

mitoosi

meioosi

fertilisaatio

replikaatio
repair

rekombinaatio
repair

mendelistinen genetiikka

DNA-huusholli

Geenien toiminta

molekyylogenetiikka



DNA

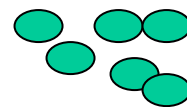
transkriptio

regulaatio



RNA

prosessori



proteiinit

translaatio



*kehitysgenetiikka
immunogenetiikka
syöpägenetiikka
= **elämä & vaivat***

CELL 309

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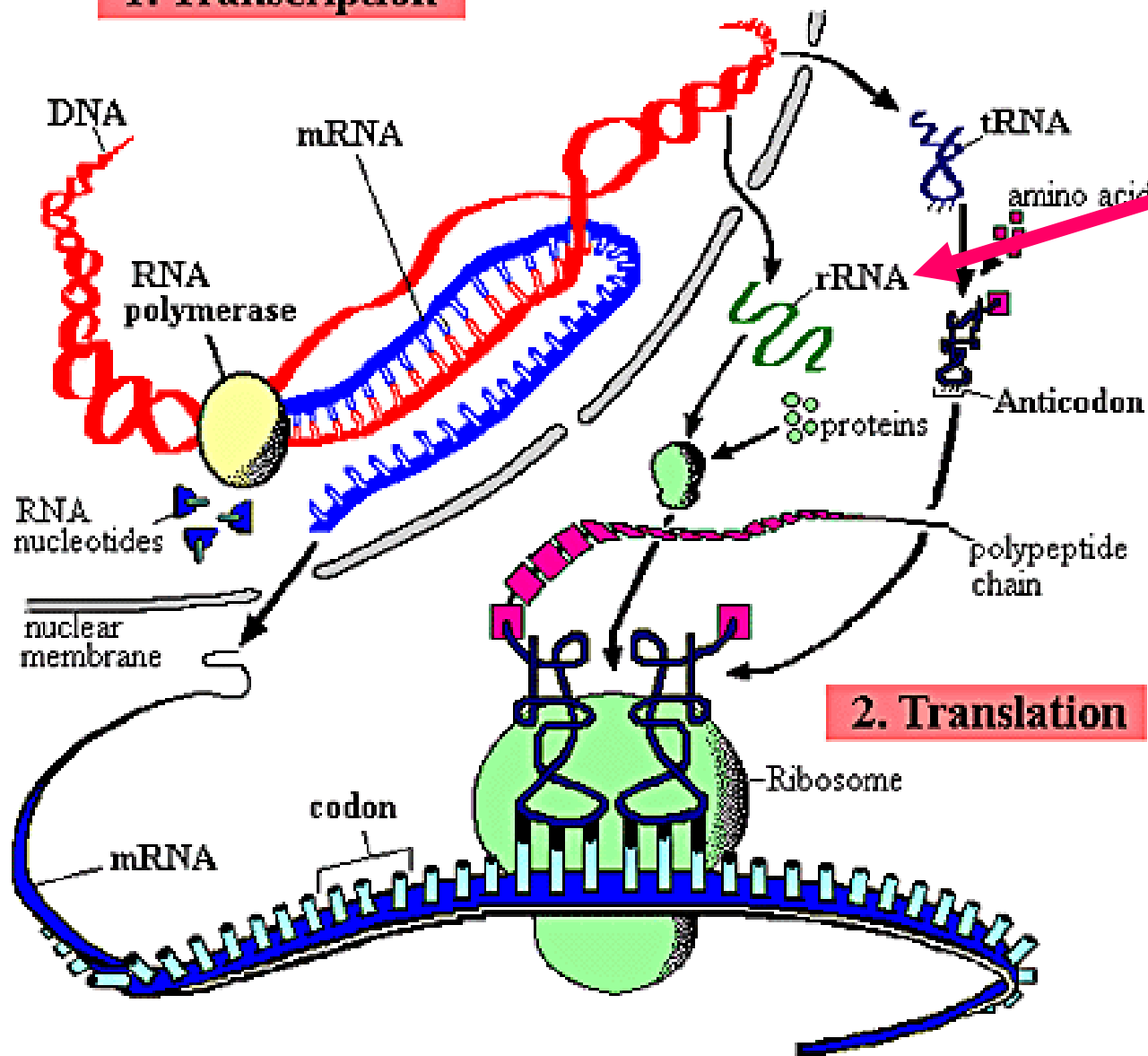
kehitysgenetiikka
immunogenetiikka
syöpägenetiikka
ELÄMÄ!

Genetiikan perusteiden miellekartta: transkriptio jatkuu

Ribosomin RNA eli rRNA

- Koodia sanotaan rDNA:ksi
- Ei mitään tekemistä triplettikoodin kanssa
- Useita alayksiköitä
- Eräs kaikkein konservatiivisimmista informaatiopaketeista
- Todistaa vahvasti *kaikkien* eliöiden yhteisestä alkuperästä

1. Transcription



Protein synthesis

Table 6–1 Principal Types of RNAs Produced in Cells

TYPE OF RNA	FUNCTION
mRNAs	messenger RNAs, code for proteins
rRNAs	ribosomal RNAs, form the basic structure of the ribosome and catalyze protein synthesis
tRNAs	transfer RNAs, central to protein synthesis as adaptors between mRNA and amino acids
snRNAs	small nuclear RNAs, function in a variety of nuclear processes, including the splicing of pre-mRNA
snoRNAs	small nucleolar RNAs, used to process and chemically modify rRNAs
scaRNAs	small cajal RNAs, used to modify snoRNAs and snRNAs
miRNAs	microRNAs, regulate gene expression typically by blocking translation of selective mRNAs
siRNAs	small interfering RNAs, turn off gene expression by directing degradation of selective mRNAs and the establishment of compact chromatin structures
Other noncoding RNAs	function in diverse cell processes, including telomere synthesis, X-chromosome inactivation, and the transport of proteins into the ER

Table 6-1 Molecular Biology of the Cell 5/e (© Garland Science 2008)

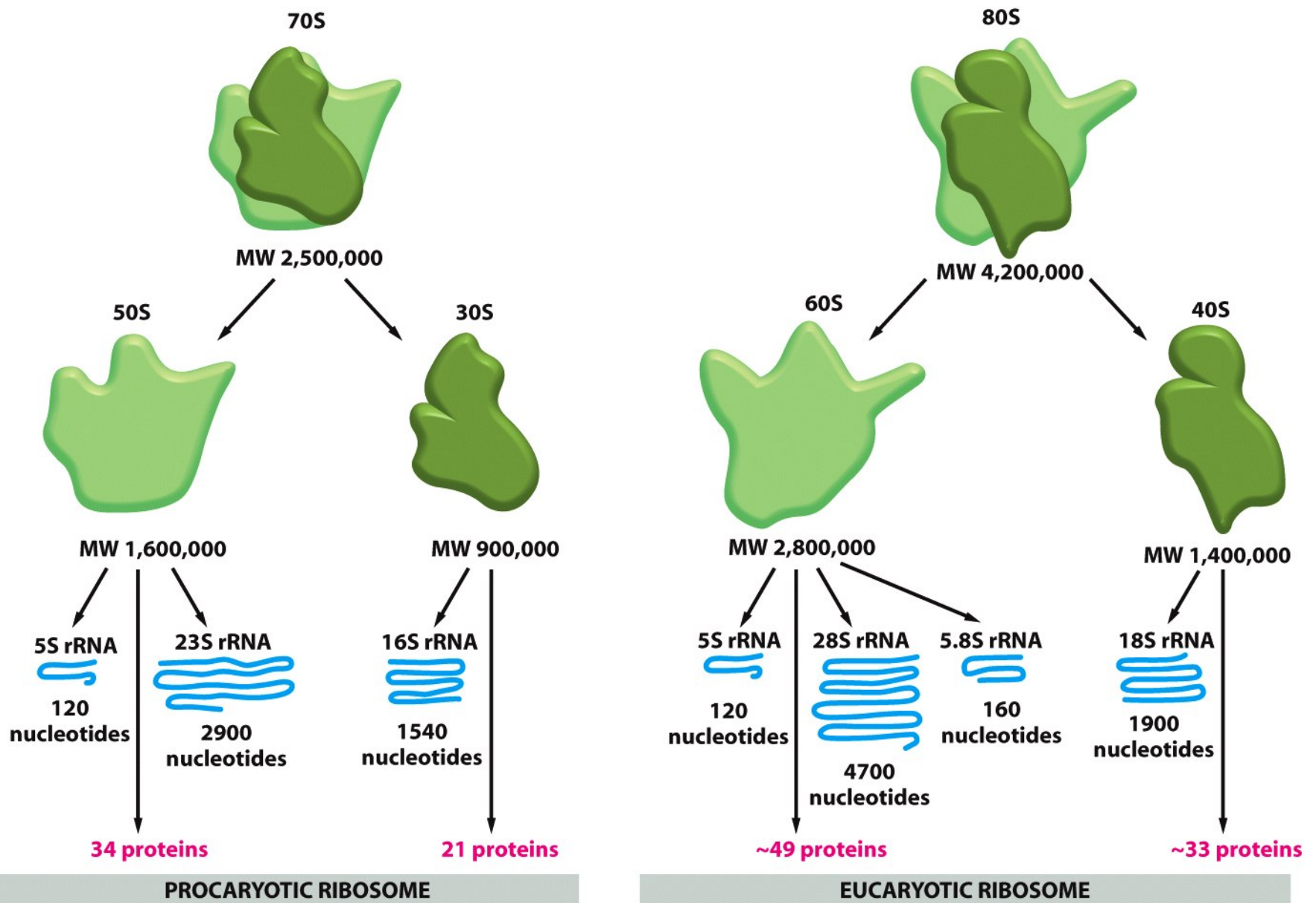


Figure 6-63 Molecular Biology of the Cell 5/e (© Garland Science 2008)

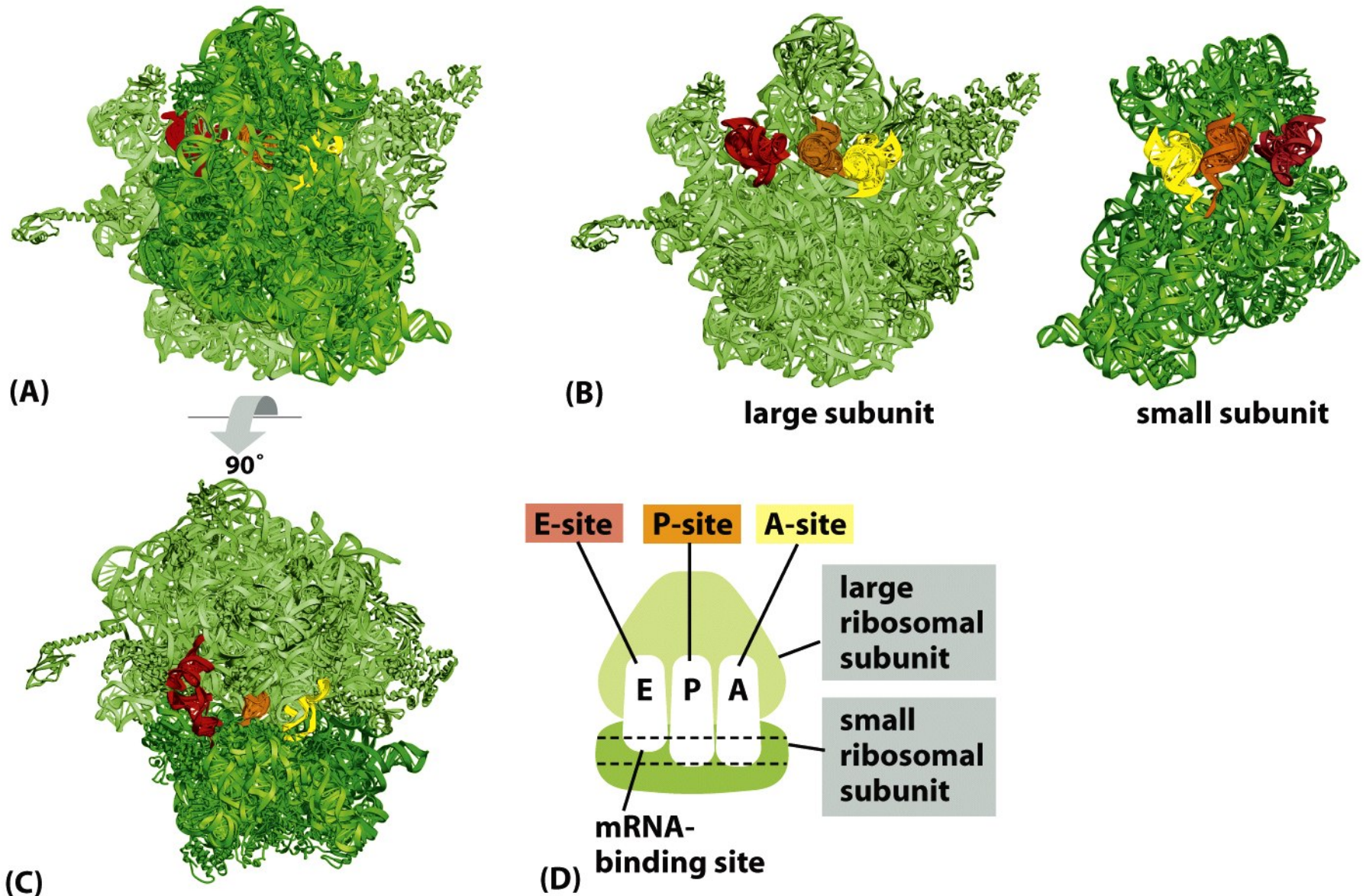
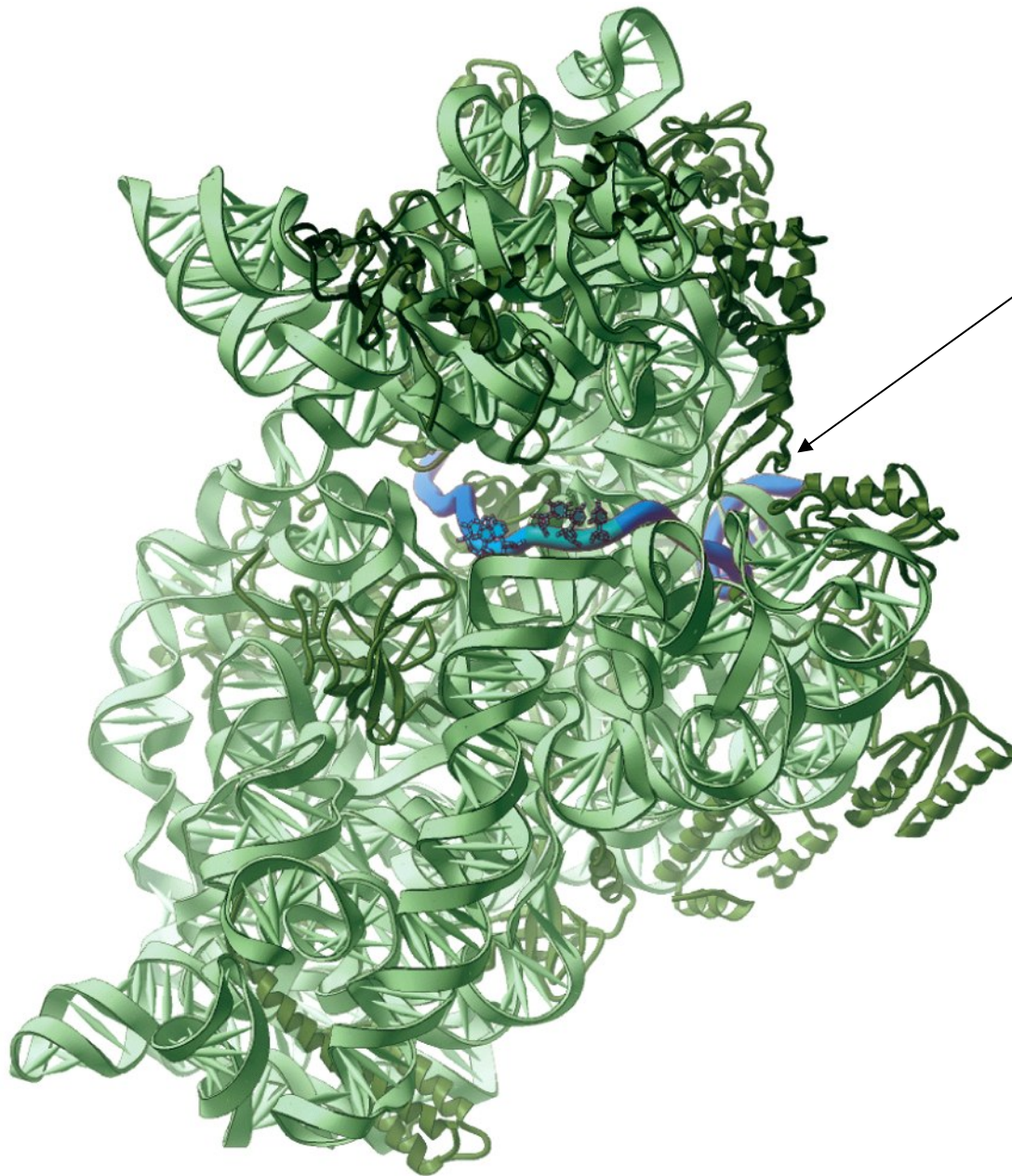


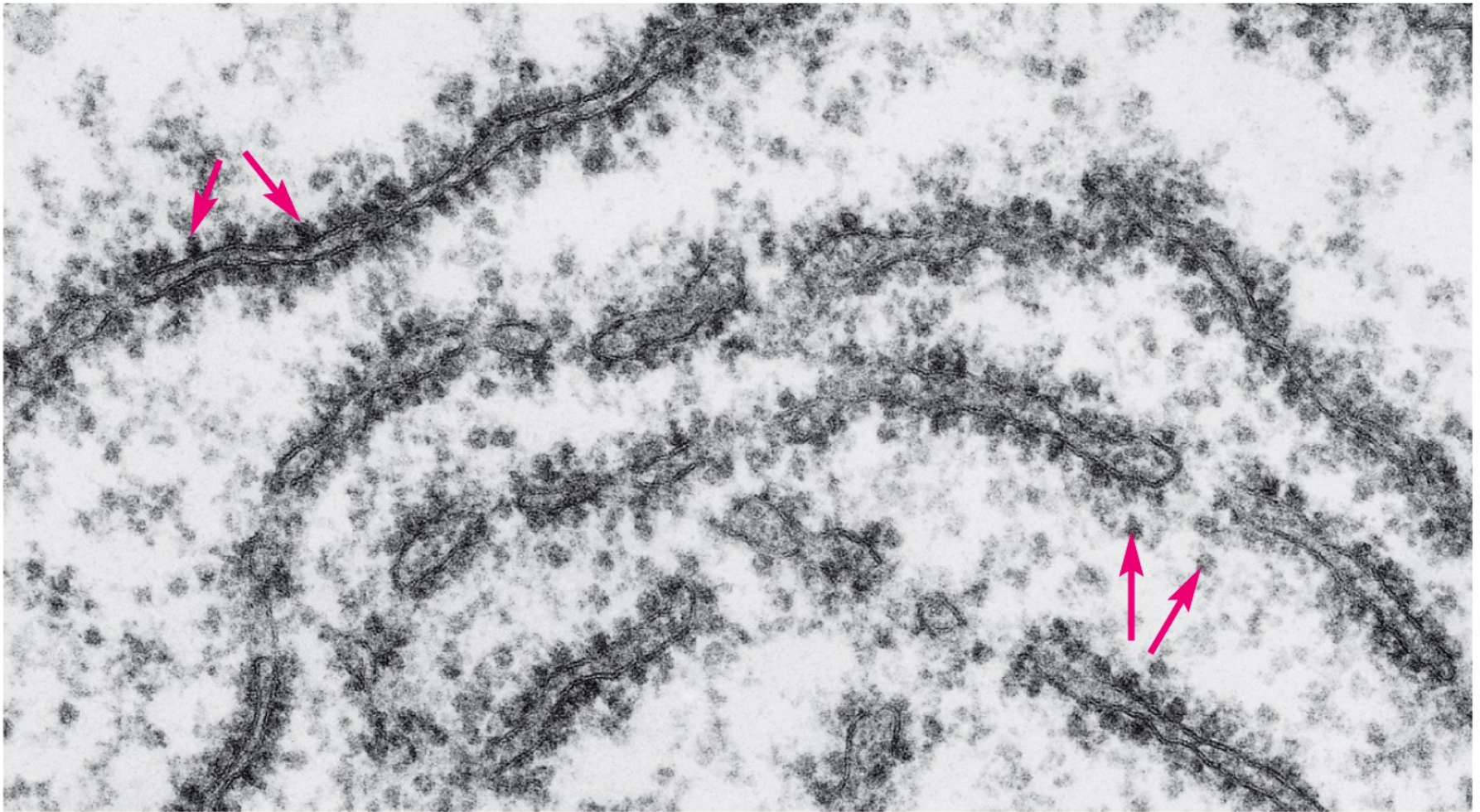
Figure 6-64 Molecular Biology of the Cell 5/e (© Garland Science 2008)



Small subunit

mRNA luikertaa

CELL 376



400 nm

Figure 6-62 Molecular Biology of the Cell 5/e (© Garland Science 2008)

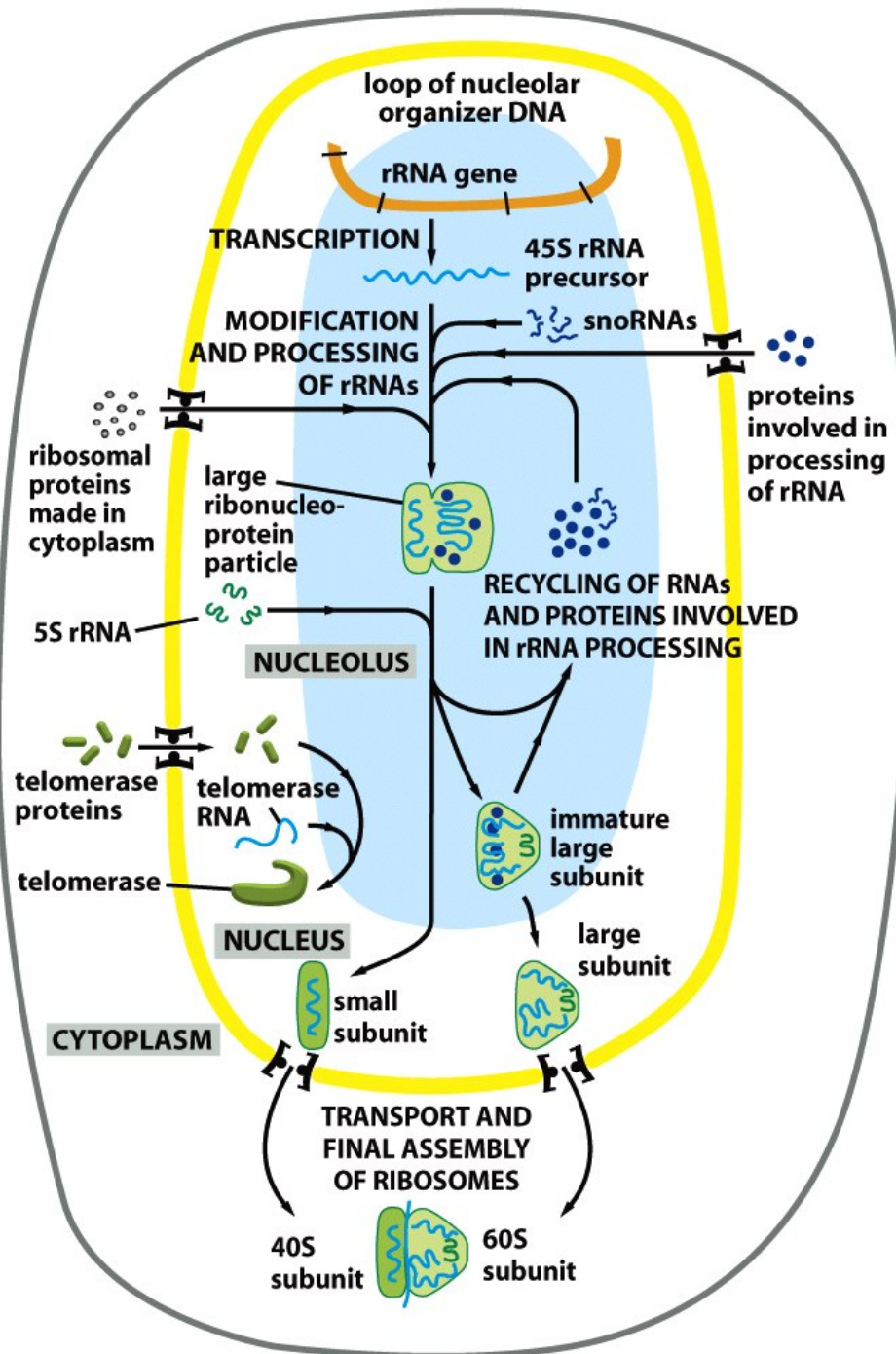


Figure 6–47 The function of the nucleolus in ribosome and other ribonucleoprotein synthesis. The 45S precursor rRNA is packaged in a large ribonucleoprotein particle containing many ribosomal proteins imported from the cytoplasm. While this particle remains in the nucleolus, selected pieces are added and others discarded as it is processed into immature large and small ribosomal subunits. The two ribosomal subunits are thought to attain their final functional form only as each is individually transported through the nuclear pores into the cytoplasm. Other ribonucleoprotein complexes, including telomerase shown here, are also assembled in the nucleolus.

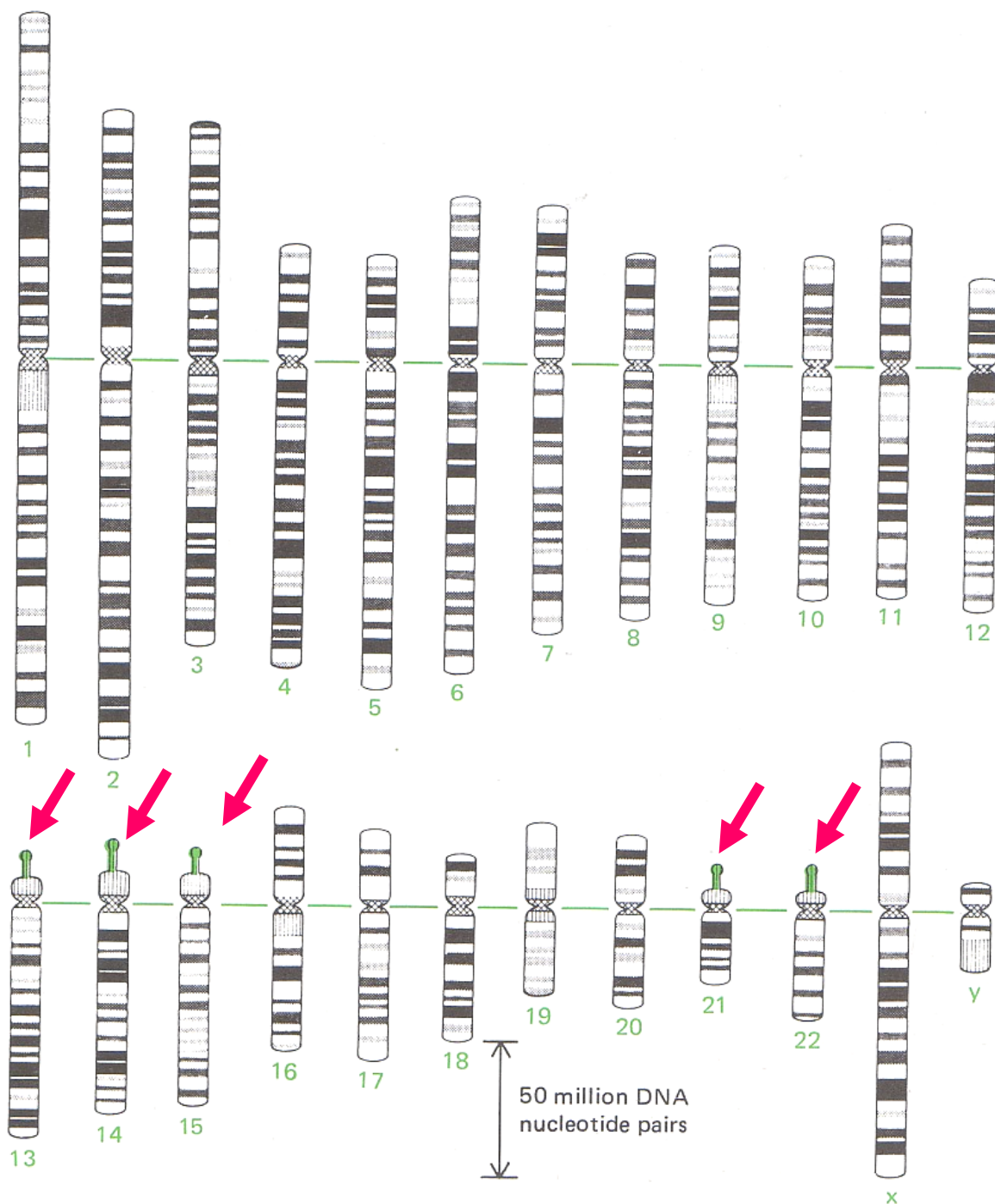


Figure 8-32 A standard map of the banding pattern of each chromosome in the human karyotype. This map was determined at the prometaphase stage of mitosis. Chromosomes 1 through 22 are labeled in the approximate order of their size; a diploid cell contains two of each of these autosomes plus two sex chromosomes—two 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 red knobs on chromosomes 13, 14, 15, 21, and 22 indicate the positions of the genes that encode the large ribosomal RNAs; the red lines mark the centromere on each chromosome. (Adapted from U. Franke, *Cytogenet. Cell Genet.* 31:24–32, 1981.)

CELL 203

fragile X:
Musco et al Cell 85:

rDNA-geenit

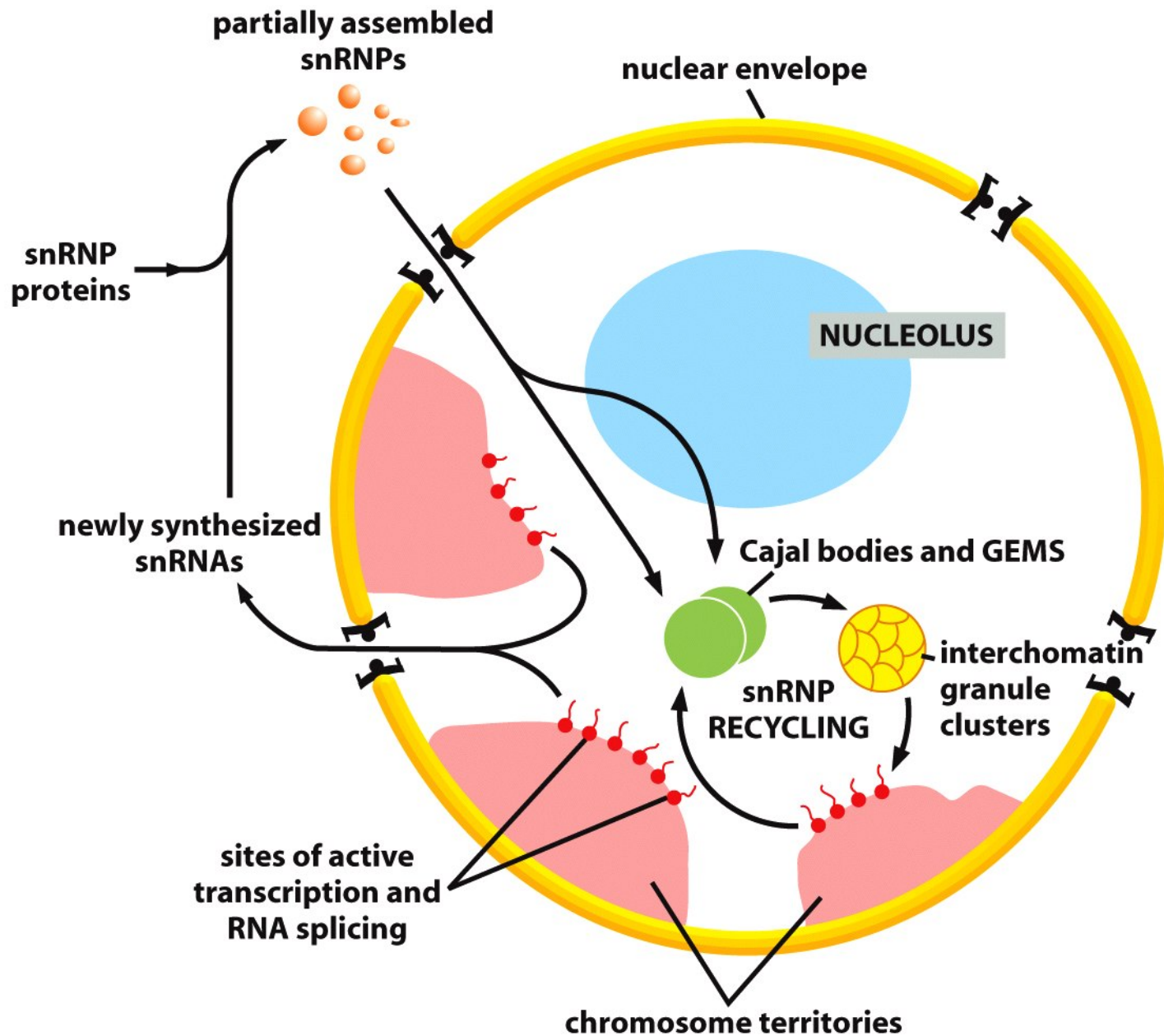


Figure 6-49 Molecular Biology of the Cell 5/e (© Garland Science 2008)

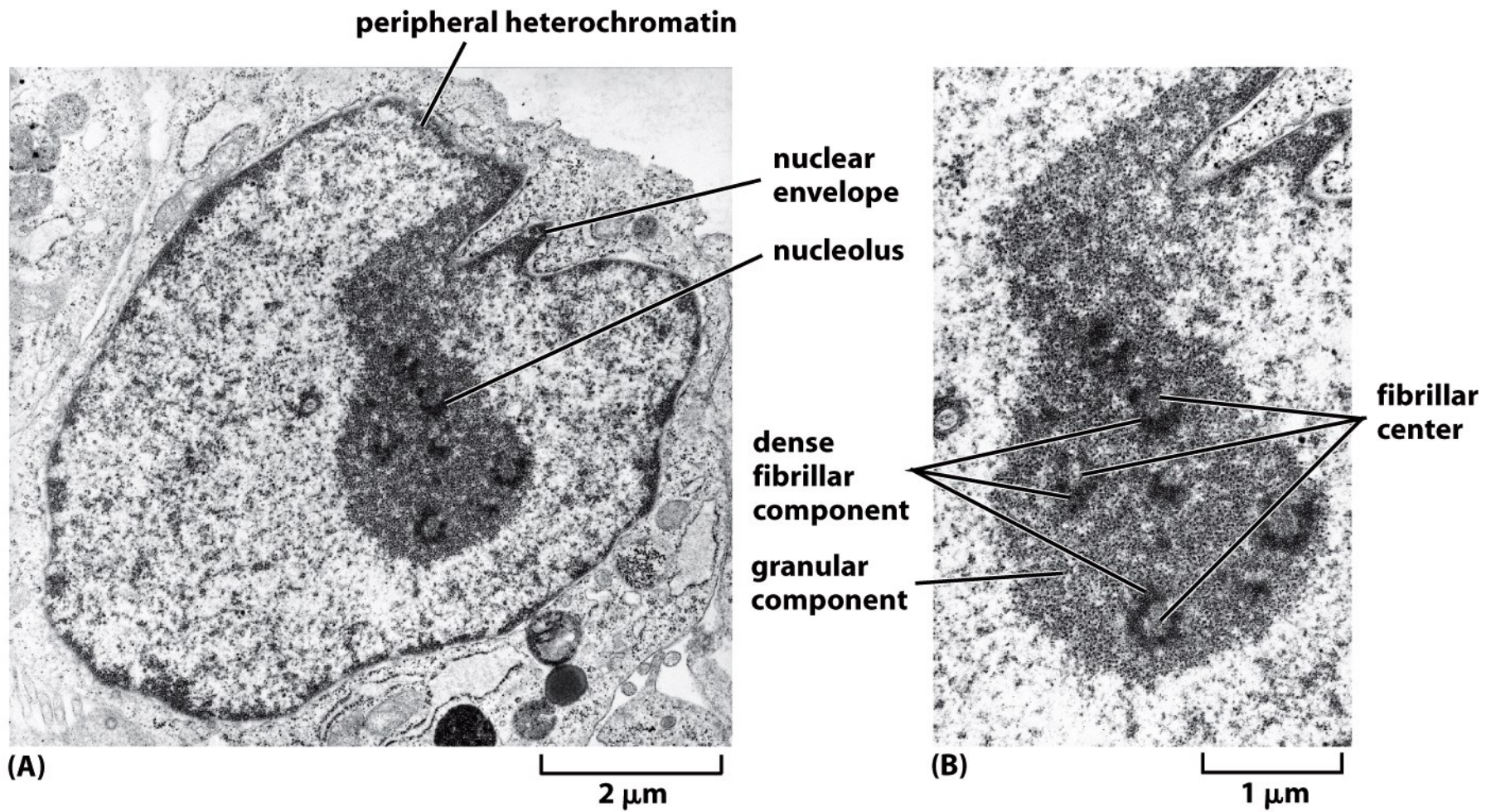


Figure 6-44 Molecular Biology of the Cell 5/e (© Garland Science 2008)

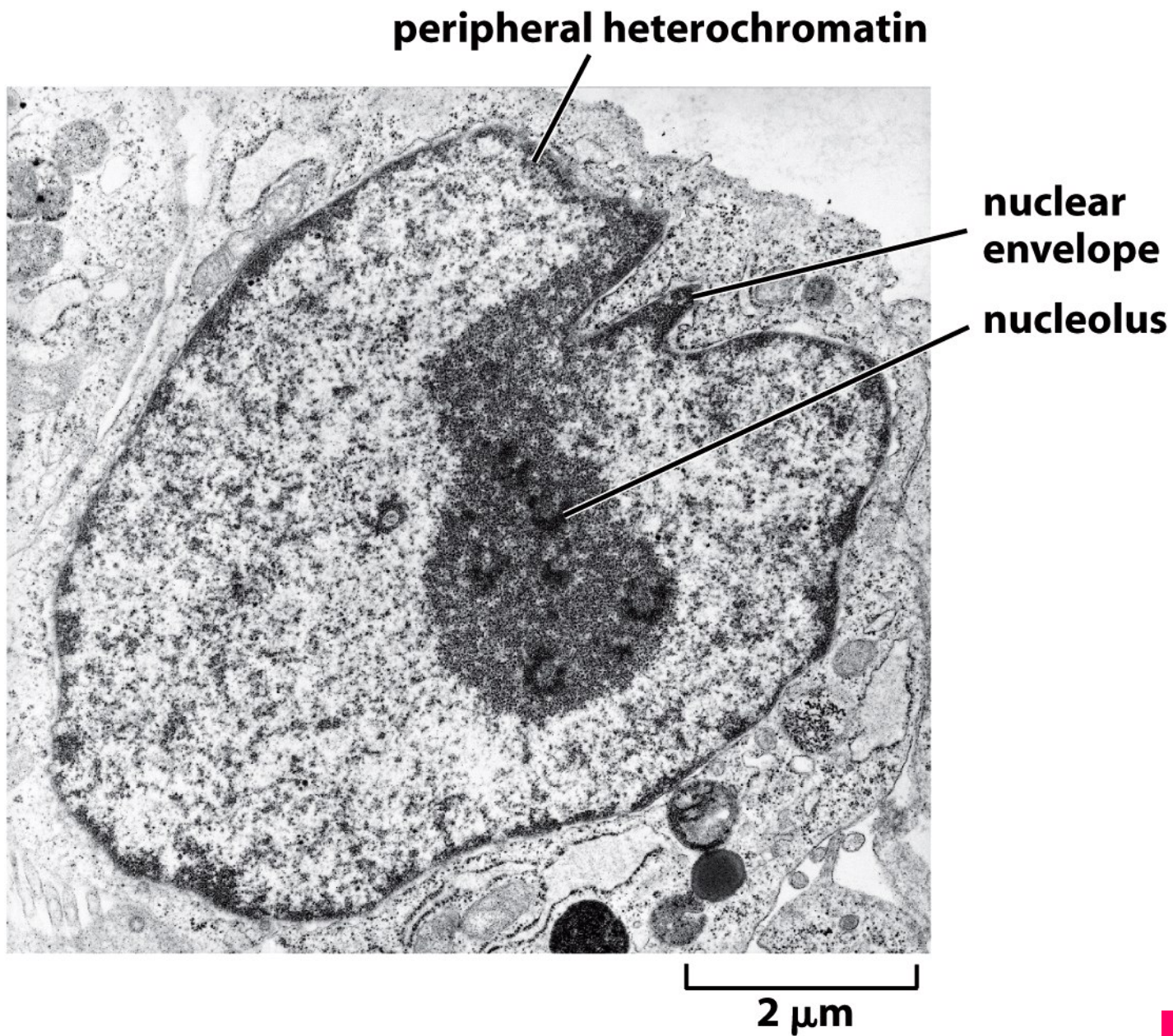


Figure 6-44a Molecular Biology of the Cell 5/e (© Garland Science 2008)

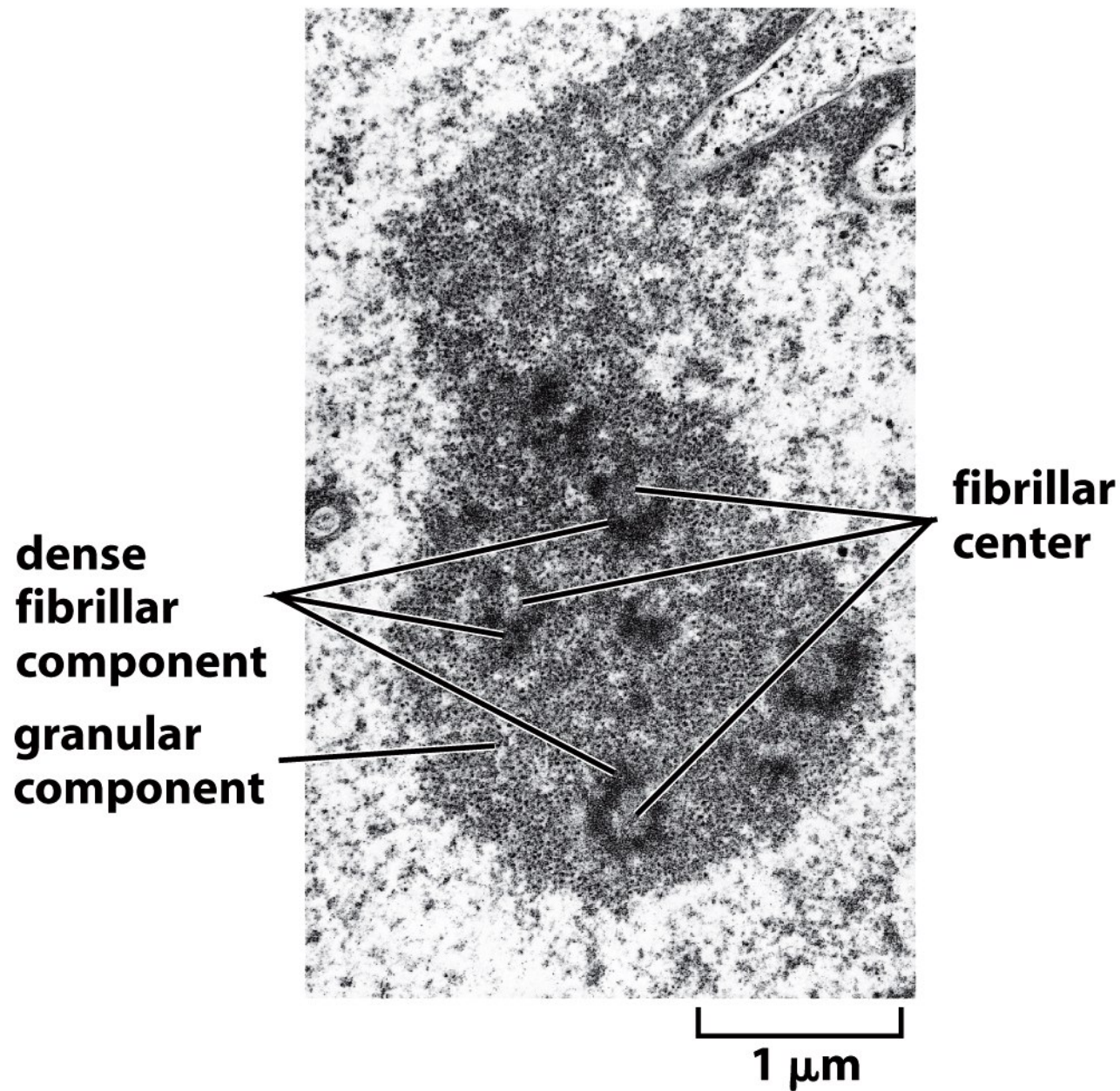


Figure 6-44b Molecular Biology of the Cell 5/e (© Garland Science 2008)

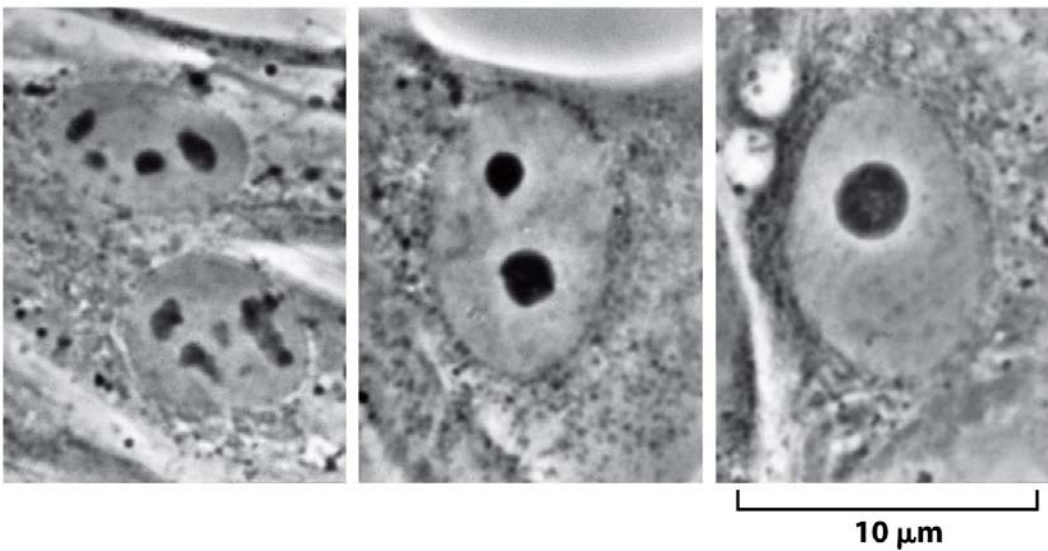


Figure 6-46 Molecular Biology of the Cell 5/e (© Garland Science 2008)

Mitoosin jälkeen kaikki 10 ihmisen NOR- segmenttiä alkavat muodostaa nukleolusta, jotka sitten fuusioituvat yhdeksi kalvottomaksi rykelmäksi

CELL 363

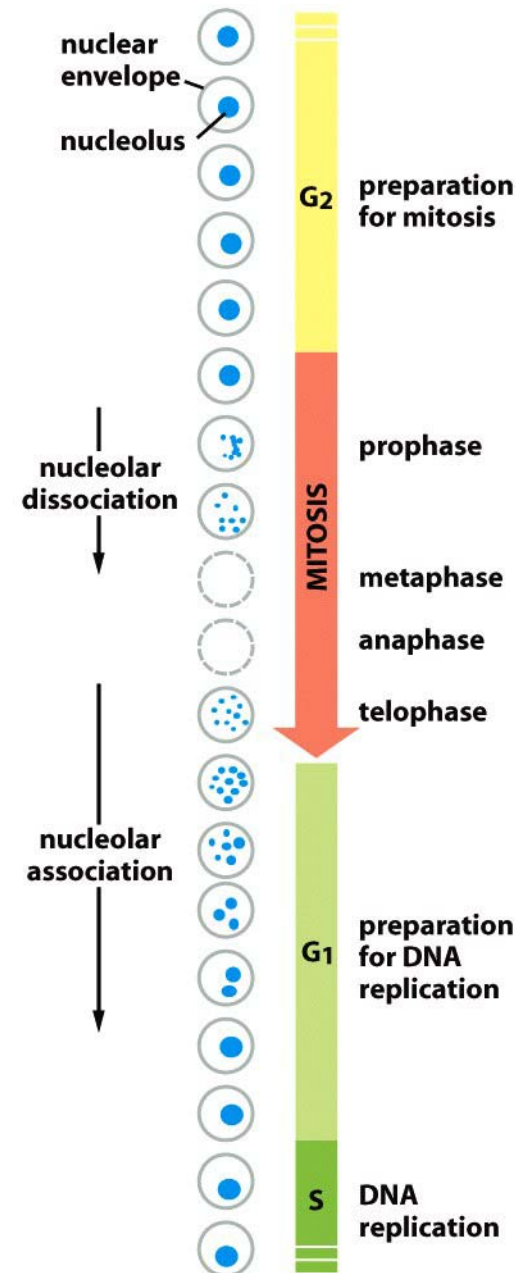


Figure 6-45 Molecular Biology of the Cell 5/e (© Garland Science 2008)



2 μm

Figure 6-41 Molecular Biology of the Cell 5/e (© Garland Science 2008)

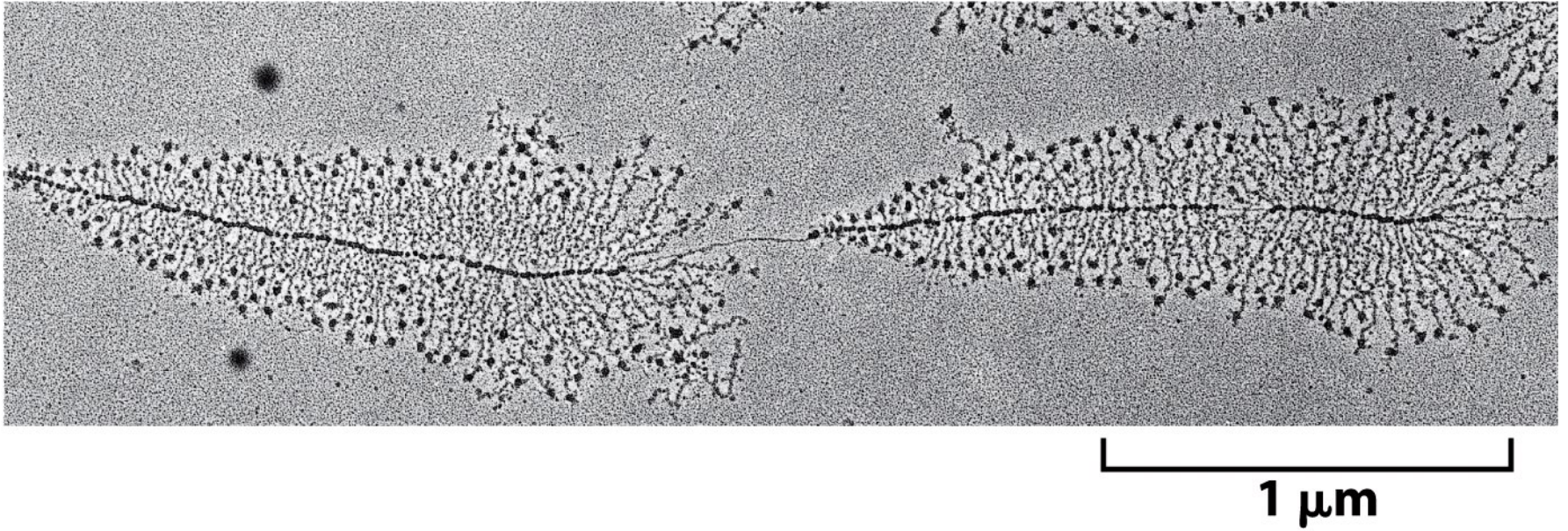


Figure 6-9 Molecular Biology of the Cell 5/e (© Garland Science 2008)

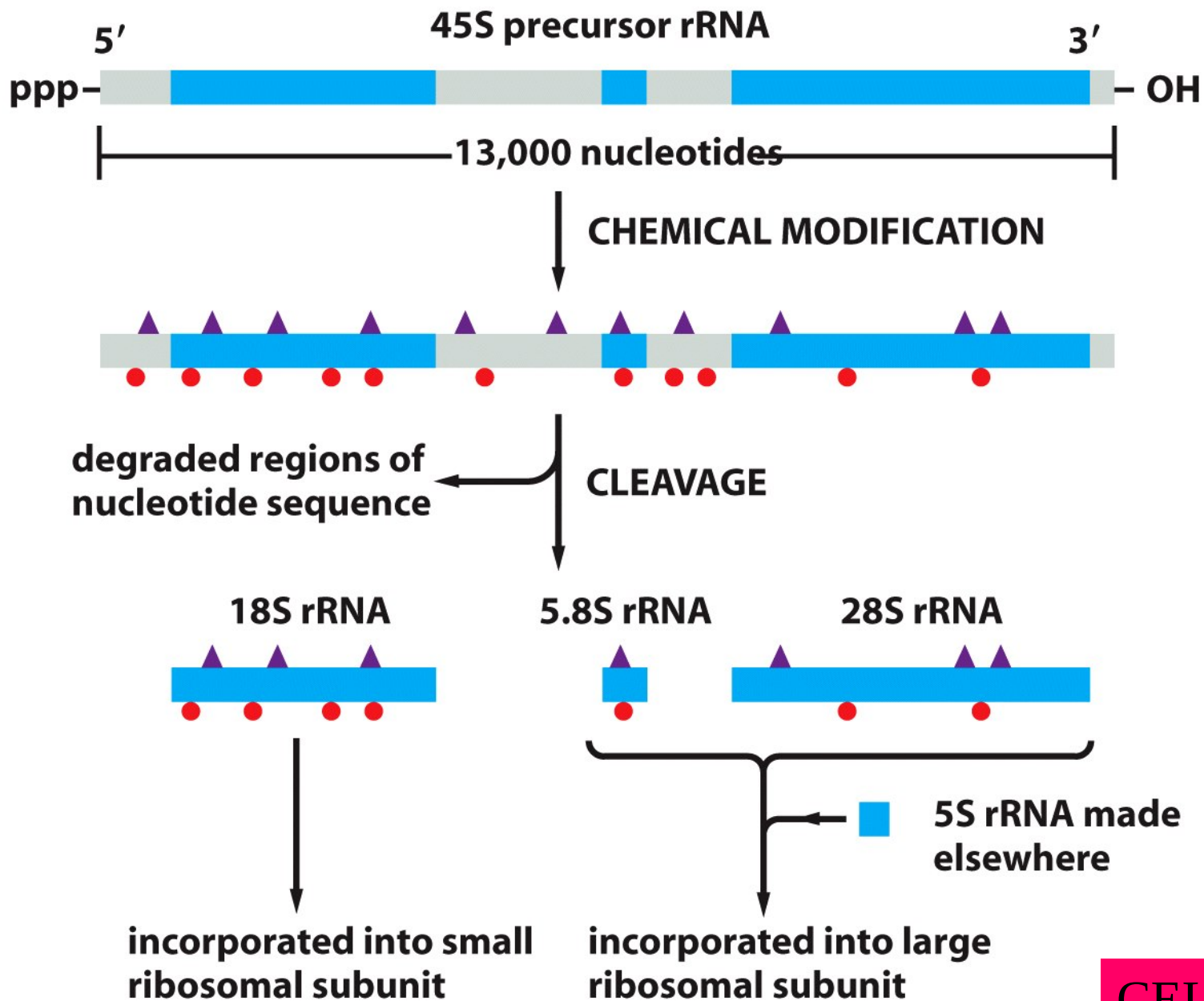
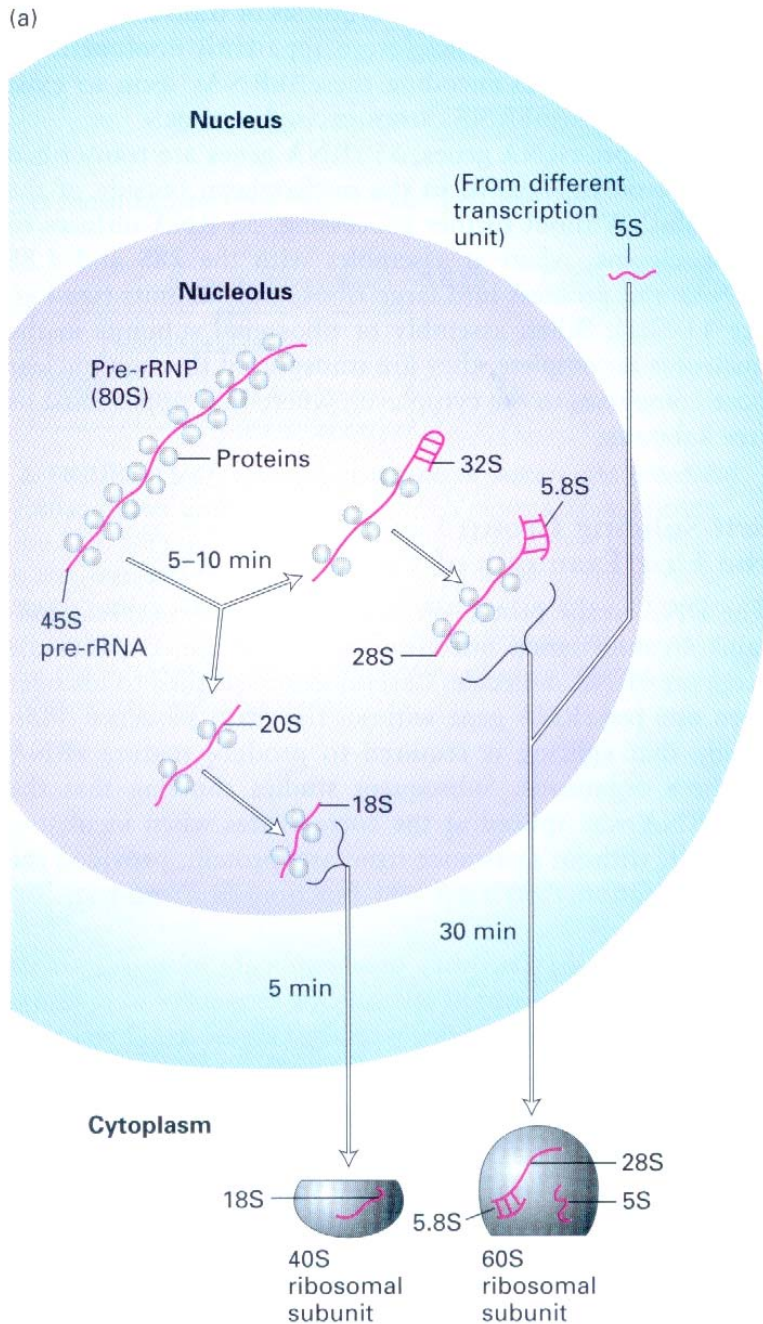


Figure 6-42 Molecular Biology of the Cell 5/e (© Garland Science 2008)

Tumajyvänen (nucleolus) on ribosomi- tehdas

(a)



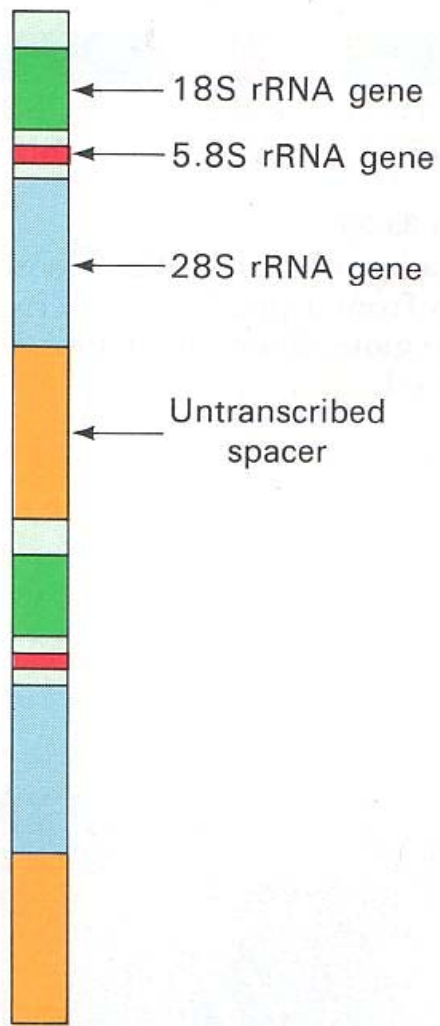


Figure 33-26

Organization of the genes for the 40S precursor of 18S, 5.8S, and 28S rRNAs in *Xenopus*. The tandemly repeated genes are separated by untranscribed spacers (yellow). The repeating unit is about 13 kb long.

RibosomiRNA –geenit ovat järjestäytyneet tandem-toistoiksi

Evoluution kuluessa jotkut voimat tai tapahtumat pitävät toistot identtisinä (concerted evolution), mikä on yksi ihmeteltävistä asioista

Ribosomigeenien eri segmenttejä käytetään paljon erilaisissa evoluutiotutkimuksissa

Koodaavat alueet ovat konservatiivisia

Välikkeet nopeasti muuttuvia:

- ITS internal transcribed spacer
- IGS tai UTS intergenic/untranscribed spacer

rDNA transkriboidaan 'kasetteina'

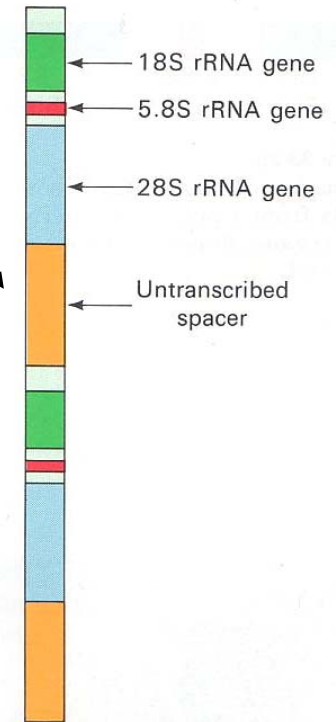
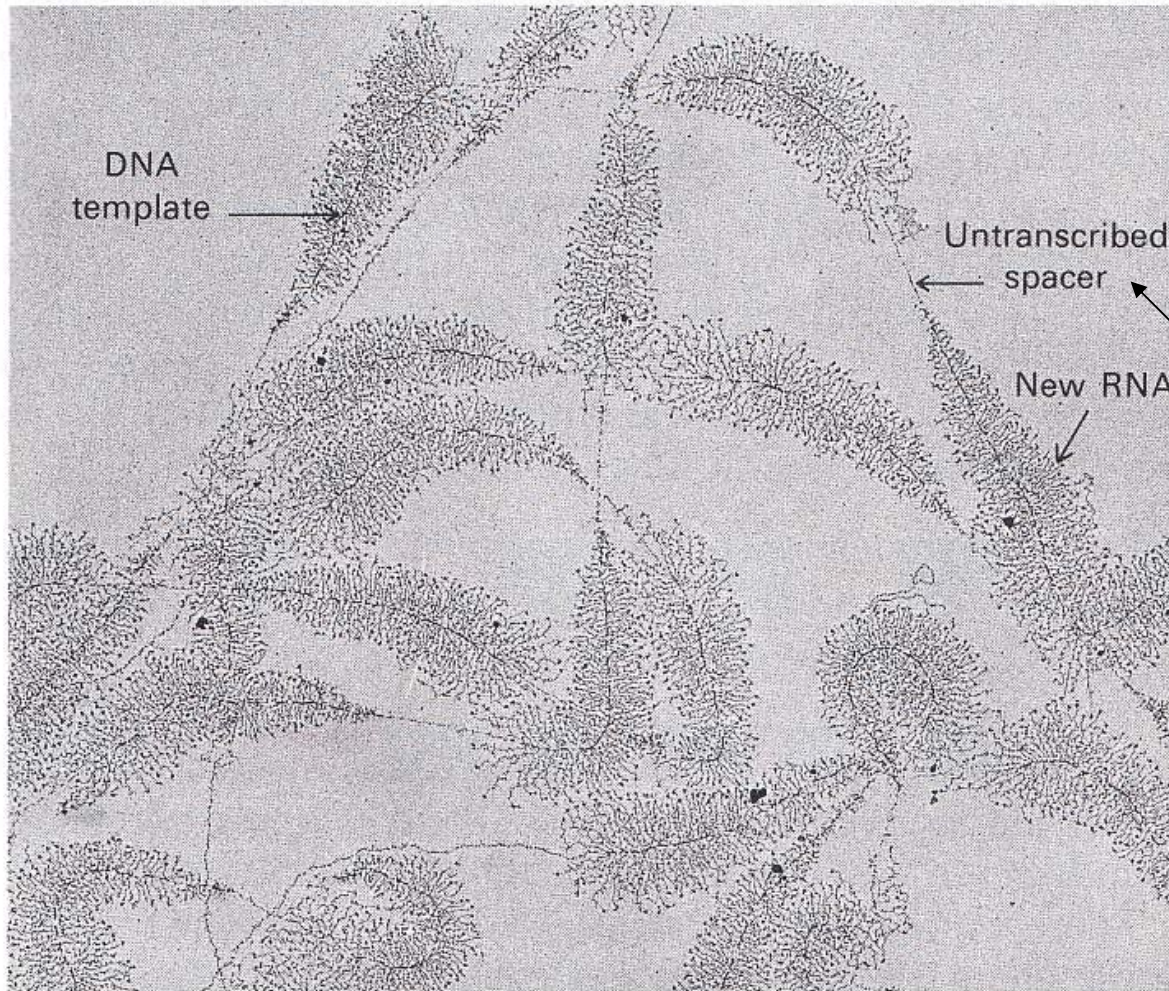


Figure 33-27

The tandem array of genes for 18S, 5.8S, and 28S rRNA is evident in this electron micrograph of nucleolar DNA. The dense axial fiber is DNA. The fine lateral fibers are newly synthesized RNA molecules with bound proteins. The tip of each arrowhead of the RNA molecules corresponds to an initiation point for transcription. The bare regions between arrowheads are the untranscribed spacers. [From O. L. Miller, Jr., and B. R. Beatty. Portrait of a gene. *J. Cell Physiol.* 74(supp. 1, 1969):225.]

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Organization of the genes for the 40S precursor of 18S, 5.8S, and 28S rRNAs in *Xenopus*. The tandemly repeated genes are separated by untranscribed spacers (yellow). The repeating unit is about 13 kb long.

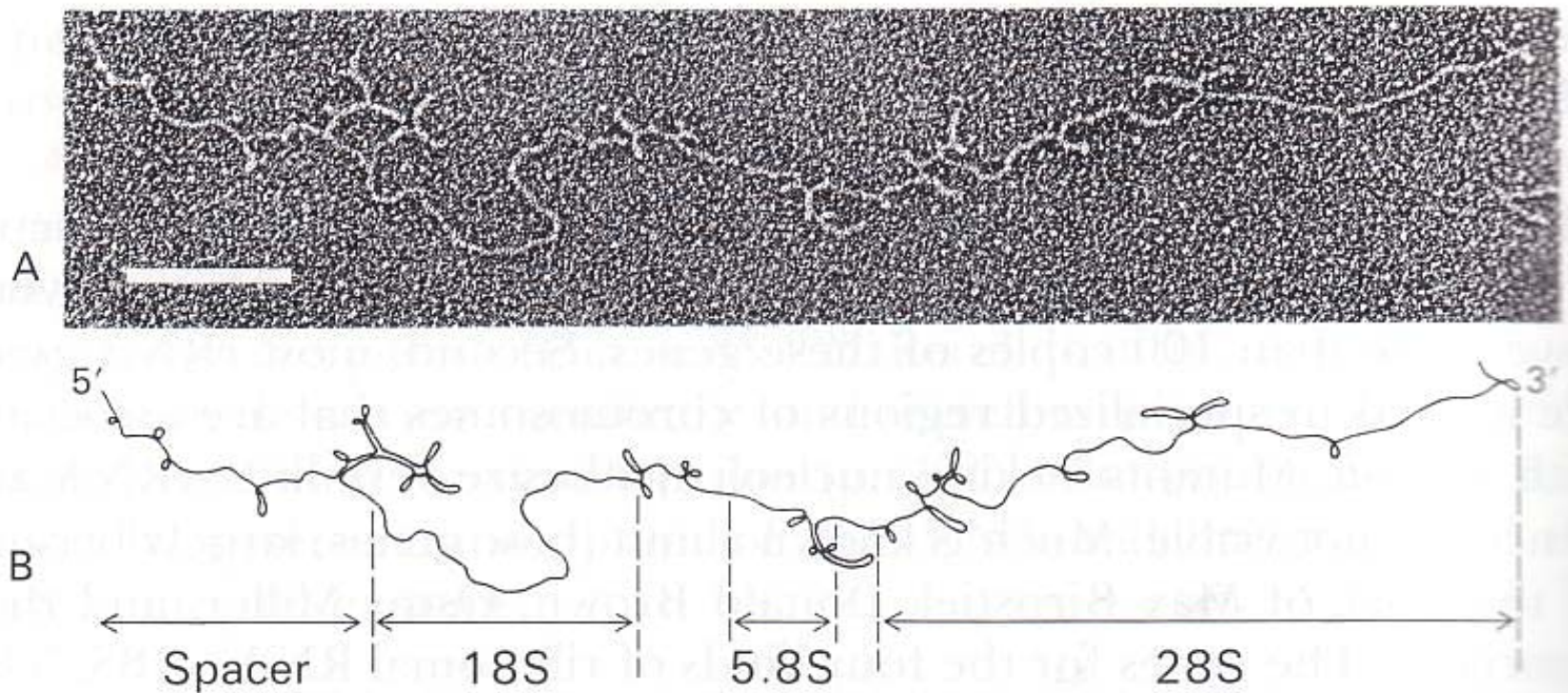
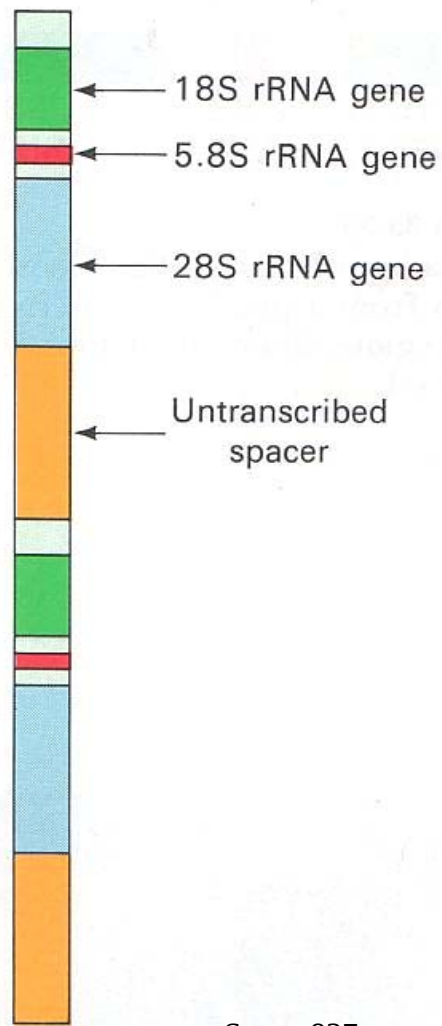


Figure 33-28

The 45S precursor of ribosomal RNA in HeLa cells has a highly distinctive pattern of hairpin loops when spread and examined by electron microscopy. This pattern makes it feasible to map the linear arrangement of 28S and 18S RNA molecules derived from this precursor. Part A is an electron micrograph of the 45S precursor (bar = 2000 Å). Part B is a tracing of the molecule shown in part A. [From P. K. Wellauer and I. B. Dawid. *Proc. Nat. Acad. Sci.* 70(1973):2828.].

Primaaritranskripti on 45S RNA, joka silputtautuu alayksiköiksi tumajyvässä sijaitsevan tehtaan koneissa



Stryer 837

Figure 33-26

Organization of the genes for the 40S precursor of 18S, 5.8S, and 28S rRNAs in *Xenopus*. The tandemly repeated genes are separated by untranscribed spacers (yellow). The repeating unit is about 13 kb long.

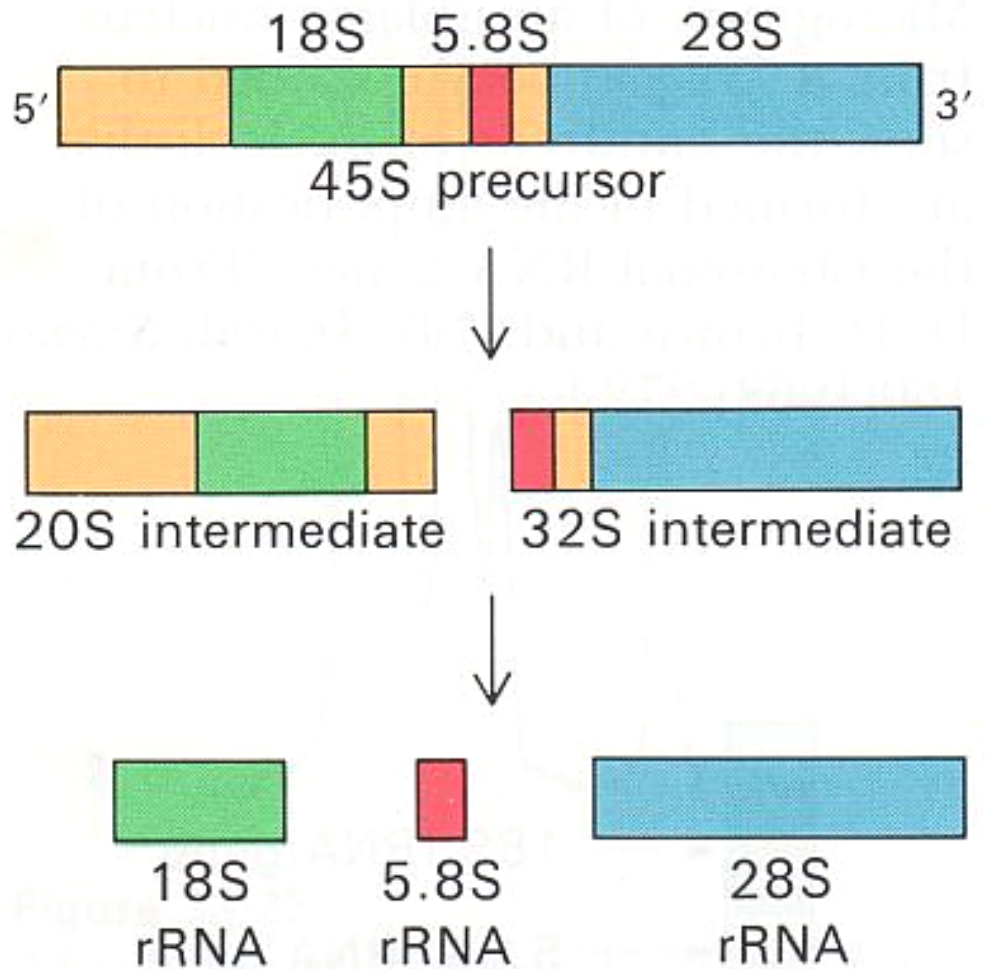


Figure 33-29

Formation of mammalian ribosomal RNAs from a primary transcript. The regions shown in yellow are removed.

Stryer 838

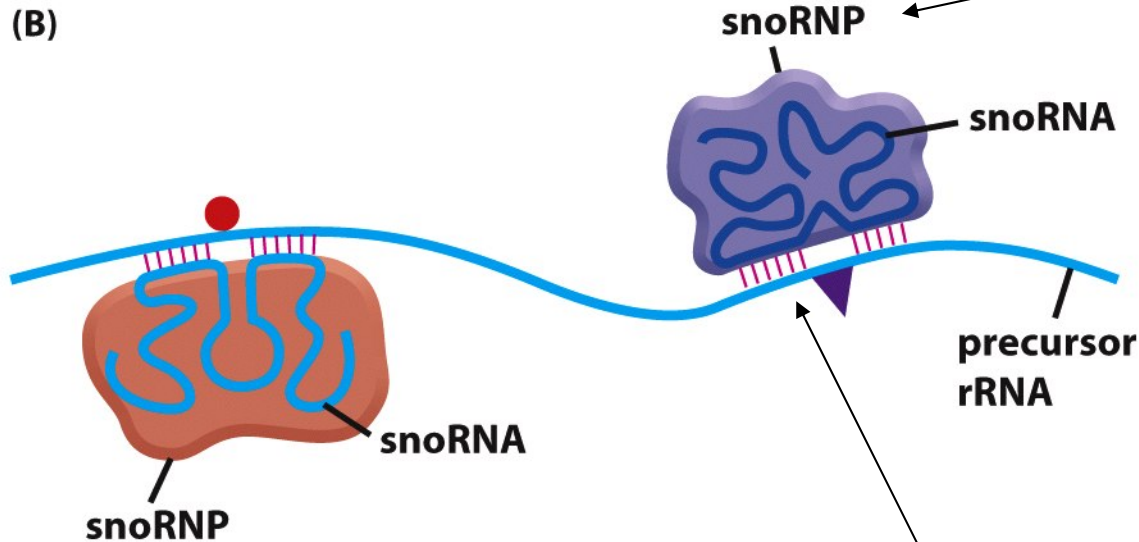
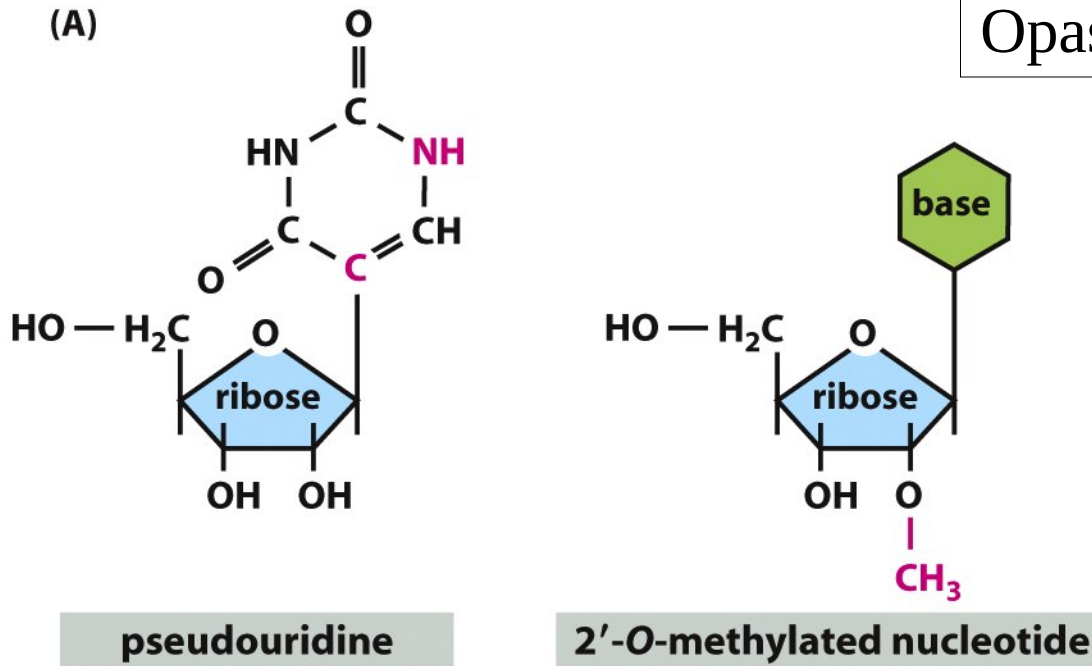
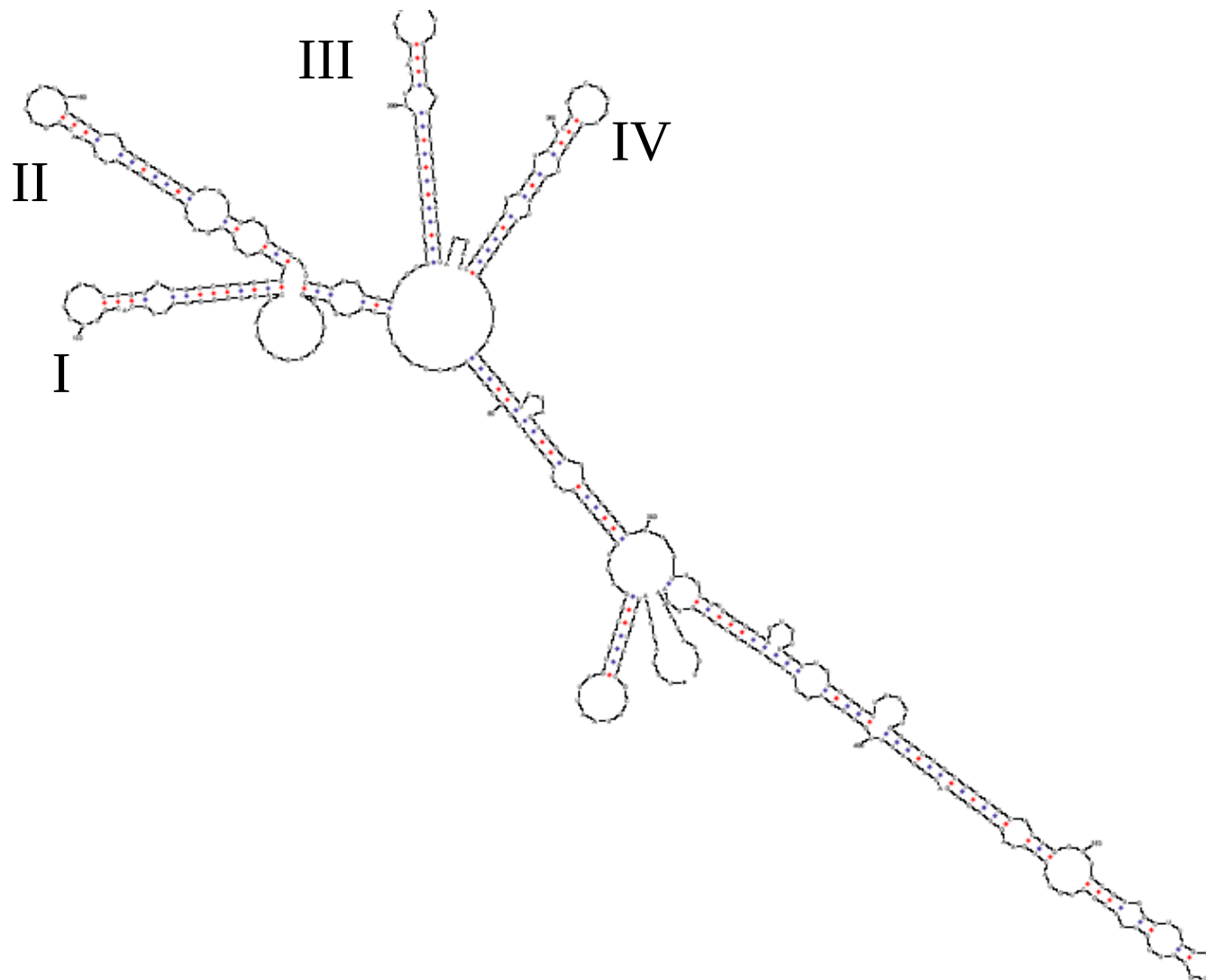
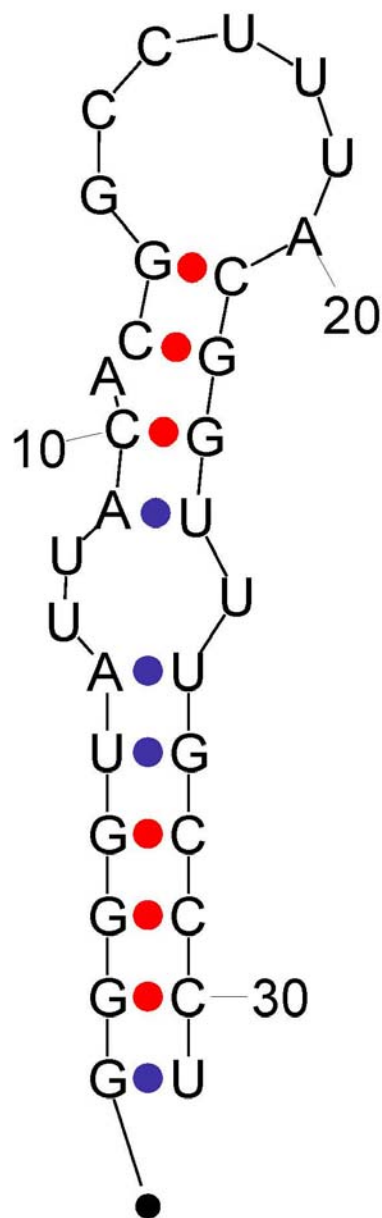


Figure 6-43 Molecular Biology of the Cell 5/e (© Garland Science 2008)

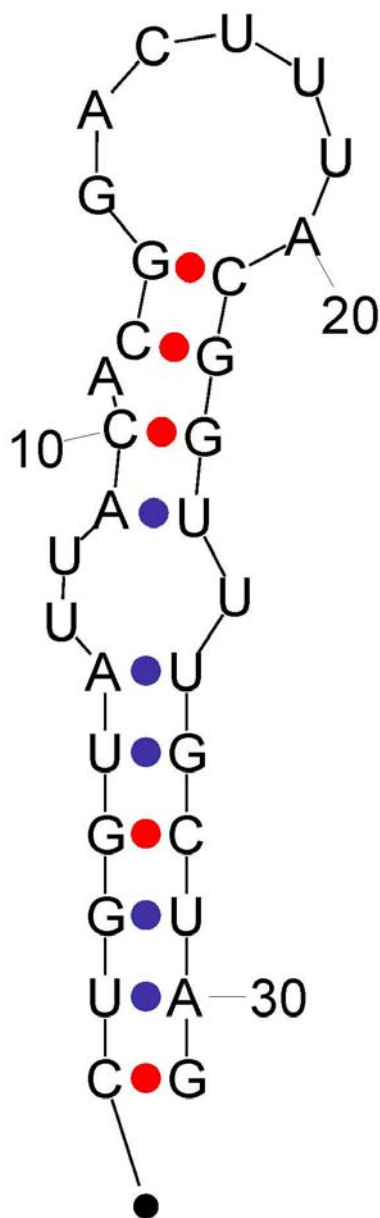


Lohen *Gyrodactylus*-loisen ITS2 rRNA:n sekundaaristruktuuri. Ajatellaan, että tiukat hiuspinnit helpottavat tämän jakson poistoa, mutta voi se toimittaa jotain aktiivistakin. Ei tiedetä.

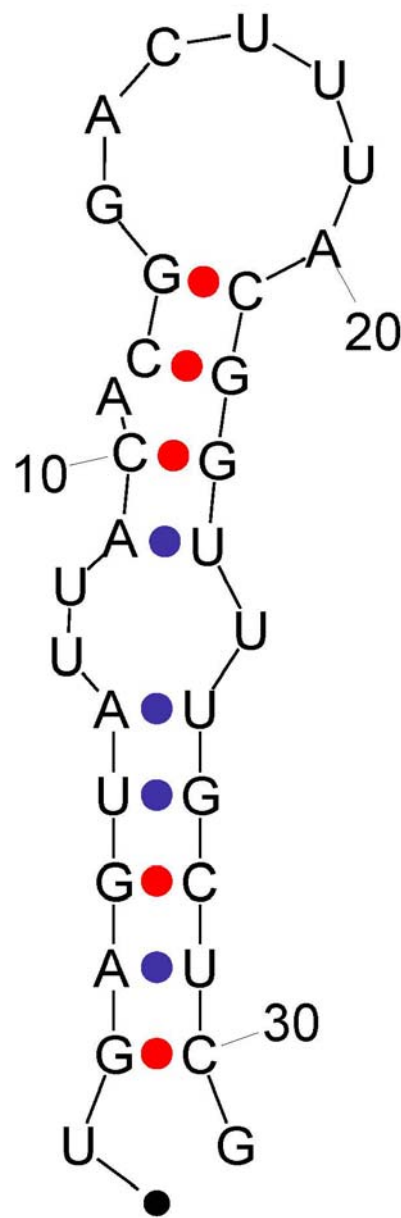
Yksityiskohtia edellisestä: neljä samanlaisena toistuvaa sormea



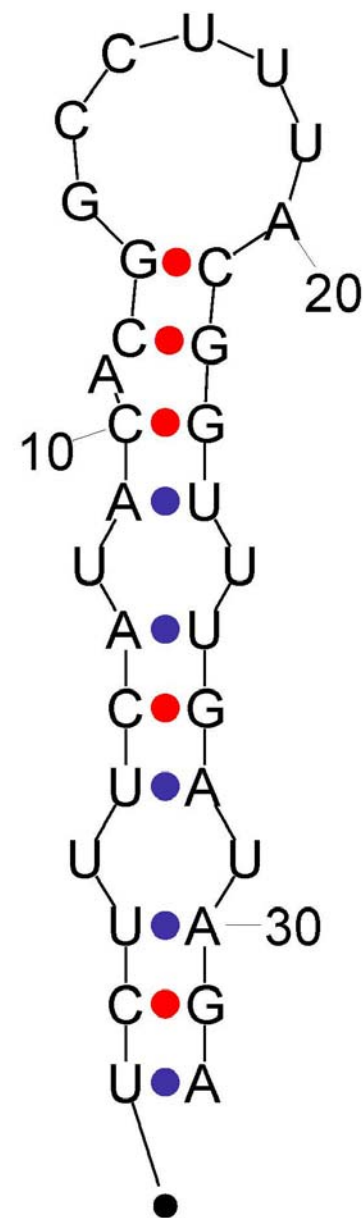
-10.1 [initially -9.6] Sal-finger1



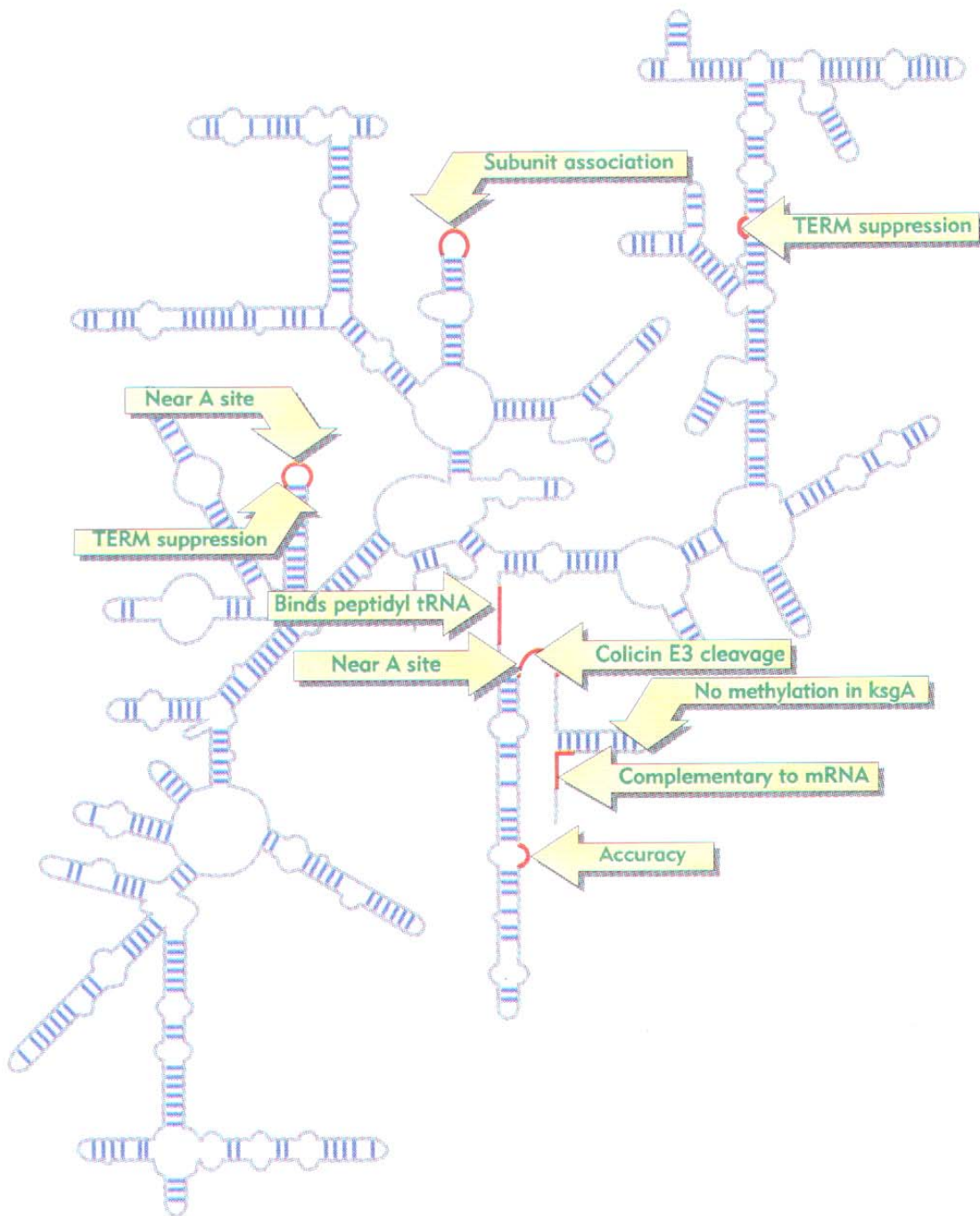
6.6 [initially -6.6] Sal-finger2



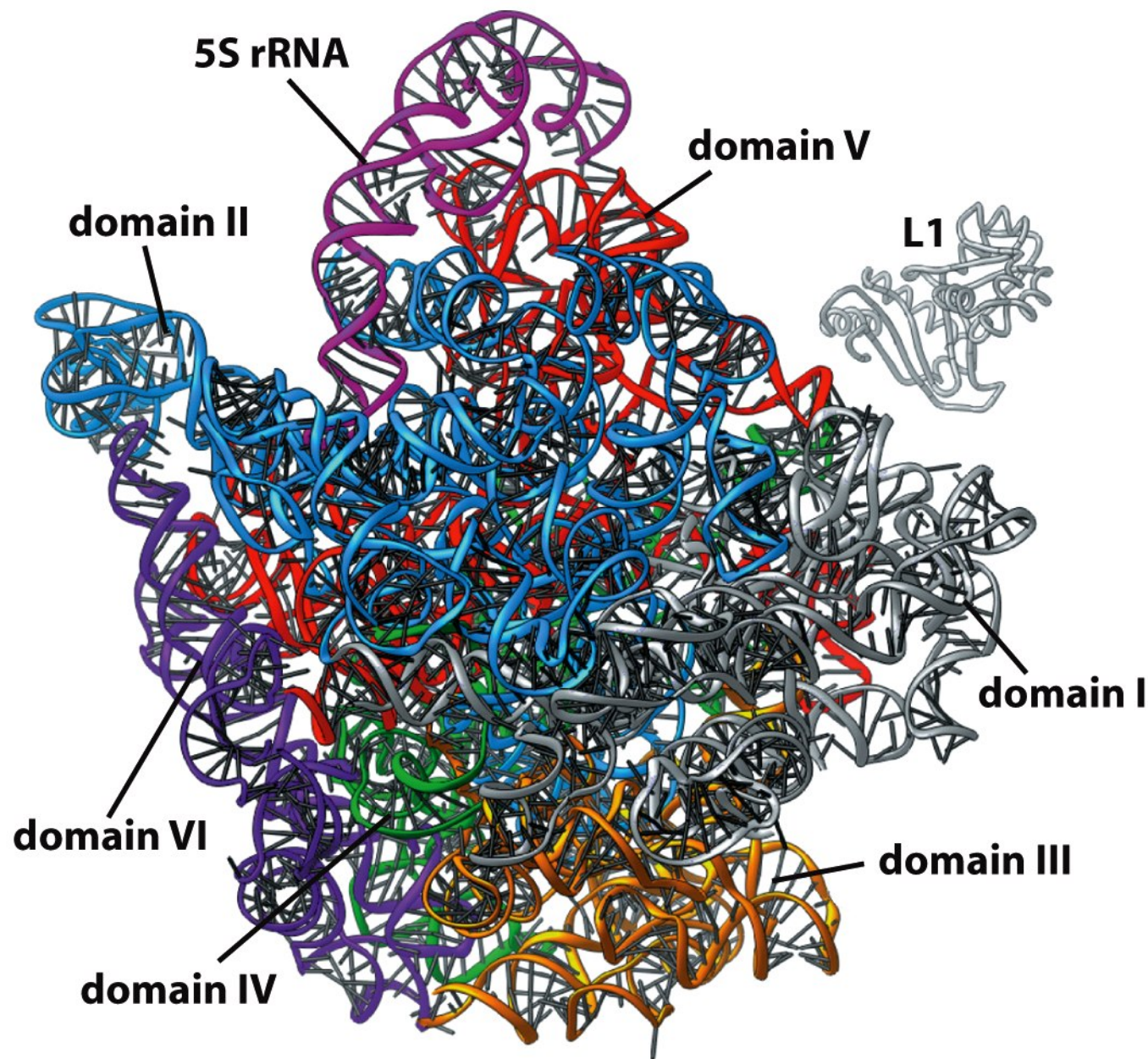
-7.6 [initially -7.6] Sal-finger3



5 [initially -6.1] Sal-finger4



Silputuksen jälkeen
rRNA alayksiköt
hankkiutuvat omiin
omituisiin
sekundaariasentoihin,
missä tietysti niillä
lukuisilla proteiineilla
on oma osuutensa



CELL 378

Figure 6-69a Molecular Biology of the Cell 5/e (© Garland Science 2008)

Bakteeri-ribosomin isomman alayksikön RNA:n laskostukset

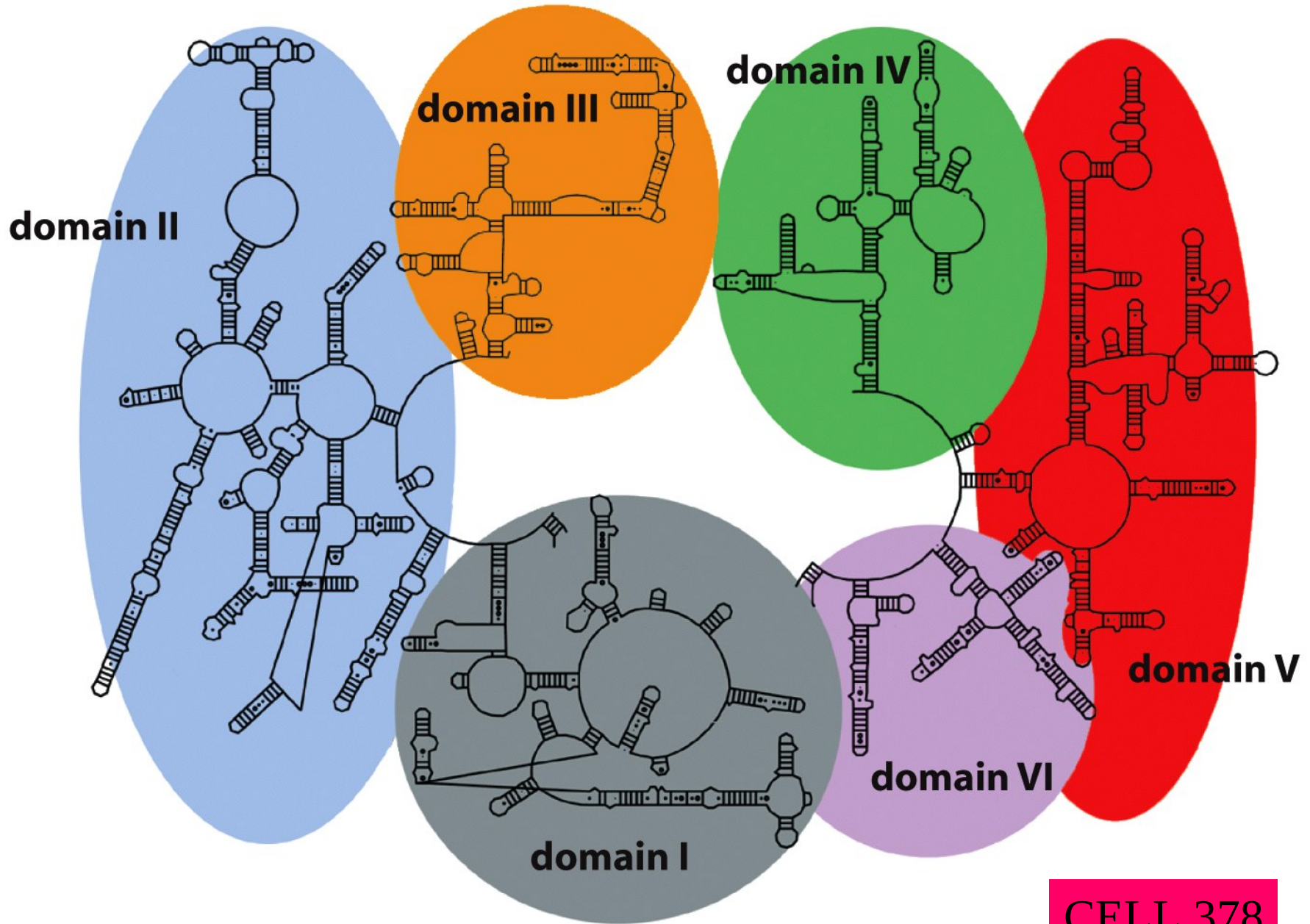


Figure 6-69b Molecular Biology of the Cell 5/e (© Garland Science 2008)

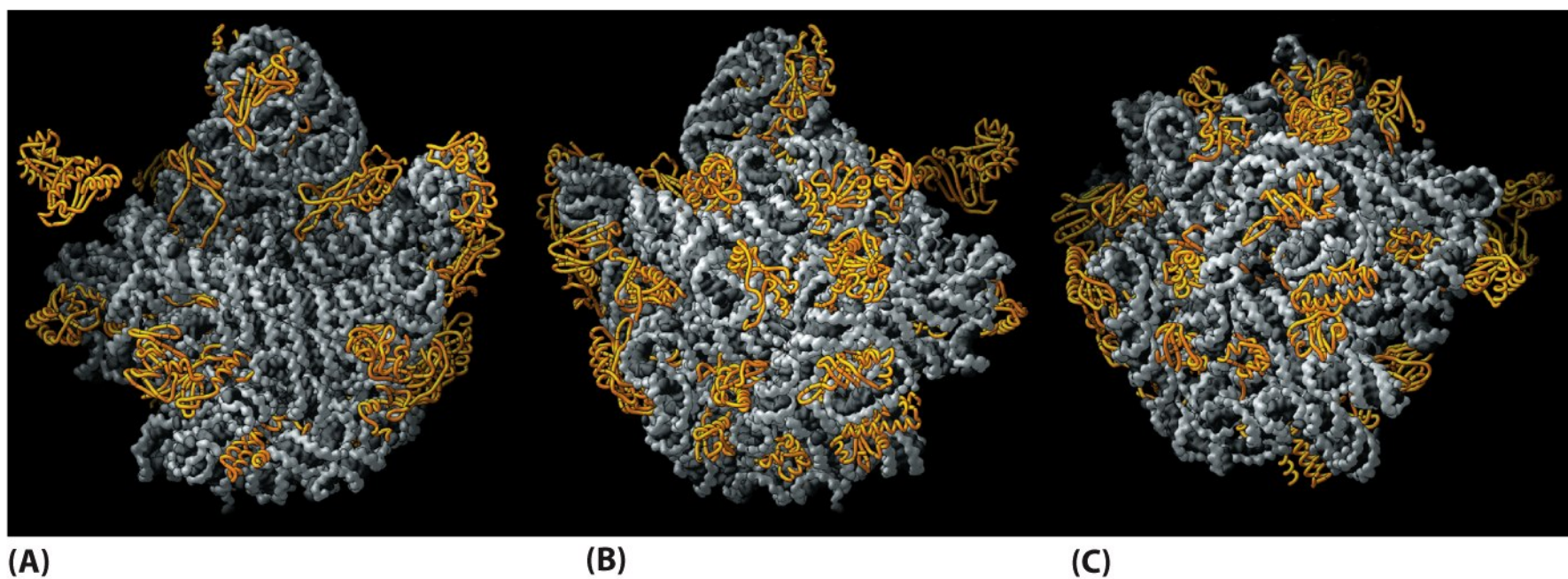
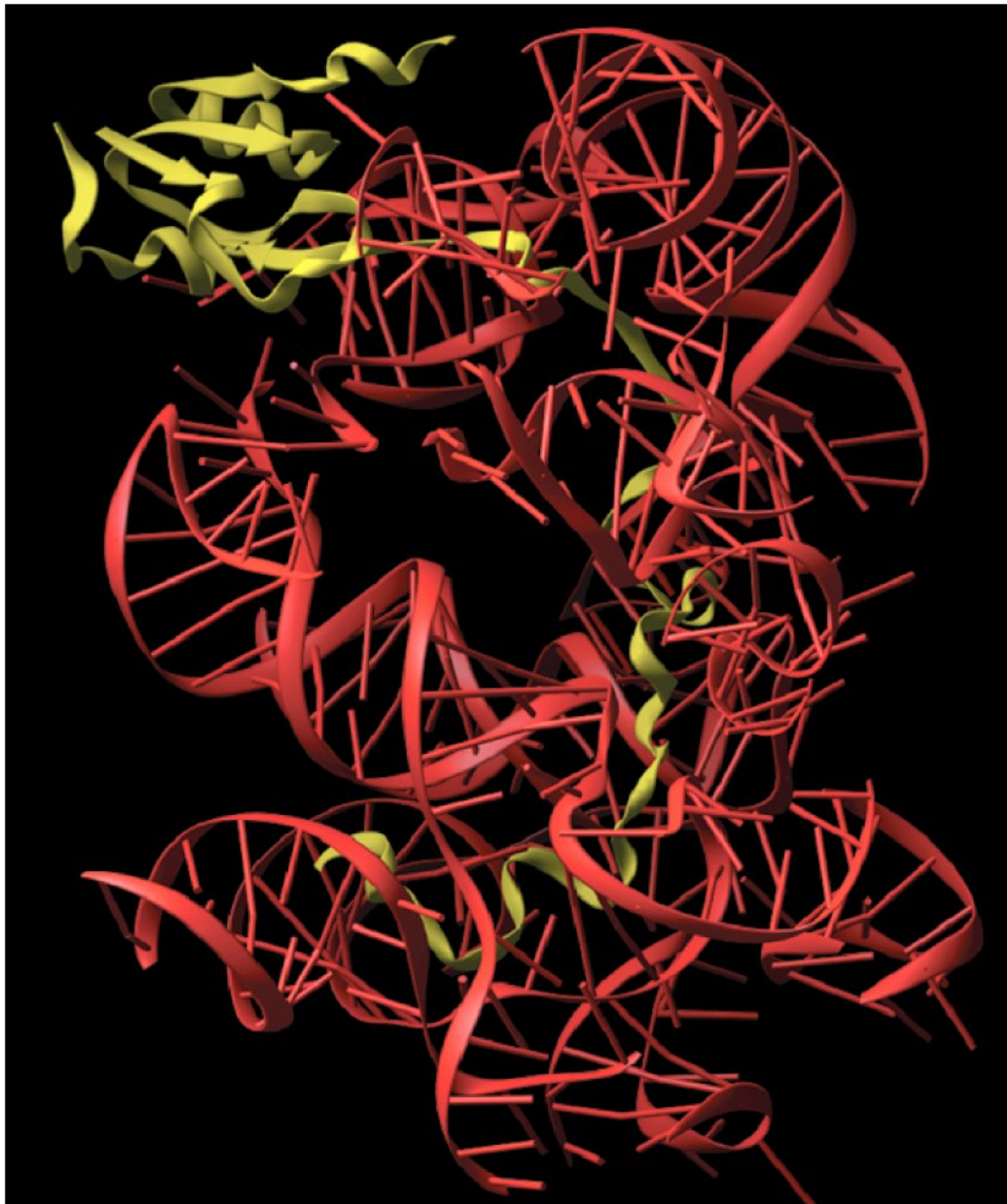


Figure 6-70 Molecular Biology of the Cell 5/e (© Garland Science 2008)

Proteiinit bakteerin LSU:ssa. Harmaa RNA, keltaiset proteiineja



Yksi ribosomin
proteiineista malliksi

L15 (keltainen)
bakteerin LSU:ssa
(osa)

CELL 379

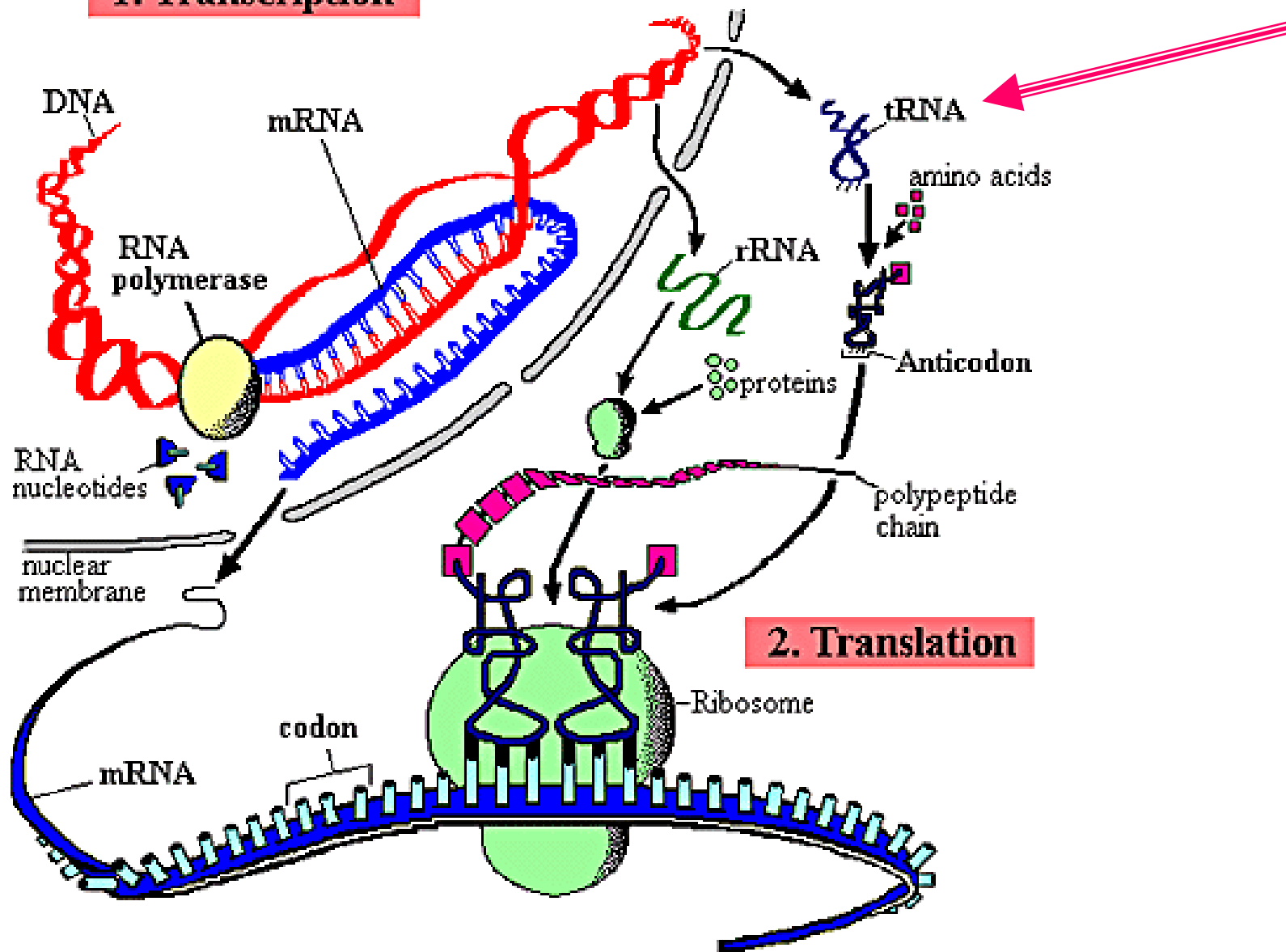
Siirtäjä-RNA eli tRNA



Siirtäjä-RNA:n keksi Robert Holley, Nobel 1968

[Nobel-luento](#)

1. Transcription



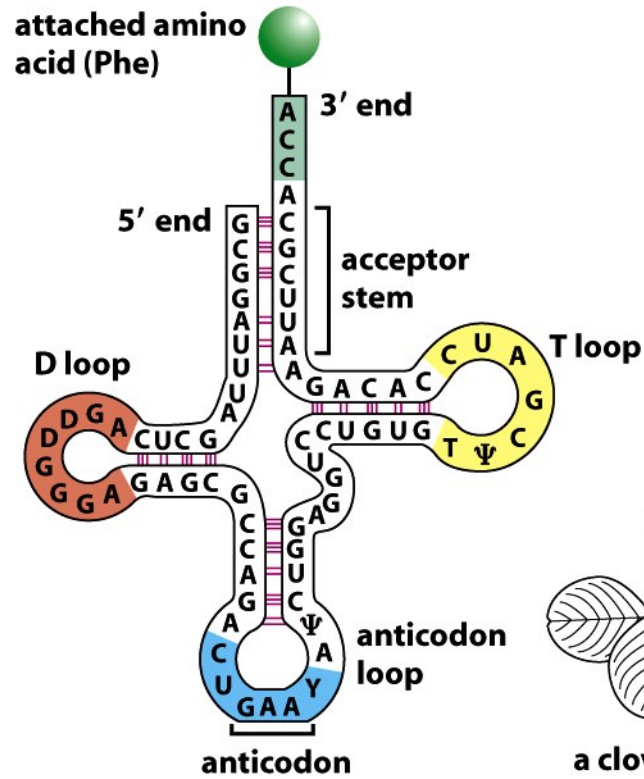
Protein synthesis

Table 6–1 Principal Types of RNAs Produced in Cells

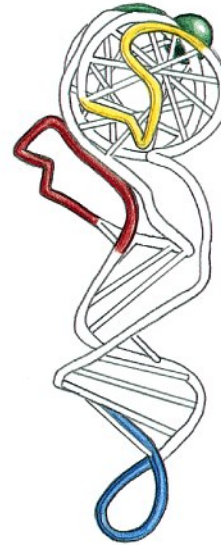
TYPE OF RNA	FUNCTION
mRNAs	messenger RNAs, code for proteins
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snoRNAs	small nucleolar RNAs, used to process and chemically modify rRNAs
scaRNAs	small cajal RNAs, used to modify snoRNAs and snRNAs
miRNAs	microRNAs, regulate gene expression typically by blocking translation of selective mRNAs
siRNAs	small interfering RNAs, turn off gene expression by directing degradation of selective mRNAs and the establishment of compact chromatin structures
Other noncoding RNAs	function in diverse cell processes, including telomere synthesis, X-chromosome inactivation, and the transport of proteins into the ER

Table 6-1 Molecular Biology of the Cell 5/e (© Garland Science 2008)

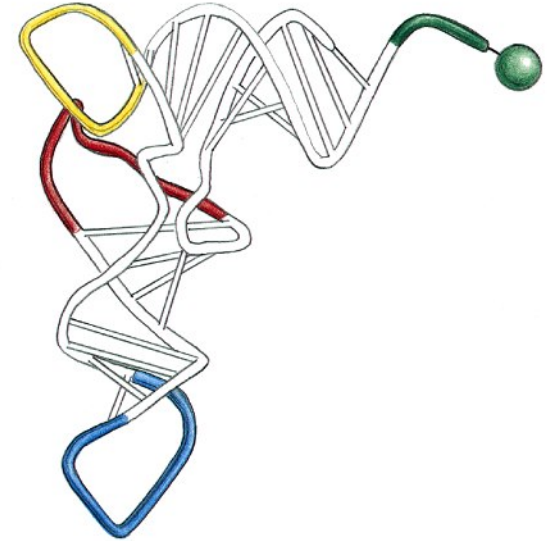
attached amino
acid (Phe)



(A)



(B)



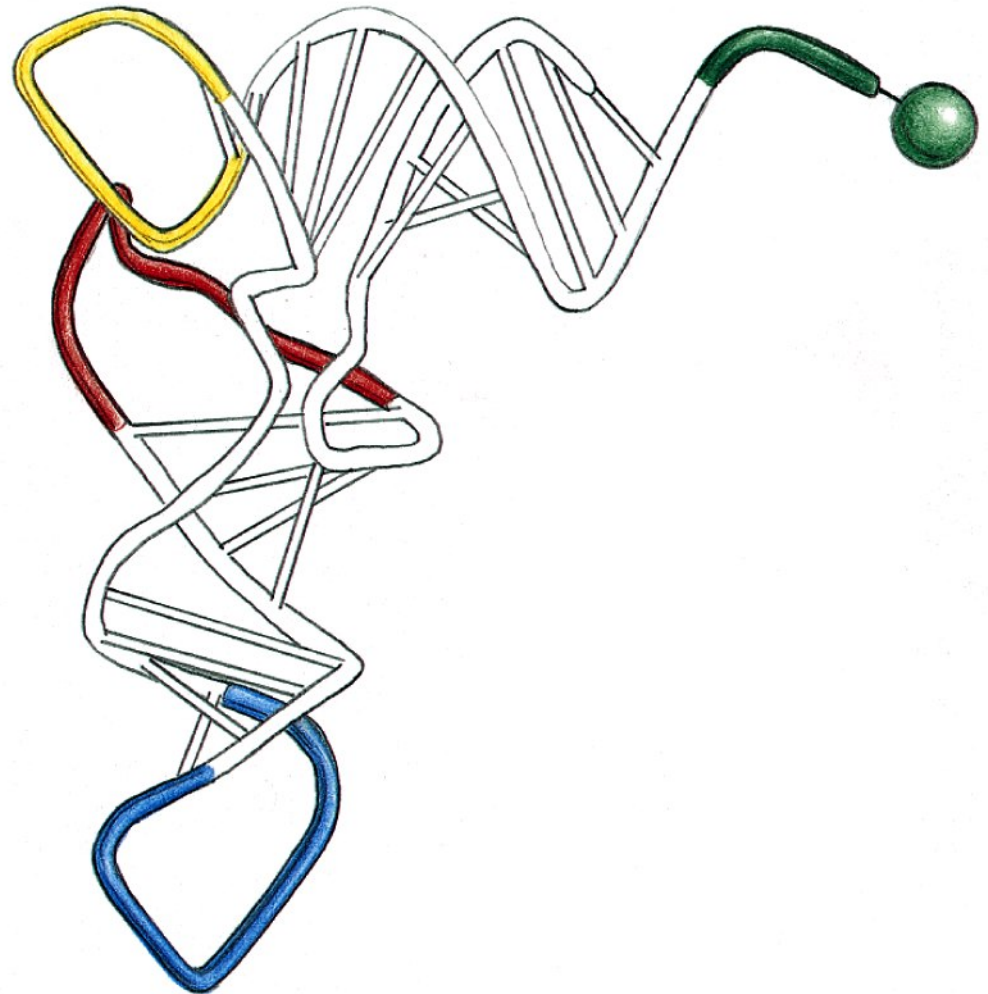
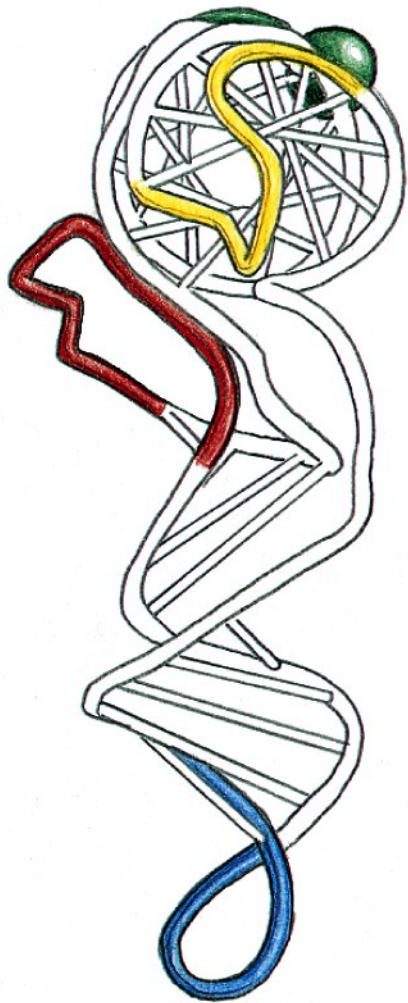
(C)

5' GCGGAUUUAGCUCAGDDGGGAGAGCGCCAGACUGAAYAΨCUGGAGGUCCUGUGTΨCGAUCCACAGAAUUCGCACCA 3'

anticodon

(D)

Figure 6-52 Molecular Biology of the Cell 5/e (© Garland Science 2008)

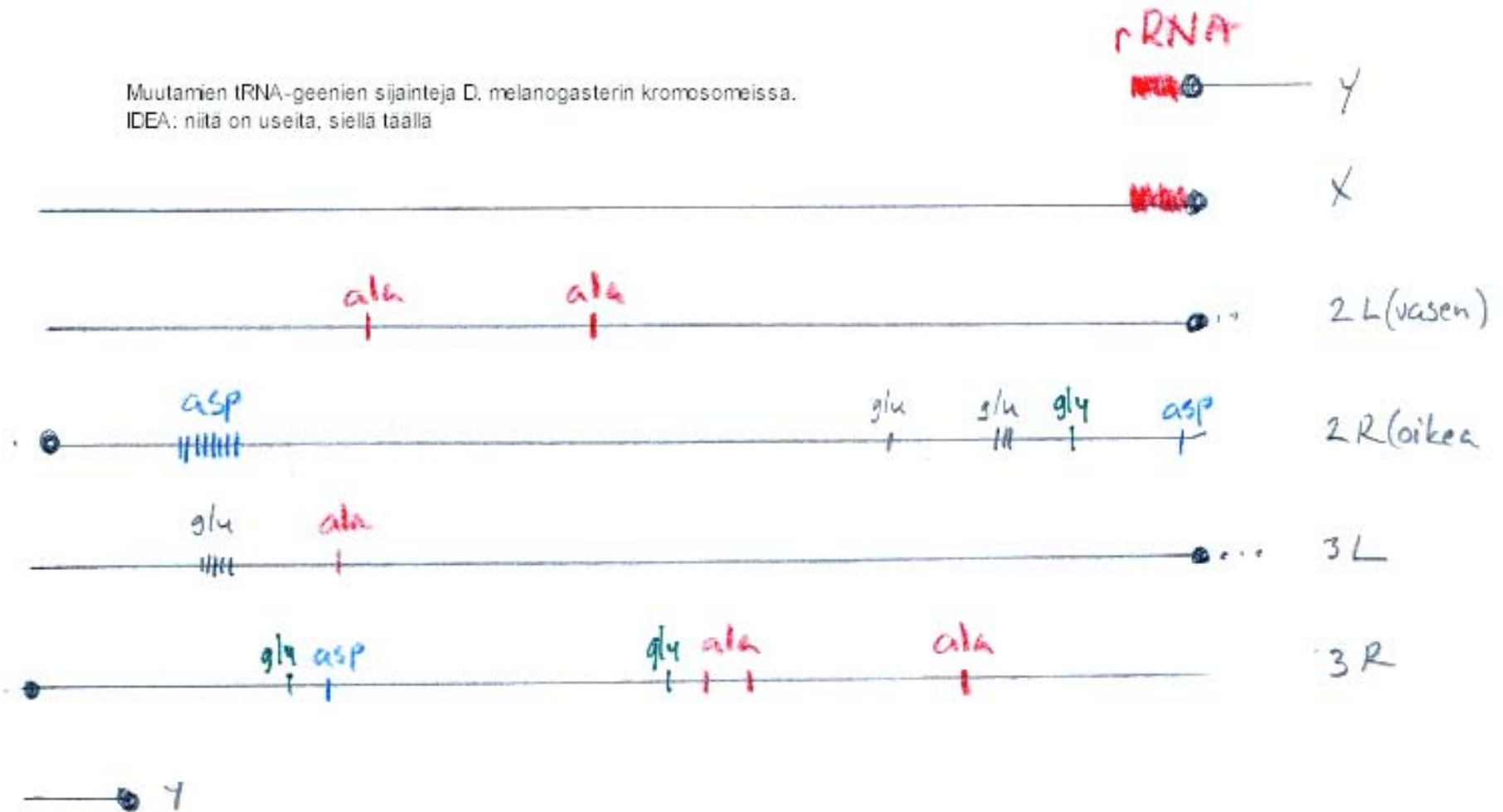


5' GCGGAUUUAGCUCAGDDGGGAGAGCGCCAGACUGAAYAΨCUGGAGGUCCUGUGTΨCGAUCCACAGAAUUCGCACCA 3'

anticodon

Figure 6-52d Molecular Biology of the Cell 5/e (© Garland Science 2008)

Muutamien tRNA-geenien sijainteja *D. melanogasterin* kromosomeissa.
 IDEA: niitä on useita, siellä täällä



Drosophilalla on 292 erilaista tRNA-geeniä, jotka sijaitsevat ihan hajallaan kromosomeissa, ilman mitään loogista järjestystä. rDNA on kahtena blokkina, X kromosomissa ja Y:ssä

tRNA eli siirtäjäRNA geenejä transkriboidaan pitkinä hnRNA-laatuina, joista sitten silputaan varsinaisia tRNA molekyylejä

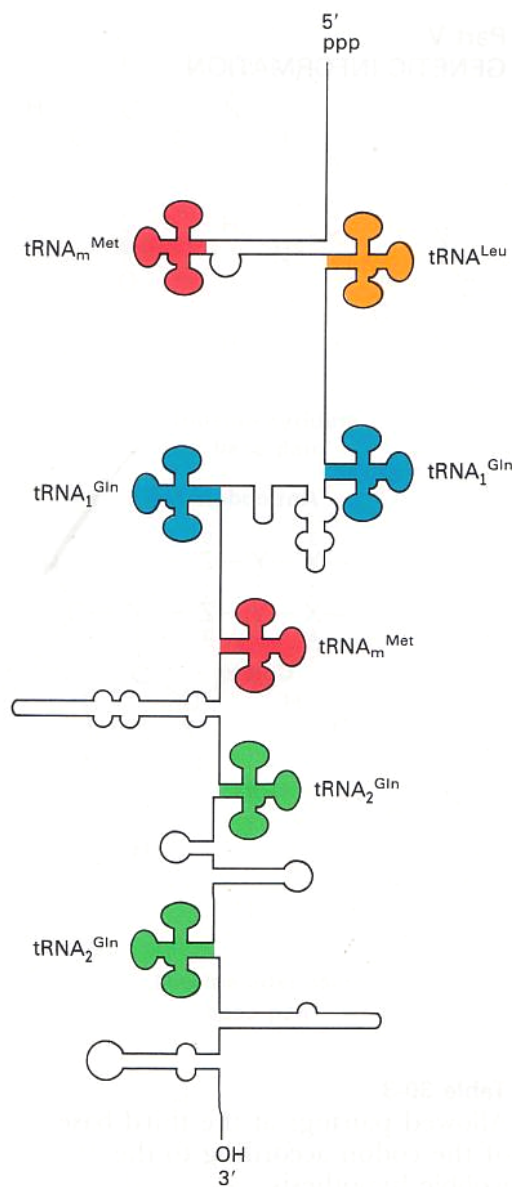


Figure 30-13

Seven tRNA molecules are formed by cleavage of this 950-nucleotide primary transcript. [After N. Nakajima, H. Ozeki, and Y. Shimura. *Cell* 23(1981):245.]



Figure 6-54 Molecular Biology of the Cell 5/e (© Garland Science 2008)

tRNA:ssa voi olla introneita, jotka silputaan pois (sininen)

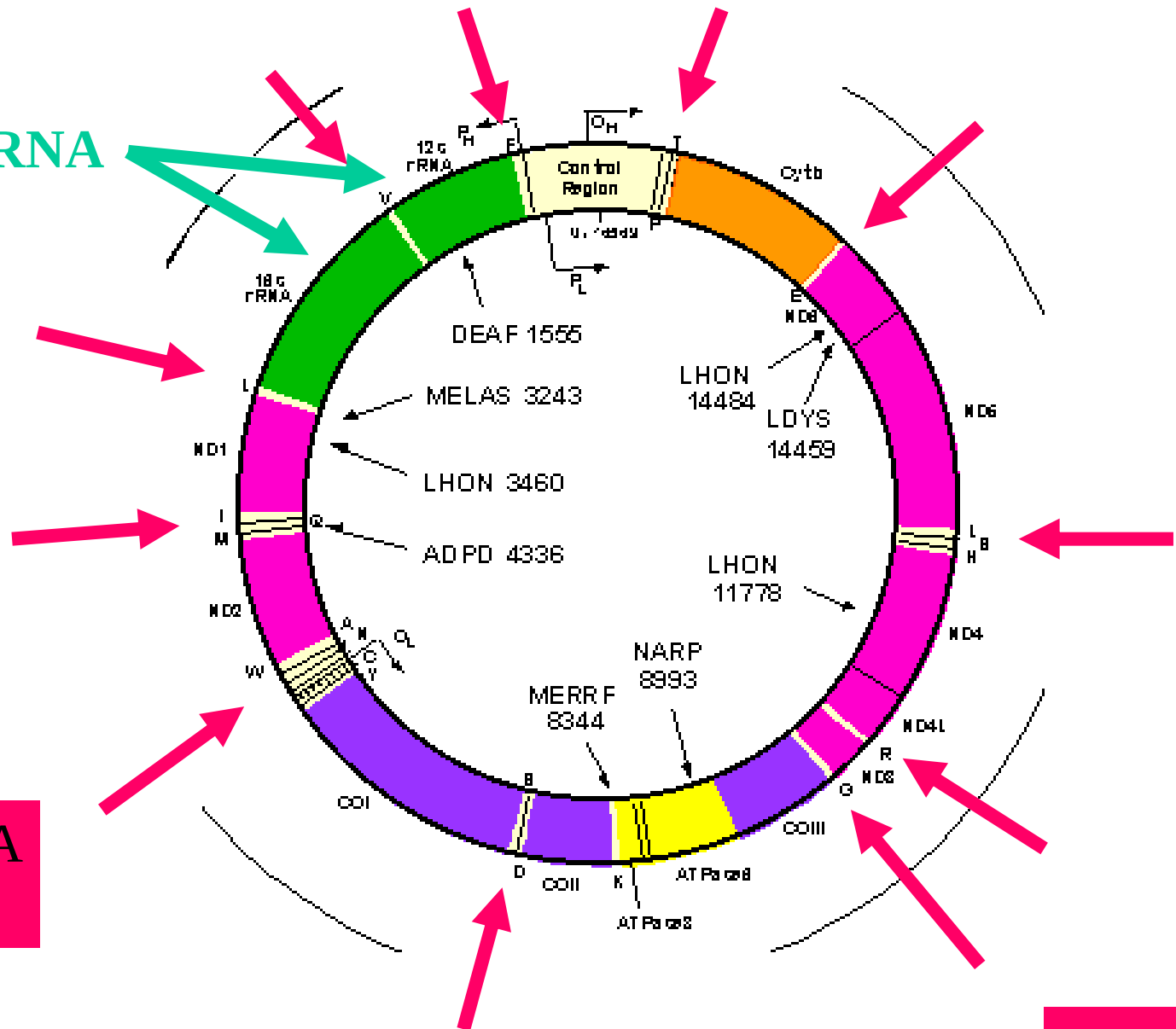


tRNA:ssa voi olla
introneita, jotka
silputaan pois
(sininen)

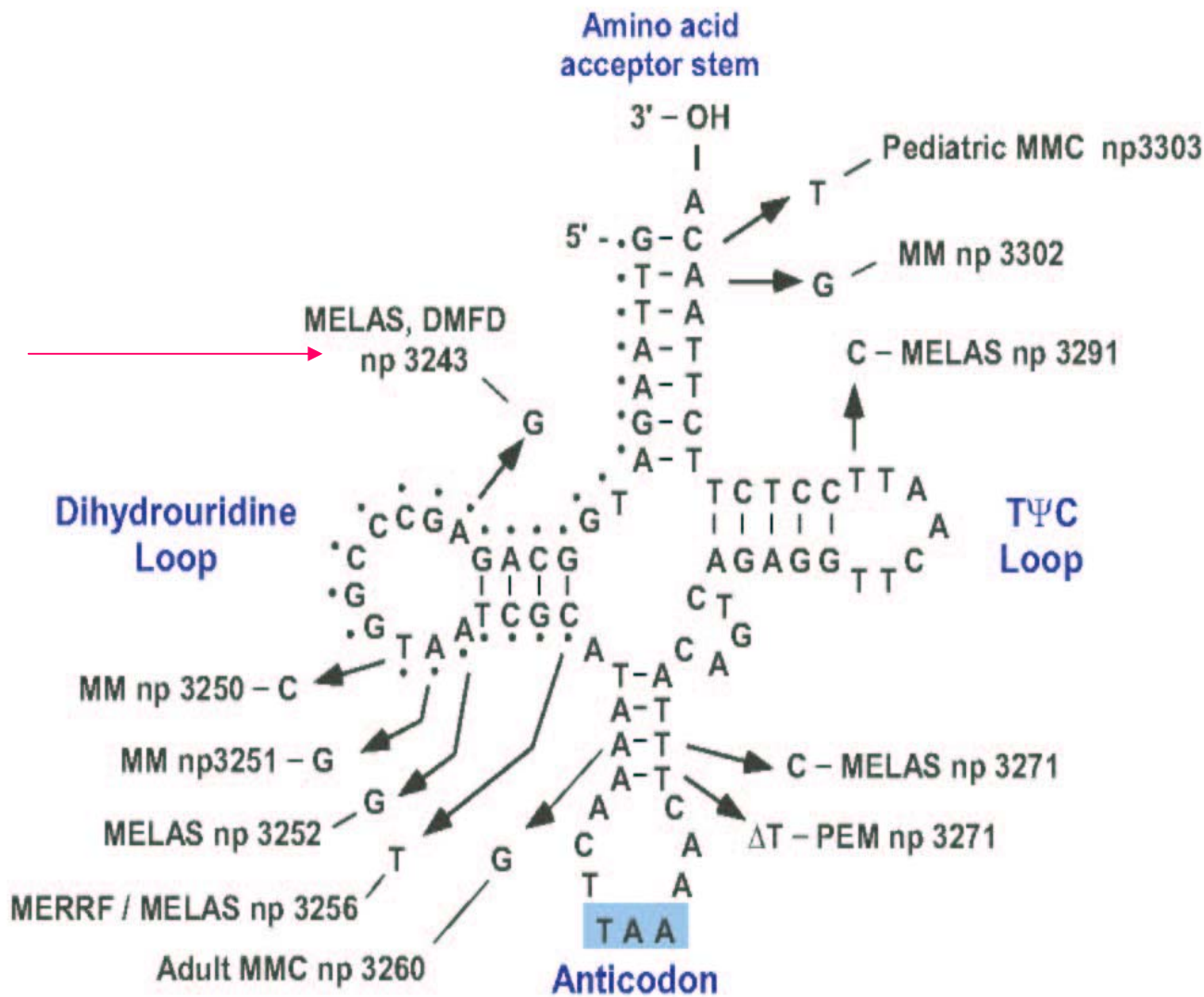
Figure 6-54 Molecular Biology of the Cell 5/e (© Garland Science 2008)

Ihmisen mitokondrio

ribosomiRNA



transferRNA
22 kpl



Pathological Mutations in tRNA^{Leu(UUR)}

<http://www.gen.emory.edu/MITOMAP/tRNAleu.pdf>
Copyright © Emory University, Atlanta, GA 30322

One of the most perplexing aspects of mitochondrial genetics is the marked clinical variability associated with mtDNA mutations. This is dramatically demonstrated for the *MTTL1* gene where base substitutions at np 3243, 3252, 3271, and 3291 give MELAS, but the np 3243 mutation can also result in maternally inherited diabetes and deafness. The *MTTL1* mutations at np 3303 and 3260 result in hypertrophic cardiomyopathy and myopathy, but the former has a pediatric onset while the latter is adult-onset. While alteration of functions embedded within the gene such as the *MTTER* for the np 3243 mutation and a muscle specific tRNA processing activity for the np 3302 mutation have been proposed as partial explanations for these phenotypic differences, much of the clinical variability remains unexplained. The mitochondrial transcription terminator binding site is indicated by black dots.

14. His gtg 636 to 699	---	ATTAAAGTTAAAGTTAAATTC	CAAACTGTTAGGTT	GTG	GGGCTAAAAATAAACATTTT	ACTTAATAC	---
15. Phe gaa 3213 to 3278	---	TTCTCTTAGCTTAAGTTTAAAG	CATTAAATTT	GAA	GAGTTAAAGTTAGTTTAAATT	ACTAGAGGAAA	---
16. Cys aca 5437 to 5502 SHOULD	---	TTTGGTAAAGTTCTTCAGAA	TATATGTGTT	ACA	AGCATAAAGGGTTTATTATT	TATATGCCAAAAAC	---
17. Ala tgc 5500 to 5569	---	AACAAGGTAGTTATTATAGGT	AGTAATAAAAAATTT	TGC	GTATTTTTAGGTGGGTGAGGT	CACCCCTTGTTA	---
18. Asp gtc 5569 to 5637	---	AATAGGGTTAGTTAATAAATA	TAAATATGTACTT	GTC	GTGTATAAGTAGTTTACAT	CAAAACACCTATTTA	---
19. Asn gtt 6479 to 6545	---	GGGGTTATAGTTTAAATCTAAA	CCGTAAAGCT	GTT	AACTTTTAAAAATGCTACT	CCAATGGCTTACCCCT	---
20. Pro tgg 6551 to 6616	---	TTTAAGATAGTTTATTAAATA	AAAAATATTATTTT	TGG	GTAATAAAGATCTCTGTAA	AGAGTCTTACTG	---
21. Ile gat 6612 to 6679	---	TACTGATAGGGCTGCTCAAG	CAGGTTGCTTT	GAT	ATAGCAAAATCGTAAAAAT	TACATTTTCGTCAGTAT	---
22. Lys ctt 6683 to 6750	---	AAGGGTATAGCTATAGGTAT	TAAAGTAACAGACT	CTT	ACTCTGTAGAGGGGCACAG	CTCTACCCTTACC	---
23. Ser gct 7102 to 7163 D-loop	---	GGGAAAAATATTATAGGTTT	TACT	GCT	AAATAAGCCTAAGAAAAC	CTACGAGTTTTCATTTT	CCCTTC
24. Trp tca 7165 to 7230	---	CGGGGGGTTACGTTAAATAT	AGACGATTTGTTT	TCA	AAACAAAAAGTGCATAAT	TGTGCACCCCTCTGT	---
25. Thr tgt 8772 to 8837	---	GTCTAGTTAGTTTTTATAGT	AAAAACATGGTTTTT	TGT	AAATACCAAGTAATCTGT	TATGGGTACTAGGCT	---
26. Cys gca 9793 to 9854	---	AGTGTATGCCATAAGCTTA	TATTTT	GCA	AAAATAAGTACGGTAGTTT	TATTTTACCCATACAC	TTT
27. Glu 11047 to 11118	---	ATTATGTTAGTGTAAAATGTT	AAAGCACATGAACCTT	TTC	GTGTTTCAGGGAAGCGGT	AAATCGCTATGTAATA	---
28. Tyr gta 11609 TO 11673	---	CTAGTTTTAGTATAAAATA	AAGTGCCTAGAAATT	GTA	GCTTCTAAAGAAAATGTT	AACTCATTATCTAGA	---
29. Leu tag 11675 to 11742	---	TTAGAGATGTTAGAAAGTT	GAATAAGTTTGT	TAG	GTACAAAAAATGGGGGT	TATCCCCCTCTTTAAG	---
30. Gln ttg 11743 to 11806	---	TATAGAGTGATGTATCATT	AGCATAATGCTTTT	TTG	GTAGCATAGGAGGTAGAA	ACCCTCTATAG	---
31. Met cat 11810 to 11874	---	AAAAAGGTAAGTTAATAAAA	CTTCTTGATT	CAT	GATCAAAAAATACACTTT	TAAAGTGTCTTTT	TTA
32. Trp tca REVERSE 12697 to 12	---	TGTTAGCTAAATTGTATT	TAGTCAGCTTAGCT	TCA	AACTAAGCTATGTGTCT	AAAC	---
33. Ser 3 tga 12641 to 12697 Fo	---	GTGTTAGACACATAGCTT	AGTT	TGA	AGCTAAGCTGACTAAAAT	ACAATTTAGCTAAACA	---
34. Leu taa 12709 to 12777	---	ACATTAGTGTCTCAGAGA	ATTATGAATCGATTTT	TAA	GCCTCGAATACGAAAG	CTTGCCCTTCCCTAGT	GTTT
35. Arg tcg 12778 to 12844	---	GCCAAATGCTTGTATTCA	AGGATAAATGTT	TCG	GCCGTATTTATGTAG	GTGAGAGCTACCTTT	GGT
36. Gly tcc 14409 to 14477	---	ACAACATTTATTATATTCA	ATACTAACTT	TCC	AAGTTAGAGAGCCTT	AAAAATAAGTAGGAT	GTTGTAC
37. Sequence 37							

*Gyrodactylus salarix*en mitokondrion tRNA-geenit.

Täsmälleen samat kuin ihmisellä, ei kuitenkaan ihan identtiset.

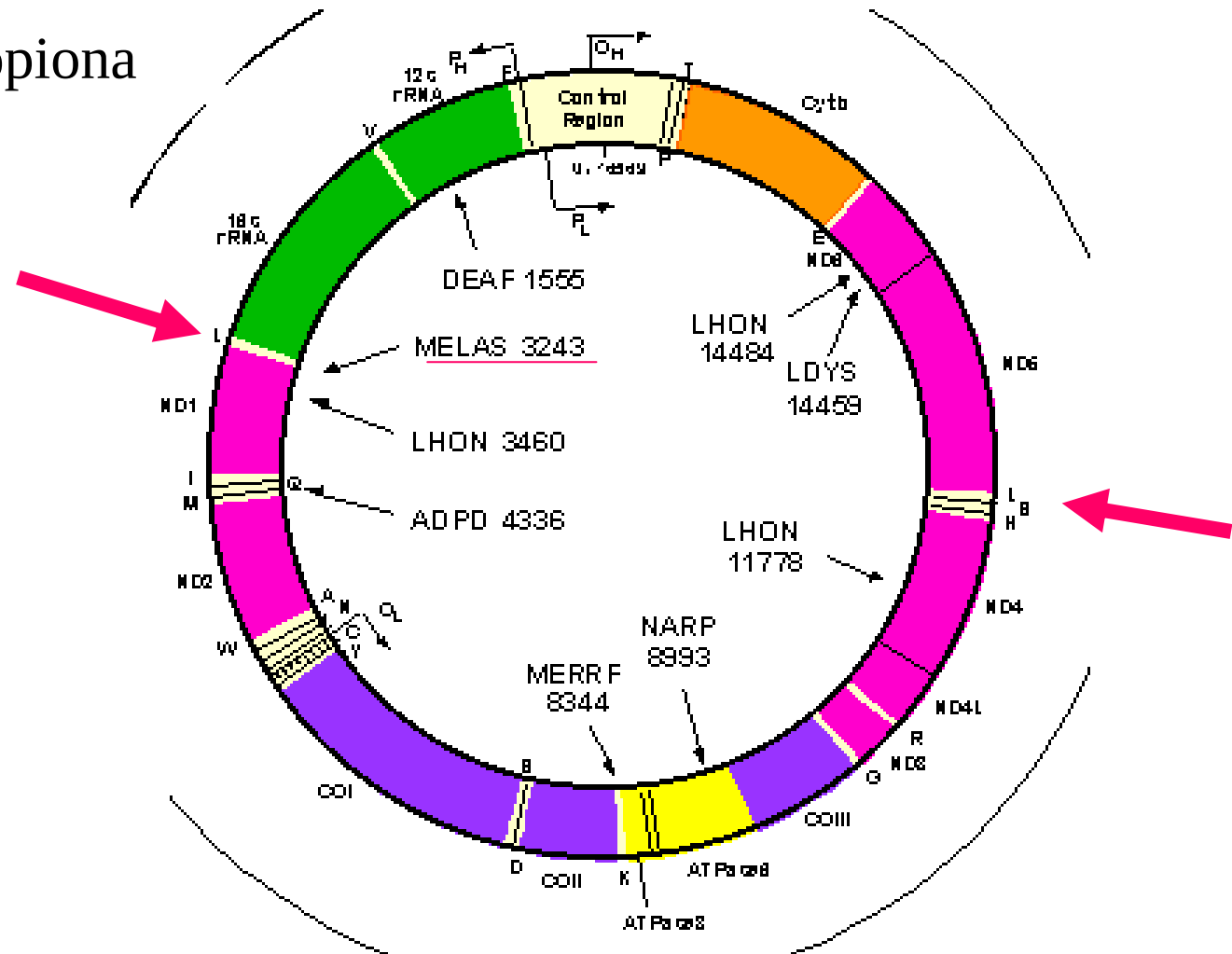
Kahtena ovat seriinin ja leusiinin tRNA:t, ihan niinkuin ihmiselläkin

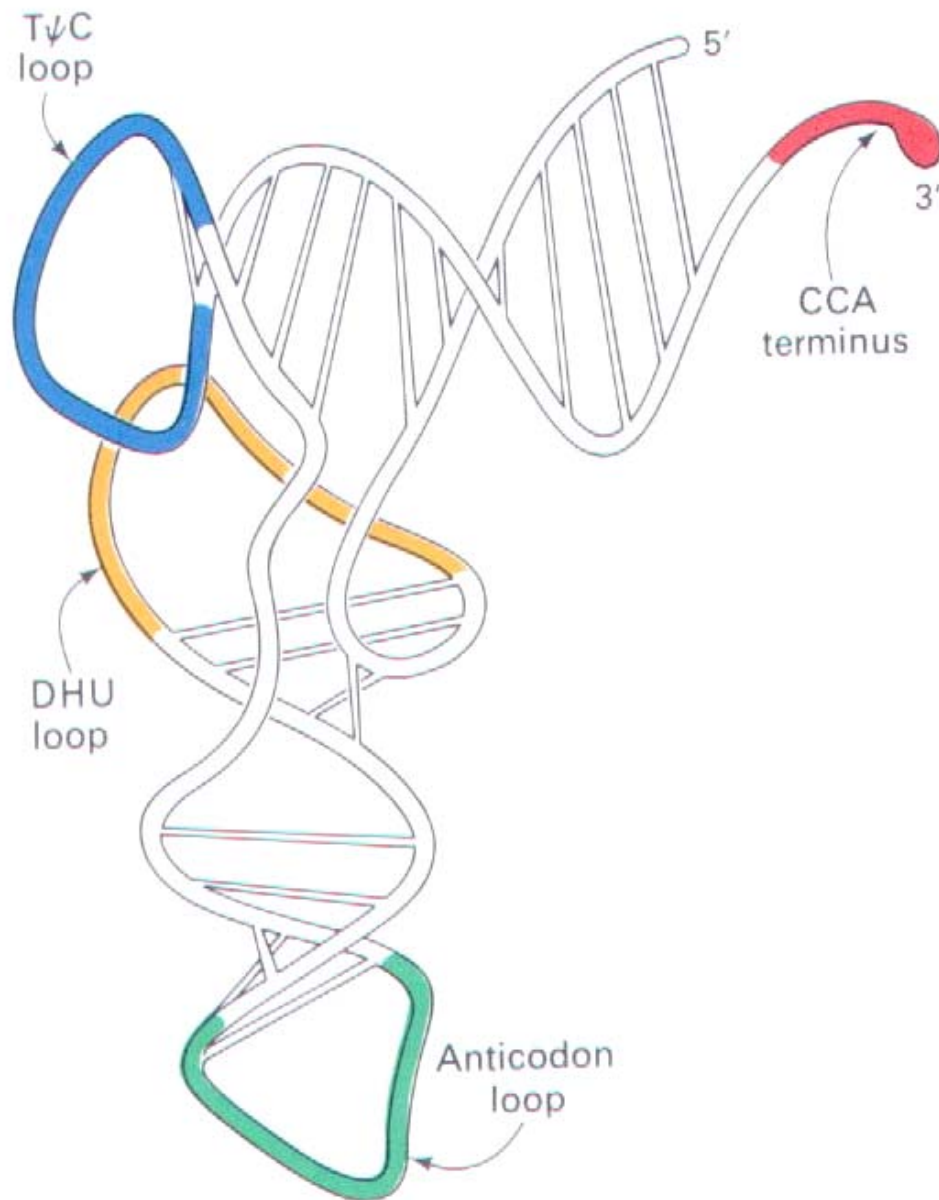
14. His gtg 636 to 699	---	ATTAAAGTTTAAAGTTAAATTC	CAAACTGTTAGGTT	GTG	GGGCTAAAAATAAACATTTT	ACTTAATAC	---
15. Phe gaa 3213 to 3278	---	TTCTCTTAGCTTAAGTTTAAAG	CATTAAATTT	GAA	GAGTTAAAGTTAGTTTAAATT	ACTAGAGGAAA	---
16. Cys aca 5437 to 5502 SHOULD	---	TTTGGTAAAGTTCTTCAGAA	TATATGTGTT	ACA	AGCATAAAGGGTTTATTATT	TATATGCCAAAAAC	---
17. Ala tgc 5500 to 5569	---	AACAAGGTAGTTATTATAGGT	AGTAATAAAAAATTT	TGC	GTATTTTTAGGTGGGTGA	GGTCACCCCTTGTTA	---
18. Asp gtc 5569 to 5637	---	AATAGGGTTAGTTAATAAATA	TAAATATGTACTT	GTC	GTGTATAAGTAGTTTACAT	CAAAACACCTATTTA	---
19. Asn gtt 6479 to 6545	---	GGGGTTATAGTTTAAATCTAAA	CCGTAAAGCT	GTT	AACTTTTAAATGCTACT	CCAATGGCTTACCCCT	---
20. Pro tgg 6551 to 6616	---	TTTAAGATAGTTTATTAAATA	AAAAATATTATTTT	TGG	GTAATAAAGATCTCTGTAA	AGAGTCTTACTG	---
21. Ile gat 6612 to 6679	---	TACTGATAGGGCTGCTCAAG	CAGGTGCTTT	GAT	ATAGCAAAATCGTAAAAAT	TACATTTTTCGTCA	GTAT
22. Lys ctt 6683 to 6750	---	AAGGGTATAGCTATAGGTAT	TAAAGTAACAGACT	CTT	ACTCTGTAGAGGGGCACAG	CTCTACCCTTACC	---
23. Ser gct 7102 to 7163 D-loop	---	GGGAAAAATATTATAGGTTT	TACT	GCT	AAATAAGCCTAAGAAACCT	ACGAGTTTTCATTTT	CCCTTC
24. Trp tca 7165 to 7230	---	CGGGGGGTTACGTTAAATAT	AGACGATTTGTTT	TCA	AAACAAAAAAGTGCATAAT	TGTGCACCCCTCTGT	---
25. Thr tgt 8772 to 8837	---	GTCTAGTTAGTTTTATAGT	AAAAACATGGTTTTT	TGT	AAATACCAAGTAATCTGT	TATGGGTACTAGGCT	---
26. Cys gca 9793 to 9854	---	AGTGTATGCCATAAGCTTA	TATTTT	GCA	AAAATAAGTACGGTAGTTT	TATTTTACCCATAC	CACTT
27. Glu 11047 to 11118	ATTATGTTAGTGTAAAATGTT	AAAGCACATGAACTT	TTC	GTGTTTCAGGGAAGCGGT	AAATCGCTATGTAATA	---	---
28. Tyr gta 11609 TO 11673	---	CTAGTTTTAGTATAAAATA	AAGTGCCTAGAAATT	GTA	GCTTCTAAAGAAAATGTT	AACTCATTATCTAGA	---
29. Leu tag 11675 to 11742	---	TTAGAGATGTTAGAAGTTGA	AATAAGTTTGTTTT	TAG	GTACAAAAAATGGGGGGT	TATCCCCCTCTTTAAG	---
30. Gln ttg 11743 to 11806	---	TATAGAGTGATGTATCATT	AGCATAAATGCTTTT	TTG	GTAGCATAGGAGGTAGAA	ACCCTCTATAG	---
31. Met cat 11810 to 11874	---	AAAAAGGTAAGTTAATAAAA	CTTCTTGATT	CAT	GATCAAAAAAATACACTT	TAAAGTGTCTCTTTTA	---
32. Trp tca REVERSE 12697 to 12	---	TGTTAGCTAAATTGTATT	TAGTCAGCTTAGCT	TCA	AACTAAGCTATGTGTCTA	AAC	---
33. Ser 3 tga 12641 to 12697 Fo	---	GTGTTAGACACATAGCTT	AGTT	TGA	AGCTAAGCTGACTAAAAT	ACAATTTAGCTAAACA	---
34. Leu taa 12709 to 12777	---	ACATTAGTGTCTCAGAGAATT	ATGAATCGATTTT	TAA	GCCTCGAAATACGAAAGCT	TGCTTTCCTAGTGTTC	---
35. Arg tcg 12778 to 12844	---	GCCAAATGCTTGTATTCAAG	GATAATGTT	TCG	GCCGTATTTTATGTAGGT	GAGAGCTACCTTTGGTT	---
36. Gly tcc 14409 to 14477	---	ACAACATTTATTATATTCA	AATACTAACTT	TCC	AAGTTAGAGAGCCTTAA	AATAGTAGGATGTTGTAC	---
37. Sequence 37							

Kotitehtävä #6: valitse joku tai joitakin ja värkkää sekundaari-struktuurin apilanlehtimalli!

Aloita antikodonista, muista että parit on G=C, A=U(T) ja mahdollinen G=U.

Leusiinin
transferRNA
on kahtena kopiona





tRNA:n kolmiulotteinen rakenne

Aminohappo sitoutuu CCA-päähän, joka on kaikilla tRNA-laaduilla samanlainen. Miten se aminohappo sitten voi olla oikea????

Otetaan se vielä esille translaatioprosessin yhteydessä:
aminoasyyli-tRNA-syntetaasi