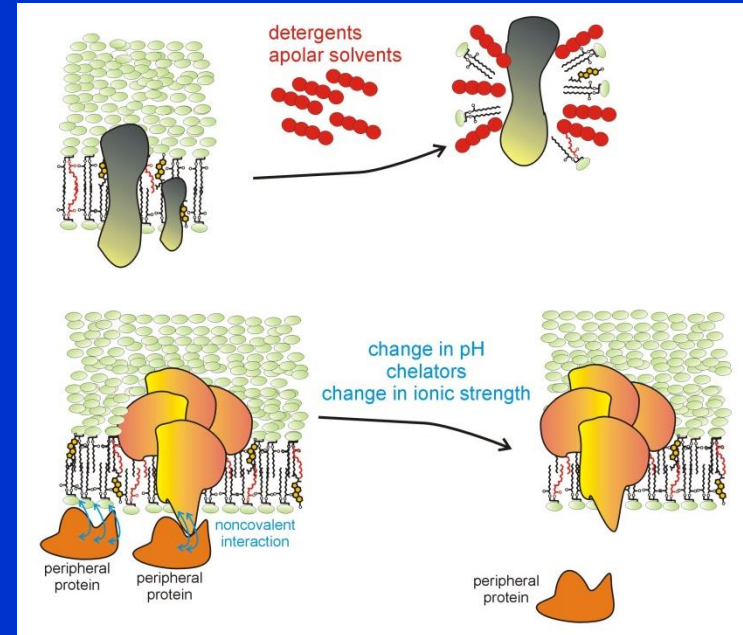
transporters, ion channels, receptors, G-proteins...

Peripheral proteins

no direct interactions with membrane PL
– salts with ionic strength
interactions with hydrophilic parts of integral proteins
spectrin, ankyrine....

Lipid anchored proteins

bound to lipid bilayer via lipid-modified amino acids



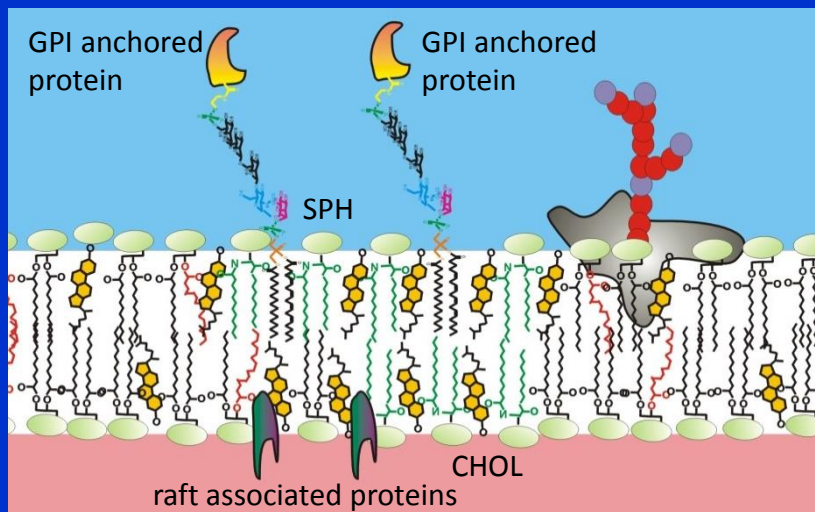
Membrane structures – lipid rafts

1973 membranes are not homogeneous – in ery there are regions that are resistant to detergents

1980 membrane lipids have assymetric distribution

1994 GPI-proteins in CH/SPH rich membrane regions

2006 Pike: Membrane rafts = small (10–200 nm), heterogeneous, dynamic domains rich on CH and SPH, which are able to compartmentalize cellular processes



Membrane structures – caveolae

Caveolae = main type of membrane rafts

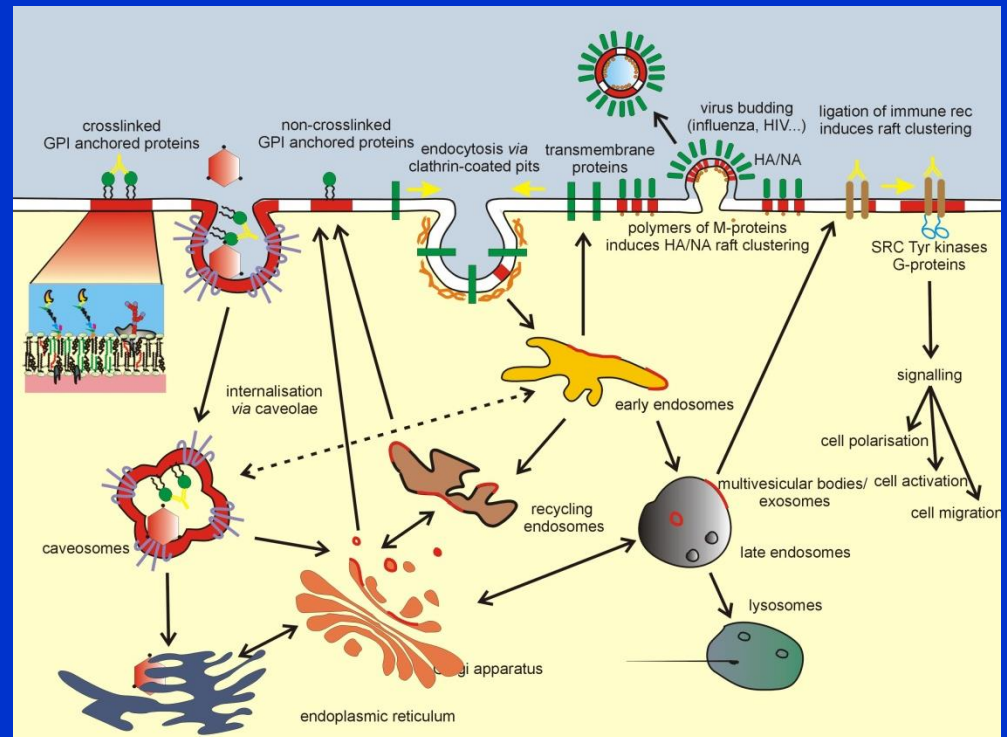
invaginations of cellular membranes containing caveolin

Caveolins

three isoforms of caveolin – 1,-2,-3

protein is palmitoylated

causes raft accumulation

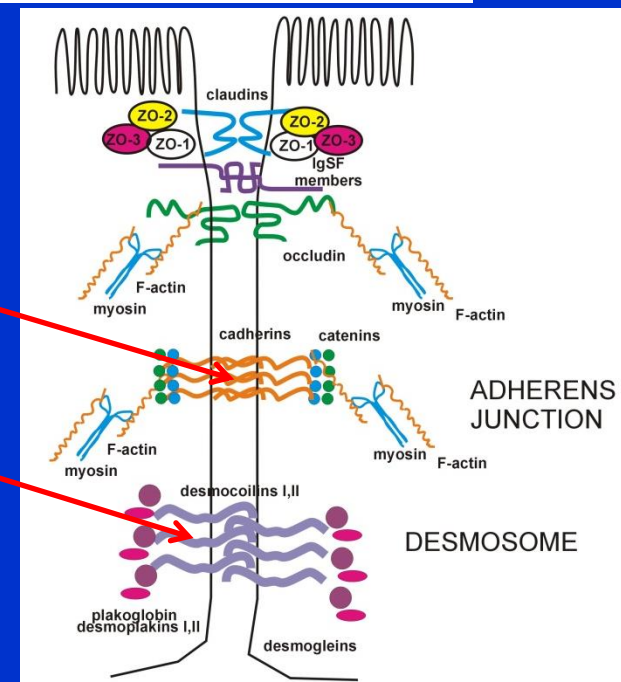
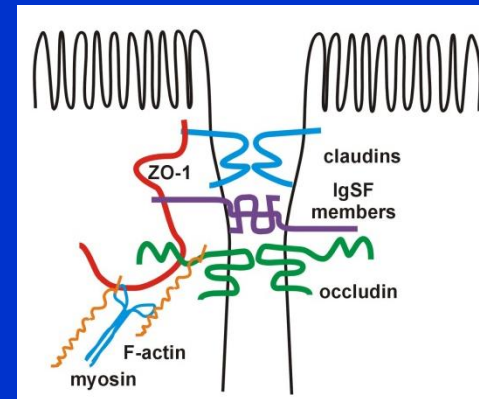


Membrane structures – tight junctions

on apical face of epithelial cells
belt-like, circumferential structure
prevent diffusion of macromolecules
between cells
= crucial for function of epithelial barrier

cell „sticking“ is further strengthened by
adherent regions
„adherent junctions“
desmosomes

- initial adhesive attractions of cells
- do not close cell layer



Membrane structures – microvilli

microvilli = stable protrusions from plasma membrane

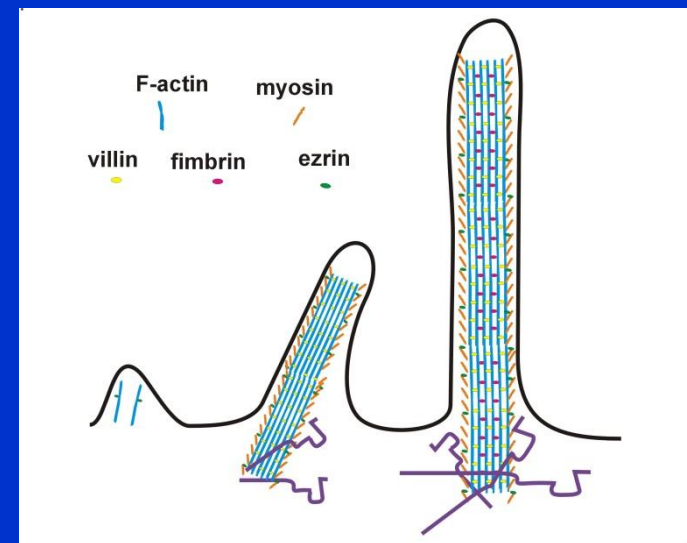
high membrane surface area – absorption

increased interaction with informative molecules – signal perception

coated with glycocalyx – glycoprotein layer

supported with actin filaments, which are crosslinked by fimbrin and villin

villin – important for microvillar morphogenesis



Membrane structures – gap junctions

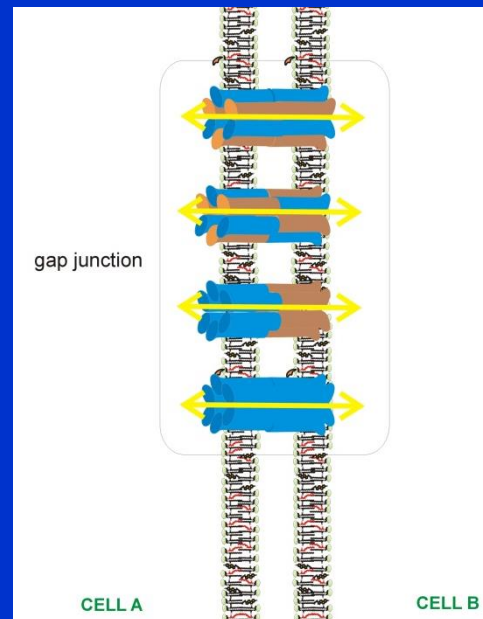
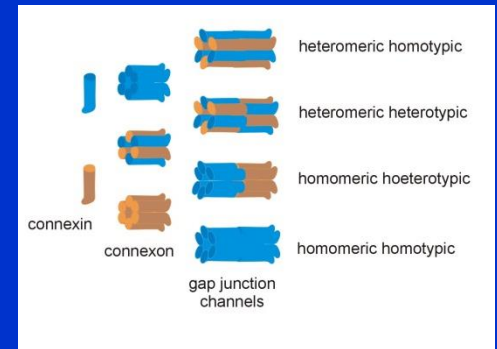
gap junctions = structures enabling **direct transfer** of small molecules (to 1200 Da) between adjacent cells

contain connexins

$6 \text{ connexins}_{\text{cell1}} + 6 \text{ connexins}_{\text{cell2}} = \text{connexon}$

one region of gap junction contains more connexons

connexon channel formation needs 2-4 nm proximity of membranes

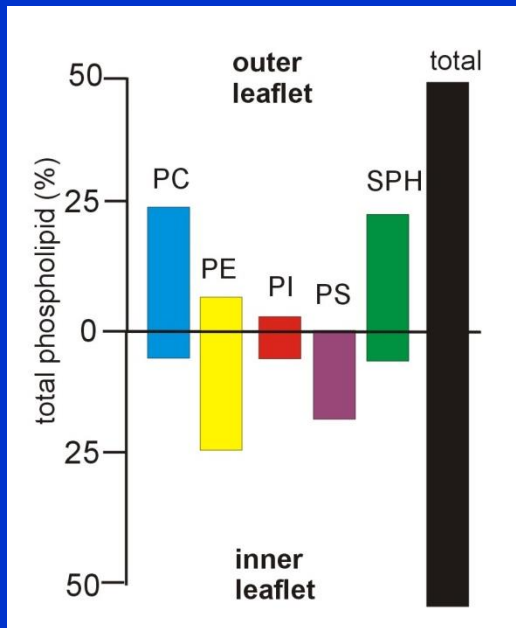


Membrane asymmetry

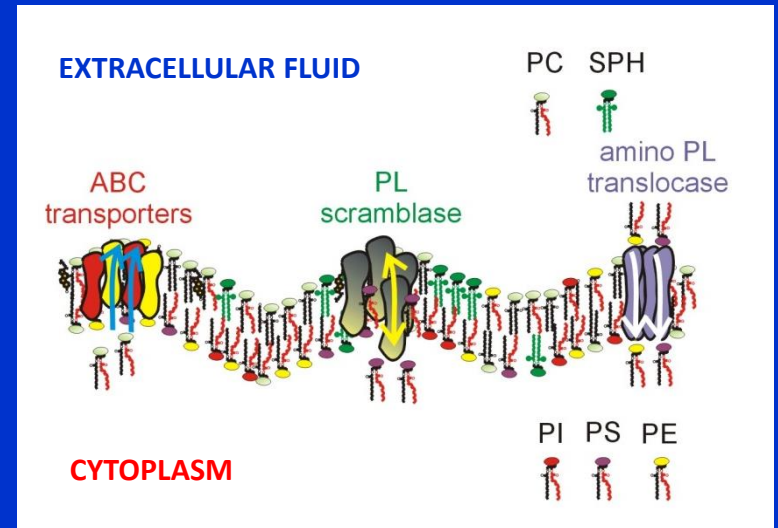
lipids

generally choline PL (PC, SPH) on outer side of membrane
aminoPL (PE, PS) on inner side of membrane (anionic PL)

mammalian PM



←
assymetry
is kept



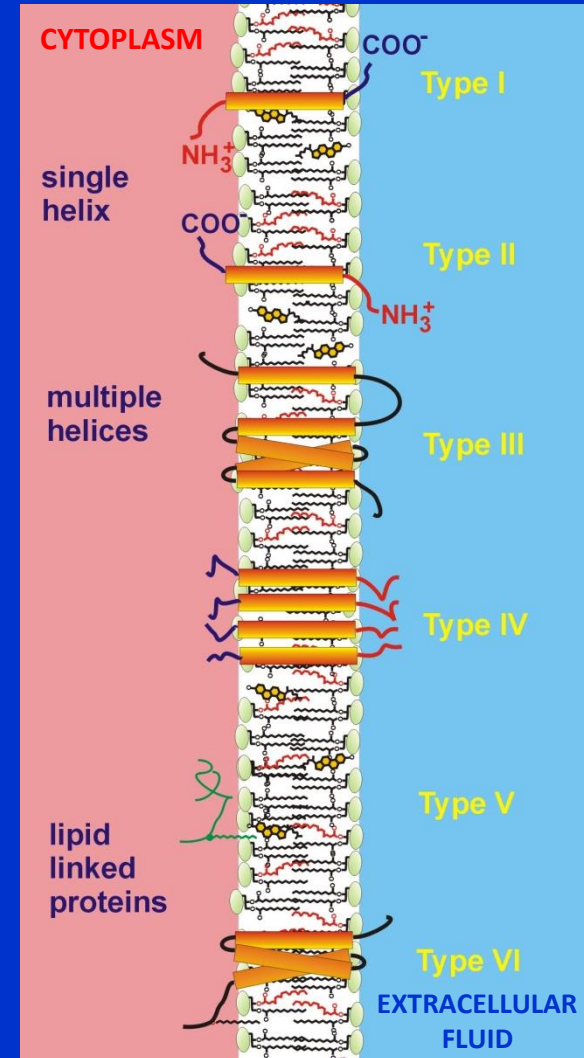
Membrane asymmetry

proteins

assymetry of peripheral proteins is based on their interaction with membrane structures
assymetry of integral proteins results from membrane orientation
(types I-VI of integral proteins)

saccharides

saccharide moiety always on exofacial side



G-proteins

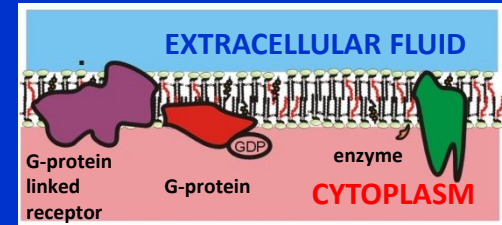
G proteins

heterotrimeric complex with subunits α_s , β , γ
 subunits $\beta\gamma$ anchored with prenylation

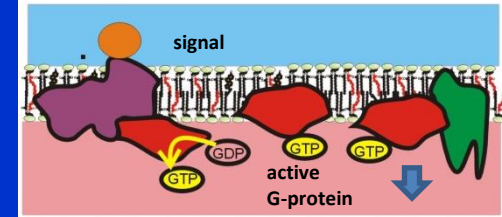
GPCR

receptors coupled with G-proteins
 typically 7 membrane helices

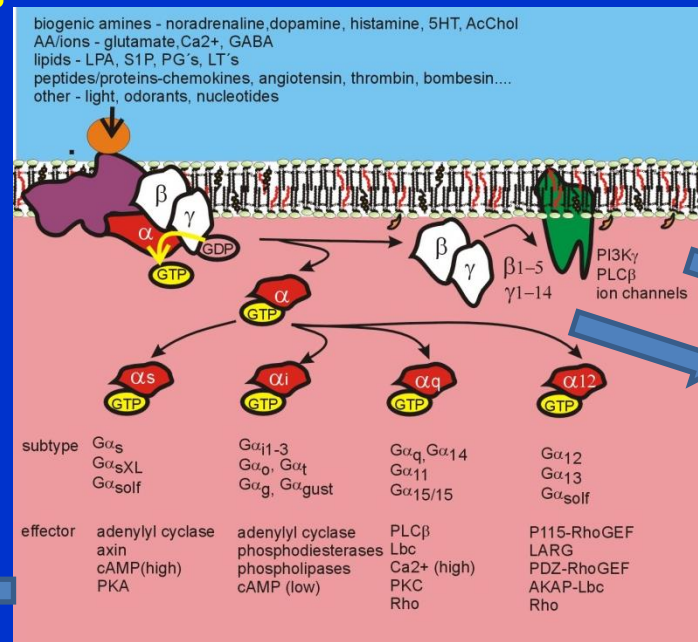
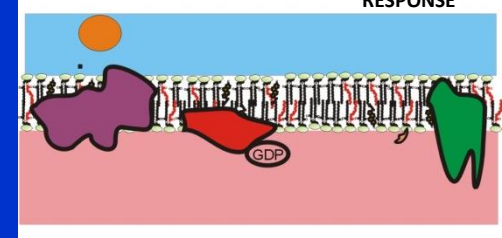
INACTIVE state



ACTIVATED state



return to INACTIVE state



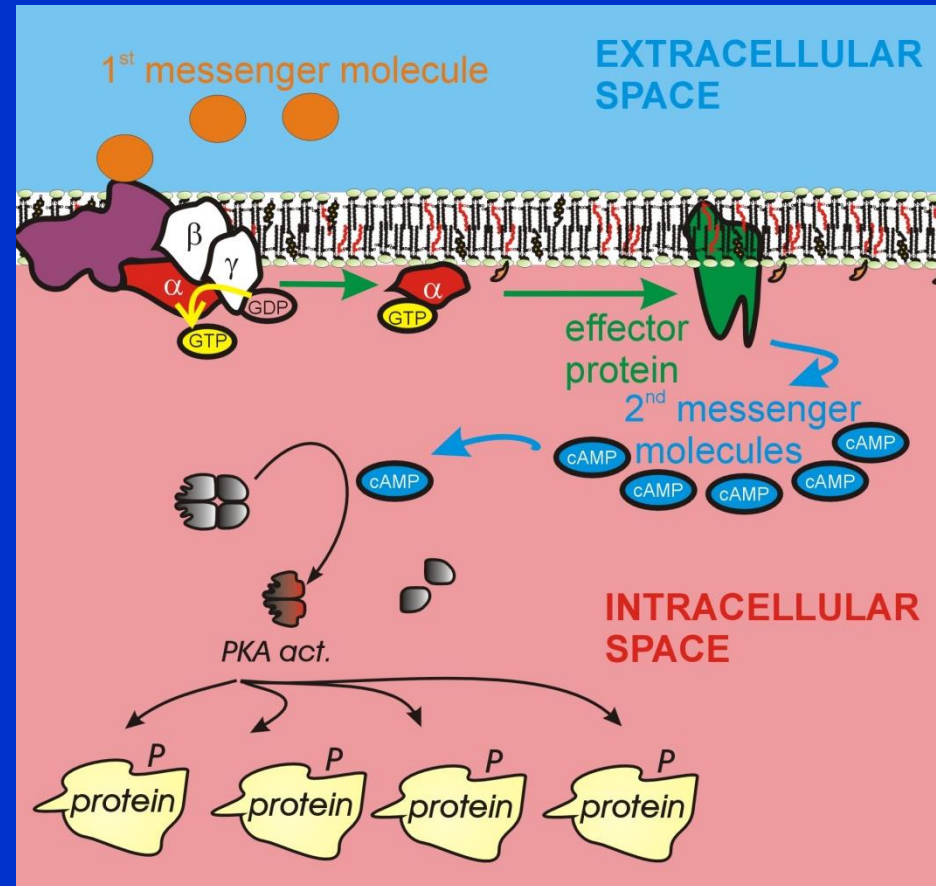
cellular responses

cellular responses

Second messengers

Second messengers = molecules that

1. **relay signals received** at receptors on the cell surface (hormones, growth factors, etc.) — to target molecules in the cytosol and/or nucleus
2. greatly **amplify the strength** of the signal synthesized/released from stores
3. cause (= **presence is signal**) changes in the biochemical activities (protein characteristics) **within the cell**



Second messengers

Types of second messengers:

I. Cyclic nucleotides

cAMP by adenylyl cyclase (*needs* G-protein) from ATP
adrenaline, glucagon, LH...

cGMP by guanylyl cyclase (*does not need* G-protein) from GTP
ANP, NO, hv in retina...

II. Lipids

IP₃ and DAG from PIP₂ by PLC

DAG recruits PKC

IP₃ releases Ca²⁺ from ER/“calciosomes”

TSH, vasopresin, GABA, angiotensin...

III. Ca²⁺

Ca²⁺ released by IP₃ rec/ryanodine rec

high Ca²⁺ binding to troponin C, calmodulin

muscle contraction, T/B cell activation, exocytosis

IV. Other (eicosanoids, Mg²⁺, Ser-P, Chol-P, NO, CO, H₂S...)

Saccharide structure of biological membranes

Membrane saccharides

- always on **exofacial side** of membrane
- monomer sequences are considerably variable
- **2 - 10% weight** of the membranes

I. Glycolipids

usually minor part (~7% of saccharides in glycolipids)

II. Glycoproteins

majority of saccharide moiety ~93% of saccharides in glycoproteins

Saccharide structure of biological membranes

x proteoglycans: saccharide >> protein

I. Glycoproteins

Protein + short saccharide part (can be branched , < 15 units)

1. Sialic acid usually on end – negative charge
2. Bonding with several AA: 2 types of linkage

N-glycosidic bond to Asn

O-glycosidic bond to Ser/Thr

important for half-life of serum glycoproteins

Functions of glycoproteins in membranes

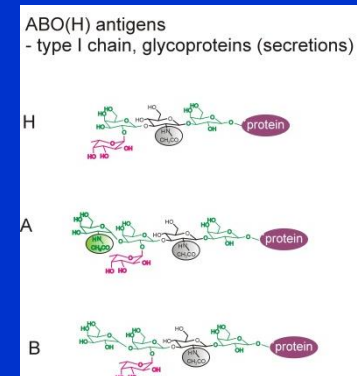
determination of immune response

host-virus/bacteria interaction

HIV entry into immune cells: *via* chemokine rec

Helicobacter pylori adhesion to gastric mucosa cells: *via* Lewis blood antigen

play a role in cell adhesion



Saccharide structure of biological membranes

II. Glycolipids

short (branched) oligosaccharide chain + ceramid → sphingolipids
(+ prenol, + acylglycerol)

Functions of glycolipids in membranes

1. membrane anchors, cell distribution targeting

2. cell recognition

Erythrocytes – ABO antigen system

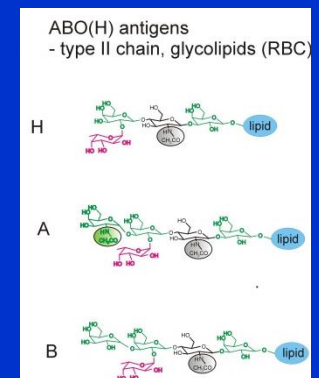
3. parts of lipid rafts (cell signalling functions)

involved infectious diseases

cholera toxin

influenza virus binding to gangliosides)

if secreted into serum: glycoproteins with ABO oligosaccharides



Membrane transport

permeability coefficients
for lipid bilayer

Small molecules

I. Passive transport

1. Simple diffusion

2. Facilitated diffusion

2.1. transporting molecules/peptide structures

2.2. via ion channels

II. Active transport

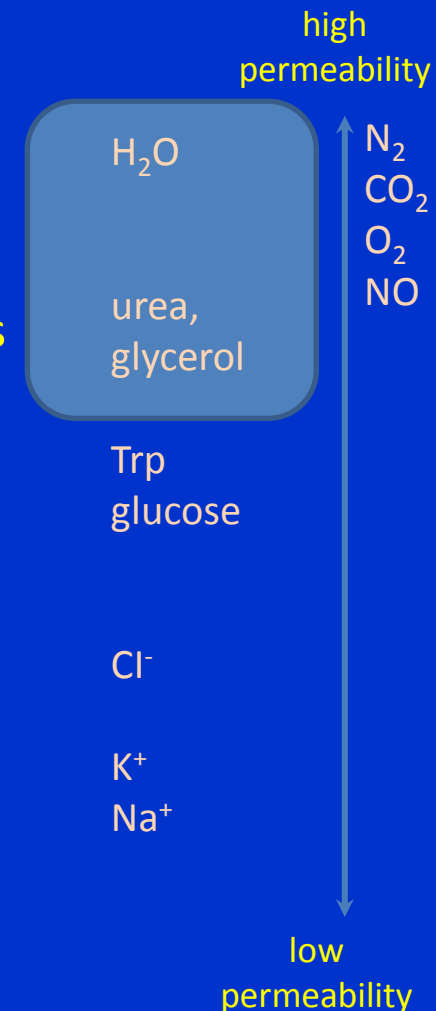
1. most often via ATP coupled transporters

Large molecules/supramolecular structures

not transferred across membrane

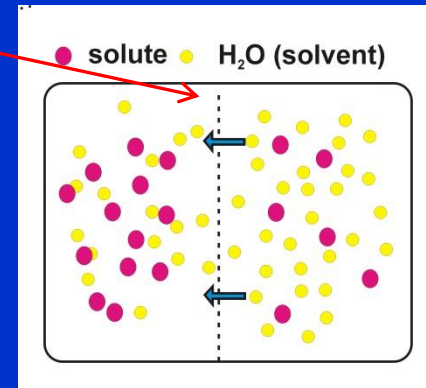
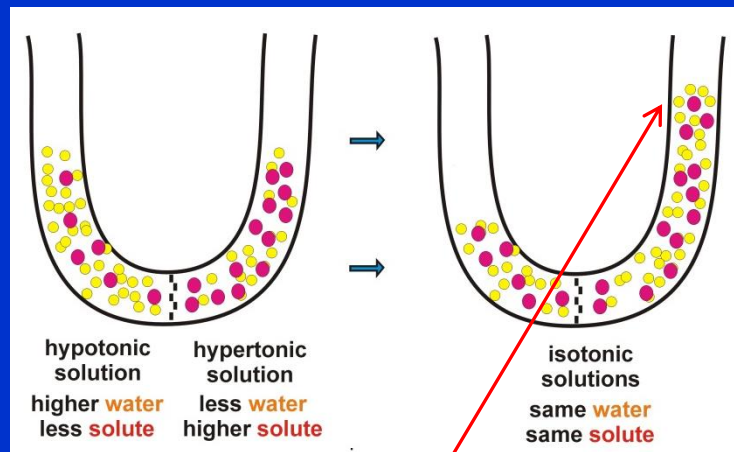
I. Endocytosis

II. Exocytosis



Osmosis

Osmosis = passive process, when molecules of **water** move from area with **higher** concentration of water into the area with **lower** concentration
semipermeable membrane does not allow solute transfer
= molecules of water dilute solute



Reverse osmosis

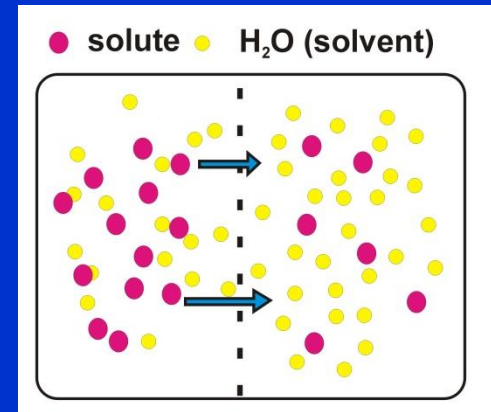
E must be supplied

pressure on the semipermeable membrane

(sea water desalting; high pure water production)

Facilitated diffusion

Diffusion = passive process, when the molecules from the area with **higher** concentration move into the area with **lower** concentration



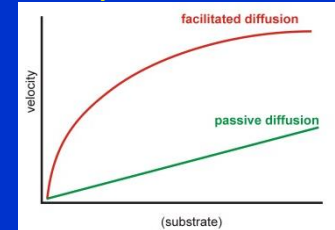
Facilitated diffusion (ion channels/transporters)

movement across membrane is augmented with ion channels/transp. proteins
also passive = no need for E (voltage gated neuronal ion channels)
saturable system

velocity of facilitated diffusion is proportional to:

1. concentration gradients across membrane
2. number (N) of active transporters/channels (e.g. hormones)
3. affinity of linkage between structure transporting and being transported
4. velocity of conformational changes of transporting structure

insulin – increases N of Glu transporters via mobilization from intracellular space
growth hormone, estrogens - increasing N of AA transporters



Simple diffusion

Diffusion = passive process, when the molecules from the area with **higher** concentration move into the area with **lower** concentration

Simple diffusion

v diffusion \sim concentration gradient

- persistent supply of molecules + removal away

(lungs: O_2 + CO_2 ; intestine: glucose lumen + port. circulation)

\sim area – area increase

(lung alveolae; mt cristae; intestinal villi...)

\sim temperature (not easily accomplished)

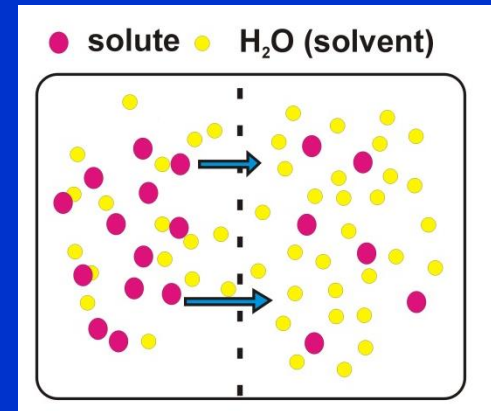
\sim electric potential across membrane – abstraction of ions

(formation of ATP)

\sim hydrostatic pressure over membrane - (...?..)

1/ \sim distance – more folds

(thin membranes – max. 7-10 nm; foldings – more membranes)



Membrane transporters

Uniport

transport of one type of molecule
(GLUT1, Valinomycin)

Symport

coupling of transfer of 2 different molecules

gradient of 1st molecule  transfer of 2nd molecule

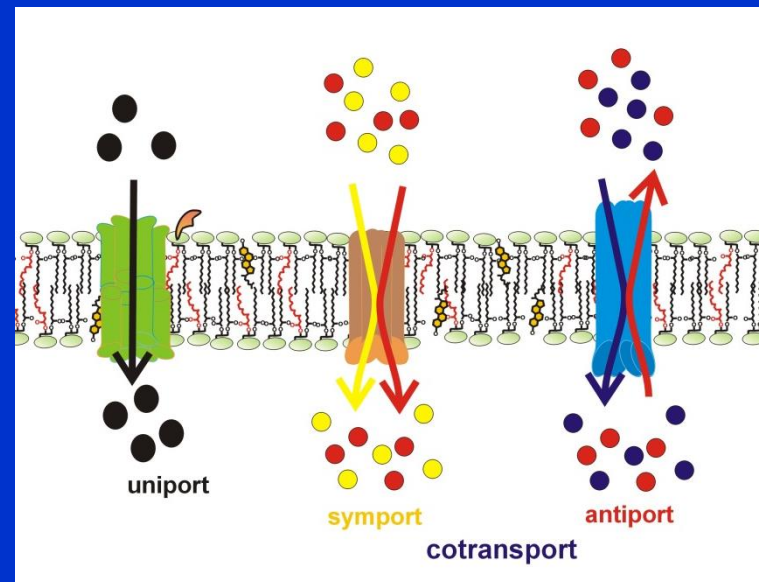
(glucose – Na⁺ symport)

Antiport

confers only exchange (S₁ for S₂)

usually ping-pong kinetics

(ATP/ADP 1:1.....)



Membrane transporters

Transport of glucose into myocytes/adipocytes

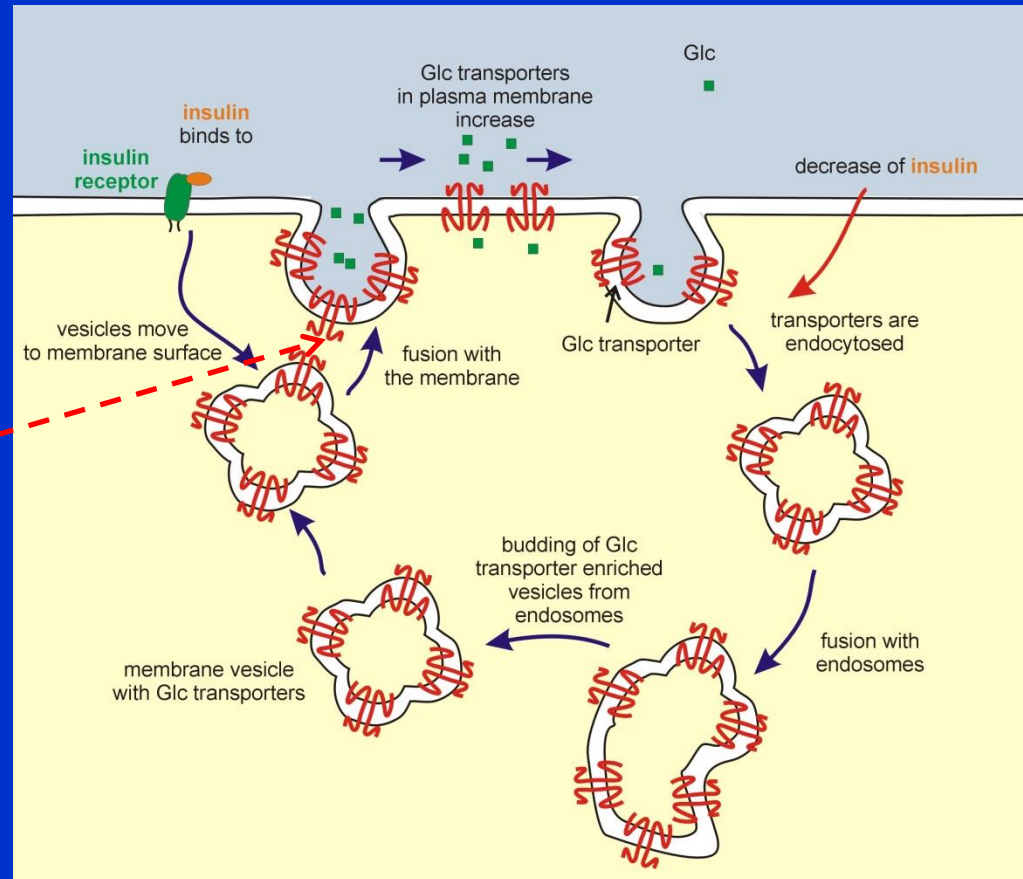
GLUT4 regulated by insulin

increase $[\text{glucose}]_{\text{plasma}} > 5 \text{ mmol/l}$

increase $[\text{insulin}]_{\text{plasma}}$

mobilization of GLUT4

DM type I



Ion channels

Transmembrane structures resembling pores (diameter cca 6 nm)

specific for given ion (Na^+ , K^+ , Ca^{2+} , Cl^-)

mechanism of selectivity varies
working transiently

– open/closed channel

Relative permeability to the three
voltage gated channels ($P_{\text{ion X}}/P_{\text{ion}}$)

Ion X	Na^+ channel	K^+ channel	Ca^{++} channel
Li^+	0.93	0.018	0.0024
Na^+	1	0.010	0.0008
K^+	0.086	1	0.0003
Rb^+	0.012	0.91	
Cs^+	0.016	0.07	0.00002
Ca^{++}	too small	too small	1
Sr^{++}			0.67
Ba^{++}			0.40
Tl^{3+}	0.33	2.30	
NH_4^+	0.16	0.13	

Ion channels

Transmembrane structures resembling pores (diameter cca 6 nm)

regulation of ion channel activity

1. ligand gated channels (neurotransmitters in synapses)

inhibition: AcChol – tubokurarin, cobrotoxin

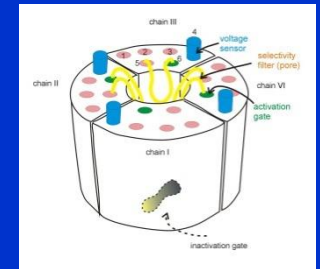
2. voltage gated channels (Na^+ in neurons)

inhibition: Na^+ - tetrodotoxin, K^+ - dendrotoxin

3. mechanically gated channels – change in pressure, touching
membrane curvature change (osmotic homeostasis)

4. light gated channels (types of rhodopsins - phototaxis)

voltage gated Na^+ channel
in neurones



flow velocity of ions \sim diffuse velocity (10^6 - 10^7 ions/s)

Ionophores

small cyclic molecules/complexes capable of destroying the ion gradients
synthesized in some microbes and animals

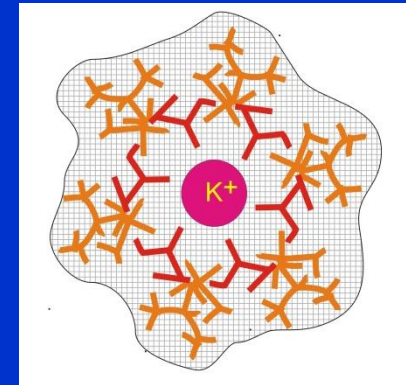
1. Shuttle system

packing the ion and carrying across membrane
selectivity mechanisms also variable

valinomycin

specifically for K^+

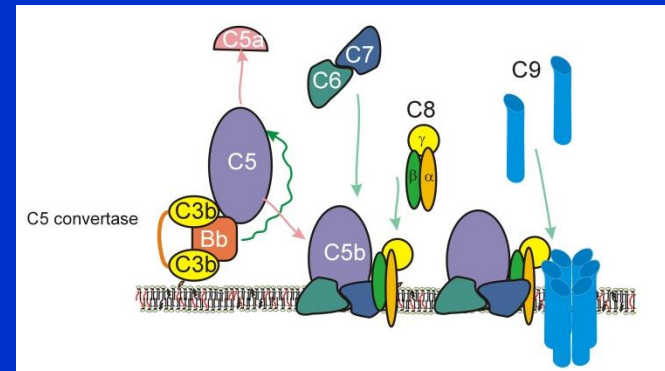
valinomycin



2. Channel formation  cell destruction
antibiotics – *gramicidine*

3. Formation of huge pores
diphtheria toxin
activated parts of complement

complement activation



Aquaporins

Augment transport of H₂O across membranes

Selective for H₂O (some also with glycerol) , ions are not passed through (even H⁺)
protons – H₂O interaction with Asn prevents H⁺ further relay

Aquaporin	location	function
AQP-1	proximal renal tubule	fluid reabsorption
	lung	water homeostasis
	eye	secretion of aqueous humor
	CNS	secretion of cerebrospinal fluid
AQP-2	renal collecting duct	water permeability
AQP-3	renal collecting duct	water retention
AQP-4	CNS	reabsorption of cerebrospinal fluid
		regulation of brain oedema
AQP-5	salivary/lachrymal glands	fluid secretion
	alveolar epithelium	fluid secretion
AQP-6,7,8,9	kidney, fat cells testis, liver, leukocytes	? transport of glycerol ? not established

ADH regulates
N of pores
(reabsorption of H₂O)

↓ mutation
lower reabsorption

Active transport

Active transport = active process, when molecules from the area

with **lower** concentration move into the area

with **higher** concentration

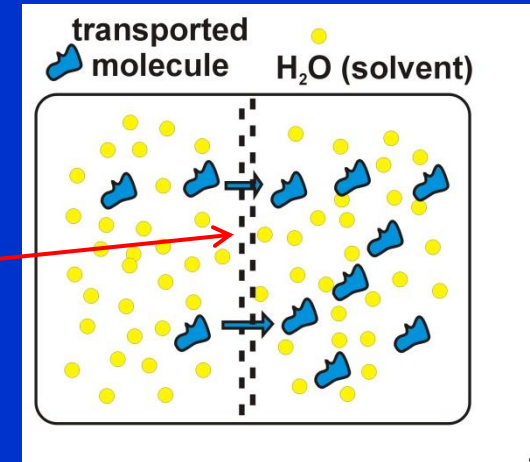
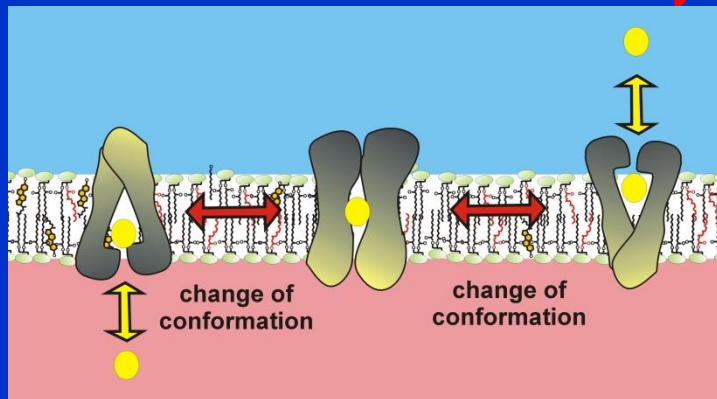
with the help of membrane pumps **and E**

Membrane **not** permeable for transported molecule

Membrane proteins - pumps

1. Specific for transported molecule

2. Binding of transported molecule  conformational change of protein



3. In the membrane, there is not open space left

4. Transport kinetics can be described with Michaelis-Menten approach

5. Number of transported molecules at a time reaches units of ions

Energetics of active membrane transport

Hydrolysis of ATP – most often used process in mammals

Na^+ - K^+ pump: consumes up to 33% of resting E of mammalian cells (67% in neurons) – keeping of electrochemical gradient is highly important

Types of ATP-coupled active transporters

1. Type P

Ca^{2+} ATPase in SR

Na^+ / K^+ ATPase in PM

2. Type F

mt ATPase - oxidative phosphorylation

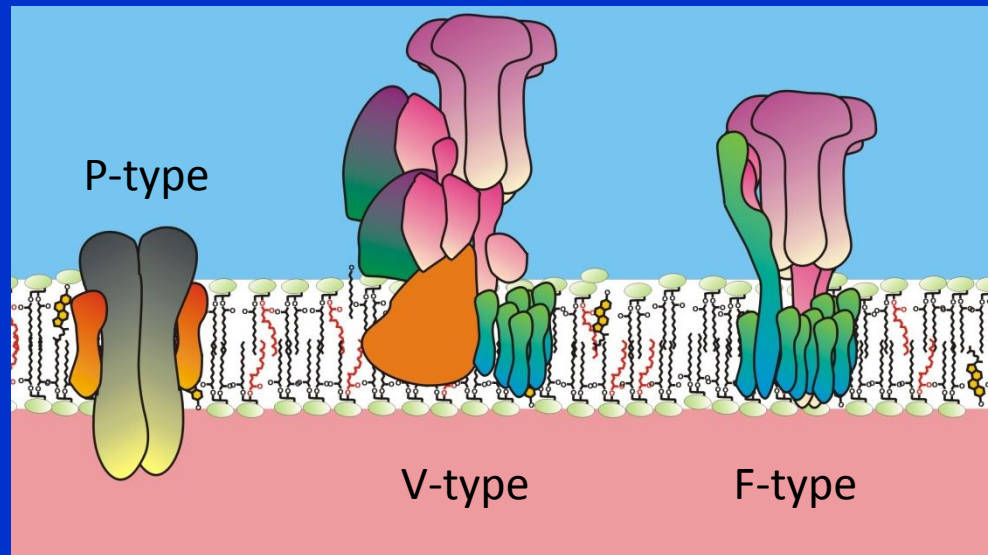
3. Type V

ATPase H^+ into lysosomes

4. ABC transporters

cystic fibrose transporter in PM

multidrug resistance (MDR-1) in PM



Energetics of active membrane transport

Active transport must be coupled with exergonic process

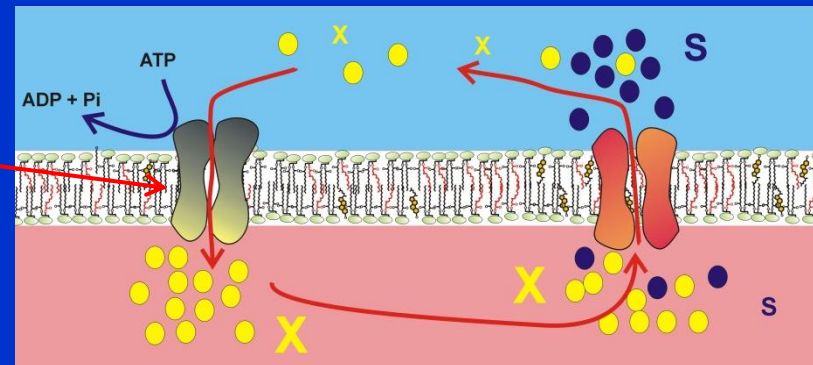
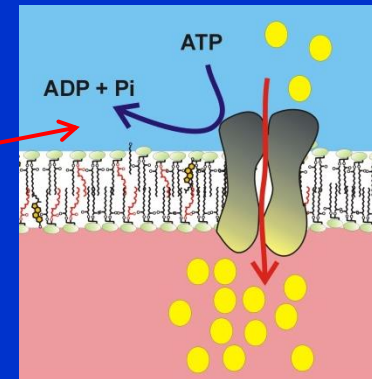
1. hydrolysis of ATP
2. absorption of light
3. oxidative reaction – electron transfer

Primary active transport

accumulation of solute is directly coupled
with exergonic reaction

Secondary active transport

endergonic transport of solute (S) is coupled
with exergonic flow of another solute (X)
initially transported via
primary active transport

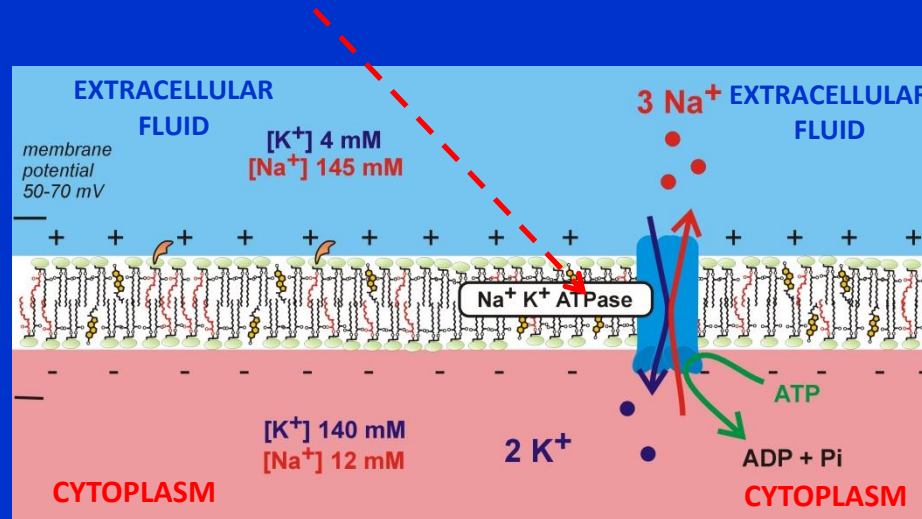


Energetics of active membrane transport

Na⁺/K⁺ ATP pump: consumes up to 33% of resting E of mammalian cells (67% in neurons) and maintains:

1. negative inner potential of cell (2 K⁺ for 3 Na⁺)
2. favourable concentrations of K⁺ and Na⁺

Inhibited by cardiac glycosides (ouabaine, digitalis)



Energetics of active membrane transport

Na⁺/K⁺ ATP pump: consumes up to 33% of resting E of mammalian cells
can be coupled with other transports:

Oral rehydration therapy

- used in acute diarrhea/cholera

Na⁺/K⁺ ATP pump maintains
low Na⁺ within epithelial cells

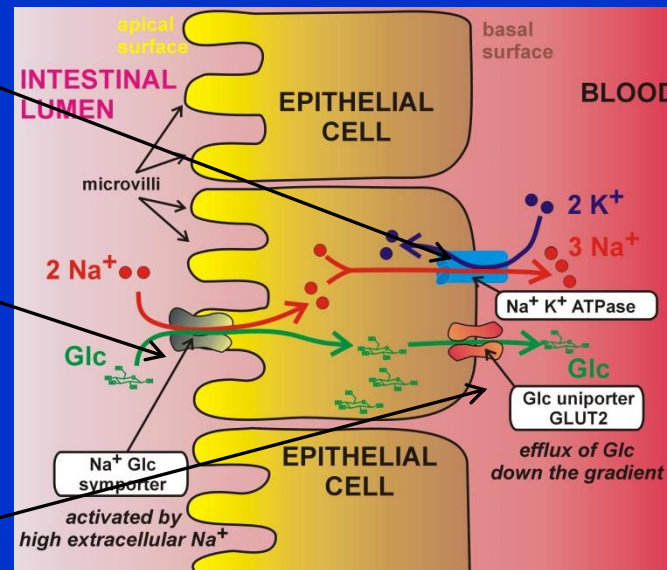
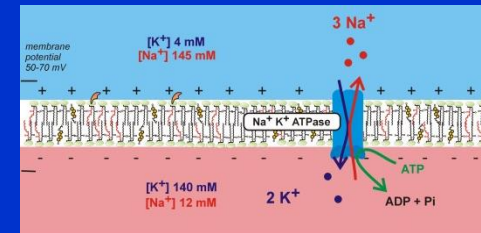
The patient is provided with solutions
with glucose **and** Na⁺
= substrates for Na⁺/Glc **co**transport



Na⁺ is driven to blood (ATP pump)

glucose is transported via GLUT2

Cl⁻/H₂O are driven via osmotic gradient



overall
transport of:

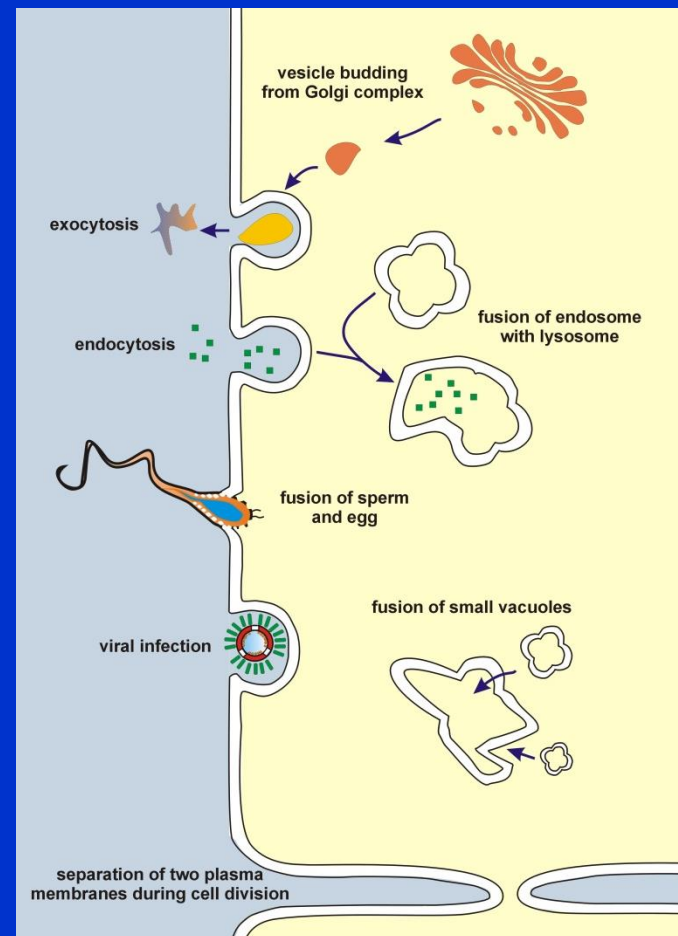
1. Na⁺
2. glucose
3. Cl⁻
4. H₂O

Cl⁻/water – via osmosis

Fusion of membranes

Membranes are able to fuse without disruption of cell membrane integrity

1. vesicle budding from Golgi complex
2. exocytosis
3. endocytosis
4. fusions of endosomes/lysosomes
5. fusion of sperm and egg
6. viral infections
7. vacuole fusions
8. cell division – separation of PM



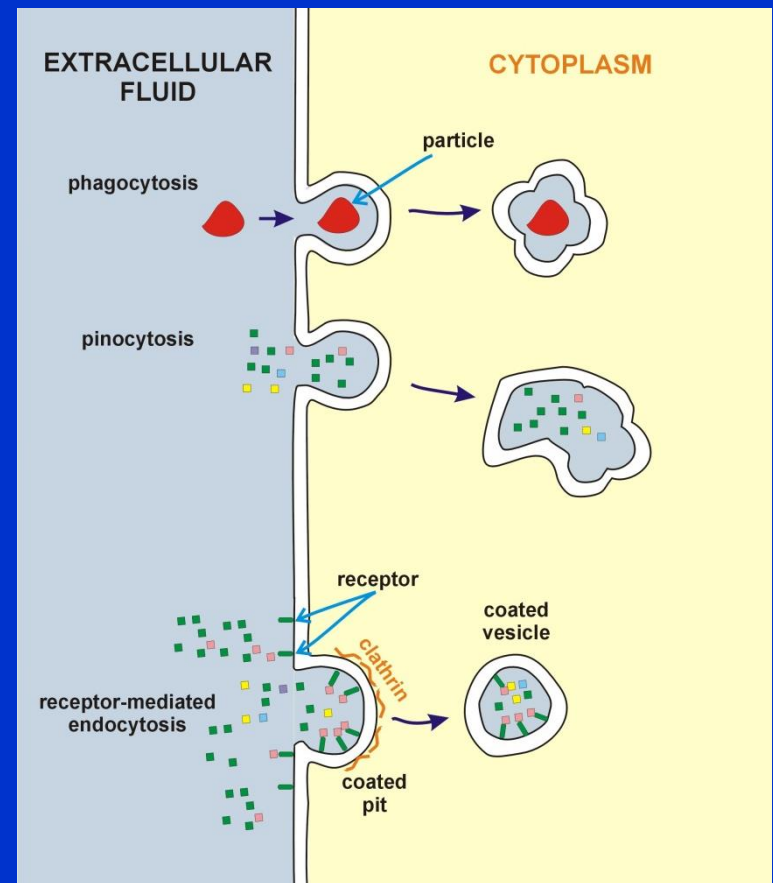
Endocytosis

Internalizing process for large molecules/structures
nutrient intake (after processing)
receptor storage
part of immune defense

1. Random endocytosis
2. Receptor mediated endocytosis

A. Pinocytosis

B. Phagocytosis



Pinocytosis

All cells have this ability, usually for fluid-phase substrates



ingested fluids directed into endosomes

Fluid phase pinocytosis

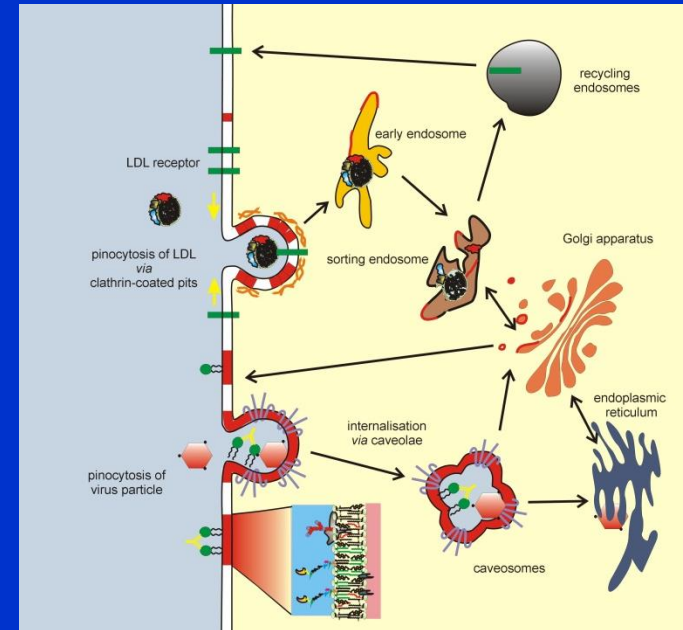
Non-selective process, very rapid

Solute entry into cell is proportional to its concentration within extracellular fluid

Absorptive pinocytosis

Receptor mediated process

Invagination of membrane – coated pits (clathrin)
(LDL uptake; absorption of extracellular GlyProt)
(infection with HIV; hepDNA; poliomyelitis)

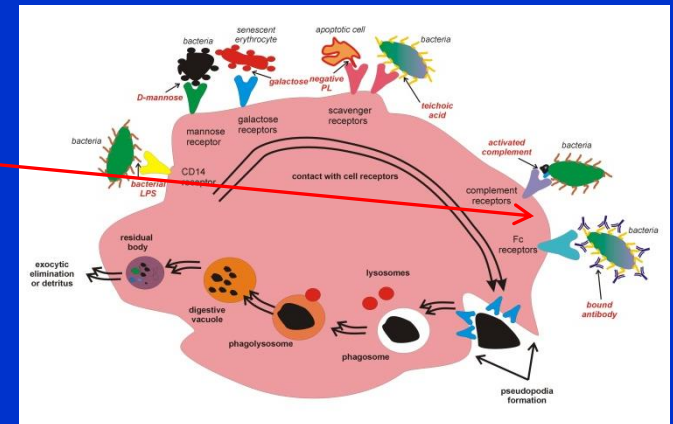


Phagocytosis

Only specialised cells (macrophages, granulocytes)

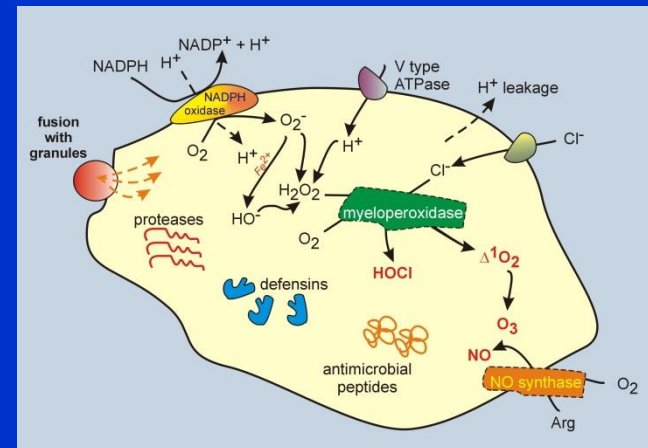
Large particles (viruses, cells, cell debris ... solid particles)

process can be accelerated via opsonization (IgG...)



Destructive mechanisms in phagolysosomes

1. Oxygen radical formation
2. NO formation
3. Antimicrobial peptides (proteases...)
4. Fe binding (lactoferrin)



Exocytosis

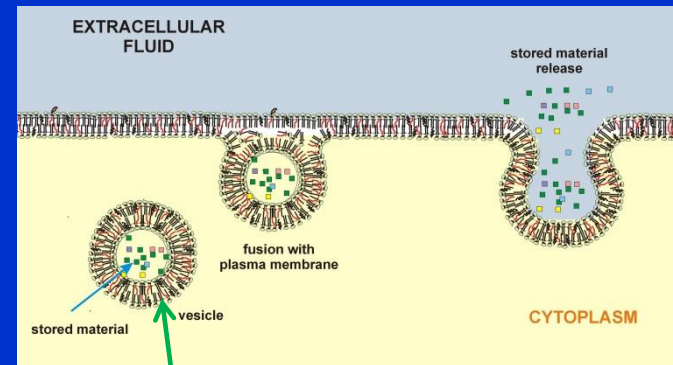
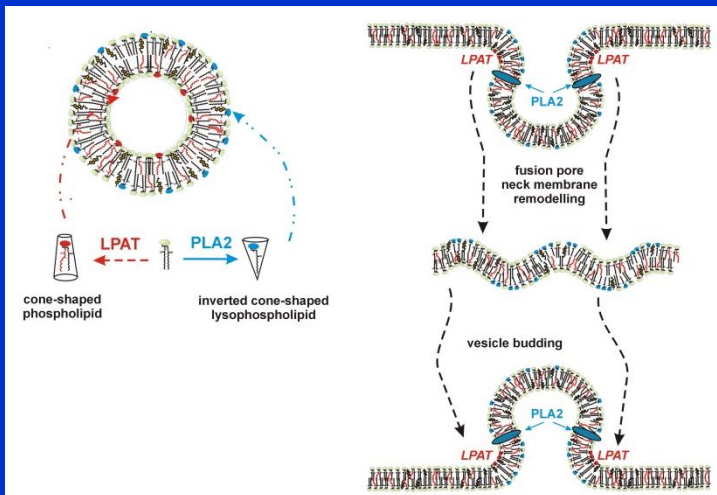
Most cells use for macromolecule expelling into extracellular space

1. attaching to the cell surface – peripheral proteins (antigens)
2. part/joining extracellular matrix – collagen, glycosaminoglycans
3. information transfer through extracellular space – hormones etc.

Remodelation of membranes (Golgi – vesicles – PM)

often triggered by changes in Ca^{2+} concentrations

(Ca^{2+} dep channels; hormonally controlled)



sometimes special coating proteins needed

Further reading

Textbooks

- Biochemistry of Lipids, Lipoproteins and Membranes (5th Ed)*; Vance DE, Vance JE (Eds.), Elsevier, Amsterdam (The Netherlands) 2008
- Lehninger Principles of Biochemistry (6th Ed)*; Nelson DL, Cox MM (Eds.), Susan Winslow, New York (U.S.A.) 2013
- Harper's Illustrated Biochemistry (28th Ed)*; Murray RK, Bender DA, Botham KM, Kennelly PJ, Rodwell VW, Weil PA (Eds.), McGraw-Hill, New York (U.S.A.) 2009
- Roitt's Essential Immunology (12th Ed)*; Delves PJ, Martin SJ, Burton DJ, Roitt M (Eds.), Wiley-Blackwell, Chichester (UK) 2011

Articles

- Van Meer G, Voelker DR, Feigenson GW: Membrane lipids: where they are and how they behave. *Nat Rev Mol Cell Biol* 2008; **9**: 112-124.
- Lane KT, Beese LS. Structural biology of protein farnesyltransferase and geranylgeranyltransferase type I. *J Lipid Res* 2006; **47**: 681-699.
- Ulmschneider MB, Sansom MSP, Di Nola A: Properties of Integral Membrane Protein Structures: Derivation of an Implicit Membrane Potential. *PROTEINS Struct Funct Bioinfo* 2005; **59**: 252-265.
- Simons K, Sampaio JL: Membrane Organization and Lipid Rafts. *Cold Spring Harb Perspect Biol* 2011; doi: 10.1101/cshperspect.a004697
- Rajendran L, Simons K: Lipid rafts and membrane dynamics. *J Cell Sci* 2005; **118**: 1099-1102.
- Le Shen: Tight junctions on the move: molecular mechanisms for epithelial barrier regulation. *Ann NY Acad Sci* 2012; **1258**: 9-18.
- Alexander JS, Elrod JW: Extracellular matrix, junctional integrity and matrix metalloproteinase interactions in endothelial permeability regulation. *J Anat* 2002; **200**: 561-574.
- Fath KR, Burgess DR: Microvillus assembly: Not actin alone. *Curr Biol* 1995; **5**: 591-593.
- Meşe G, Richard G, White TW: Gap Junctions: Basic Structure and Function. *J Invest Dermatol* 2007; **127**: 2516-2524.
- von Heijne G: Membrane-protein topology. *Nat Rev Mol Cell Biol* 2006; **7**: 909-918.
- Fadeel B, Xue D: The ins and outs of phospholipid asymmetry in the plasma membrane: roles in health and disease. *Crit Rev Biochem Mol Biol* 2009; **44**: 264-277.
- Heeren J, Beisiegel U: Intracellular metabolism of triglyceride-rich lipoproteins. *Curr Opin Lipidol* 2001; **12**: 255-260.
- LaPlante JM, Falardeau JL, Brown EM, Slaugenhaupt SA, Vassilev PM: The cation channel mucolipin-1 is a bifunctional protein that facilitates membrane remodeling via its serine lipase domain. *Exp Cell Res* 2011; **317**: 691-705.

Web sources

<http://www.vivo.colostate.edu/molkit/hydropathy/>