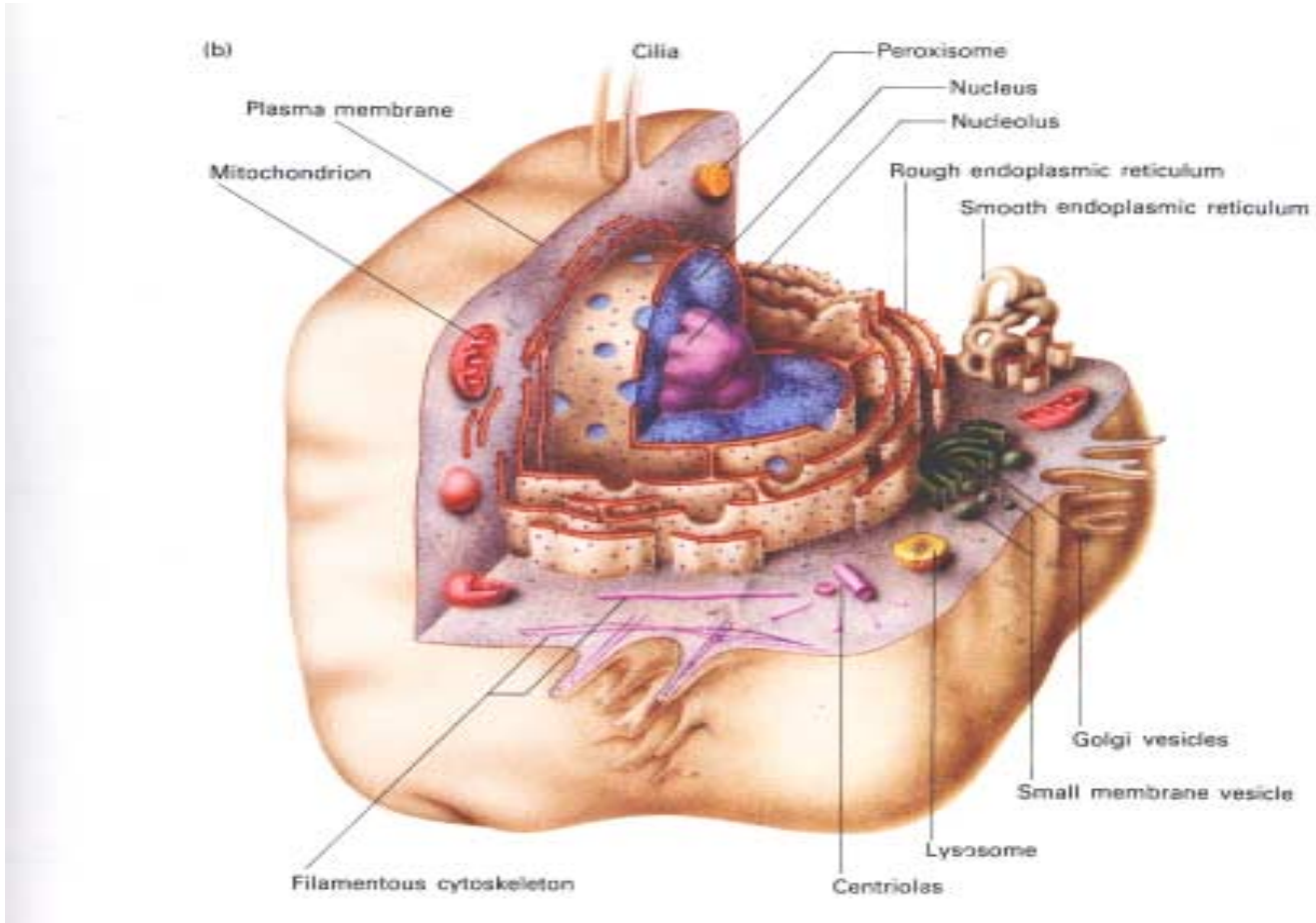
Rakuteooria ajalugu.

- **Athanasius Kircher-**vaatles vaklade ja teiste elusolendite arengut kõdunevates organismides (1658).
- **Jan Swammerdam**-kirjeldas esimesena punaseid vererakke.
- **Antoni van Leeuwenhoek** (1632-1723)- avastas mikroobid.
- **Robert Hook-**kirjeldas esimesena rakku (1665) ning nimetas need *cella*.
- **Lazzaro Spallanzani**-”organism pärineb alati teisest organismist”, kummutas elu isetärkamise teooria.
- **Louis Pasteur** (1822-1895)-kummutas lõplikult elu isetärkamise teooria.
- **Robert Brown**-kirjeldas esimesena rakutuuma (1831).
- **Matthias Jakob Schleiden**-”kõik taime osad koosnevad rakkudest või nende produktidest” (1838).
- **Theodor Shwann**-”kõik loomade koed koosnevad rakkudest või nende produktidest” (1839).
- **Rudolf Virchow**-”rakk tekib rakust” (*omnis cellula e cellula*).

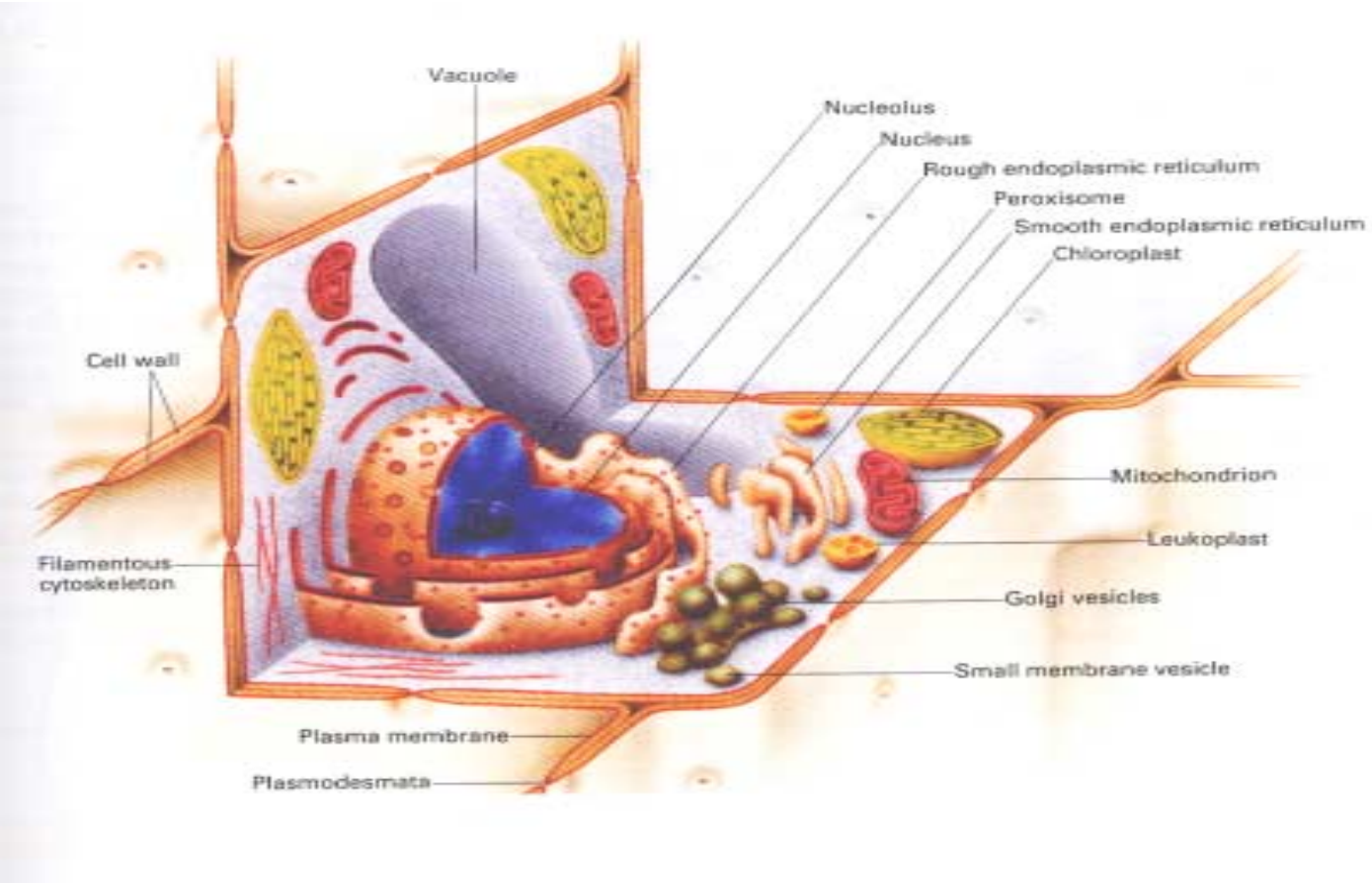
Elu tekke eeldused:

- pidid olema moodustunud isereplitseeruvad polümeerid (ilmselt RNA)
- pidi olema tekkinud mehhanism, mille abil RNA suunaks valgusünteesi, s.o. geneetiline kood
- pidid olema tekkinud molekulid (lipiidid), mis moodustaksid membraani ning eraldaks keskonnast isereplitseeruva valkude ja RNA segu

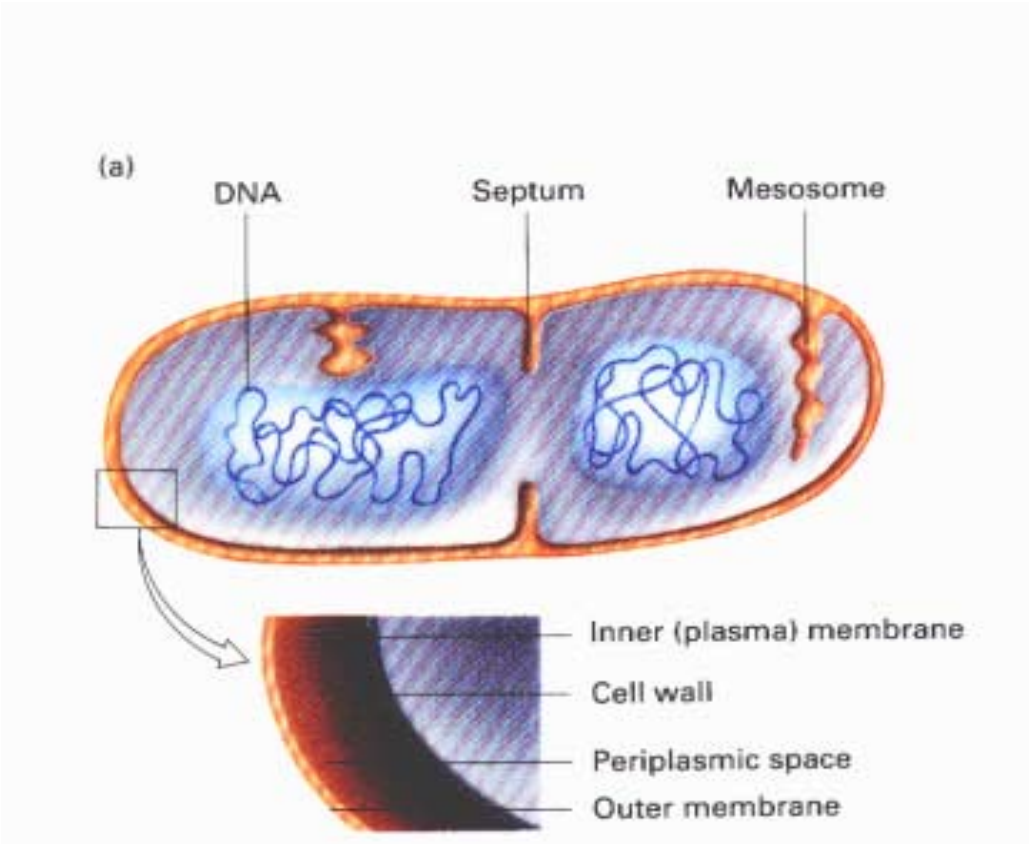
Loomarakk


(b)
Cilia
Peroxisome
Nucleus
Nucleolus
Plasma membrane
Mitochondrion
Rough endoplasmic reticulum
Smooth endoplasmic reticulum
Golgi vesicles
Small membrane vesicle
Lysosome
Filamentous cytoskeleton
Centriolas

Taimerakk.


Vacuole
Nucleolus
Nucleus
Rough endoplasmic reticulum
Peroxisome
Smooth endoplasmic reticulum
Chloroplast
Cell wall
Mitochondrion
Leukoplast
Filamentous cytoskeleton
Golgi vesicles
Small membrane vesicle
Plasma membrane
Plasmodesmata

Prokarüoot (bakter)



Rakutuum.

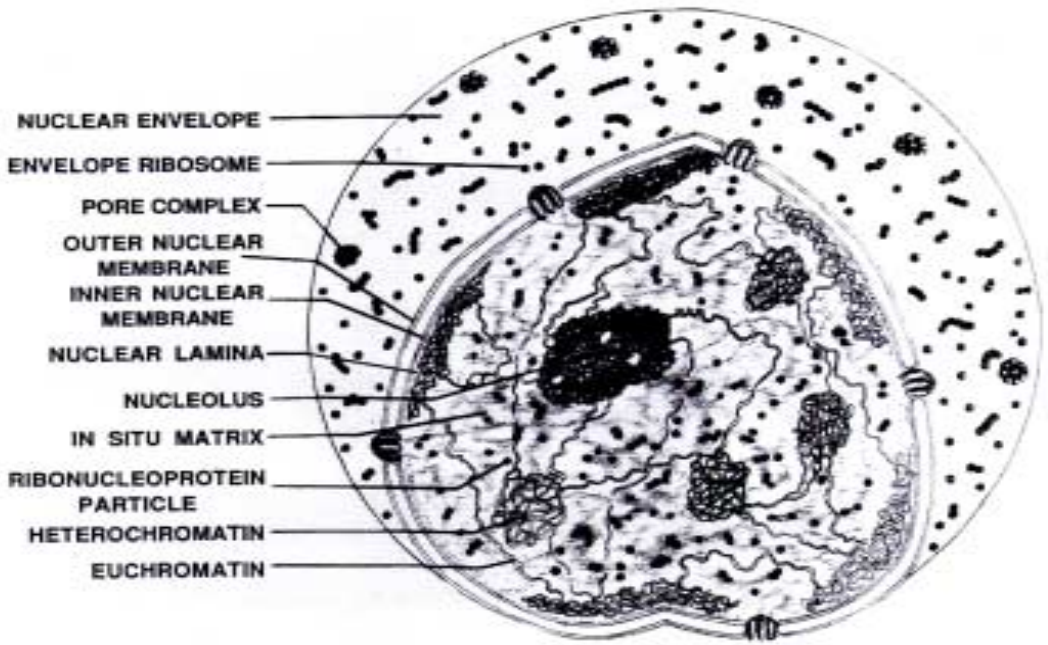


FIG. 3 Schematic model of a typical cell nucleus. The nucleus is surrounded by a double-membraned nuclear envelope containing nuclear pore complexes. Ribosome-like structures are found on the surface of the outer nuclear membrane as individual particles and "polysome-like" arrays. The chromatin in the nuclear interior is interpreted as a continuous system of condensed (heterochromatin) and diffuse (euchromatin) regions. The nonchromatin regions of the nuclear interior are simplified to contain the nucleolus, RNP (ribonucleoprotein) particles, and an *in situ* matrix forming a diffuse network which associates with the chromatin and nucleoli in the interior and the nuclear pore complexes at the periphery. The peripherally localized matrix may correspond to the nuclear lamina often observed in close association with the inner nuclear membrane. Drawn by L. A. Buchholtz and from Berezney, R. (1979) *In* "The Cell Nucleus," Vol. 7, (H. Busch, ed.), p. 413. Academic Press, New York.

Tuuma poori kompleks.

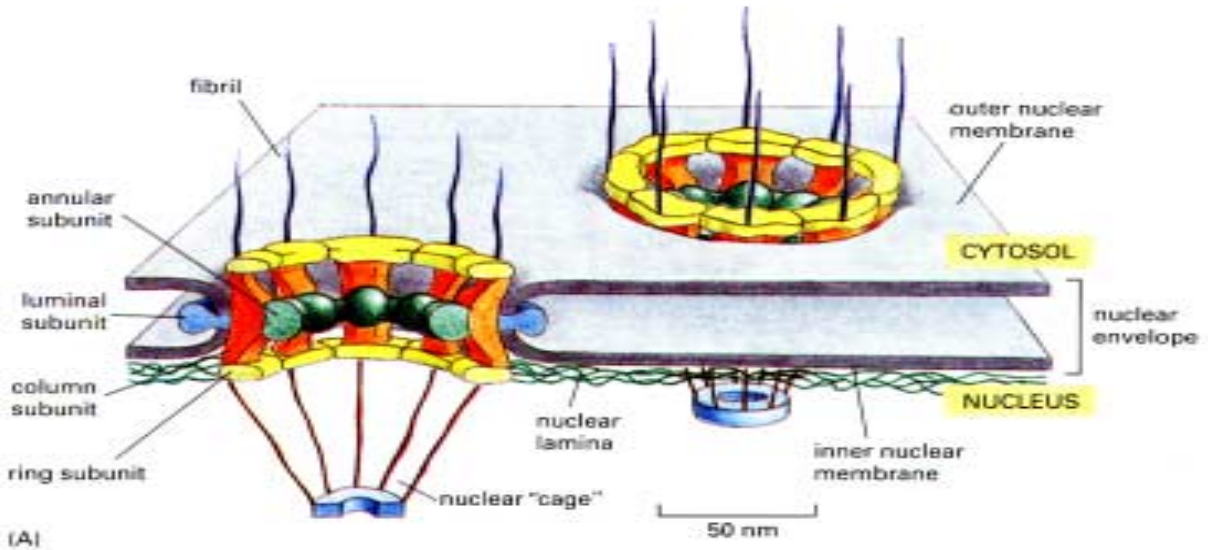


Figure 12–10 The arrangement of the nuclear pore complexes in the nuclear envelope. (A) A sketch showing a small region of the nuclear envelope. In cross-section the nuclear pore complex appears composed of three parts: (1) a column component which forms the bulk of the pore wall; (2) an annular component, which extends "spokes" toward the center of the pore; and (3) a luminal component, which is formed by a large transmembrane glycoprotein that is thought to help anchor the complex to the nuclear membrane. In addition, fibrils protrude from both the cytosolic and nuclear sides of the complex. On the nuclear side the fibrils converge to form cagelike structures, which are shown in a scanning electron micrograph of the nuclear side of the nuclear envelope of an oocyte in (B). (B, from M.W. Goldberg and T.D. Allen, *J. Cell Biol.* 119:1429–1440, 1992, by copyright permission of the Rockefeller University Press.)

Tuuma lokalisatsiooni signaal e. nukleaarne lokalisatsiooni signaal (NLS).

TABLE 19-6 Amino Acid Sequences That Act as Signals for Translocation to the Cell Nucleus

Type of Signal	Nuclear Protein	Location of Signal in Protein	Deduced Nuclear Localization Sequence*
Single	large T antigen of SV40 virus	Residues 126–132	Pro **Lys Lys Lys Arg** Lys Val
	Adenovirus E1a	C-terminus	**Lys Arg** Pro **Arg** Pro
	Influenza virus nucleoprotein (NP)	Near C-terminus; residues 336–345	Ala Ala Phe Glu Asp Leu **Arg** Val Leu Ser
Bipartite	*Xenopus* nucleoplasmin	Near C-terminus; residues 155–171	**Lys Arg** Pro Ala Ala Thr Lys Lys Ala Gly Gln Ala **Lys Lys Lys Lys** Leu
	Xenopus N1 nuclear protein	Internal; residues 534–550	**Lys Arg** Lys Thr Glu Glu Glu Ser Pro Leu Lys Asp Lys Asp Ala **Lys Lys**
	Yeast SWI 5 transcription factor	Internal; residues 636–652	**Lys Lys** Tyr Glu Asn Val Val Ile Lys Arg Ser Pro **Arg Lys Arg** Gly Arg
	Mouse poly-ADP-ribose polymerase	Internal; residues 208–224	**Arg** Lys Gly Asp Glu Val Asp Gly Thr Asp Glu Val Ala **Lys Lys Lys** Ser
	Chicken estrogen receptor	Internal; residues 250–266	**Arg Lys** Asp Arg Arg Gly Gly Glu Met Met Lys Gln **Lys Arg** Gln **Arg** Glu

*Boldface = the basic residues thought to be essential for nuclear uptake.

SOURCE: C. Dingwall and R. Laskey, 1986, *Ann. Rev. Cell Biol.* 2:367–390; and C. Dingwall and R. Laskey, 1991, *Trends Biochem. Sci.* 16:478–481.

Tuumake.

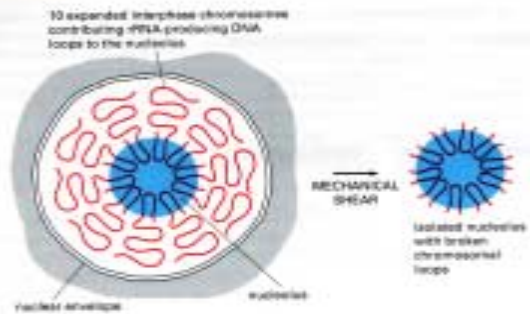


Figure 8–63 **The nucleolus.** This highly schematic view of a nucleo in a human cell shows the contributions of loops of chromat containing rRNA genes from 10 separate chromosomes. Purified nucleoli are very useful for biochemical studies of nucleolar function; to obtain such nucleoli, loops of chromatin are mechanic sheared from their chromosomes shown.

ules, which do not appear on other types of RNA transcripts, presumably reflect the first of the protein-RNA interactions that take place in the nucleolus.

The biosynthetic functions of the nucleolus can be traced by briefly labeling newly made RNA with ^{3}H-uridine. After varying intervals of further incubation without ^{3}H-uridine, a cell fractionation procedure can be used to break the rRNA genes free of their chromosomes, thereby allowing the radioactive nucleoli to be isolated in relatively pure form (Figure 8–63). Such experiments show that the

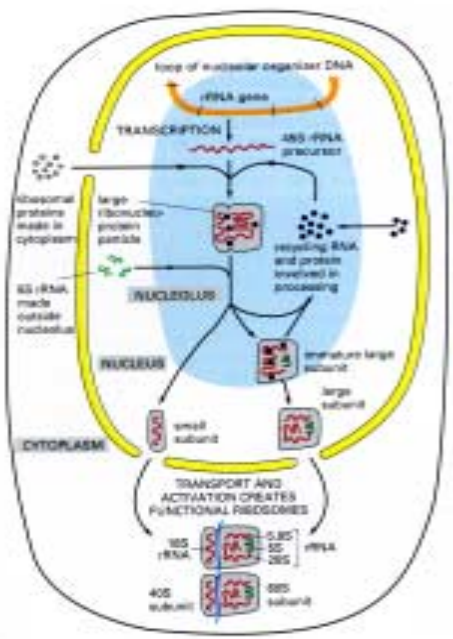


Figure 8–64 **The function of the nucleolus in ribosome synthesis.** 45S rRNA transcript is packaged large ribonucleoprotein particle containing many ribosomal prote imported from the cytoplasm. W this particle remains in the nucle selected pieces are discarded as processed into immature large a small ribosomal subunits. These subunits are thought to attain th final functional form only as each individually transported through nuclear pores into the cytoplasm.

Kromatiin.

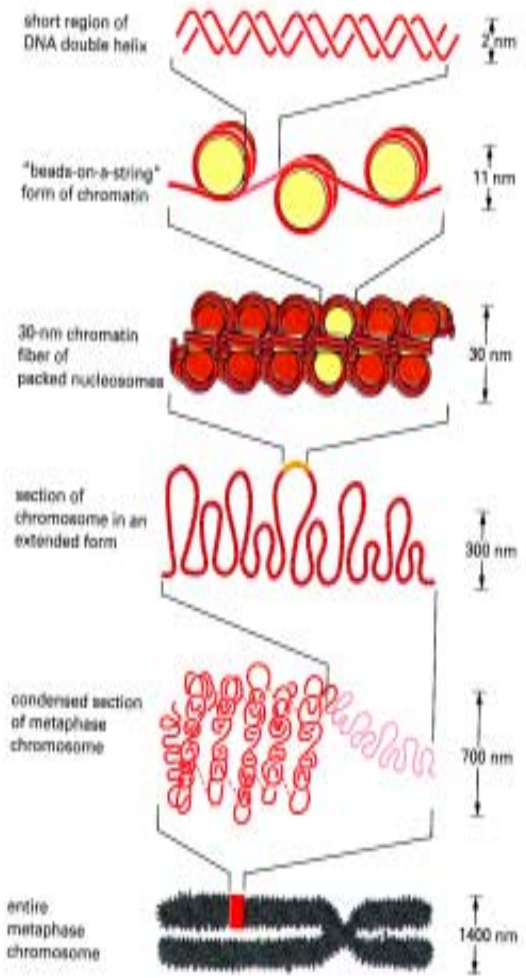
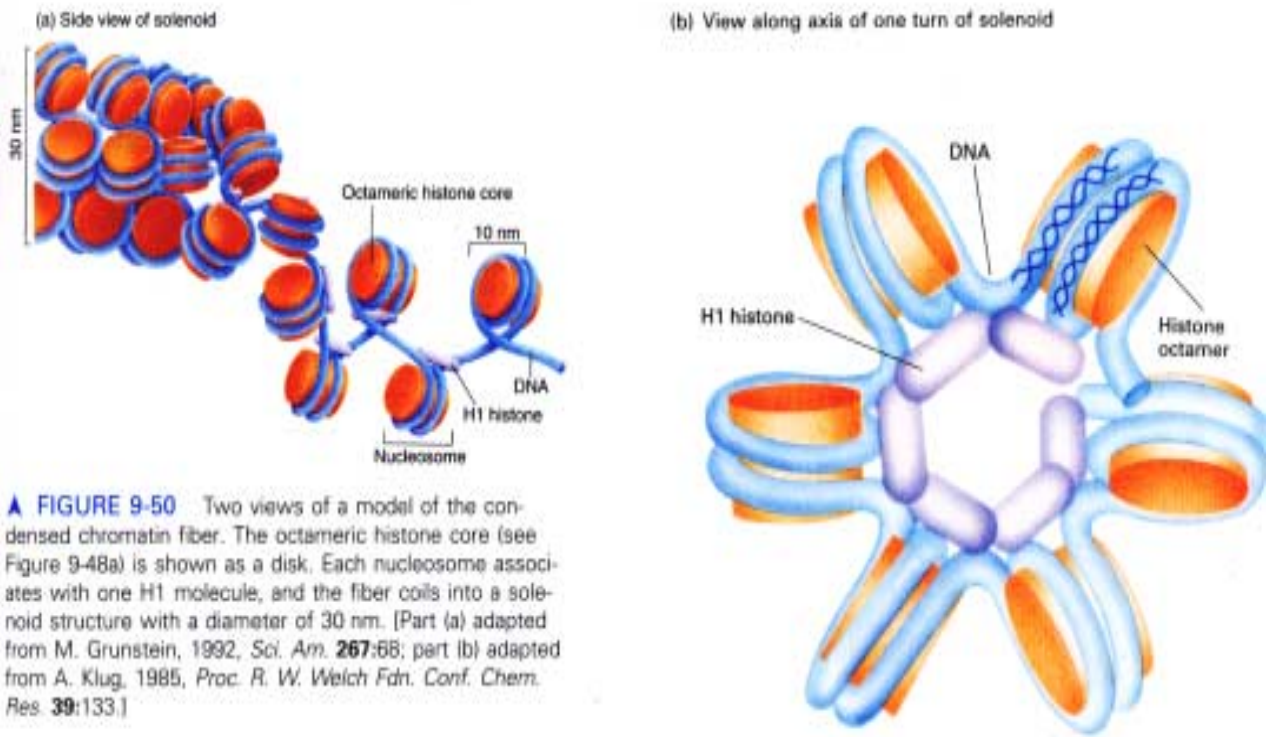


Figure 8–30 Model of chromatin packing. This schematic drawing shows some of the many orders of chromatin packing postulated to give rise to the highly condensed mitotic chromosome.

Nukleosoomid (1).



▲ FIGURE 9-50 Two views of a model of the condensed chromatin fiber. The octameric histone core (see Figure 9-48a) is shown as a disk. Each nucleosome associates with one H1 molecule, and the fiber coils into a solenoid structure with a diameter of 30 nm. [Part (a) adapted from M. Grunstein, 1992, *Sci. Am.* **267**:68; part (b) adapted from A. Klug, 1985, *Proc. R. W. Welch Fdn. Conf. Chem. Res.* **39**:133.]

Nukleosoomid (2).

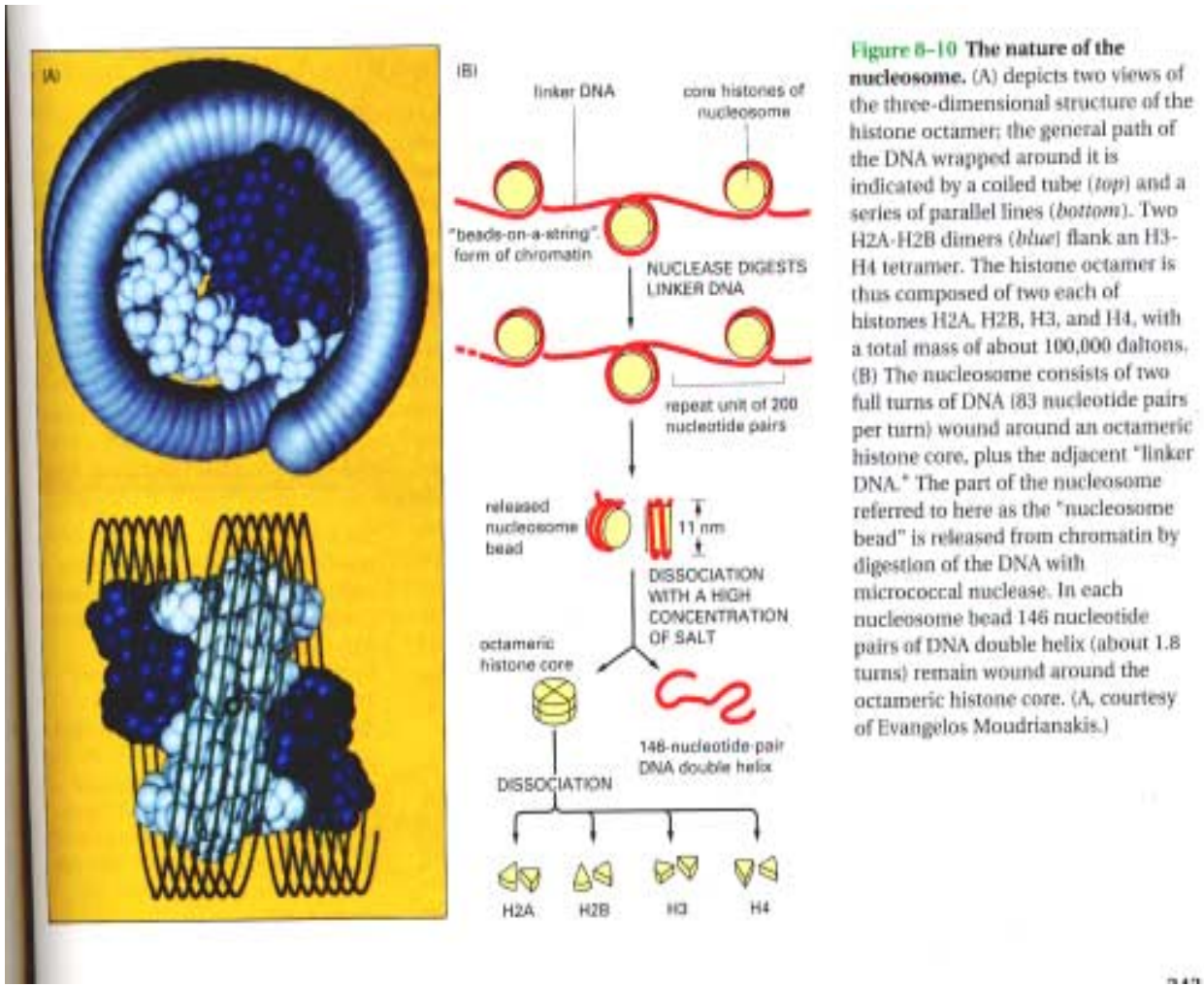


Figure 8–10 The nature of the nucleosome. (A) depicts two views of the three-dimensional structure of the histone octamer; the general path of the DNA wrapped around it is indicated by a coiled tube (*top*) and a series of parallel lines (*bottom*). Two H2A-H2B dimers (*blue*) flank an H3-H4 tetramer. The histone octamer is thus composed of two each of histones H2A, H2B, H3, and H4, with a total mass of about 100,000 daltons. (B) The nucleosome consists of two full turns of DNA (83 nucleotide pairs per turn) wound around an octameric histone core, plus the adjacent "linker DNA." The part of the nucleosome referred to here as the "nucleosome bead" is released from chromatin by digestion of the DNA with micrococcal nuclease. In each nucleosome bead 146 nucleotide pairs of DNA double helix (about 1.8 turns) remain wound around the octameric histone core. (A, courtesy of Evangelos Moudrianakis.)

X-kromosoomi inaktivatsioon.

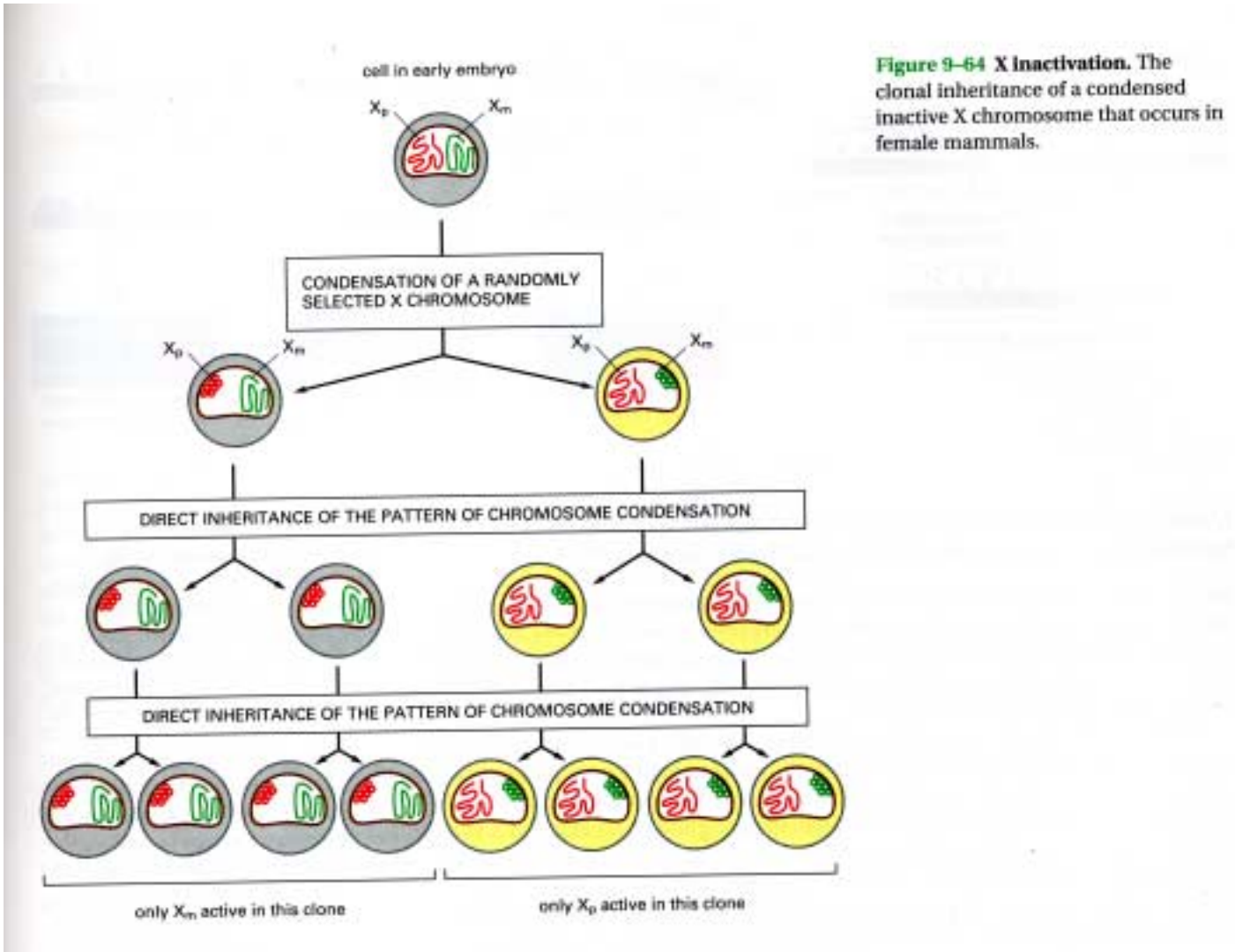


Figure 9–64 X inactivation. The clonal inheritance of a condensed inactive X chromosome that occurs in female mammals.

Inimese karüotüüp.

Figure 8–32 A standard map of the banding pattern of each chromosome in the human karyotype. This map was determined at the prometaphase stage of mitosis. Chromosomes 1 through 22 are labeled in the approximate order of their size; a diploid cell contains two of each of these autosomes plus two sex chromosomes—two X chromosomes (female) or an X and a Y chromosome (male). The 850 bands shown here are G bands, which stain with reagents that appear to be specific for A-T-rich DNA sequences. The *green knobs* on chromosomes 13, 14, 15, 21, and 22 indicate the positions of the genes that encode the large ribosomal RNAs; the *green lines* mark the centromere on each chromosome. (Adapted from U. Franke, *Cytogenet. Cell Genet.* 31:24–32, 1981.)

Tsentromeer, telomeerid ja replikatsiooni alguspunktid.

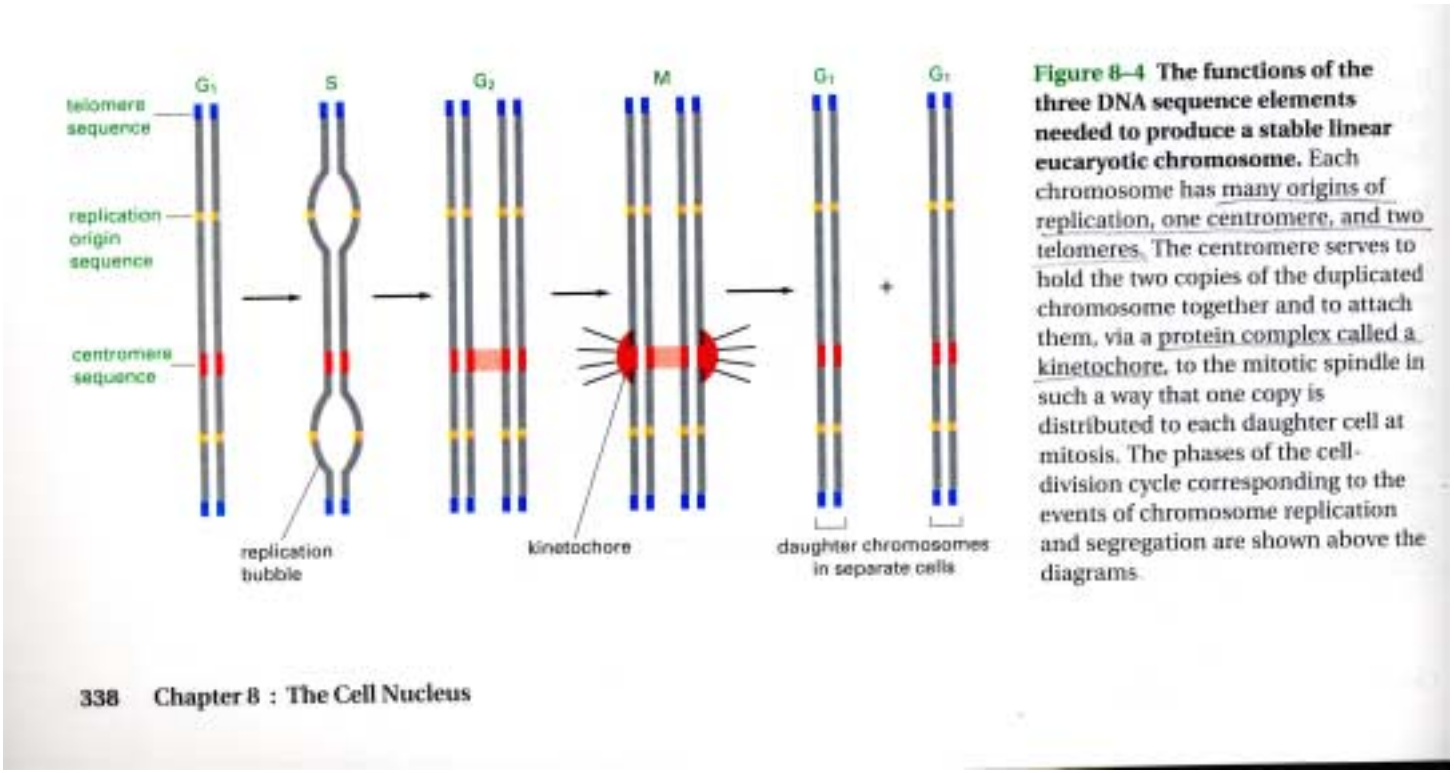


Figure 8–4 The functions of the three DNA sequence elements needed to produce a stable linear eucaryotic chromosome. Each chromosome has many origins of replication, one centromere, and two telomeres. The centromere serves to hold the two copies of the duplicated chromosome together and to attach them, via a protein complex called a kinetochore, to the mitotic spindle in such a way that one copy is distributed to each daughter cell at mitosis. The phases of the cell-division cycle corresponding to the events of chromosome replication and segregation are shown above the diagrams.

DNA replikatsiooni kahvel.

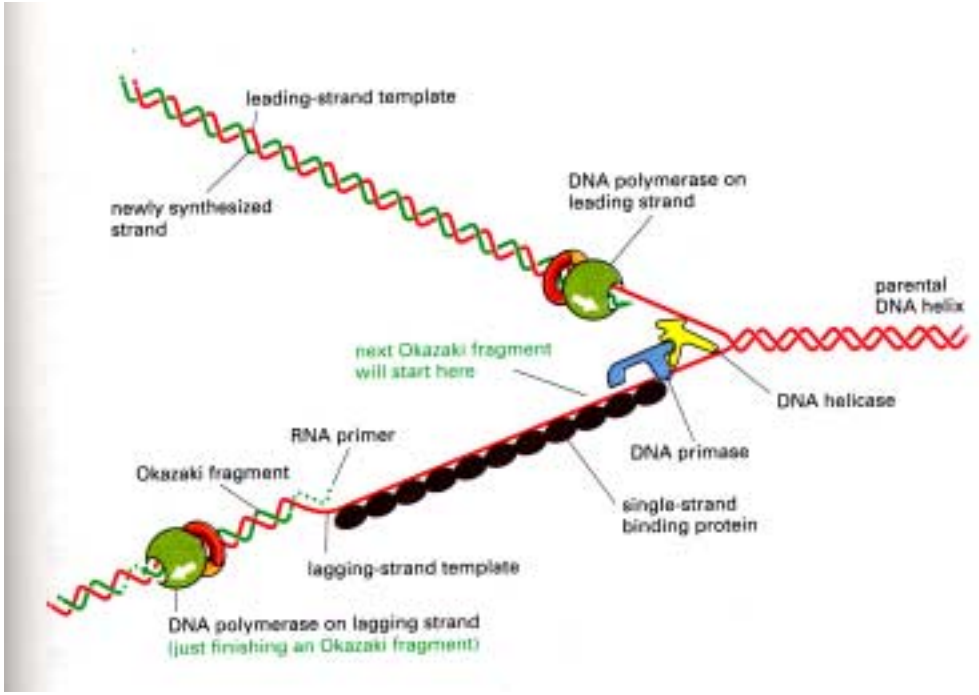


Figure 6–48 The proteins at a DNA replication fork. The major types of proteins that act at a DNA replication fork are illustrated, showing their positions on the DNA.

DNA replikatsiooni kahvli teke replikatsiooni alguspunktis.

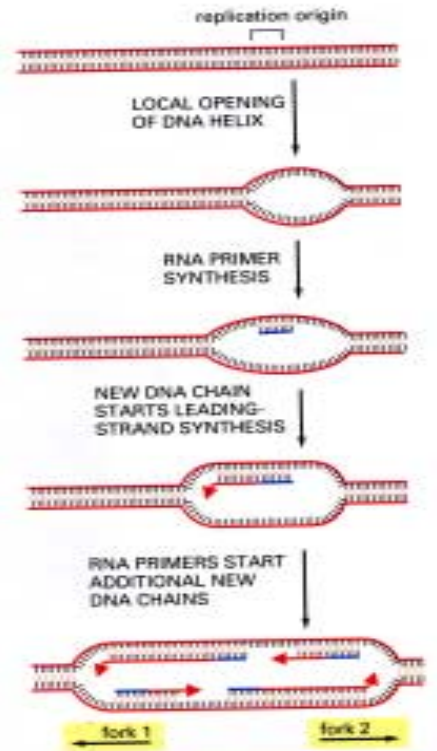
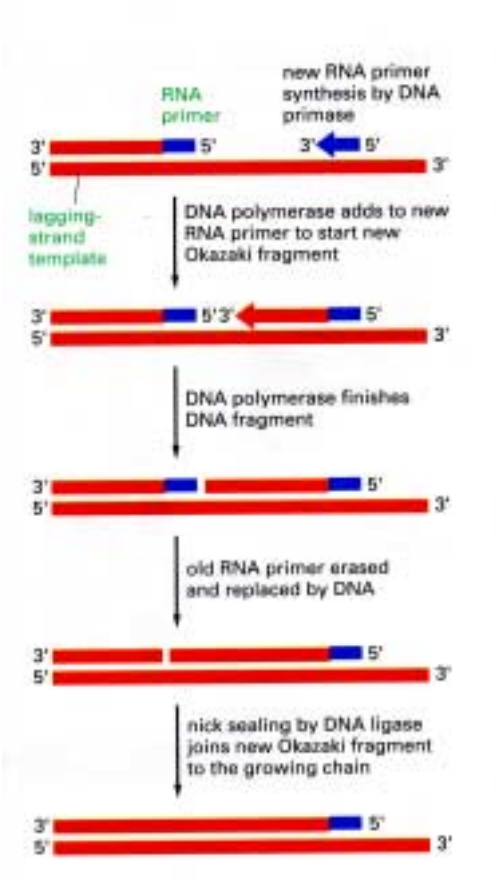


Figure 6–51 Replication fork initiation. The figure outlines the processes involved in the initiation of replication forks at replication origins. (See also Figure 6–52.)

DNA replikatsioon.



RNA süntees.

weakly to most DNA. The polymerase binds very tightly, however, when it con-

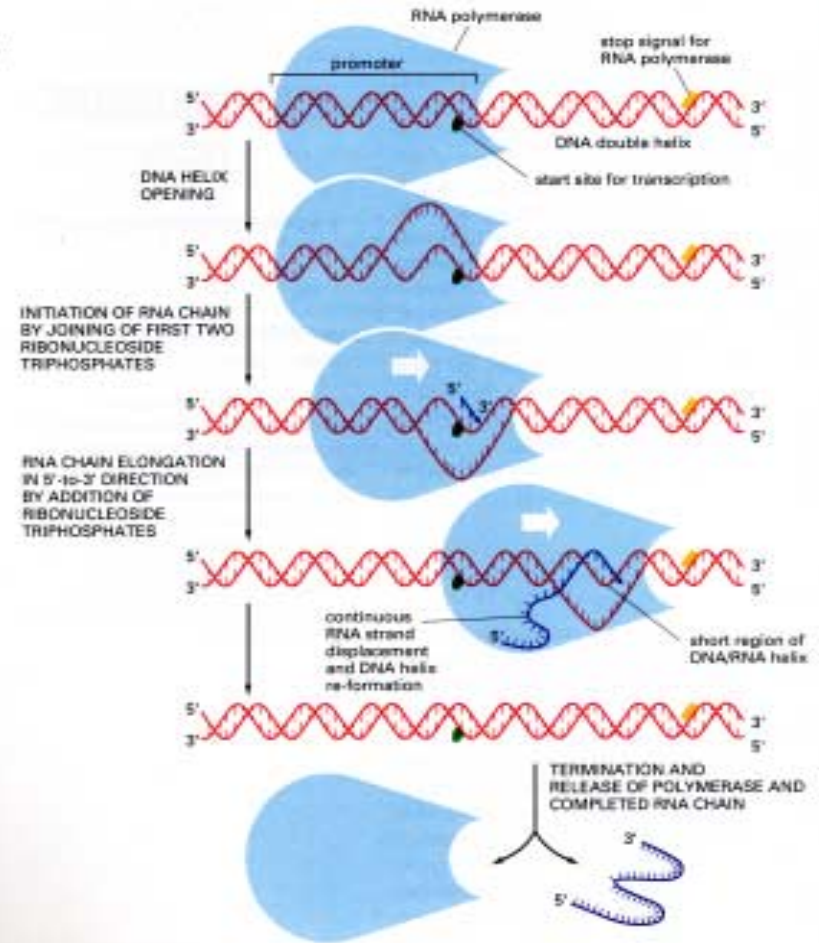


Figure 6–2 The synthesis of an RNA molecule by RNA polymerase. The enzyme binds to the promoter sequence on the DNA and begins its synthesis at a start site within the promoter. It completes its synthesis at a stop (termination) signal, whereupon both the polymerase and its completed RNA chain are released. During RNA chain elongation, polymerization rates average about 30 nucleotides per second at 37°C. Therefore, an RNA chain of 5000 nucleotides takes about 3 minutes to complete.

Eukarüootse raku biosünteesi, sekretsiooni ja endotsütoosi organellid.

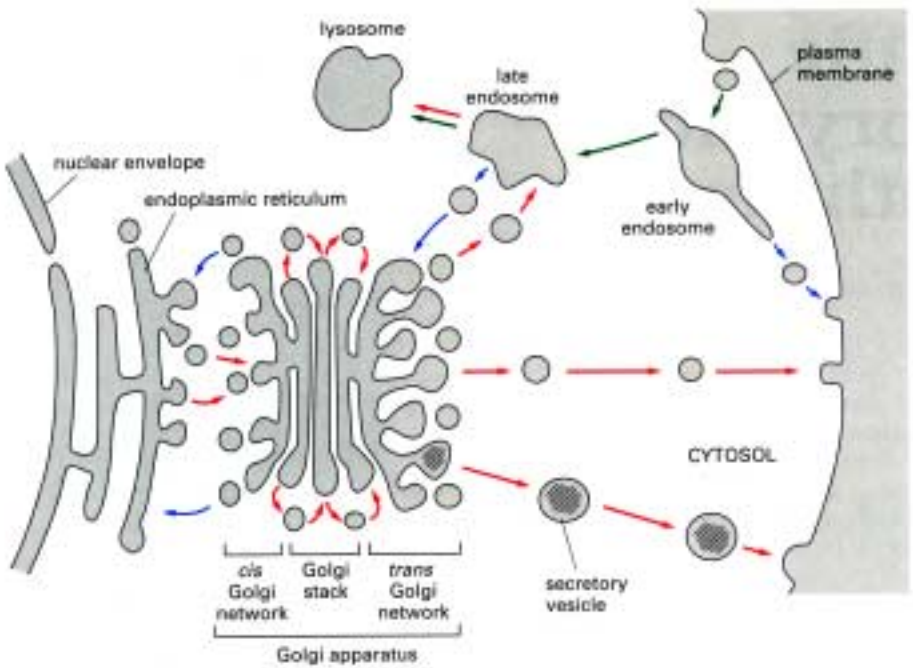
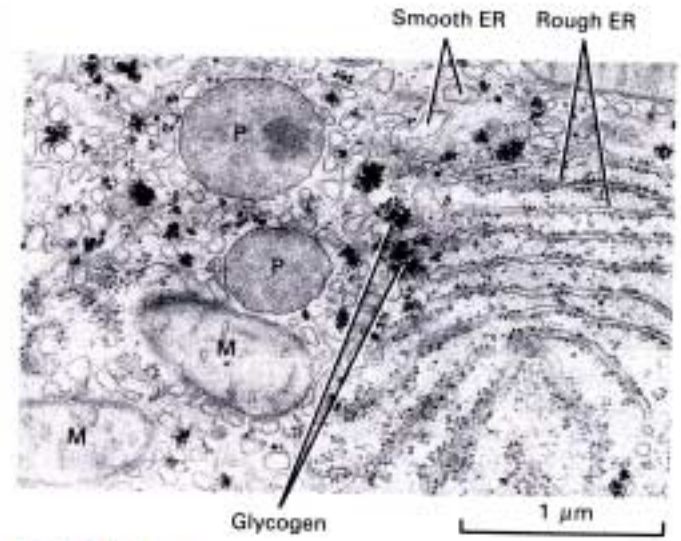
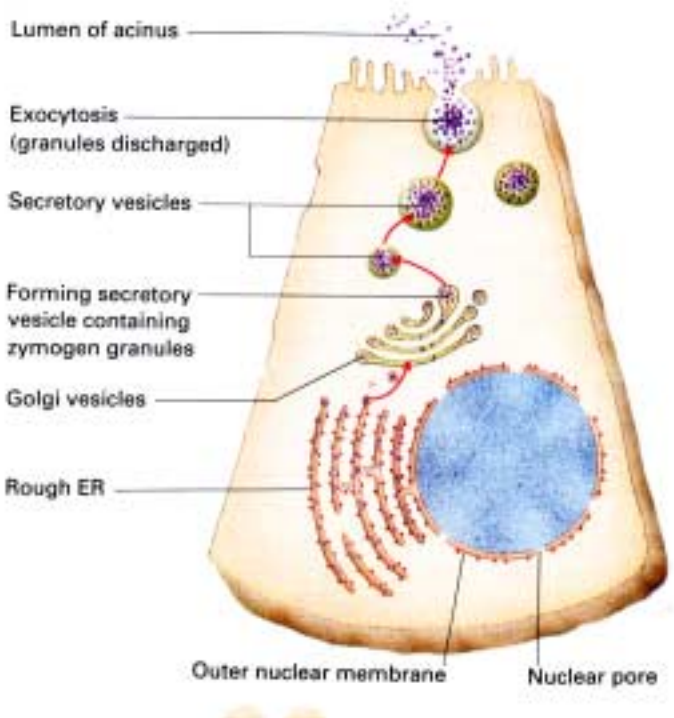


Figure 13–3 The intracellular compartments of the eucaryotic cell involved in the biosynthetic-secretory and endocytic pathways. Each compartment encloses a space that is topologically equivalent to the outside of the cell, and they all communicate with one another by means of transport vesicles. In the biosynthetic-secretory pathway (*red arrows*) protein molecules are transported from the ER to the plasma membrane or (via late endosomes) to lysosomes. In the endocytic pathway (*green arrows*) molecules are ingested in vesicles derived from the plasma membrane and delivered to early endosomes and then (via late endosomes) to lysosomes. Many endocytosed molecules are retrieved from early endosomes and returned to the cell surface for reuse; similarly, some

Endoplasmaatiline retiikulum, Golgi kompleks ja sekretoorsed vesiikulid.



▲ FIGURE 5-37 Electron micrograph of a section of a rat hepatocyte, showing two mitochondria (M), two peroxisomes (P), rough and smooth endoplasmic reticula, and glycogen rosettes. [Courtesy of P. Lazarow.]



Kare ja sile endoplasmaatiline retiikulum.

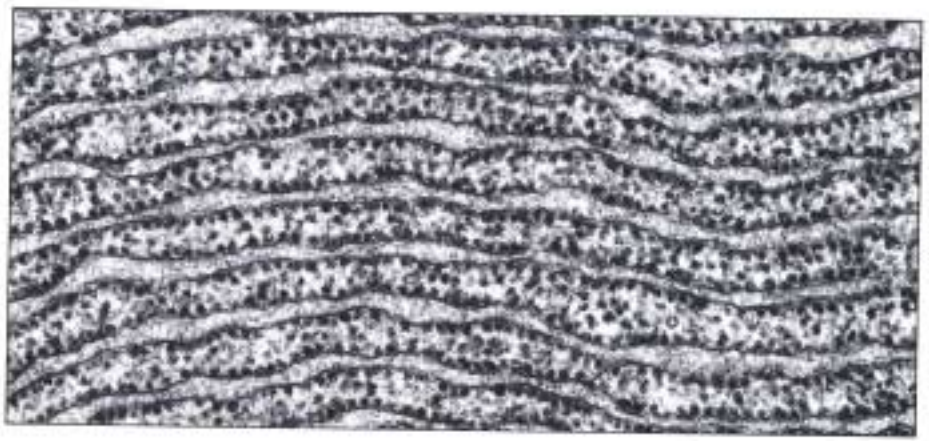


Figure 12–31 The rough ER. Electron micrograph of the rough ER, which receives its name from the many ribosomes on its cytosolic surface. (Courtesy of L. Orci.)

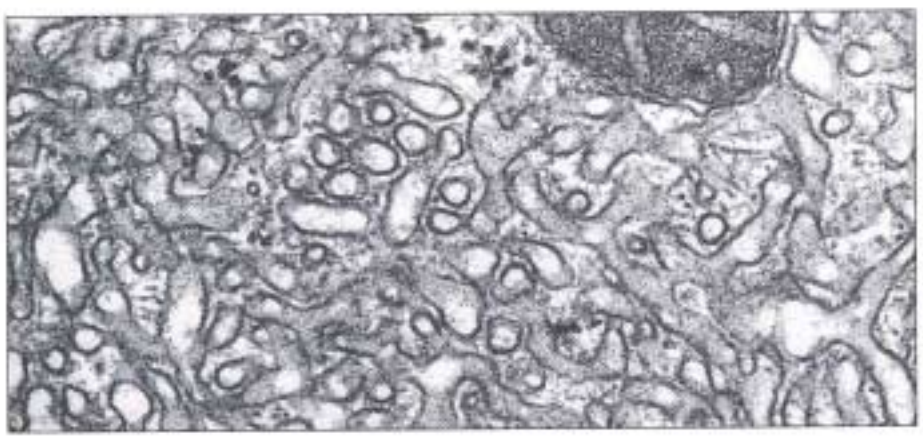


Figure 12–34 Abundant smooth ER in a steroid-hormone-secreting cell. This electron micrograph is of a testosterone-secreting Leydig cell in the human testis.

Kare ja sile endoplasmaatiline retiikulum.

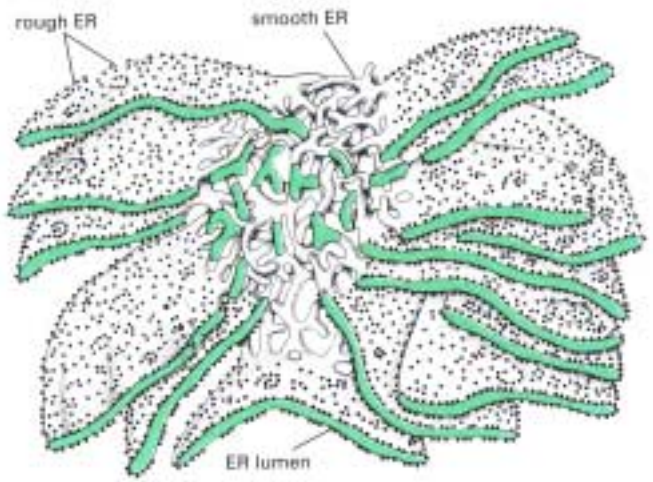


Figure 12–35 Three-dimensional reconstruction of a region of the smooth and rough ER in a liver cell. The rough ER forms oriented stacks of flattened cisternae, each having a luminal space 20 to 30 nm wide. The smooth ER membrane is connected to these cisternae and forms a fine network of tubules 30 to 60 nm in diameter. (After R.V. Krstić, Ultrastructure of the Mammalian Cell. New York: Springer-Verlag, 1979.)

Vabad ja membraaniga seotud ribosoomid.

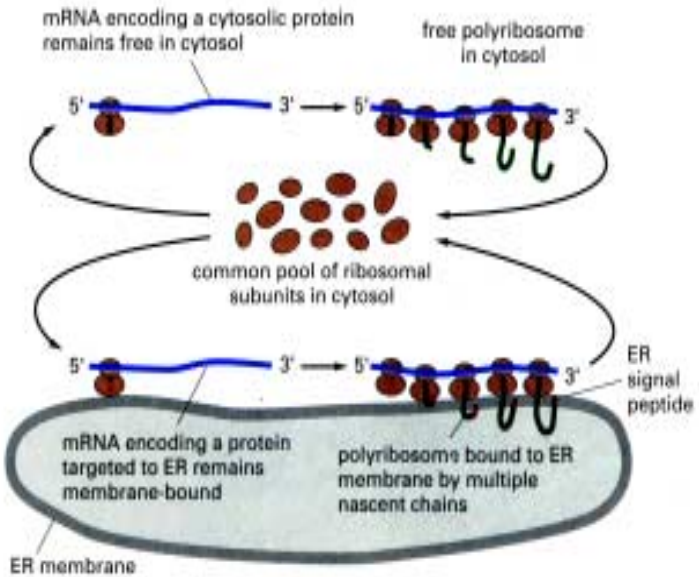


Figure 12–33 Free and membrane-bound ribosomes. A common pool of ribosomes is used to synthesize both the proteins that stay in the cytosol and those that are transported into the ER. It is the ER signal peptide on a newly formed polypeptide chain that directs the engaged ribosome to the ER membrane. The mRNA molecule may remain permanently bound to the ER as part of a polyribosome, while the ribosomes that move along it are recycled; at the end of each round of protein synthesis, the ribosomal subunits are released and rejoin the common pool in the cytosol.

Signaalpeptiidi hüpotees endoplasmaatilises võrgustikus.

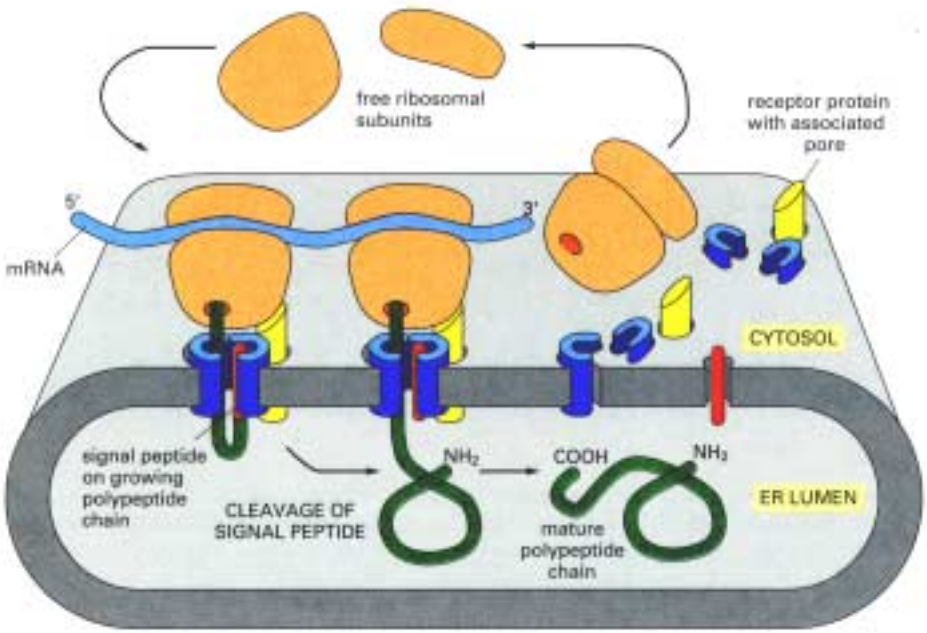


Figure 12–38 The original signal hypothesis. A simplified view of protein translocation across the ER membrane, as originally proposed. When the signal peptide emerges from the ribosome, it directs the ribosome to a receptor protein on the ER membrane. As it is synthesized, the polypeptide is postulated to be translocated across the ER membrane through a protein pore associated with the receptor. The signal peptide is clipped off during translation by signal peptidase, and the mature protein is released into the lumen of the ER immediately after being synthesized. We now know that the hypothesis is correct in outline but that additional components beside those shown in this figure are required. The signal peptidase, for example, is a complex of five differ

Signaalpeptiidid ja signaali äratundev osake (SRP) endoplasmaatilises võrgustikus.

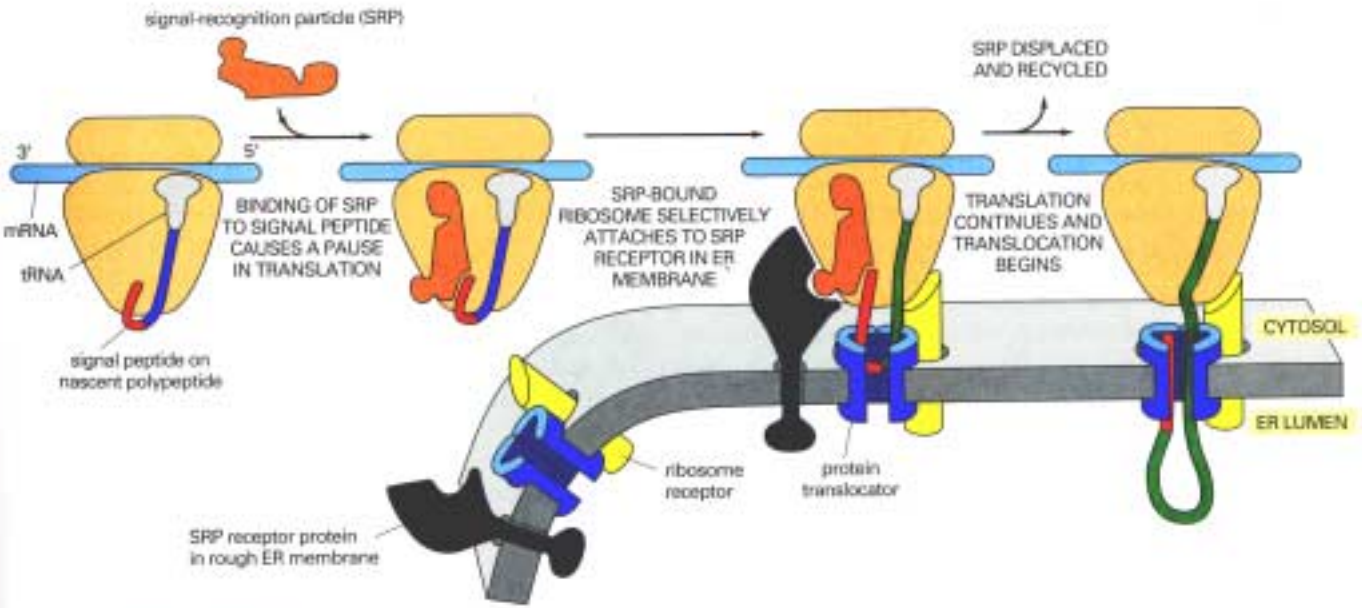


Figure 12–40 How ER signal peptides and SRP direct ribosomes to the ER membrane. The SRP and the SRP receptor are thought to act in concert. The SRP binds to the exposed ER signal peptide and to the ribosome, thereby inducing a pause in translation. The SRP receptor in the ER membrane, which is composed of two different polypeptide chains, binds the SRP ribosome complex. In a poorly understood reaction that involves multiple GTP-binding proteins, the SRP is released, leaving the ribosome on the ER membrane. A multisubunit protein translocation apparatus in the ER membrane then inserts the polypeptide chain into the membrane and transfers it across the lipid bilayer.

Transmembraanse valgu seostumine endoplasmaatilise võrgustiku membraani.

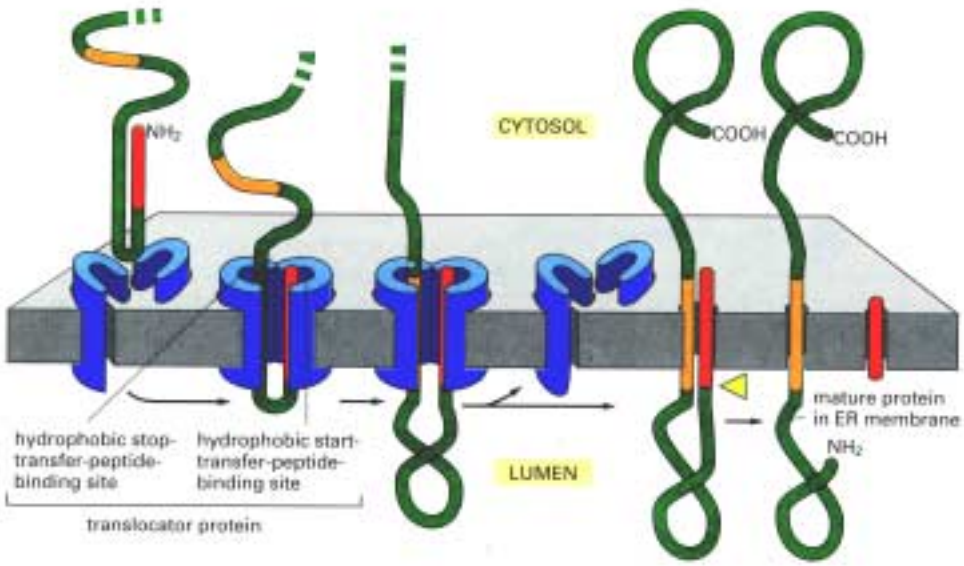


Figure 12–44 How a single-pass transmembrane protein with a cleaved ER signal peptide is integrated into the ER membrane. In this hypothetical model the co-translational translocation process is initiated by an amino-terminal ER signal peptide (*red*) that functions as a start-transfer signal as in Figure 12–43. In addition to the start-transfer peptide, however, the protein also contains a stop-transfer peptide (*orange*). When the stop-transfer peptide enters the translocator and interacts with a binding site, the translocator flips into its inactive state and discharges the protein laterally into the lipid bilayer.

Lahustuva valgu suundumine läbi endoplasmaatilise võrgustiku membraani.

translocator pore, cleaved off by the signal peptidase, and rapidly degraded to amino acids by other proteases in the ER while the protein is released into the ER lumen (Figure 12–43).

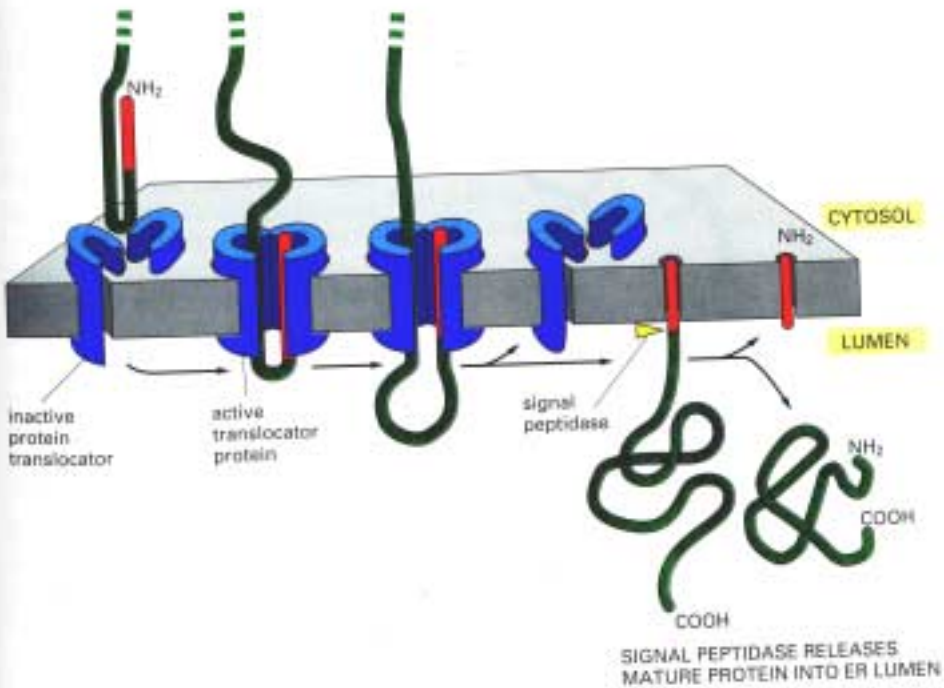


Figure 12–43 The translocation of a soluble protein across the ER membrane. In this hypothetical model the protein translocator in the membrane is postulated to exist in two alternative states—active or inactive. On binding an ER signal peptide (which acts as a start-transfer signal), the translocator adopts an active state and begins to transfer the polypeptide chain across the lipid bilayer as a loop. In this state it forms an aqueous pore across the membrane that can be detected electrophysiologically if the polypeptide chain is released (see Figure 12–42). After the protein has been completely translocated, the translocator reverts to an inactive conformation, which can no longer conduct ions across the membrane but is open to the lipid bilayer, allowing the hydrophobic signal peptide to diffuse out into the bilayer, where it is rapidly degraded. In this and the following two figures the ribosomes have been omitted for clarity.

Valgu glükosüleerimine karedas endoplasmaatilises võrgustikus.

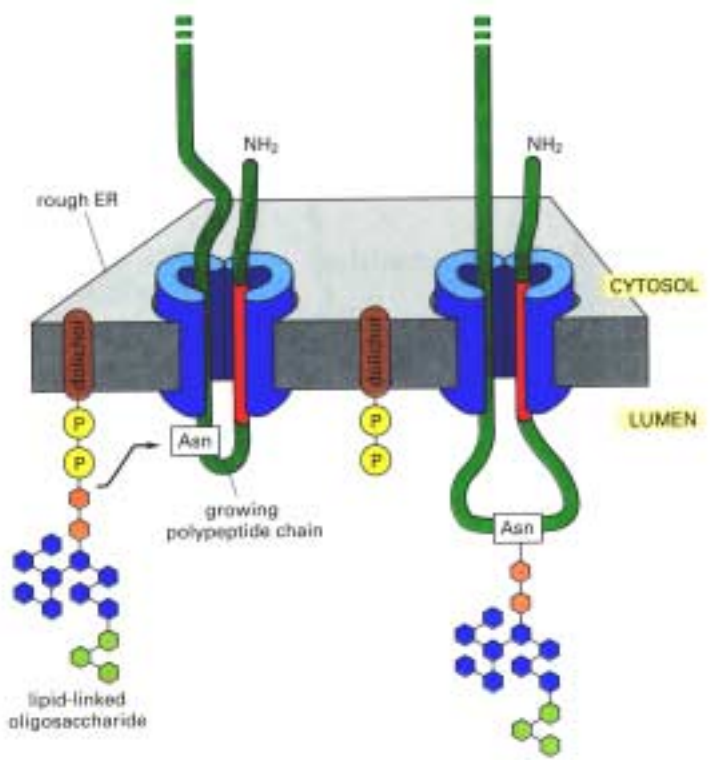


Figure 12–49 Protein glycosylation in the rough ER. Almost as soon as a polypeptide chain enters the ER lumen, it is glycosylated on target asparagine amino acids. The oligosaccharide shown in Figure 12–48 is transferred to the asparagine as an intact unit in a reaction catalyzed by a membrane-bound *oligosaccharyl transferase* enzyme. There is one copy of this enzyme associated with each protein translocator in the ER membrane.

Polüribosoom.

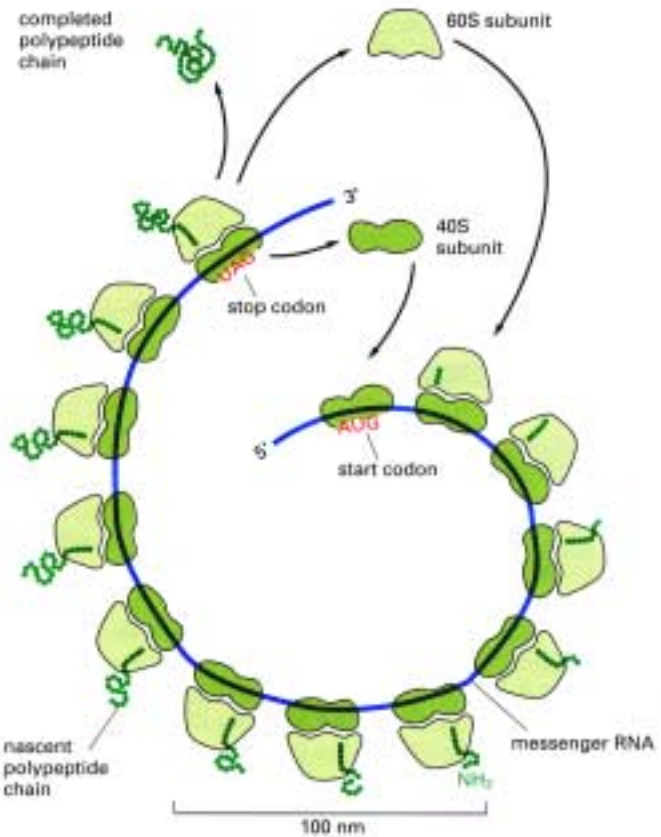


Figure 6–28 **A polyribosome.** Schematic drawing showing h
series of ribosomes can simul-
taneously translate the same r
molecule.

Lagundamise rajad lüsosoomis.

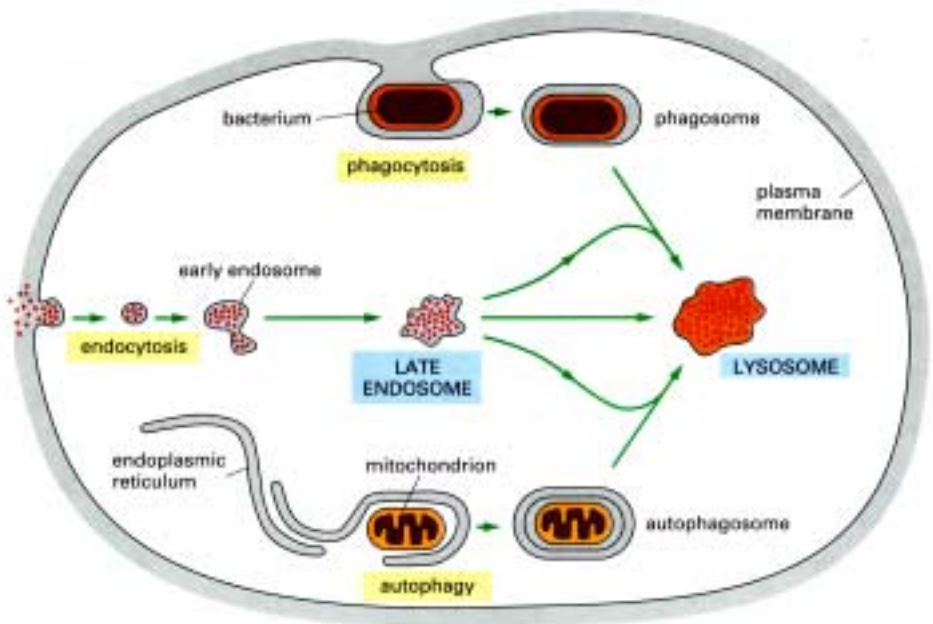
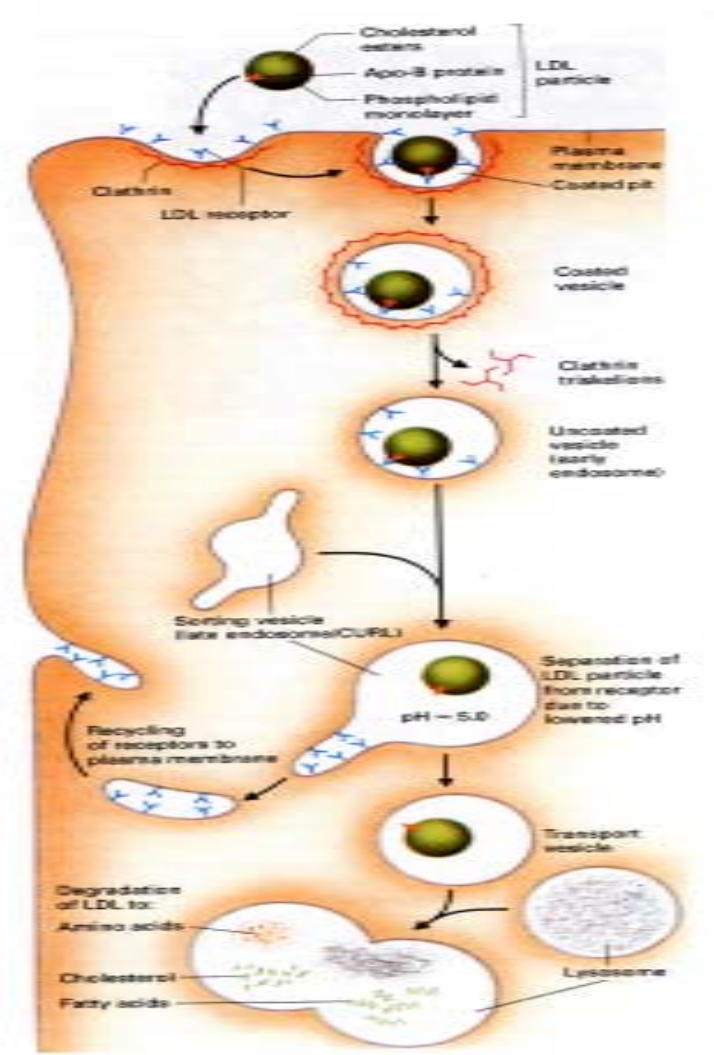
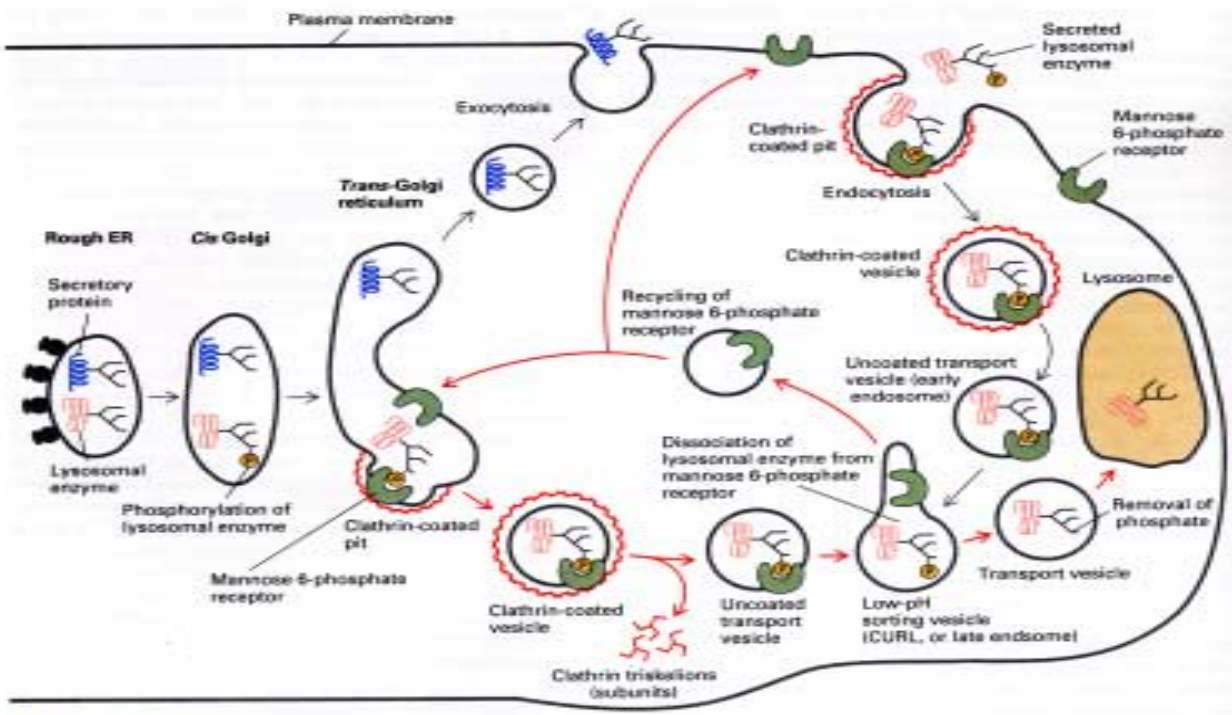


Figure 13–22 Three pathways to degradation in lysosomes. Each pathway leads to the intracellular digestion of materials derived from different source. The compartment resulting from the three pathways c sometimes be distinguished morphologically—hence the terms "autophagolysosome," "phago-lysosome," and so on. Such lysosomes, however, may differ onl because of the different materials they are digesting.

Madala tihedusega lipoproteiini (LDL) ja tema retseptori saatus pärast endotsütoosi.



Lüsosomaalsete ensüümide suundumine lüsosoomidesse.



▲ FIGURE 16-37 The targeting of lysosomal enzymes to lysosomes. During biosynthesis, lysosomal enzymes migrate from the rough ER (left) to the *cis* Golgi, in which one or more mannose residues are phosphorylated. In the *trans*-Golgi reticulum, the enzymes bind to the membrane-attached, highly specific mannose 6-phosphate receptor, which directs the enzymes into vesicles coated with the fibrous protein clathrin. The clathrin surrounding these vesicles is rapidly depolymerized to its clathrin triskelion subunits, and the uncoated transport vesicle fuses with a CURL vesicle (also called a late endosome). The low pH of the CURL vesicle (~5.5) causes the phosphorylated enzyme to dissociate from its receptor. The receptor recycles back to the Golgi, and the phosphorylated enzyme is incorporated into a different transport vesicle that buds from the CURL. In this vesicle the protein loses its phosphate group, and the vesicle soon fuses with a lysosome. The sorting of lysosomal enzymes from secretory proteins (left) thus occurs in the *trans*-Golgi reticulum, and these two classes of proteins are incorporated into different vesicles, which take different routes after they bud from the Golgi.

The mannose 6-phosphate receptor is also found on the plasma membrane (upper right), where it binds extracellular phosphorylated lysosomal enzymes that are occasionally secreted. These receptor-ligand complexes are internalized from the cell surface in clathrin-coated vesicles which also lose their clathrin coats and fuse with the CURL organelle. [See G. Griffiths et al. 1988. *Cell* **52**:329–341; S. Kornfeld. 1992 Ann. Rev. Biochem. **61**:307–330; and G. Griffiths and J. Gruenberg. 1991. *Trends Cell Biol.* **1**:5–9.]