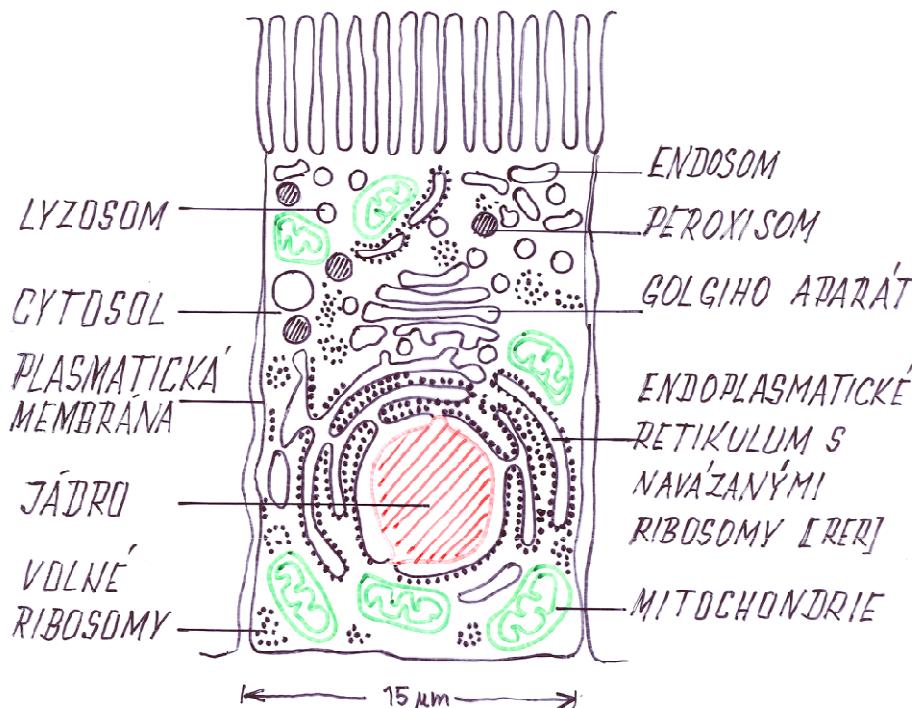


HOW MANY PROTEIN DESTINATIONS?



SMĚROVÁNÍ PROTEINŮ

DO :	% objemu buněky	pocet
CYTOSOL	54	1
MITOCHONDRIE	22	1700
ER	12	1
JÁDRO	6	1
GOLGIHO APARÁT	3	1
PEROXISOMY	1	400
LYZOSOMY	1	300
ENDOSOMY	1	200

TRANSPORTATION OF NEWLY SYNTHESIZED
PROTEINS WITHIN THE CELL - THEIR DESTINATION
IS DETERMINED GENETICALLY

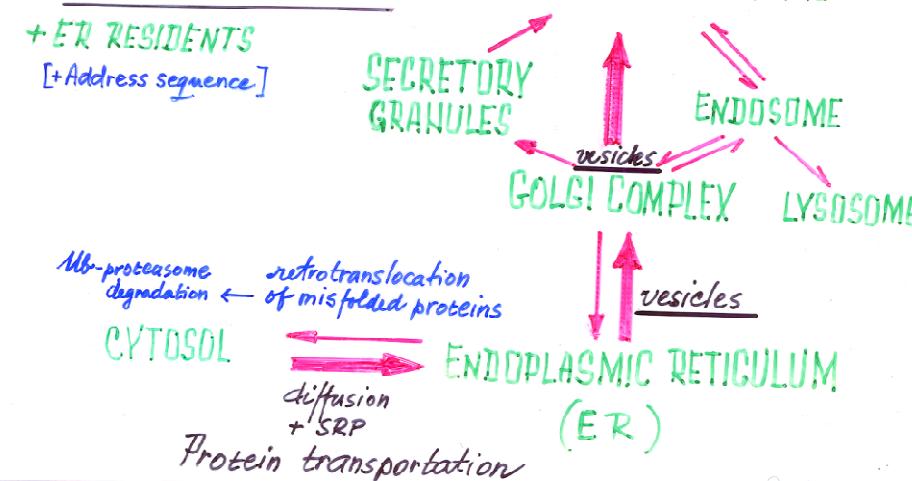
1. DIRECT TRANSPORTATION FROM THE CYTOSOL,
TARGETING TAKES PLACE ACCORDING TO
ADDRESS SEQUENCE TO :

NUCLEUS [NLS]
CHLOROPLASTS
MITOCHONDRIA
PEROXISOMES

2. INDIRECT TRANSPORTATION VIA ENDOPLASMIC RETICULUM (ER). THE PROTEINS CARRY
ADDRESS SEQUENCE CALLED SIGNAL SEQUENCE
TO BE TARGETED TO ER. MEDIATED BY SRP,
TO:

GOLGI (SIGNAL RECOGNITION
LYSOSOMES ER-Mn⁶P PARTICLE)
ENDOSOMES

NUCLEAR MEMBRANE } [Address sequence]
CELL MEMBRANE }



PROTEIN TARGETING, SORTING AND PROCESSING

Site of protein synthesis : **RIBOSOMES**

IN THE CYTOSOL

WITHIN ORGANELLES

FREE RIBOSOMES : synthesize mostly soluble proteins,
→ CYTOSOL and mitochondrial (chloroplast, peroxosomal)
proteins, and nuclear proteins

MEMBRANE-BOUND RIBOSOMES : manufacture

→ RER transmembrane proteins destined for
secretion
operation within the ER
incorporation into lysosomes

~ 40% of proteins that a cell synthesizes must be
processed (modified):

COTRANSLATIONALLY (a secretory pathway)

POSTTRANSLATIONALLY (other protein targeting
pathways; e.g. mt proteins)

(~ 30% of newly synthesized proteins are defective ribosomal
products scheduled for degradation (after Ub addition))

SOME ADDRESS SEQUENCES

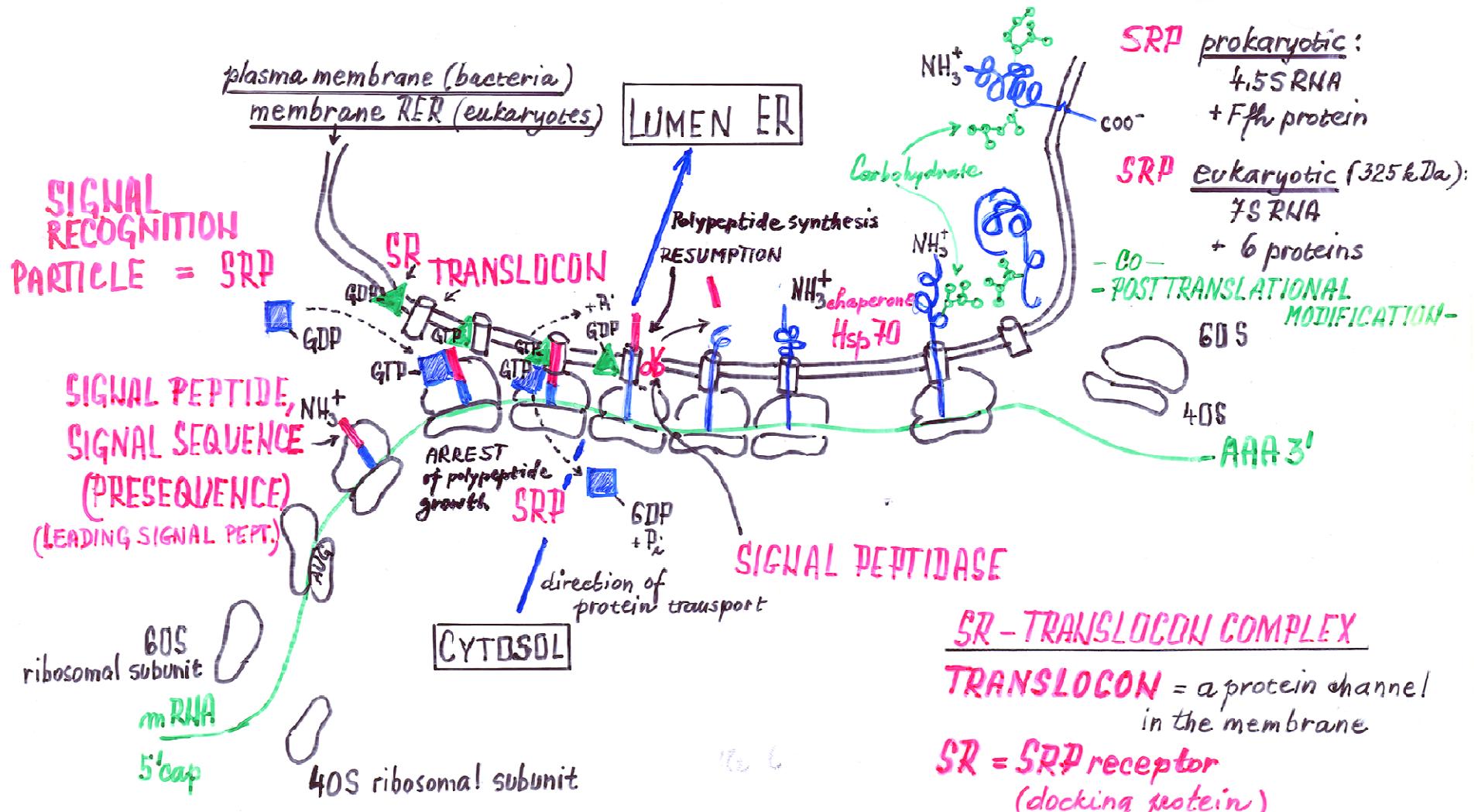
<u>SIGNAL FUNCTION</u>	<u>TARGETING SEQUENCE</u> <u>ADDRESS SEQUENCE_(res)</u> (<u>No gene specificity</u>)
A. <u>Import to nucleus</u> :	- Pro-Pro- <u>Lys⁺-Lys⁺-Arg⁺-Lys⁺-Val-</u> NLS
B. <u>Import to mitochondria matrix</u> : (20-60 residues)	<p><u>H₃N-Met-Leu-Ser-Leu-Arg⁺-Gln-Ser-Ile-Arg⁺-</u> basic + hydroxylated res.</p> <p>- Phe - Phe - <u>Lys⁺-Pro-Ala-Thr-Arg⁺-Thr-</u> Leu-Cys- These presequences do not interact with SRP</p> <p>- Ser-Ser- <u>Arg⁺-Tyr-Leu-Leu-</u> (+ lack of acidic AAs)</p>
C. <u>Retention in ER</u> :	- <u>Lys-Asp-Glu-Leu-COO-</u> KDEL (HDEL) at C-terminus
D. <u>Import into ER</u> <small>→ secretion, transmembr. pr.</small> = "SIGNAL SEQUENCE" (PRESEQUENCE) (SS) (13-36 residues) = N-terminus ⇒ PREPROTEINS, PREPROPROTEINS (e.g. proinsulin, procollagen):	<p><u>H₃N-Met-Met-Ser-Phe-Val-Ser-Leu-Leu-Leu-</u> hydrophobic res.</p> <p>- Val - Gly - Ile - Leu - Phe - Trp - Ala - Thr - Glu - Ala -</p> <p>- Glu - Gln - Leu - Thr - <u>Lys-Cys-Glu-Val-Phe-Gln-</u> Signal peptidase ↓</p> <p>MALWM<u>RLLPLALLALWGPDPAAAFVN</u></p>
<u>Membrane width</u> :	8-9 AA in an elongated form 20 AA in an α-helix
E. <u>Import to peroxisomes</u> : (Transmembrane receptors for some hormones : 7x; more times)	- Ser-Lys-Leu- ; at the C-Terminus

Modulation of Targeting:

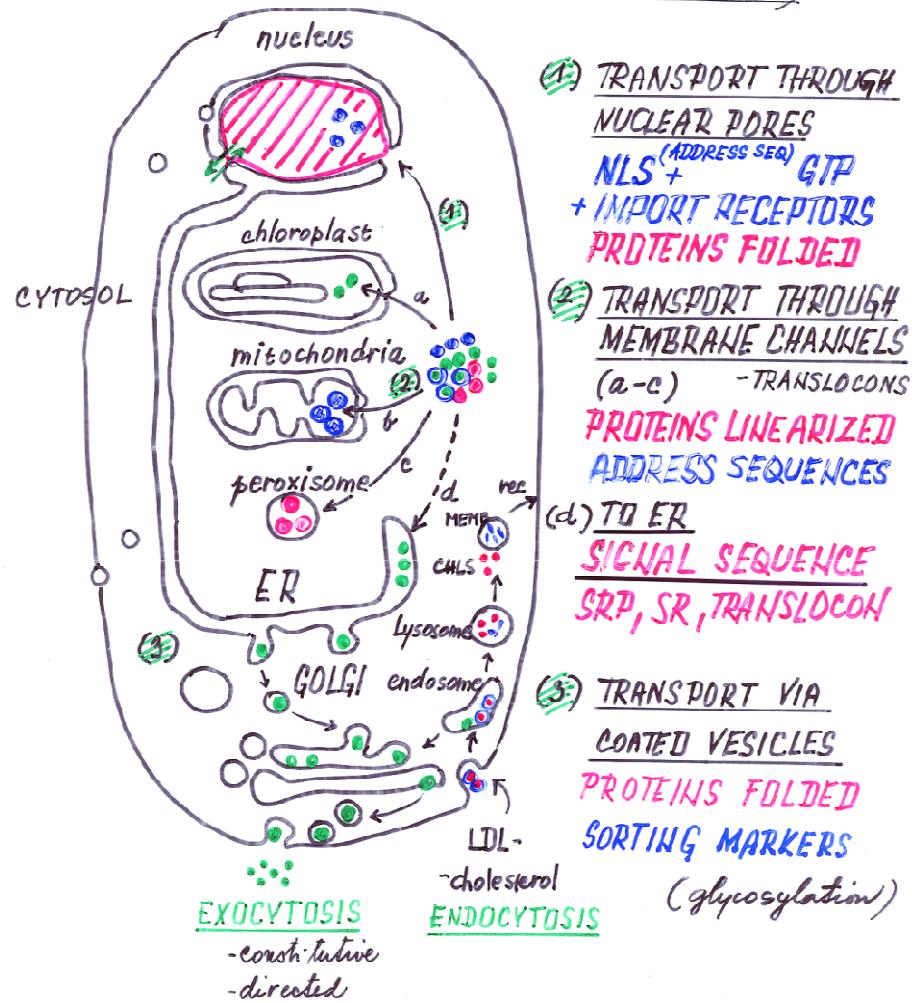
- alternative translation initiation = with or without A.S. → to mt → to cytosol
- rat liver fumarase

MEMBRANE, SECRETED AND LYSOSOMAL PROTEINS AND PROTEINS OF ENDOPLASMIC RETICULUM

are synthesized with a LEADING (N-terminal) SIGNAL SEQUENCE



Synthesis of all proteins starts in the cytoplasm and further targeting + sorting depends on the address sequence + post translational modification (glycosylation)

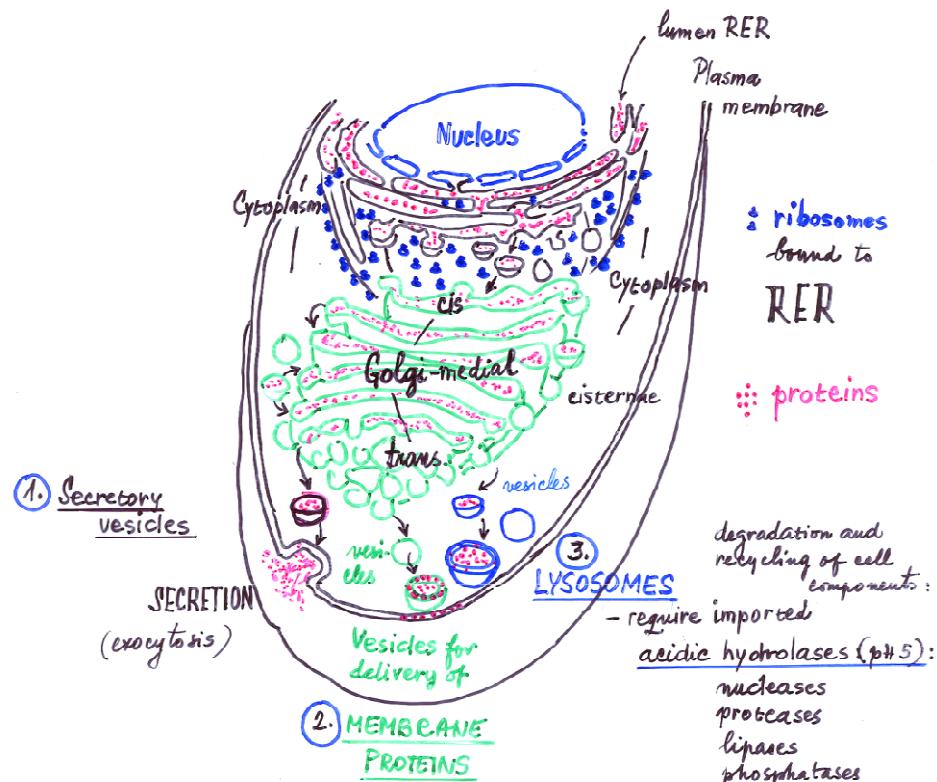


MOLECULAR MOTORS

dynein, kinesin
GTP

MICROTUBULES

PATHWAYS OF NEWLY SYNTHESIZED SECRETORY, MEMBRANE AND LYSOSOMAL PROTEINS (Glycoproteins)



On reaching the TRANS GOLGI network, the now matured proteins are sorted and sent to their final cell destinations. Membrane, secretory and lysosomal proteins are transported in vesicles known as **COATED VESICLES** (3 types).

Coated vesicles originate by budding off from ER membrane. They transport proteins also between RER and GOLGI and subsequently fuse with cis-GOLGI.

PROTEIN MISLOCATION:

The lysosomes in the connective tissues of the victims of mucolipidosis contain large inclusions of glycosaminoglycans and glycolipids as a result of the absence of several lysosomal hydrolases.

Progressive psychomotor retardation!
Skeletal deformities
Death by age 10

degradation and recycling of cell components:
- require imported acidic hydrolases (pH 5):
nucleases
proteases
lipases
phosphatases
glycosidases
phospholipases
sulfatases

MARKER FOR THE DELIVERY TO LYSOMES:

mannose 6-phosphate
(in cis-GOLGI)

Lack of an enzyme
catalyzing mannose phosphorylation
results in incomplete labeling
of enzymes: NO TRANSPORT TO LYSOMES → deficient degradative activity → genetic disease
MUCOLIPIDOSIS ↔ disease I-cell disease

MITOCHONDRIAL PROTEIN IMPORT: THROUGH ONE OR TWO MEMBRANES

(CHLOROPLASTS, PEROXISOMES)
98% of mt proteins are synthesized by cytosolic ribosomes (encoded by nuclear genes)
Posttranslational (=10-20% of all intracellular proteins)

Proteins are in unfolded states maintained by CHAPERONES (+ATP)

(Hsp70, MSF families)

N-terminal targeting sequence (presequence): 20-60 res. for matrix destin.
(rich in basic + hydroxylated amino acids)

Internal targeting sequence (poorly characterized) for directing to IMM, inter-membranous space; cytochrome c is in IMM (outer surf.)

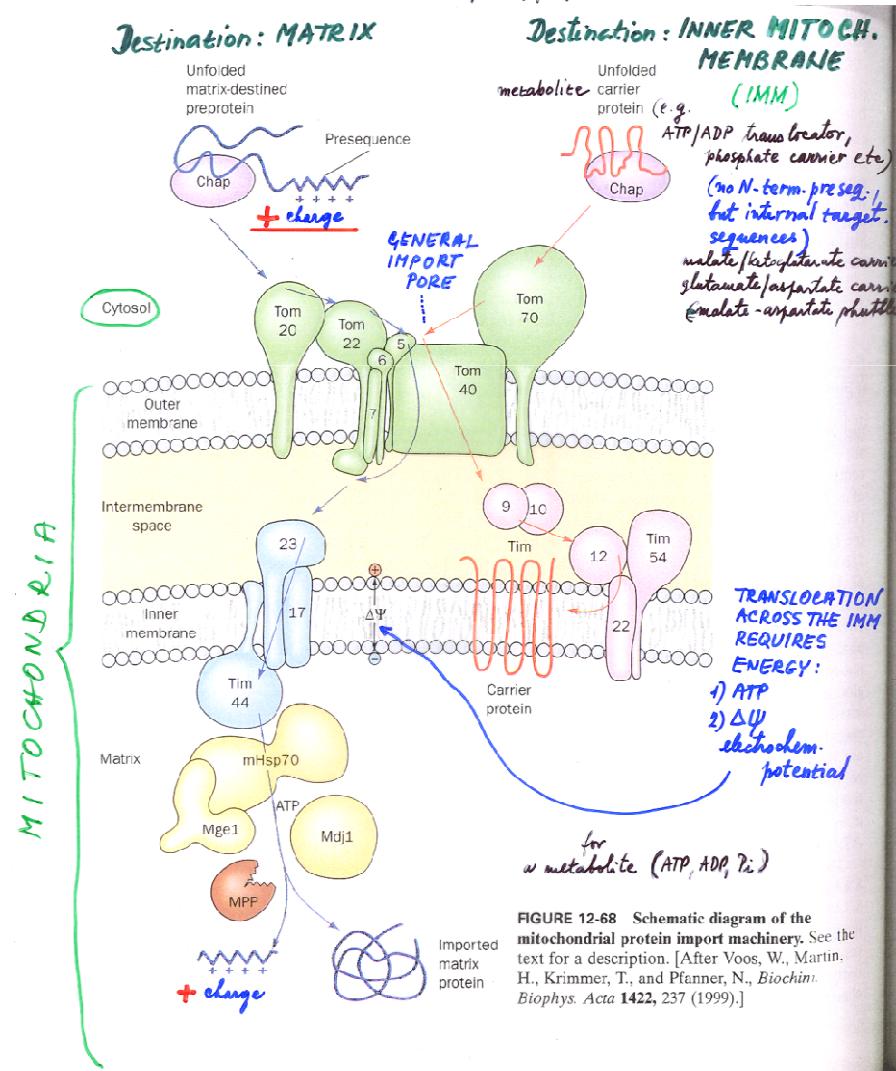
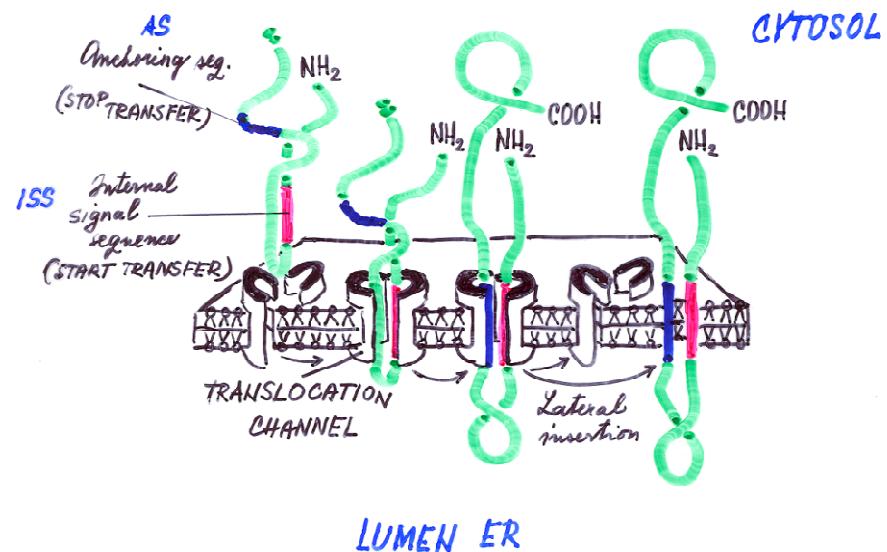


FIGURE 12-68 Schematic diagram of the mitochondrial protein import machinery. See the text for a description. [After Voos, W., Martin, H., Krimmer, T., and Pfanner, N., *Biochim. Biophys. Acta* **1422**, 237 (1999).]

INSERTION OF PROTEIN WITH TWO TRANSMEMBRANE SEGMENTS INTO MEMBRANE OF ER



Several ISS and AS allow various segments of protein to be oriented on each side of membrane = proteins with more transmembrane regions

AS : hydrophobic
always a signal for docking in the membrane

ER and GOLGI FUNCTIONS

ENDOPLASMIC RETICULUM

- 1) • correct folding of proteins in the presence of chaperones
 - only correctly folded proteins are transported/processed/used further; oxidative environment = formation of S-S bridges
- unfolded protein response (UPR): arrest of PS + misfolded proteins are retro-translocated (after reduction of S-S bridges ^(ERdj5 reduction)) to cytosol for degradation by the Ubiquitin-Proteasome system
- XBP1 (X-box binding protein 1 = TF) controls expression of genes required for UPR: binds to promoter elements of genes that encode chaperone proteins that assist with protein folding in ER ^(ERAD = ER-associated protein degradation)
- [KO of Xbp1 gene in mice: embryonic lethal
in liver in adults: reduction of biogenesis of fatty acids + cholesterol by 85-90% !!]

- 2) • glycosylation - in blocks of 14 monosaccharides to NH₂- of Asn
- 3) • formation of antibodies - assembly from 4 polypeptide chains - glycosylation: determination of Ab activity?

GOLGI APPARATUS

- 1) • completion of glycosylation - oligosaccharides serve as markers for the sorting process

mammose 6-P labelling of hydrolases (enzymes) to become recognized by receptors of vesicles traveling/delivering cargo to LYSOSOMES

<u>ABO blood group antigens</u> :	A group	antigen terminal portion of
= glycoproteins	A	: GalNAc ^{terminal antigen}
also present in saliva, urine	B group	: Gal
milk, seminal fluid, gastric juice	O group	: H
	AB group	: A+B : GalNAc + Gal

- 2) • secretion pathways:
 - secretory vesicle formation
 - membranous vesicle formation

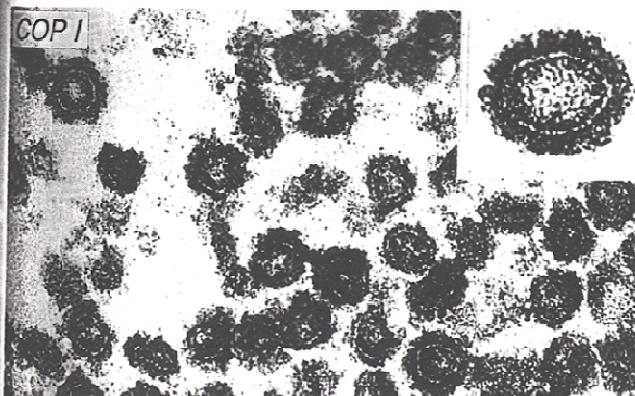
(A,B group carriers:
resistance to cholera)

23-3B). The vesicles, each containing various tubular structures opposite the side of the Golgi stack, through which vesicles bud off. These different types of vesicles, each of which contains different processing enzymes, move from the end of the Golgi stack to the

3 types of coated vesicles (60 - 150 nm diameter sacs)

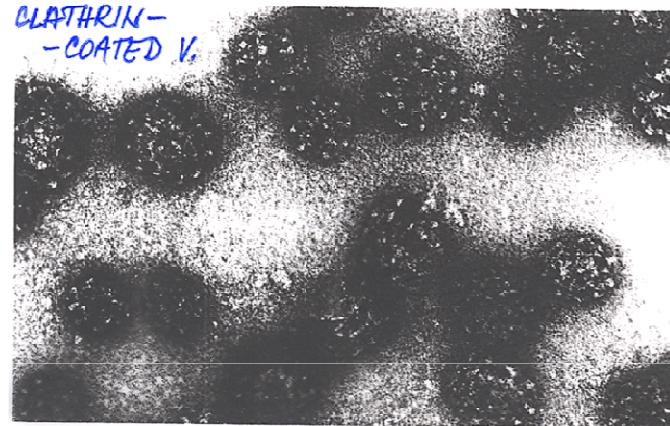
FIGURE 12-52 Electron micrographs of coated vesicles.
(a) Clathrin-coated vesicles. Note their polyhedral character. [Courtesy of Barbara Pearse, Medical Research Council, Cambridge, U.K.] (b) COP I-coated vesicles. (c) COP II-coated vesicles. The insets in Parts b and c show the respective vesicles at higher magnification. [Courtesy of Lelio Orci, University of Geneva, Switzerland.]

(b)

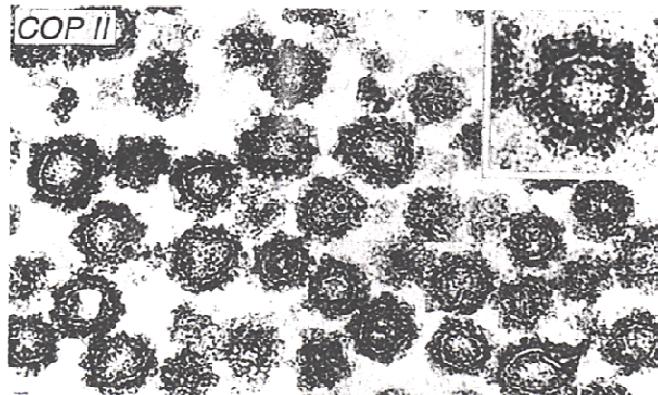


(a)

CLATHRIN-
COATED V.



(c)



CLATHRIN - FORMED CAGE

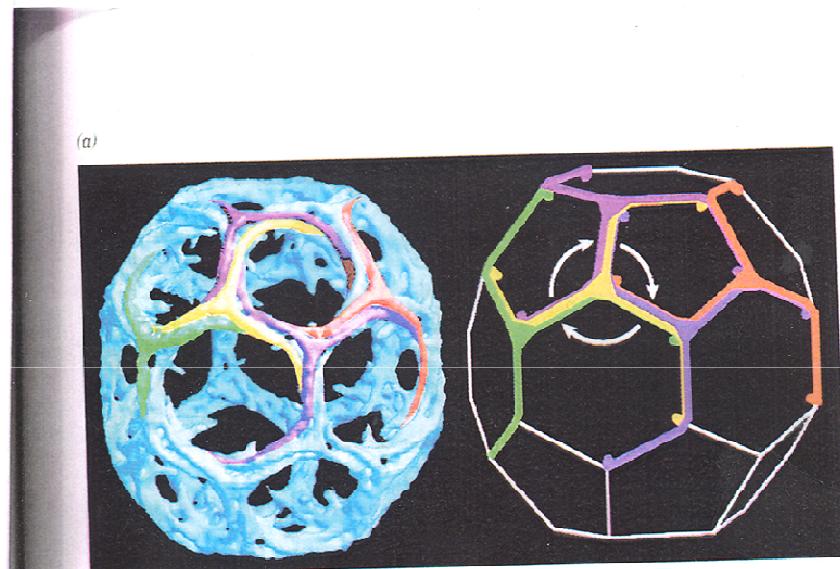
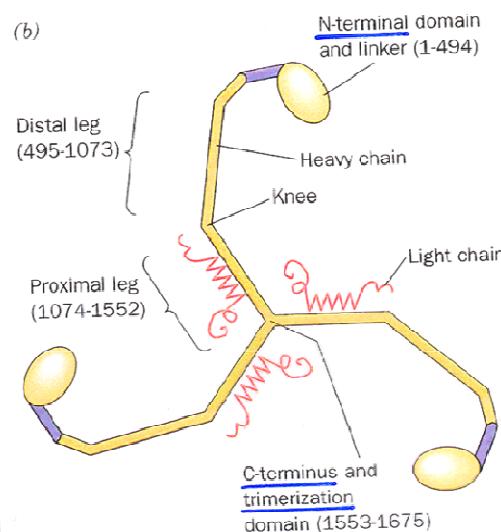


FIGURE 12-55 Anatomy of a clathrin-coated vesicle. (a) A cryo-electron microscopy-based image of a clathrin cage at 21 Å resolution with its triskelions differently colored. Its adaptor protein-containing core has been removed for clarity. As the accompanying diagram (right) indicates, a triskelion is centered on each of this polyhedral cage's 36 vertices, the cage edges are formed by the antiparallel legs of adjacent triskelions, and the linker and N-terminal domains project inward. Clathrin forms polyhedral cages with a large range of different sizes (number of hexagons).

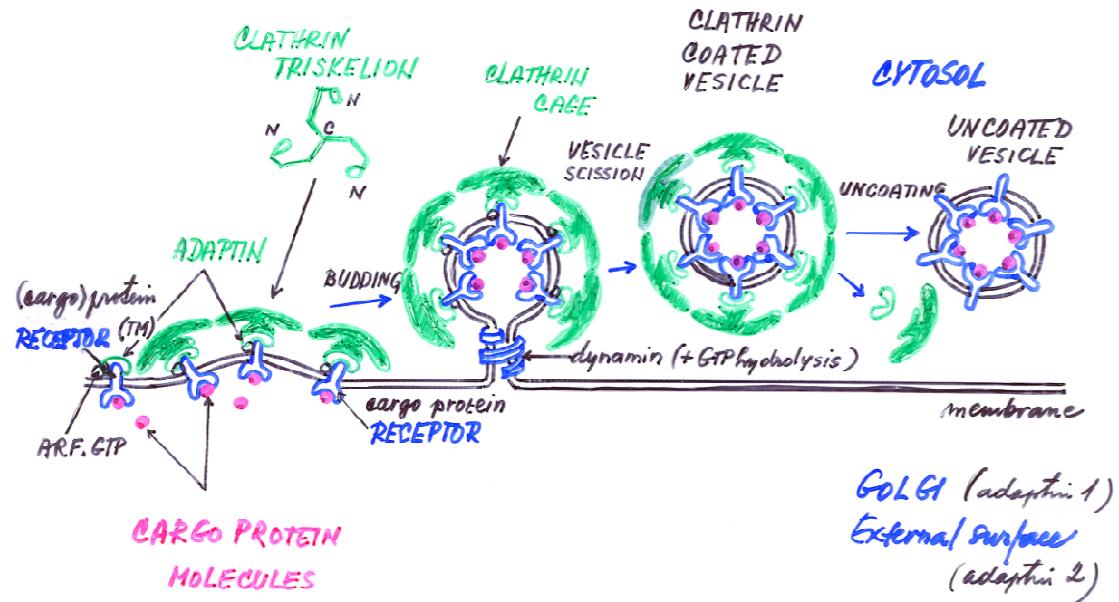


CLATHRIN HEAVY CHAIN TRIMER
=
TRISKELEION

polyhedral cages with a large range of different sizes (number of hexagons): That shown here is only ~600 Å in diameter, whereas clathrin-coated membranous vesicles are typically ~1200 Å in diameter or larger. [Electron micrograph by Barbara Pearse and courtesy of H.T. McMahon, MRC Laboratory for Molecular Biology, Cambridge, U.K.]
(b) Schematic diagram of a triskelion indicating its structural subdivisions.

FORMATION OF CLATHRIN-COATED VESICLES

= A COMPLEX PROCESS



CARGO PROTEINS carry specific TRANSPORT SIGNALS, which are recognized by CARGO RECEPTORS

mannose 6-P
latching of hydrolases
for lysosomes

Function of CLATHRIN CAGE: to determine the shape of the vesicle?

MOVEMENT OF VESICLES

- 1) by diffusion - short distances (ER → Golgi app.)
- 2) by motor proteins (myosin, dynein, kinesin) alongside of cytoskeletal + ATP driven "crawling" microtubules

Mechanisms of vesicle movement in the cell

1. Vesicles that travel only short distances ($< 1\mu\text{m}$) do so via **diffusion**, a process that typically takes from 1 to several minutes
2. Vesicles that have longer distances to commute (e.g. from trans-GOLGI to the plasma membrane) are actively transported along cytoskeletal microtubules by the **motor proteins dynein and kinesin**, which unidirectionally crawl along microtubule "tracks in an ATP - driven process.

Section 12-4. Membrane Assembly and Protein Targeting

1. SECRETORY VESICLE FUSION

In arriving at its target membrane, a vesicle fuses with it, thereby releasing its contents on the opposite side of the target membrane:

e.g. TRANSMISSION OF NERVE IMPULSES

via SYNAPSIS
(junctions between neurons, and neurons and muscles)

PROTEINS REQUIRED FOR VESICLE FUSION (ACTIVE) PROCESS :

Rab (GTPases)

SNARE

R-SNARE : assoc.

Q. with vesicle membr.
t-SNARE : assoc

with target membr.
by association they anchor vesicles to their target membranes = DOCKING

SM proteins

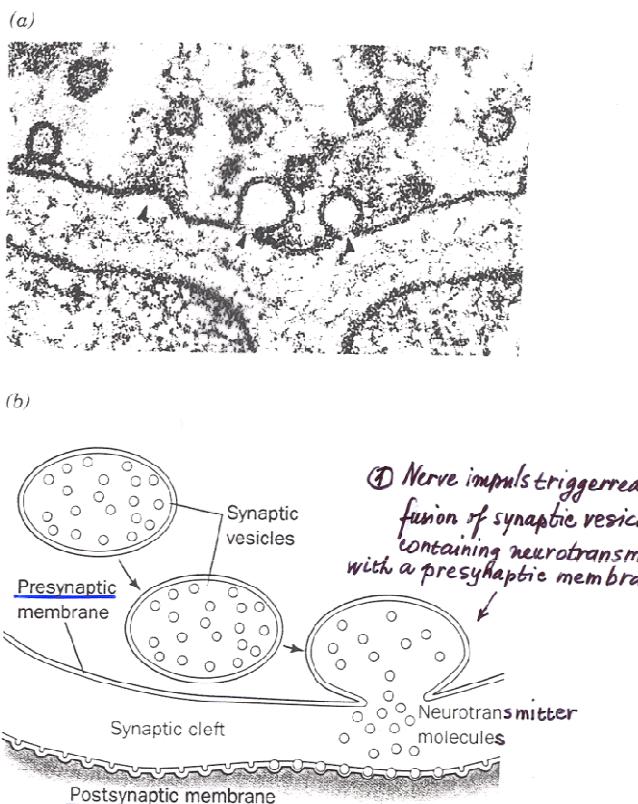
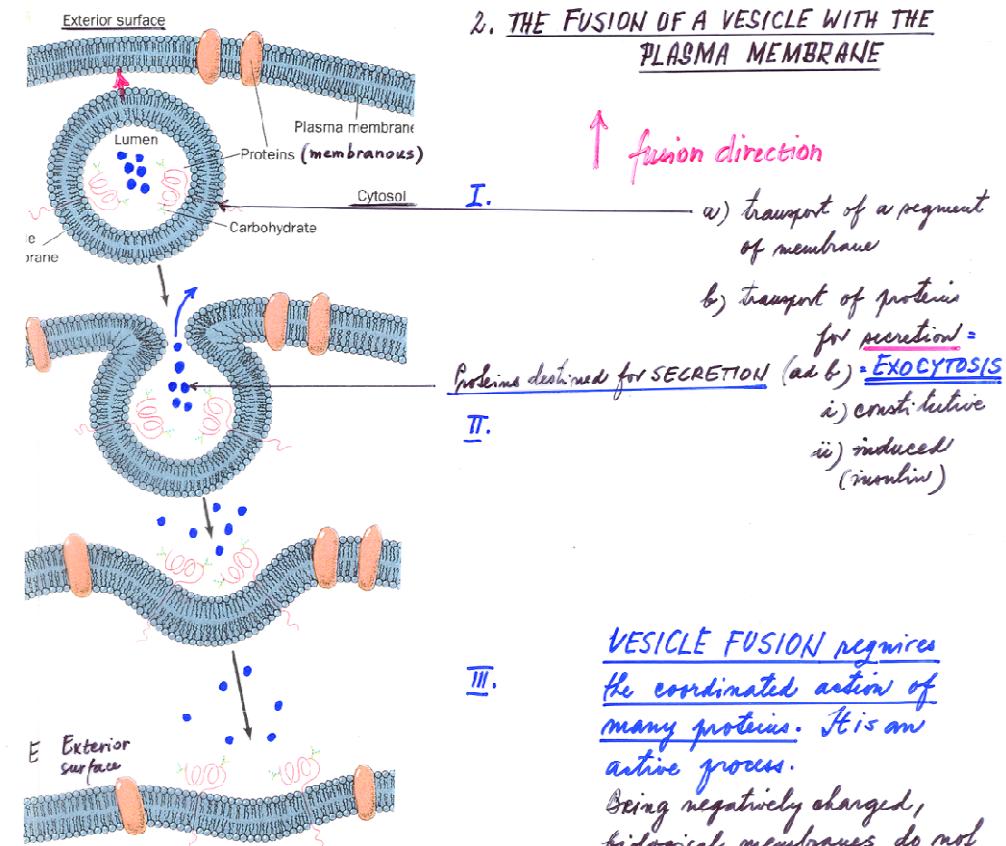


FIGURE 12-61 Transmission of nerve impulses across a synaptic cleft. (a) Electron micrograph of a frog neuromuscular junction in which the synaptic vesicles are undergoing exocytosis (arrows) with the presynaptic membrane (top). [Courtesy of John Heuser, Washington University School of Medicine, St. Louis, Missouri.] (b) The neurotransmitter, which is thereby discharged into the synaptic cleft, rapidly (< 0.1 ms) diffuses to the postsynaptic membrane, where it binds to transmembrane receptors, triggering a new nerve impulse = continuation of the nerve impulse in the postsynaptic cell.

indicating the presence of an **NEM-sensitive fus protein**. NSF is a cytosolic ATPase that does not bind to membranes unless a **soluble NSF attachment protein (SNAP)** is also present. SNAsPs bind to membr

2. THE FUSION OF A VESICLE WITH THE PLASMA MEMBRANE



12-53 The fusion of a vesicle with the plasma membrane preserves the orientation of the integral proteins embedded in the vesicle bilayer. The inside of the vesicle and the exterior of the cell are topologically equivalent because the same side of the protein is always immersed in the cytosol. Any soluble proteins contained within the vesicle will be secreted. In fact, proteins destined for secretion are packaged in membranous secretory vesicles that subsequently fuse with the plasma membrane as shown.

Tet Tx binds to inhibitory neurons →
= spastic paralysis
Bot Tx (1-7) binds to motor neurons →
= flaccid paralysis

ially encased on their outer (cytosolic) faces by proteins that act as flexible scaffolding in protein formation. A vesicle buds off from its membrane and later fuses to its target membrane, preserving the orientation of the transmembrane proteins (12-53), so that the lumens of the ER and the

4) SM proteins

↑ fusion direction

a) transport of a segment of membrane

b) transport of protein for secretion =

Proteins destined for SECRETION (at b) = EXOCYTOSIS

- i) constitutive
- ii) induced (secretion)

VESICLE FUSION requires the coordinated action of many proteins. It is an active process.

Being negatively charged, biological membranes do not spontaneously fuse! They strongly repel one another at short distances.

~ Four classes of proteins appear to participate in the fusion:

- 1) Rab (GTPases) : recognition of the target membrane
- 2) SNARE

R - SNARE : in the cargo vesicle

C - SNARE : in the target membrane.

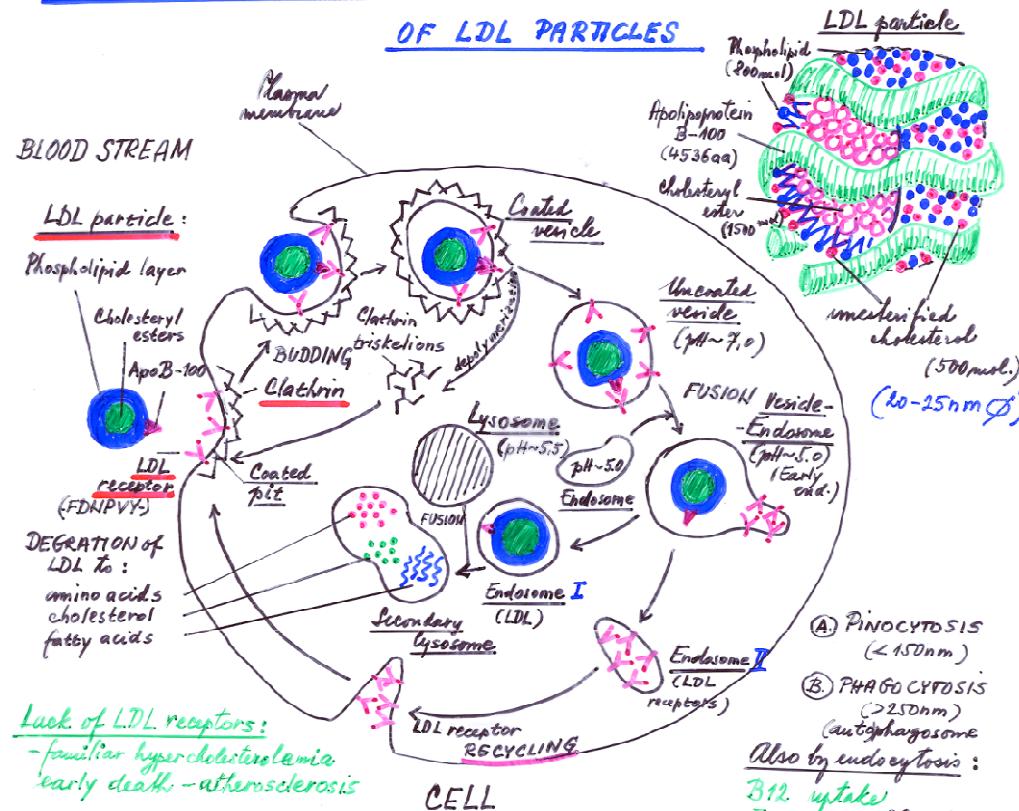
t - SNARE : in the target membrane by association (via complementarity) they anchor vesicles to their target membranes = DOCKING - TRANS-SNARE COMPLEX FORMATION

- 3) Pore forming protein V0

TETANUS and BOTULINUS TOXINS

Specifically cleave proteins
SNARES = inhibition of release of neurotransmitters into synapses

SEQUENCE OF EVENTS IN THE RECEPTOR-MEDIATED ENDOCYTOSIS



VESICLE - coated
- uncoated

ENDOSOME : dissociation of LDL from its receptor induced by $\text{pH} \sim 5.0$

- endosome I : vesicular portion of the endosome =
accumulates LDL

- endosome II : membrane portion with attached tubular structure = concentrates LDL receptors

LYSOSOME : degradation of LDL = cholesterol \rightarrow membranes

(A) PINOCYTOSIS
($< 150\text{nm}$)

(B) PHAGOCYTOSIS
($> 250\text{nm}$)
(autophagosome)

Also by endocytosis:

B12 uptake
Fe \rightarrow (transferrin)
virus internalization
(influenza, HIV, etc.)

+ active movement:
a) actin-mediated
b) myosin motor:
(molecules)