

Figure 27-1

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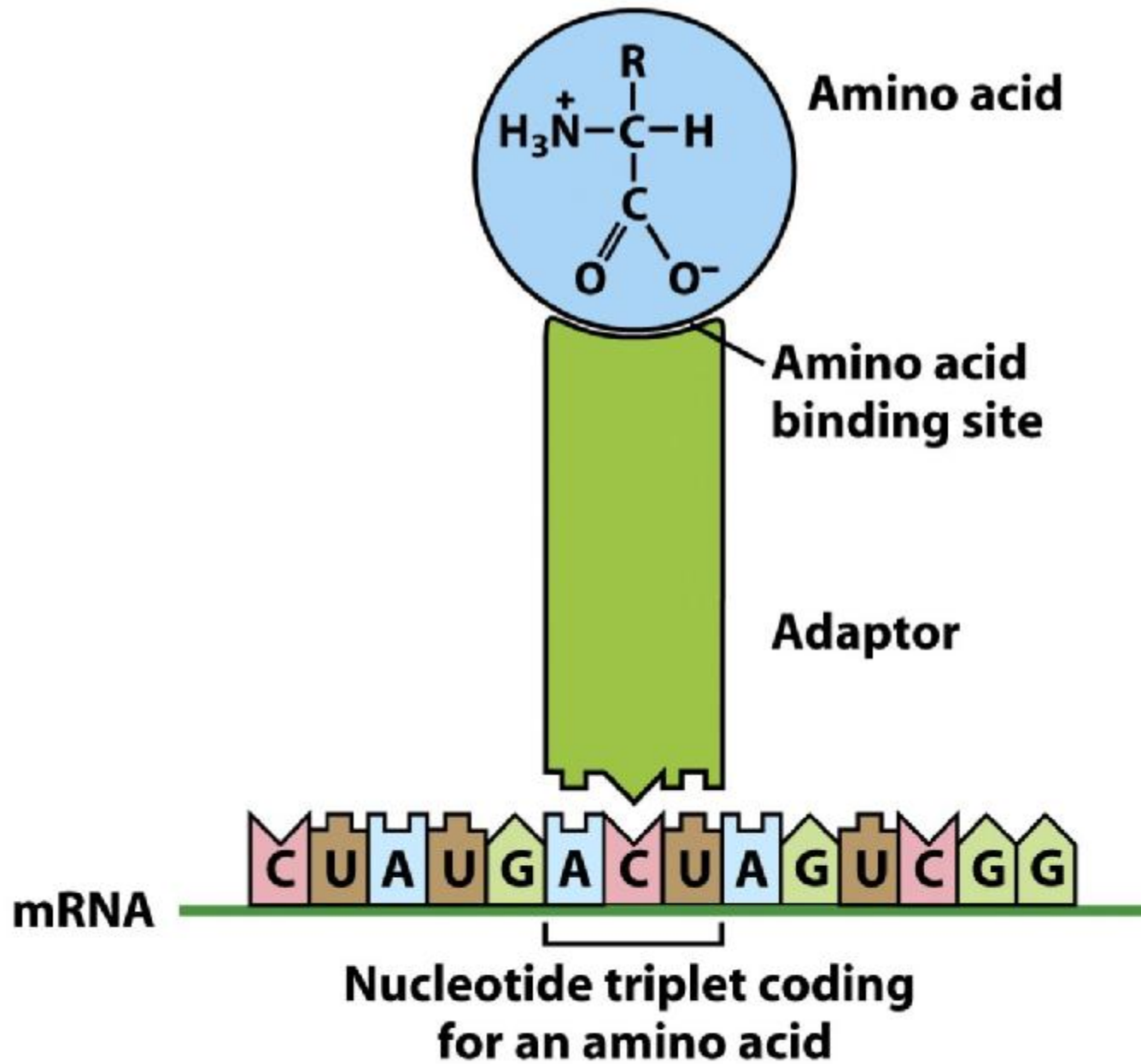


Figure 27-2
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**Nonoverlapping
code**



**Overlapping
code**

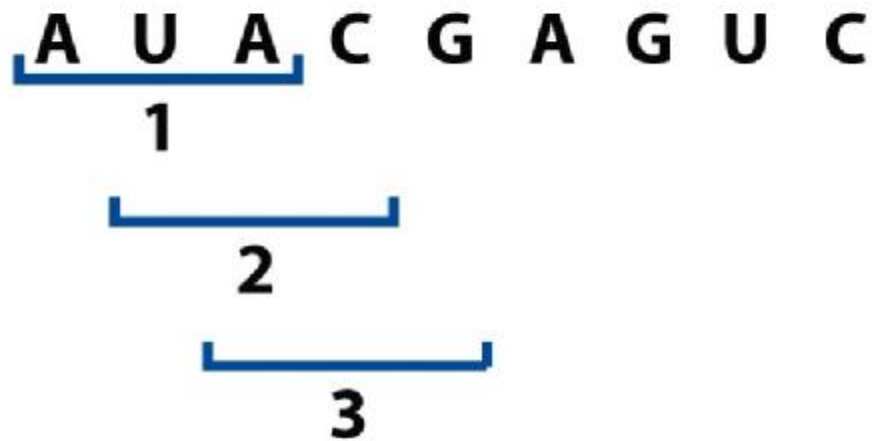


Figure 27-3

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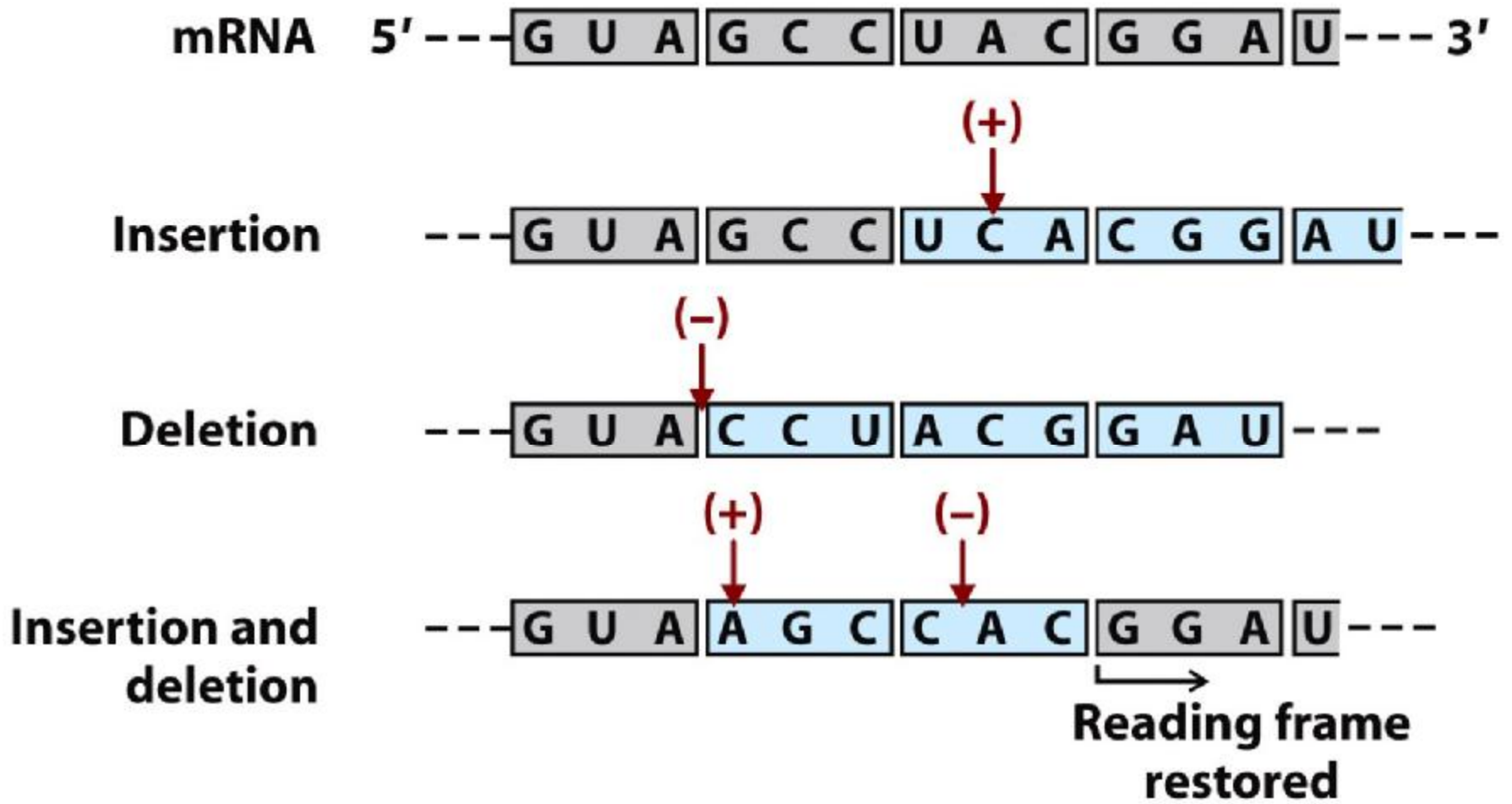


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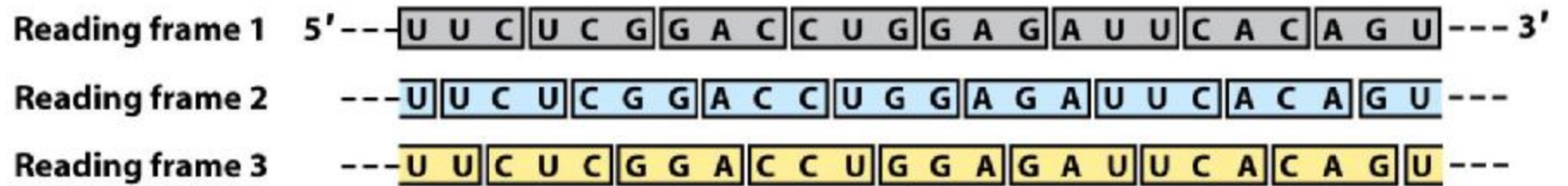


Figure 27-5

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TABLE 27-1

Incorporation of Amino Acids into Polypeptides in Response to Random Polymers of RNA

Amino acid	Observed frequency of incorporation (Lys = 100)	Tentative assignment for nucleotide composition of corresponding codon*	Expected frequency of incorporation based on assignment (Lys = 100)
Asparagine	24	A ₂ C	20
Glutamine	24	A ₂ C	20
Histidine	6	AC ₂	4
Lysine	100	AAA	100
Proline	7	AC ₂ , CCC	4.8
Threonine	26	A ₂ C, AC ₂	24

Note: Presented here is a summary of data from one of the early experiments designed to elucidate the genetic code. A synthetic RNA containing only A and C residues in a 5:1 ratio directed polypeptide synthesis, and both the identity and the quantity of incorporated amino acids were determined. Based on the relative abundance of A and C residues in the synthetic RNA, and assigning the codon AAA (the most likely codon) a frequency of 100, there should be three different codons of composition A₂C, each at a relative frequency of 20; three of composition AC₂, each at a relative frequency of 4.0; and CCC at a relative frequency of 0.8. The CCC assignment was based on information derived from prior studies with poly(C). Where two tentative codon assignments are made, both are proposed to code for the same amino acid.

*These designations of nucleotide composition contain no information on nucleotide sequence (except, of course, AAA and CCC).

Table 27-1

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TABLE 27-2**Trinucleotides That Induce Specific Binding of Aminoacyl-tRNAs to Ribosomes**

Trinucleotide	Relative increase in ¹⁴ C-labeled aminoacyl-tRNA bound to ribosome*		
	Phe-tRNA ^{Phe}	Lys-tRNA ^{Lys}	Pro-tRNA ^{Pro}
UUU	4.6	0	0
AAA	0	7.7	0
CCC	0	0	3.1

Source: Modified from Nirenberg, M. & Leder, P. (1964) RNA code words and protein synthesis. *Science* **145**, 1399.

*Each number represents the factor by which the amount of bound ¹⁴C increased when the indicated trinucleotide was present, relative to a control with no trinucleotide.

Table 27-2

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H. Gobind Khorana

Unnumbered 27 p1068

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Figure 27-6

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First letter of codon (5' end)

		Second letter of codon							
		U		C		A		G	
U	U	UUU	Phe	UCU	Ser	UAU	Tyr	UGU	Cys
	C	UUC	Phe	UCC	Ser	UAC	Tyr	UGC	Cys
C	U	UUA	Leu	UCA	Ser	UAA	Stop	UGA	Stop
	C	UUG	Leu	UCG	Ser	UAG	Stop	UGG	Trp
A	U	CUU	Leu	CCU	Pro	CAU	His	CGU	Arg
	C	CUC	Leu	CCC	Pro	CAC	His	CGC	Arg
G	U	CUA	Leu	CCA	Pro	CAA	Gln	CGA	Arg
	C	CUG	Leu	CCG	Pro	CAG	Gln	CGG	Arg
A	U	AUU	Ile	ACU	Thr	AAU	Asn	AGU	Ser
	C	AUC	Ile	ACC	Thr	AAC	Asn	AGC	Ser
G	U	AUA	Ile	ACA	Thr	AAA	Lys	AGA	Arg
	C	AUG	Met	ACG	Thr	AAG	Lys	AGG	Arg
G	U	GUU	Val	GCU	Ala	GAU	Asp	GGU	Gly
	C	GUC	Val	GCC	Ala	GAC	Asp	GGC	Gly
G	U	GUA	Val	GCA	Ala	GAA	Glu	GGA	Gly
	C	GUG	Val	GCG	Ala	GAG	Glu	GGG	Gly

Figure 27-7

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TABLE 27-3**Degeneracy of the Genetic Code**

Amino acid	Number of codons	Amino acid	Number of codons
Met	1	Tyr	2
Trp	1	Ile	3
Asn	2	Ala	4
Asp	2	Gly	4
Cys	2	Pro	4
Gln	2	Thr	4
Glu	2	Val	4
His	2	Arg	6
Lys	2	Leu	6
Phe	2	Ser	6

Table 27-3*Lehninger Principles of Biochemistry, Fifth Edition*

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TABLE 1**Known Variant Codon Assignments in Mitochondria**

	Codons*				
	UGA	AUA	AGA AGG	CUN	CGG
Normal code assignment	Stop	Ile	Arg	Leu	Arg
Animals					
Vertebrates	Trp	Met	Stop	+	+
<i>Drosophila</i>	Trp	Met	Ser	+	+
Yeasts					
<i>Saccharomyces cerevisiae</i>	Trp	Met	+	Thr	+
<i>Torulopsis glabrata</i>	Trp	Met	+	Thr	?
<i>Schizosaccharomyces pombe</i>	Trp	+	+	+	+
Filamentous fungi	Trp	+	+	+	+
Trypanosomes	Trp	+	+	+	+
Higher plants	+	+	+	+	Trp
<i>Chlamydomonas reinhardtii</i>	?	+	+	+	?

*N indicates any nucleotide; +, codon has the same meaning as in the normal code; ?, codon not observed in this mitochondrial genome.

Box 27-1 table 1

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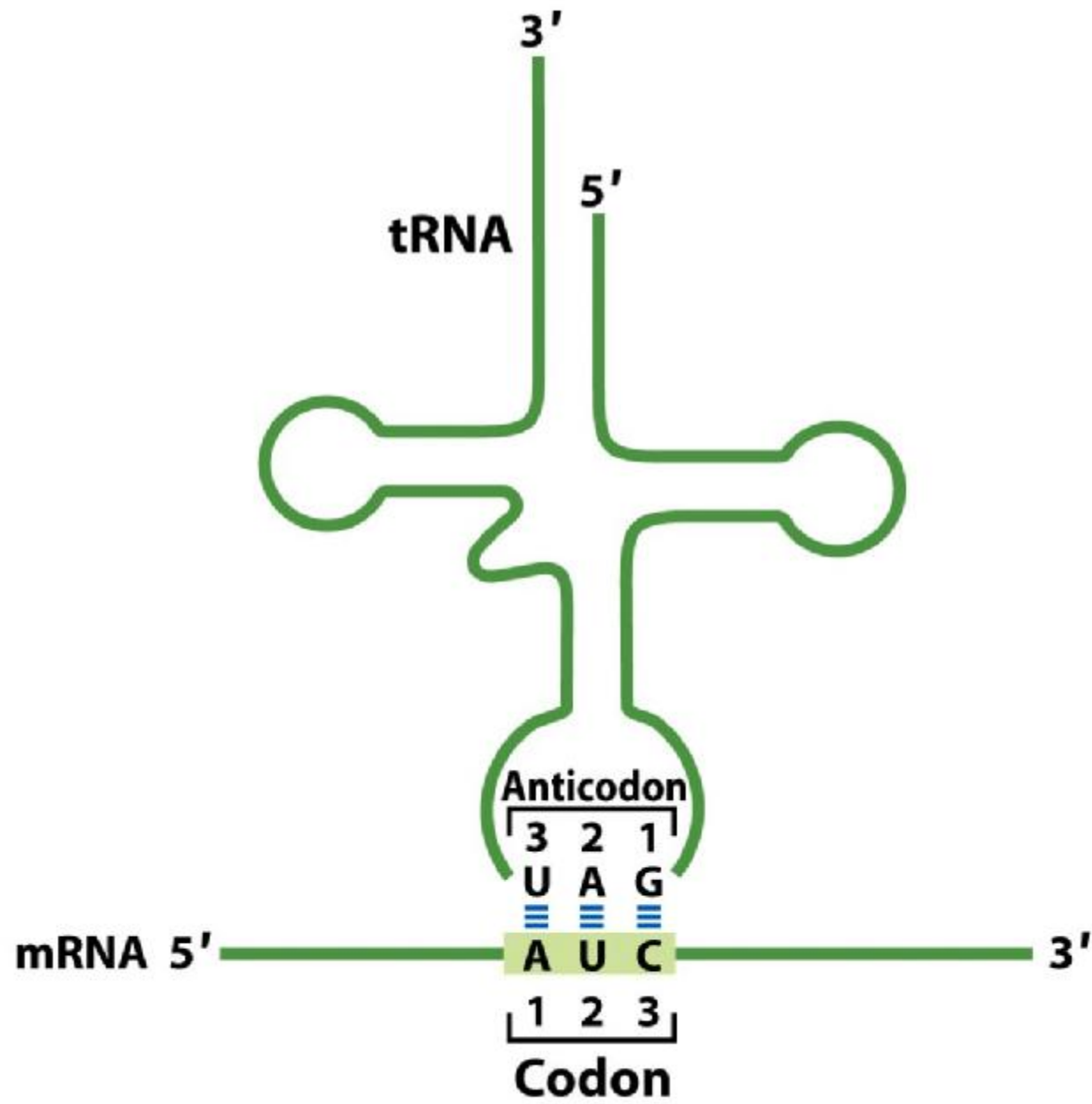


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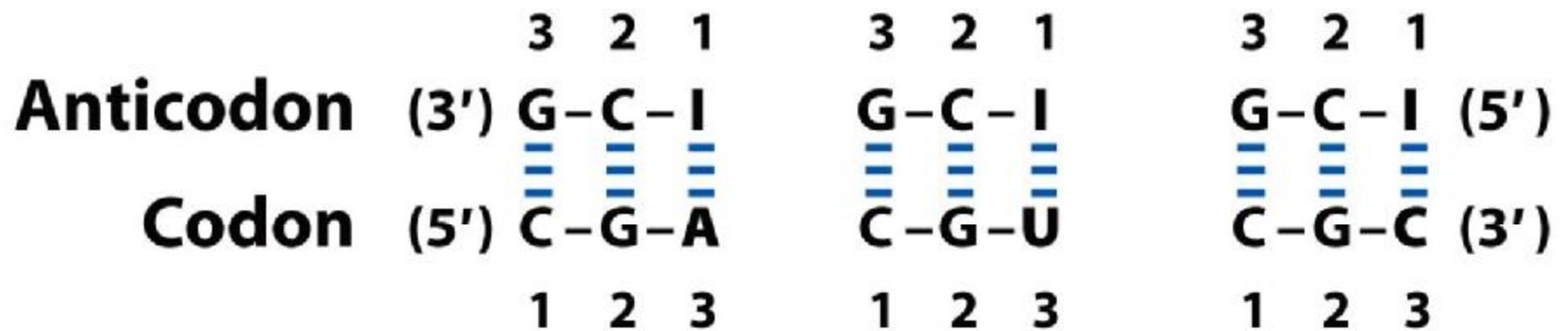


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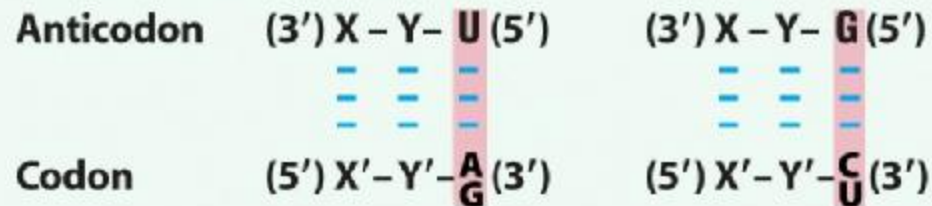
TABLE 27-4

How the Wobble Base of the Anticodon Determines the Number of Codons a tRNA Can Recognize

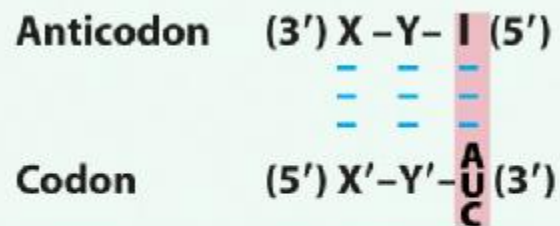
1. One codon recognized:



2. Two codons recognized:



3. Three codons recognized:



Note: X and Y denote bases complementary to and capable of strong Watson-Crick base pairing with X' and Y', respectively. Wobble bases—in the 3' position of codons and 5' position of anticodons—are shaded in pink.

Table 27-4

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***gag* reading frame**

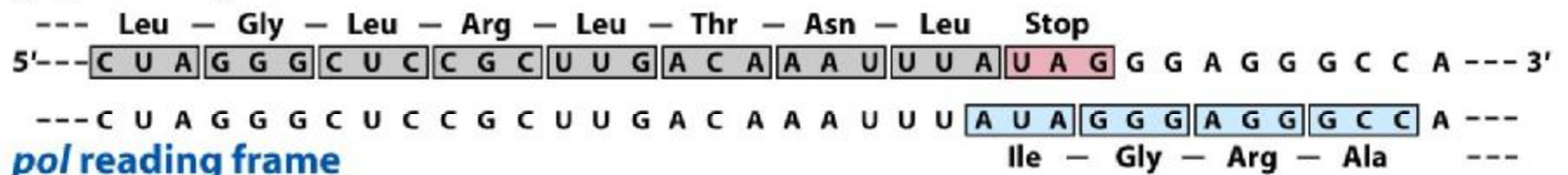
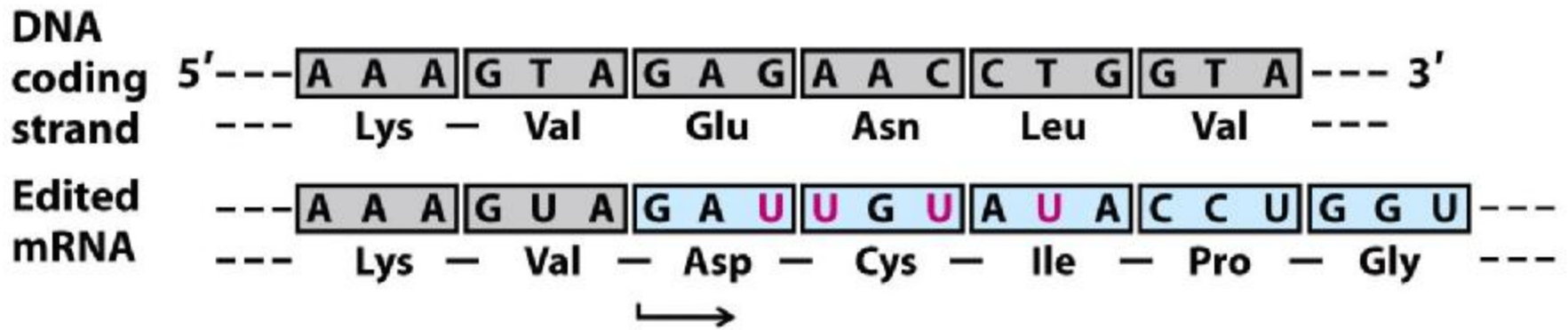


Figure 27-9

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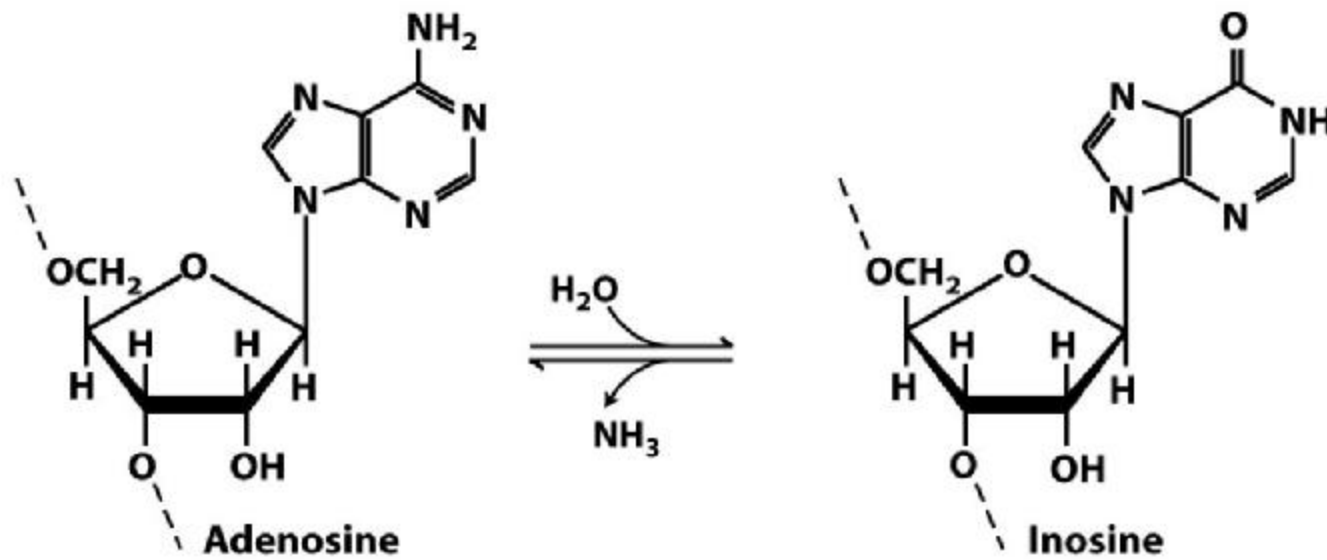


(a)

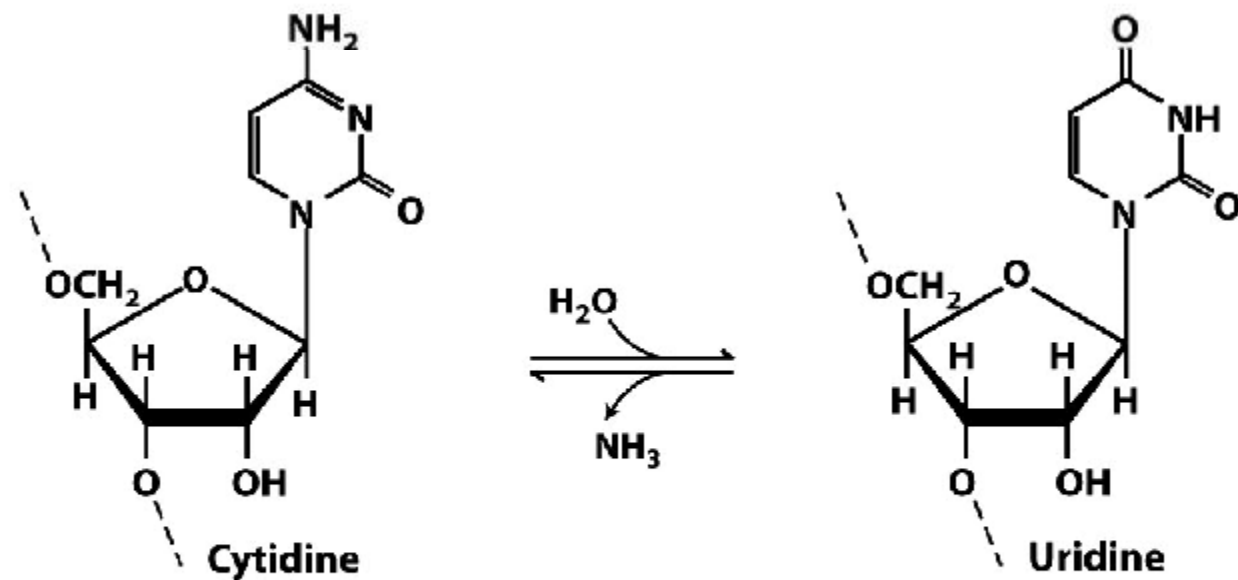


(b)

Figure 27-10
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(a)



(b)

Figure 27-11
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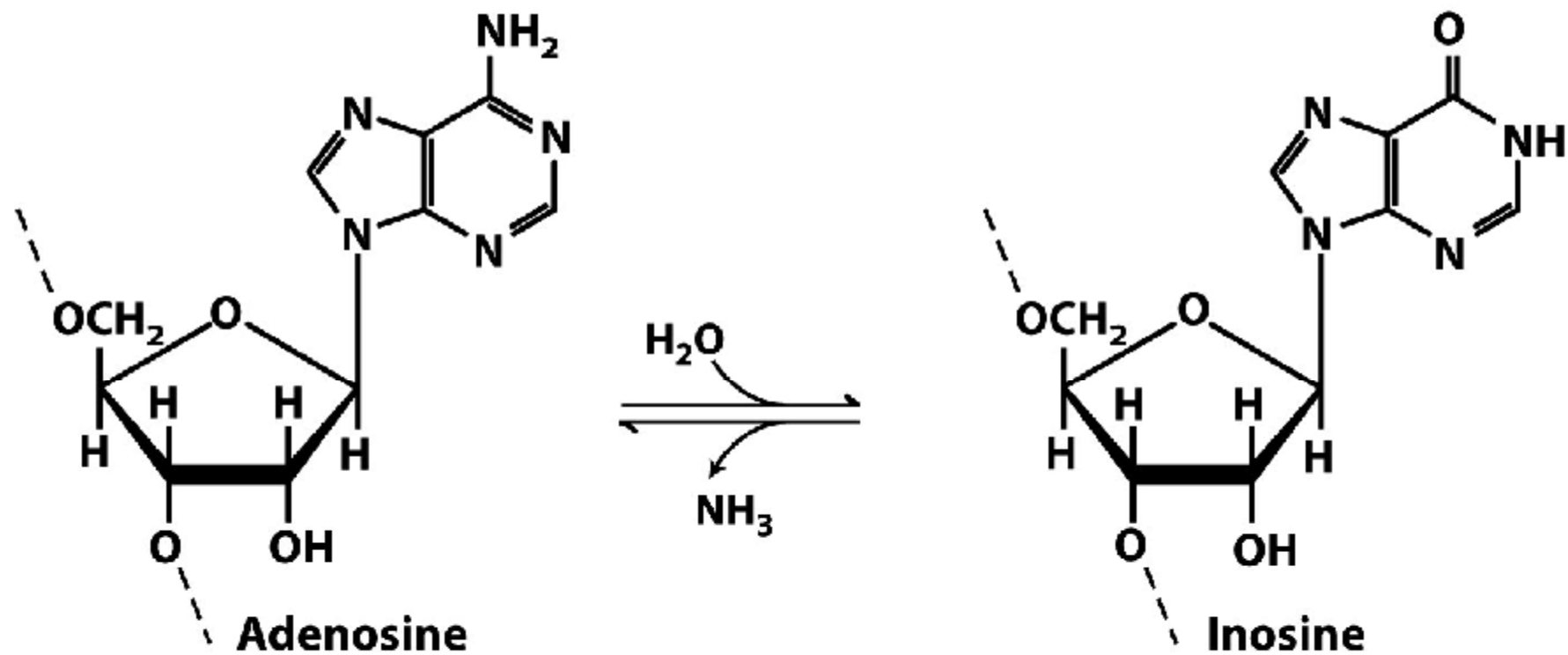


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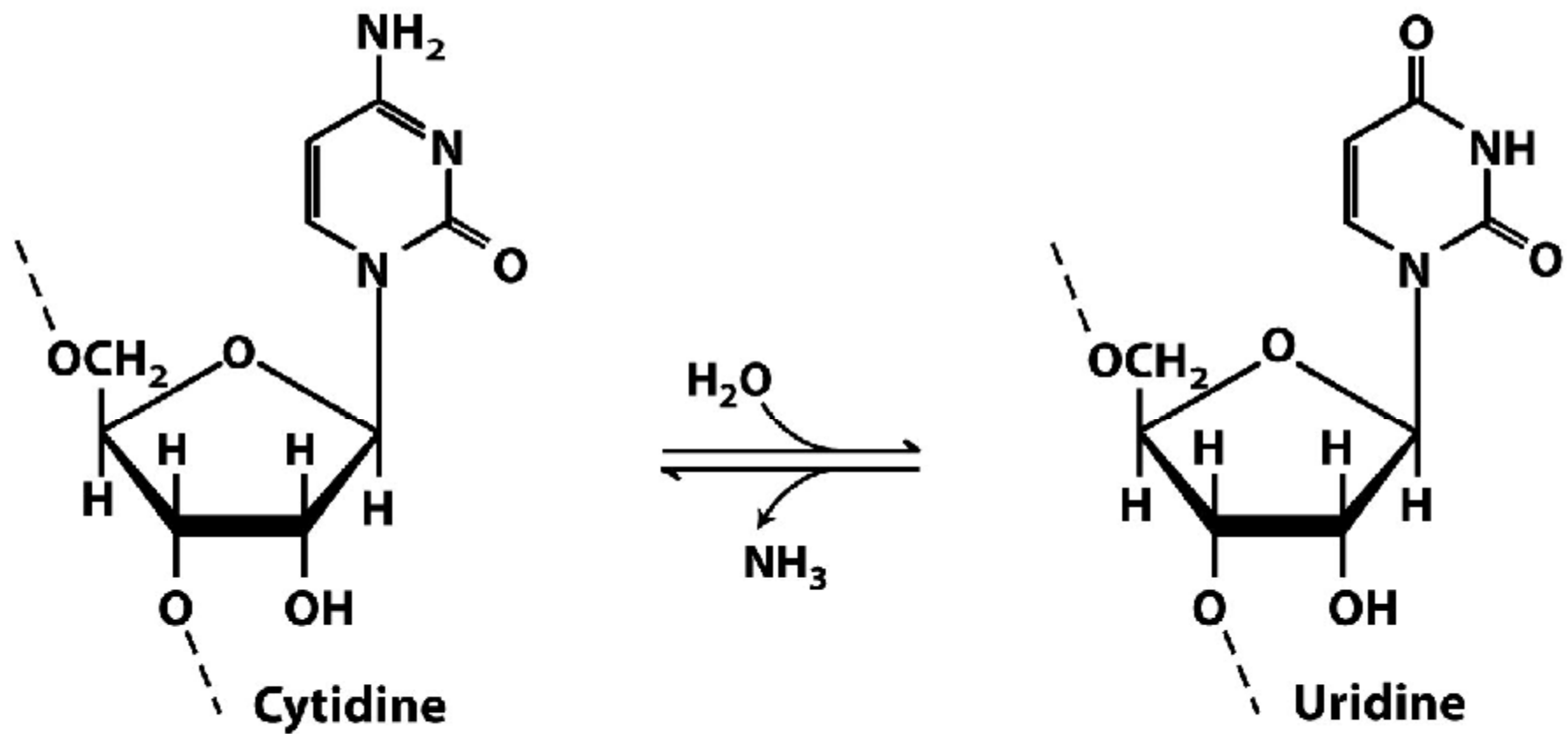


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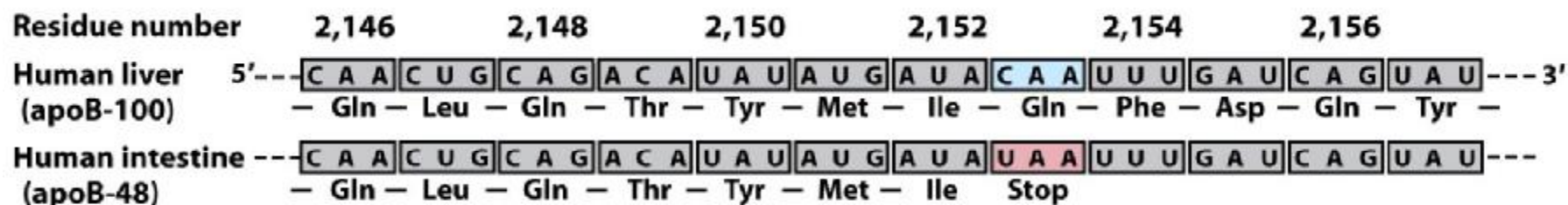


Figure 27-12

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TABLE 27-5		Components Required for the Five Major Stages of Protein Synthesis in <i>E. coli</i>	
Stage	Essential components		
1. Activation of amino acids	20 amino acids 20 aminoacyl-tRNA synthetases 32 or more tRNAs ATP Mg ²⁺		
2. Initiation	mRNA N-Formylmethionyl-tRNA ^{fMet} Initiation codon in mRNA (AUG) 30S ribosomal subunit 50S ribosomal subunit Initiation factors (IF-1, IF-2, IF-3) GTP Mg ²⁺		
3. Elongation	Functional 70S ribosome (initiation complex) Aminoacyl-tRNAs specified by codons Elongation factors (EF-Tu, EF-Ts, EF-G) GTP Mg ²⁺		
4. Termination and ribosome recycling	Termination codon in mRNA Release factors (RF-1, RF-2, RF-3, RRF) EF-G IF-3		
5. Folding and posttranslational processing	Specific enzymes, cofactors, and other components for removal of initiating residues and signal sequences, additional proteolytic processing, modification of terminal residues, and attachment of acetyl, phosphoryl, methyl, carboxyl, carbohydrate, or prosthetic groups		

Table 27-5

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TABLE 27-6		RNA and Protein Components of the <i>E. coli</i> Ribosome		
Subunit	Number of different proteins	Total number of proteins	Protein designations	Number and type of rRNAs
30S	21	21	S1-S21	1 (16S rRNA)
50S	33	36	L1-L36*	2 (5S and 23S rRNAs)

*The L1 to L36 protein designations do not correspond to 36 different proteins. The protein originally designated L7 is in fact a modified form of L12, and L8 is a complex of three other proteins. Also, L26 proved to be the same protein as S20 (and not part of the 50S subunit). This gives 33 different proteins in the large subunit. There are four copies of the L7/L12 protein, with the three extra copies bringing the total protein count to 36.

Table 27-6

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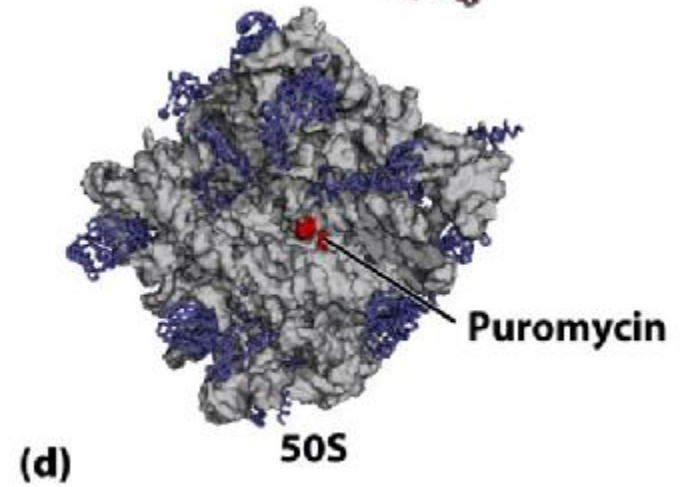
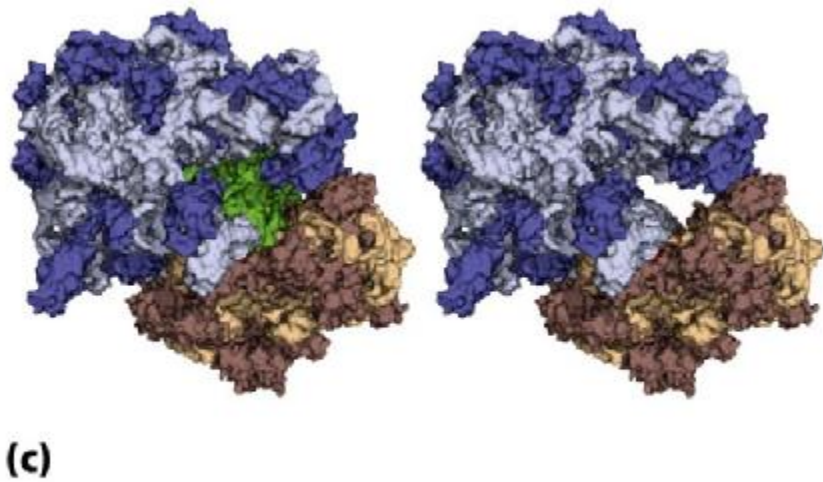
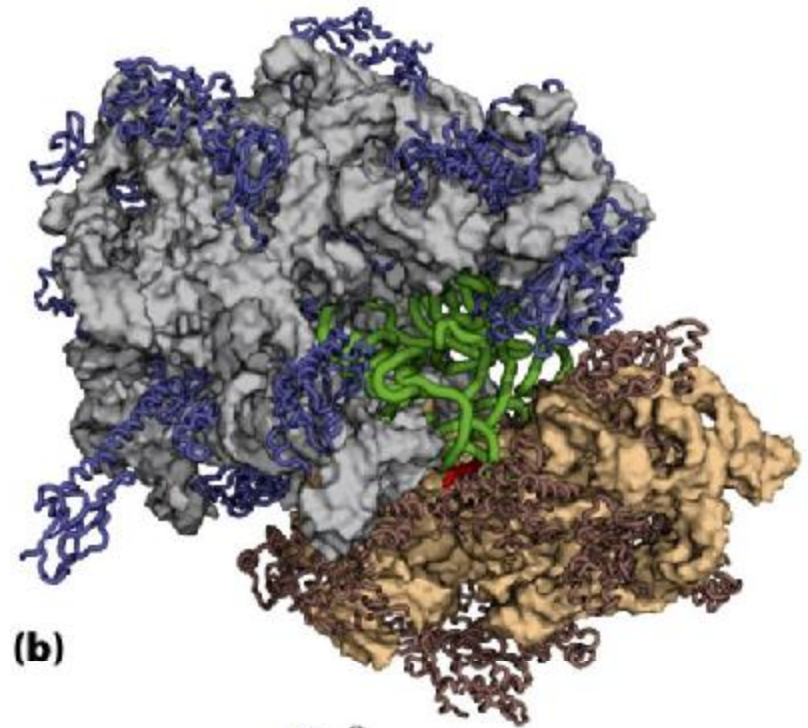
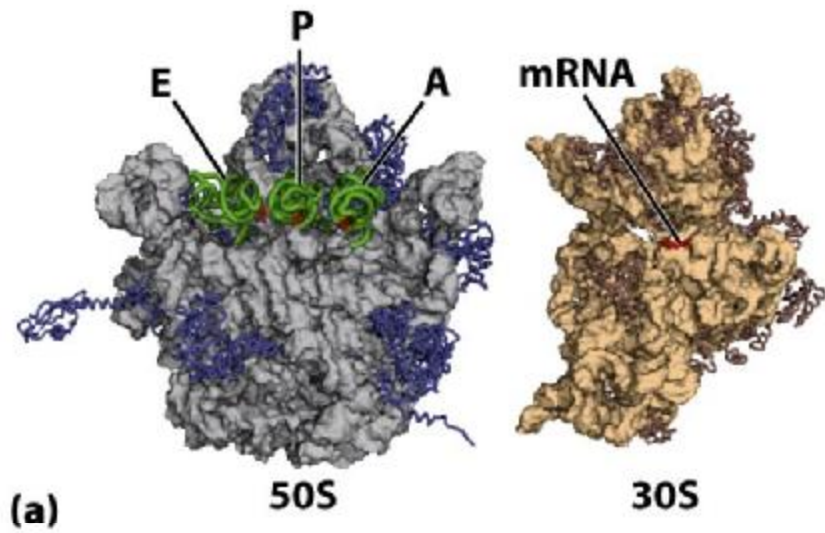


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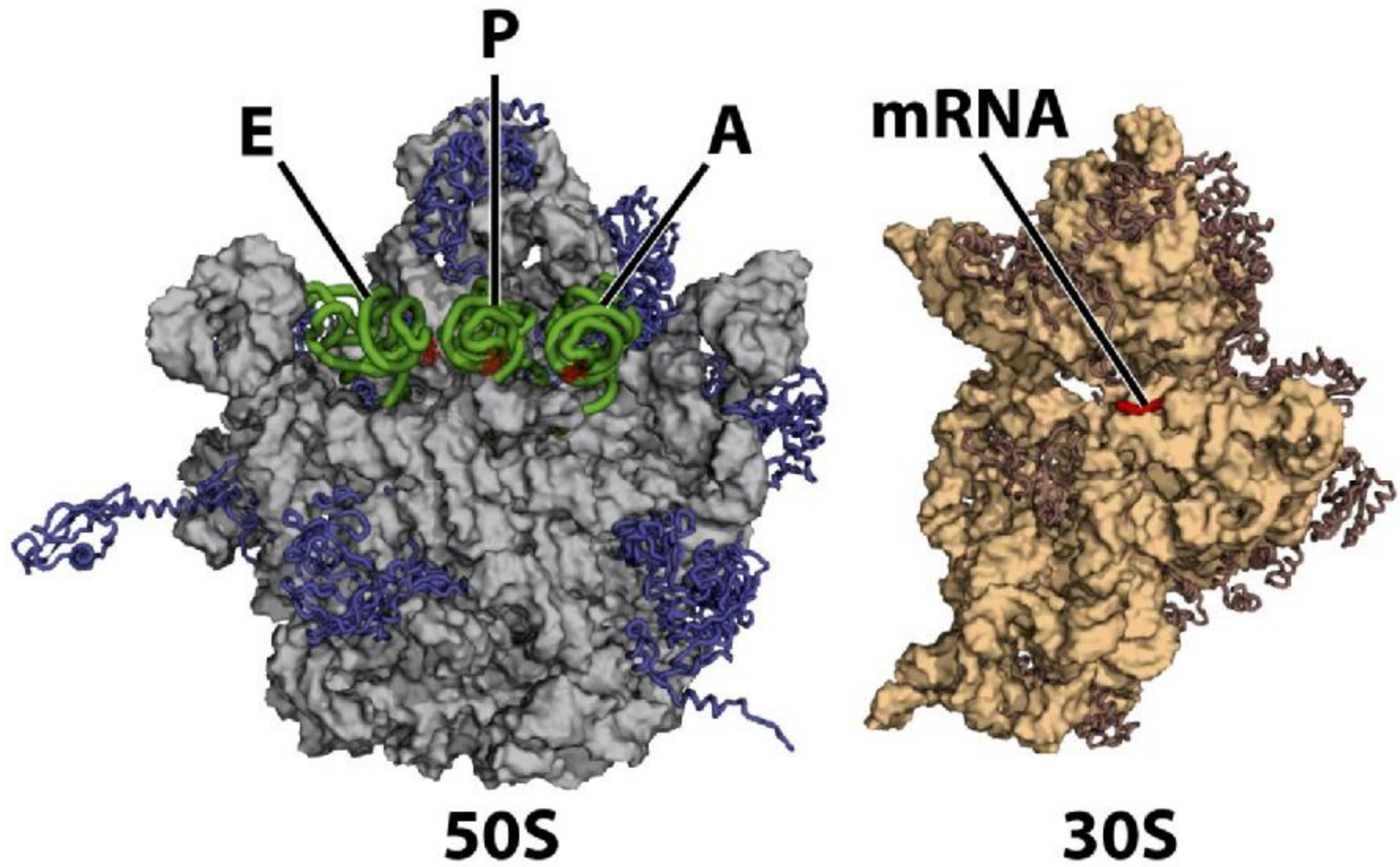


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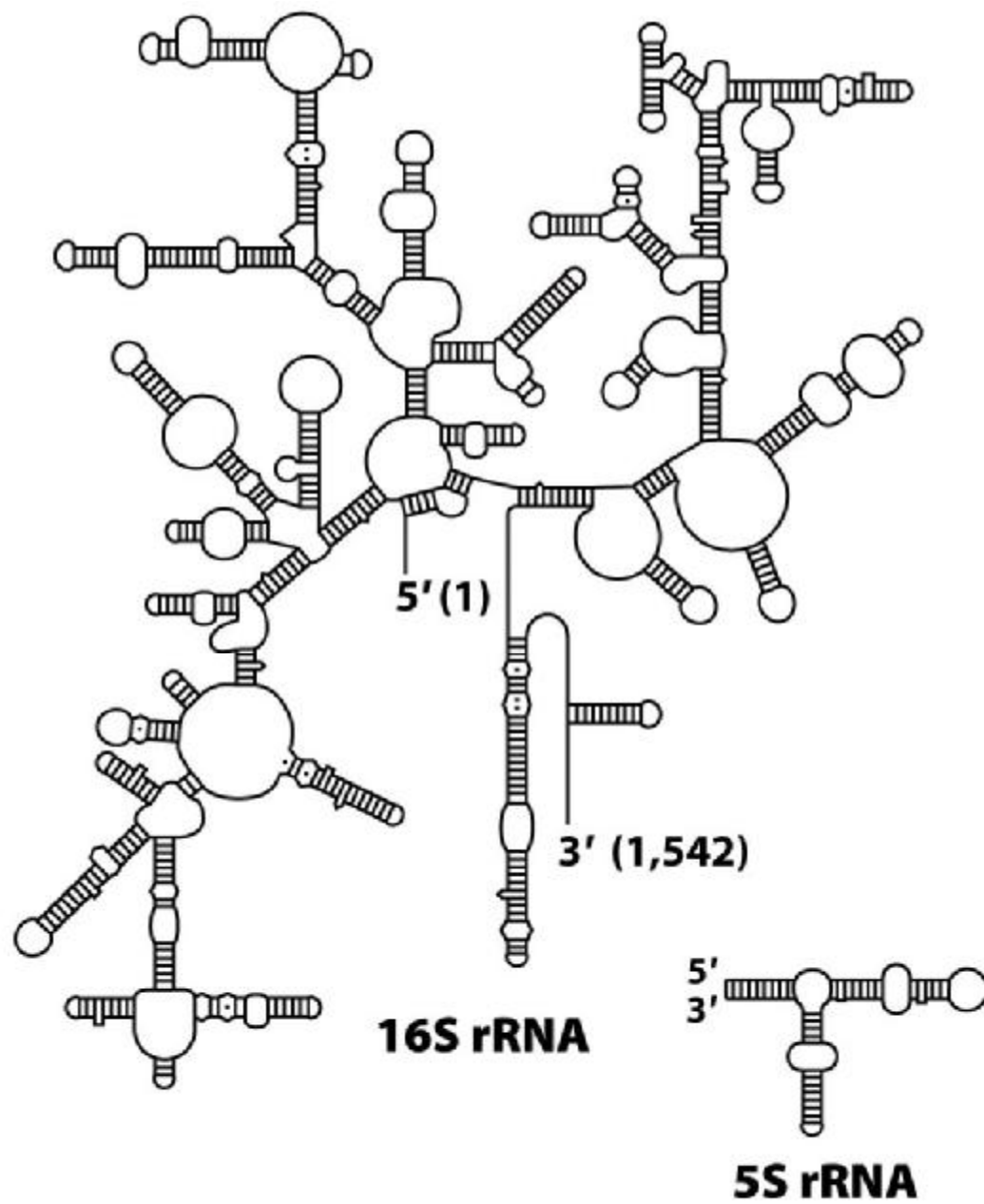


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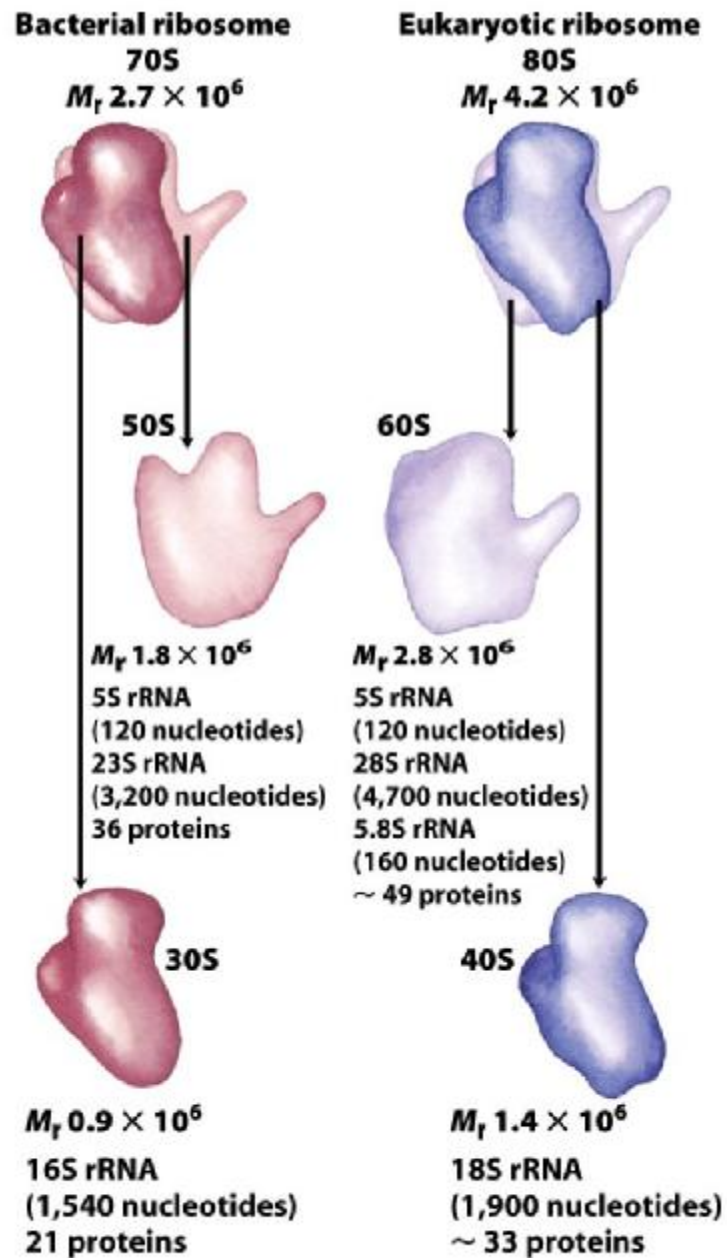


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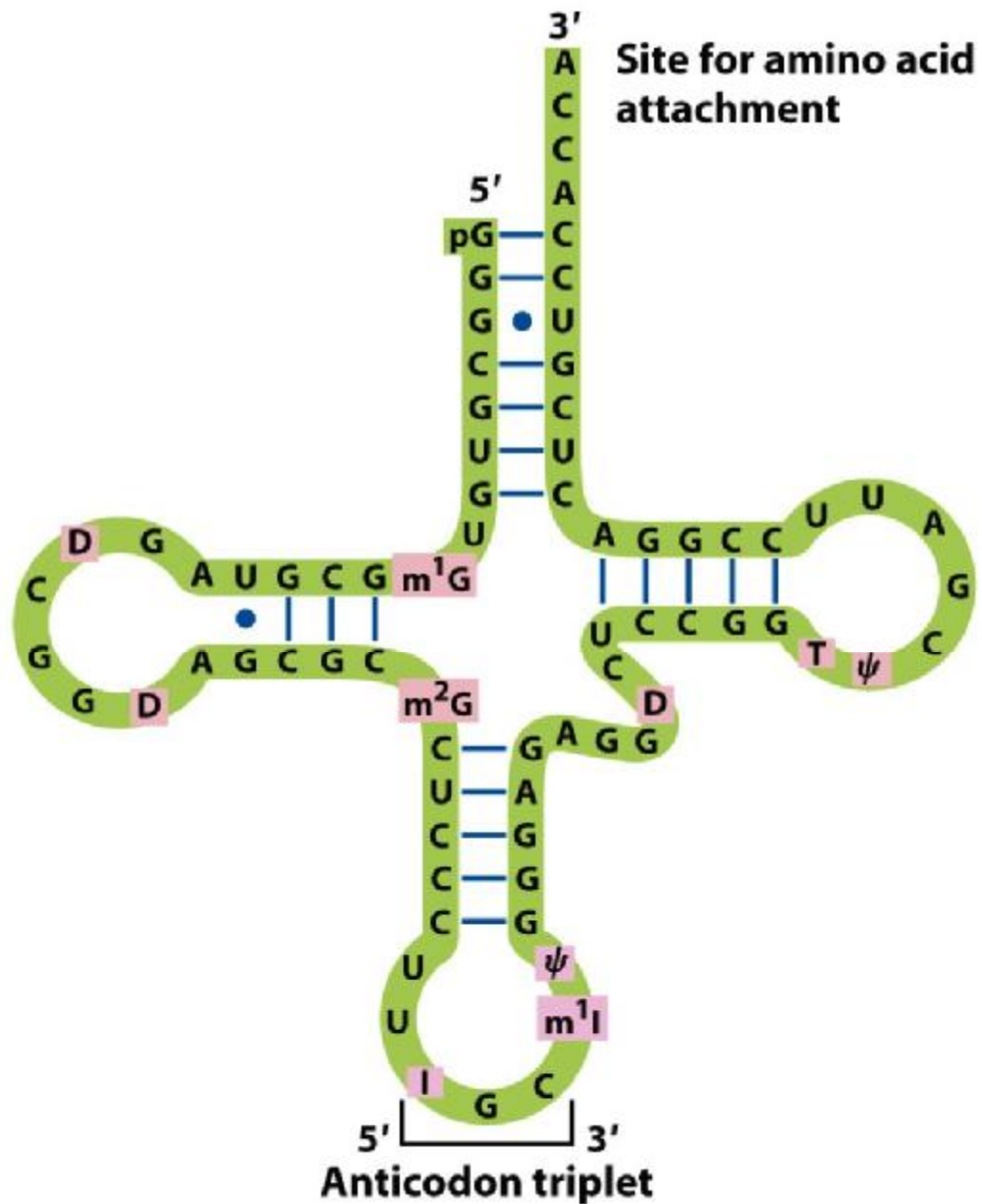


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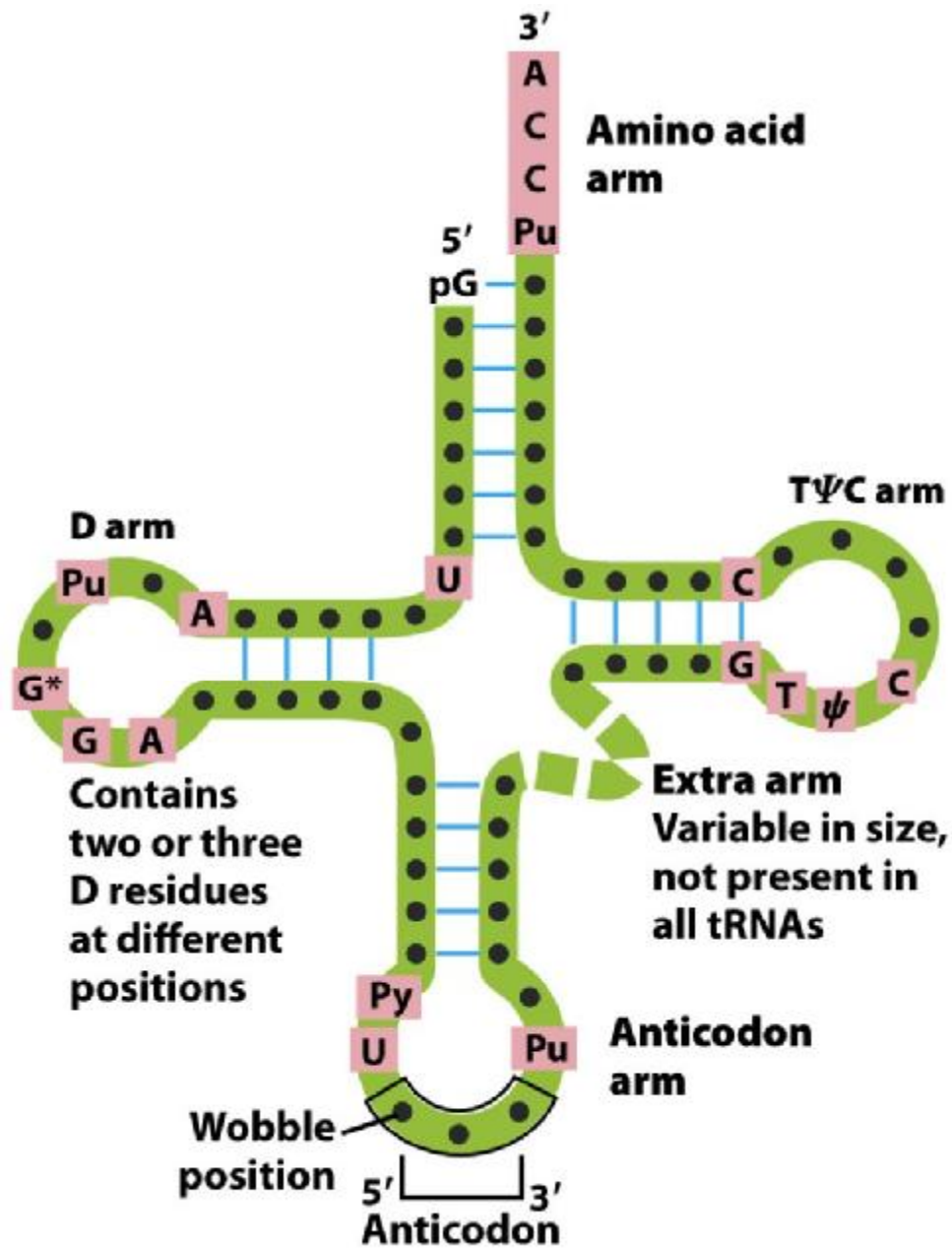


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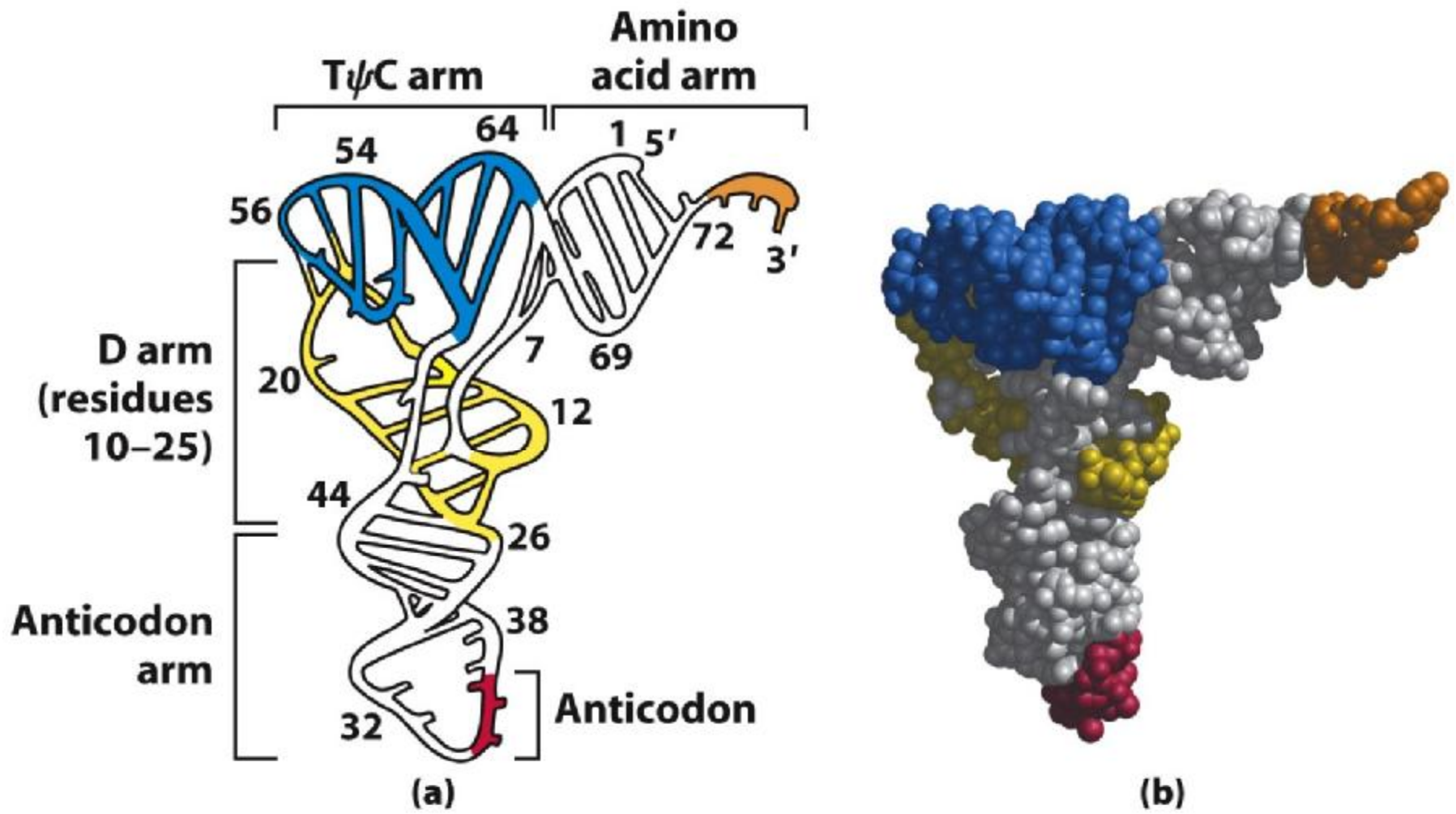


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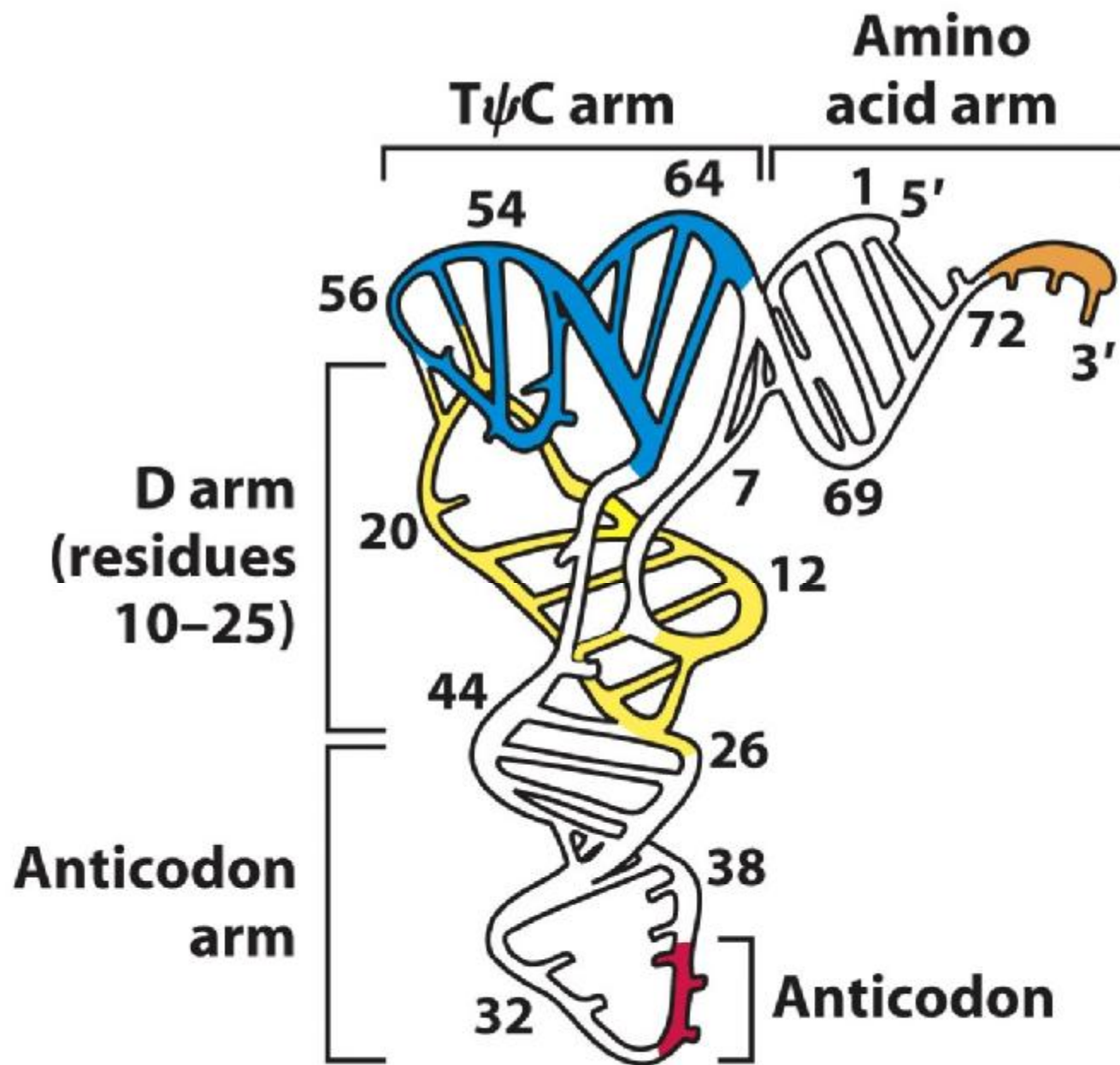


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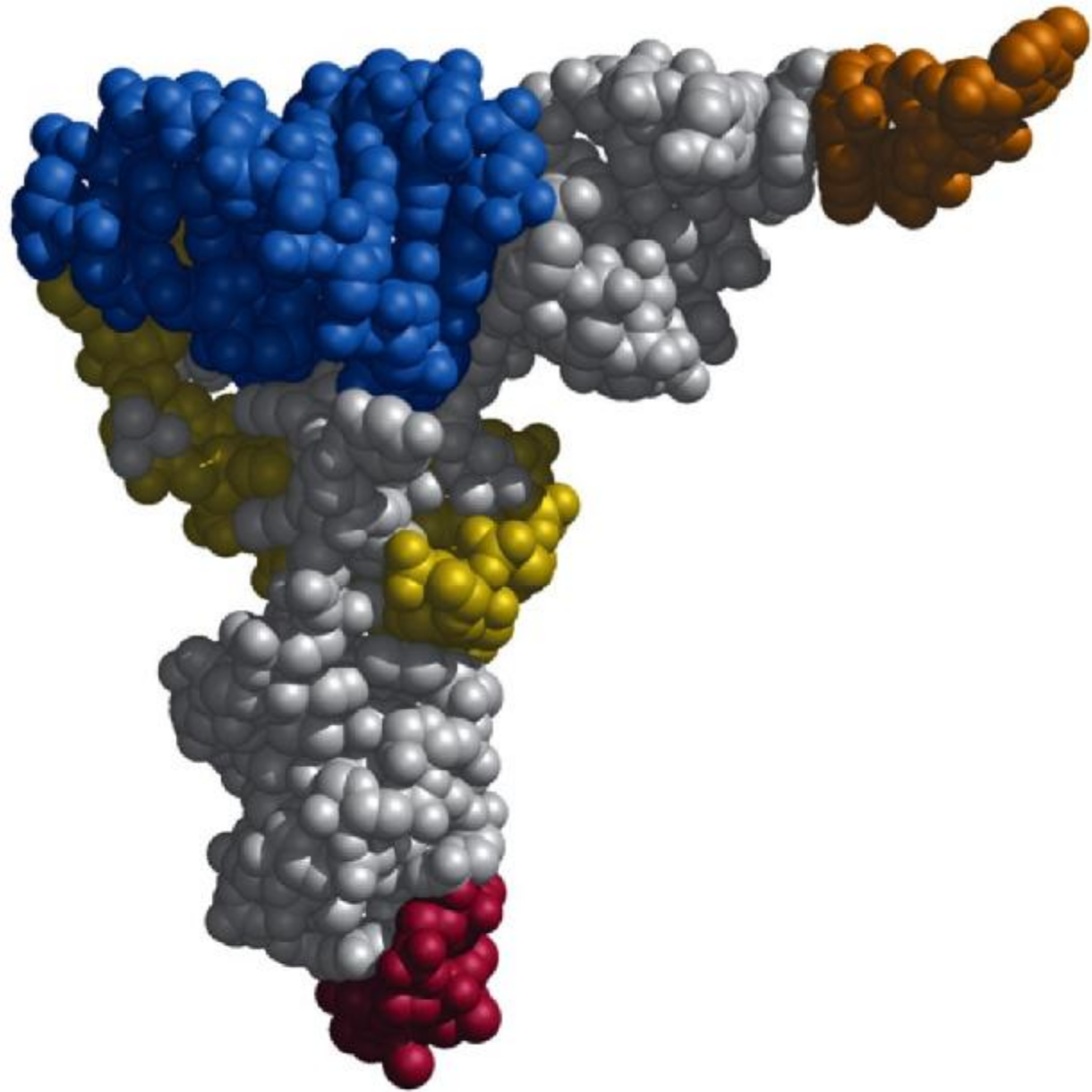


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TABLE 27-7**The Two Classes of Aminoacyl-tRNA Synthetases**

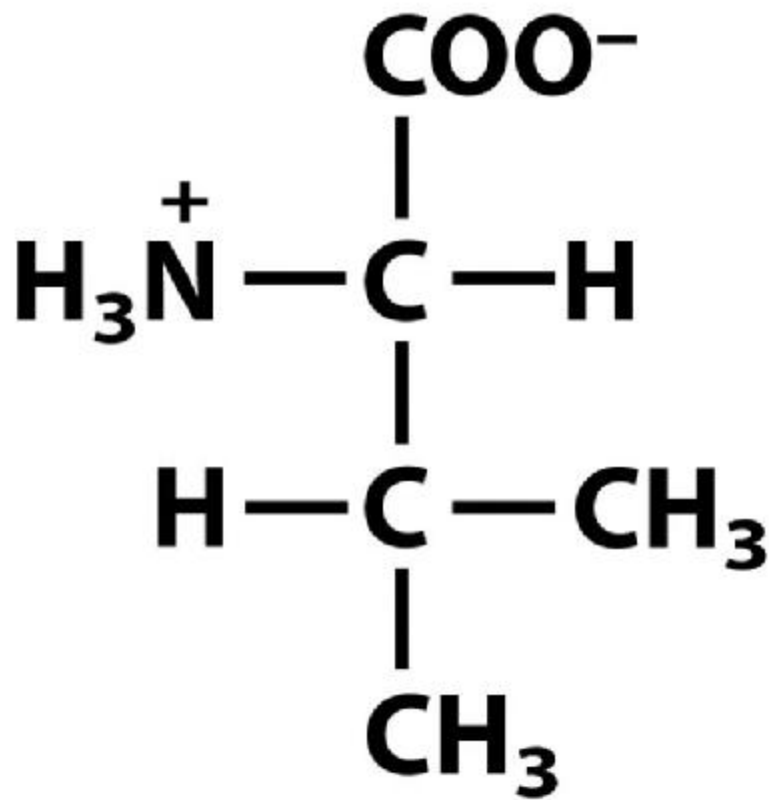
Class I		Class II	
Arg	Leu	Ala	Lys
Cys	Met	Asn	Phe
Gln	Trp	Asp	Pro
Glu	Tyr	Gly	Ser
Ile	Val	His	Thr

Note: Here, Arg represents arginyl-tRNA synthetase, and so forth. The classification applies to all organisms for which tRNA synthetases have been analyzed and is based on protein structural distinctions and on the mechanistic distinction outlined in Figure 27-19.

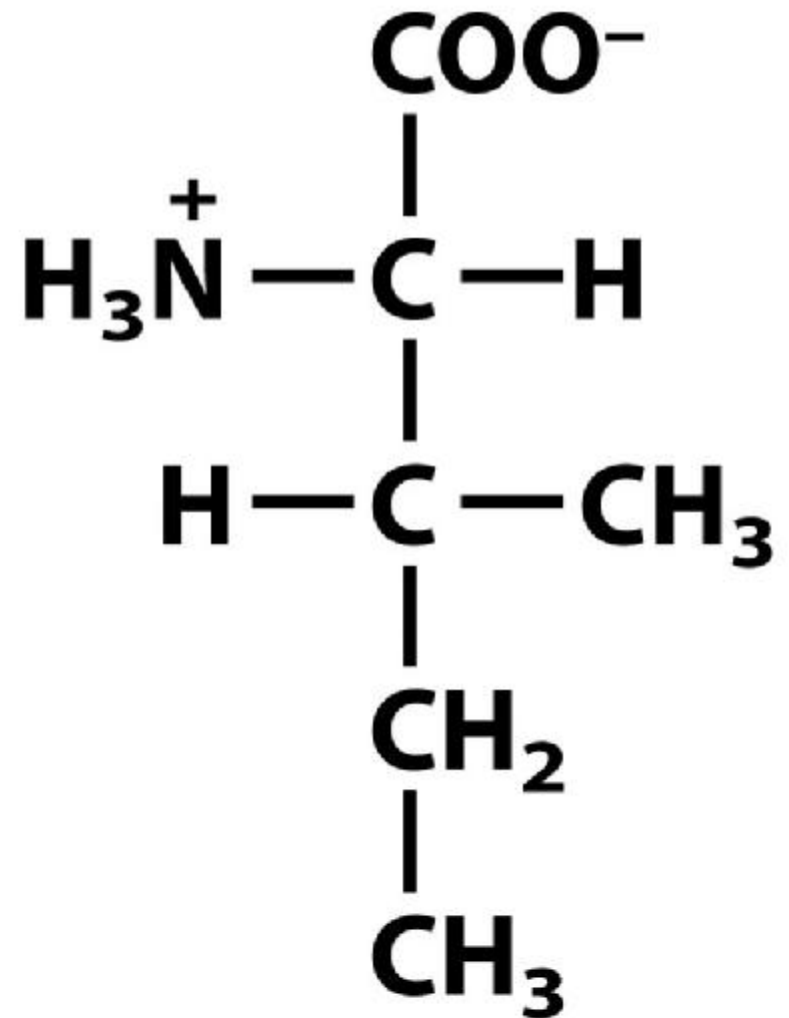
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Valine



Isoleucine

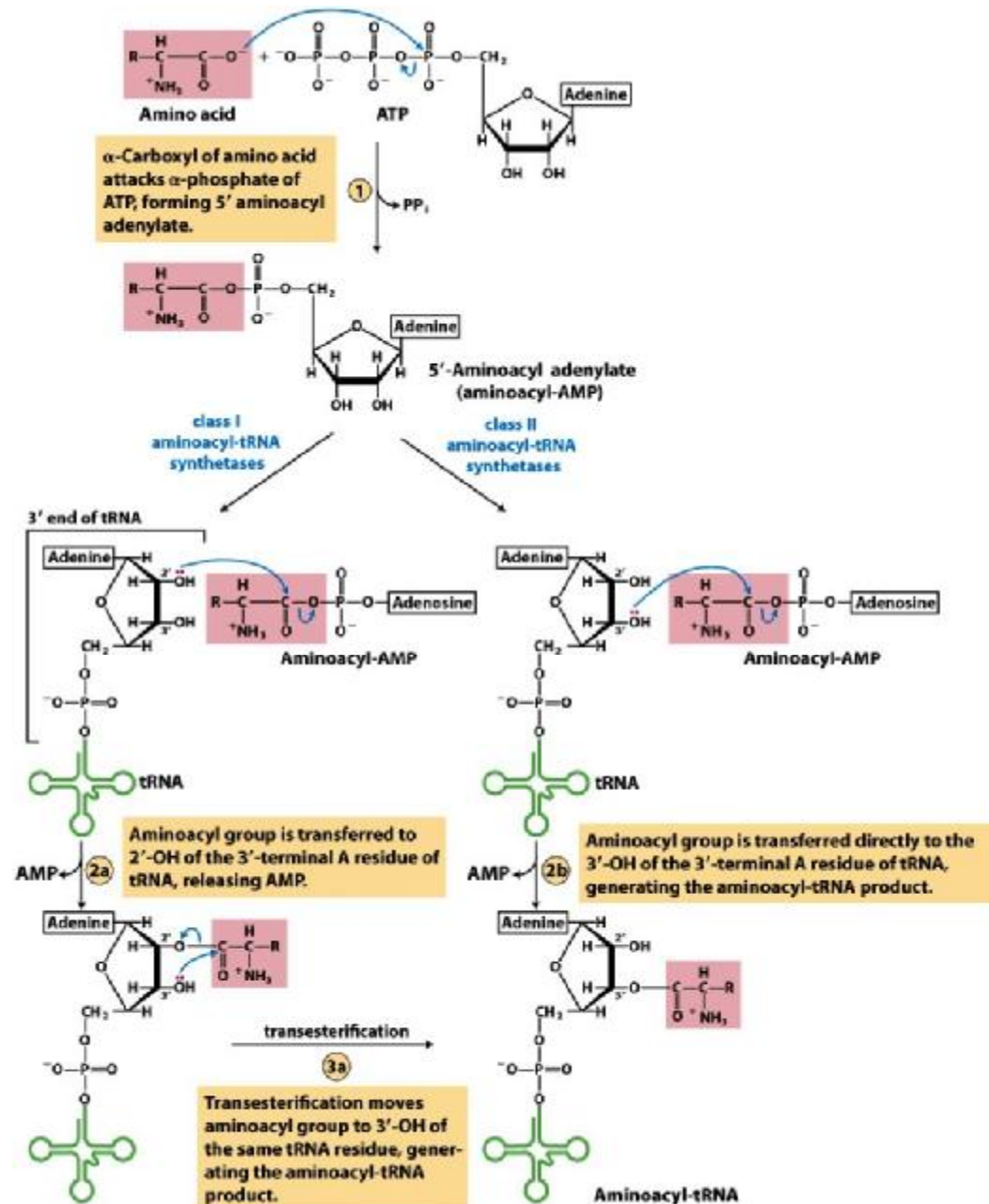


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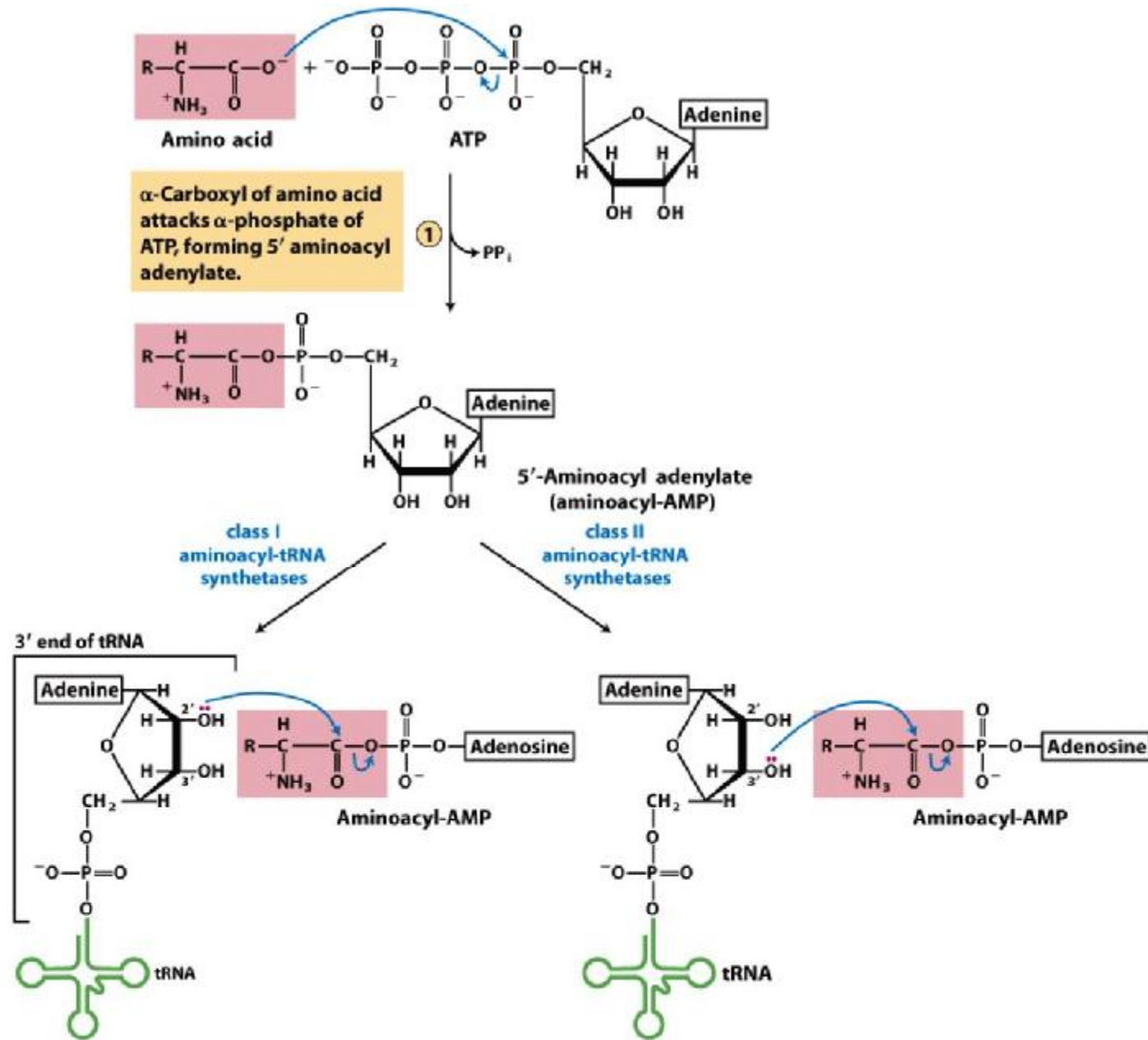


Figure 27-19 part 1

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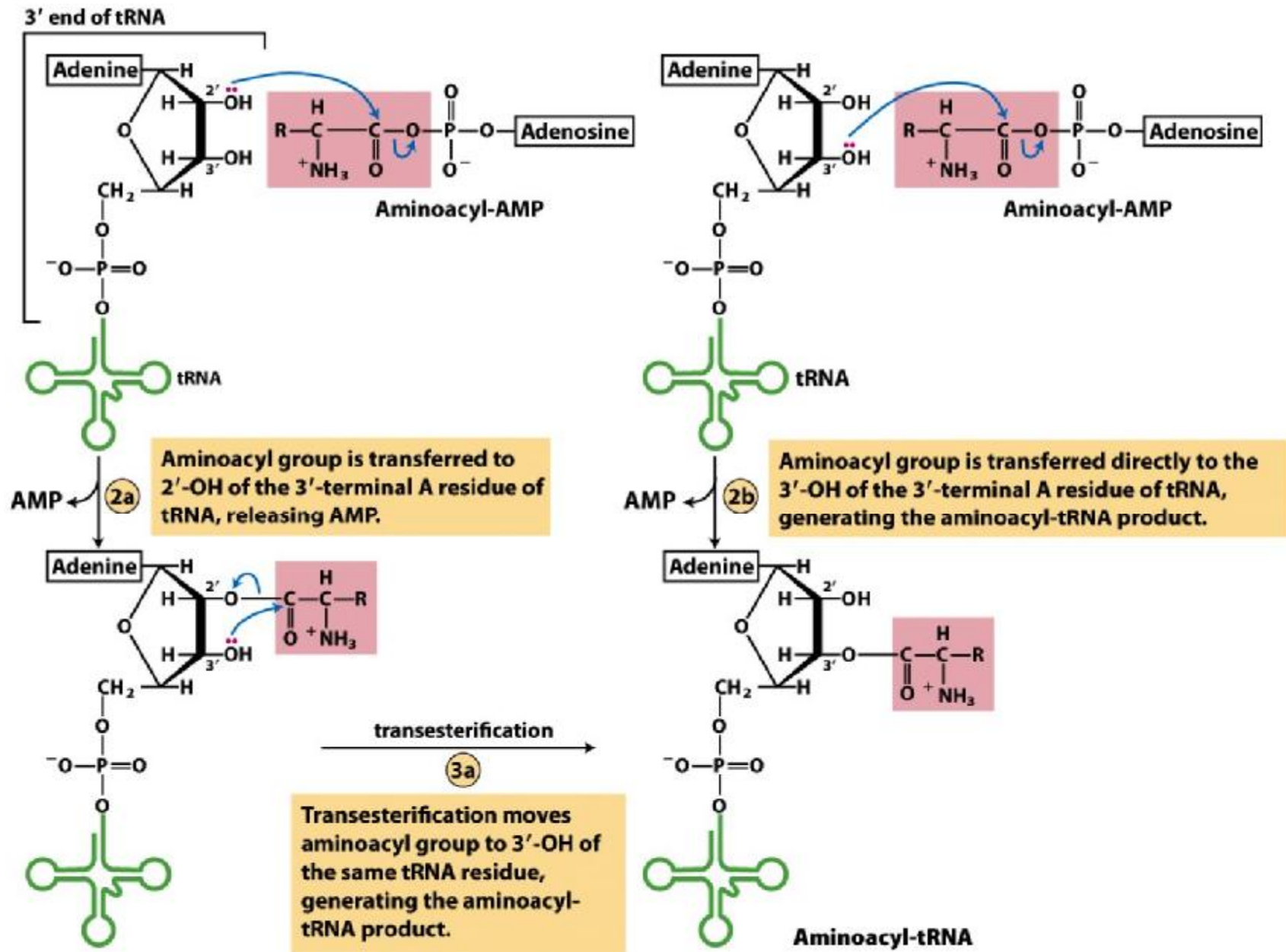


Figure 27-19 part 2

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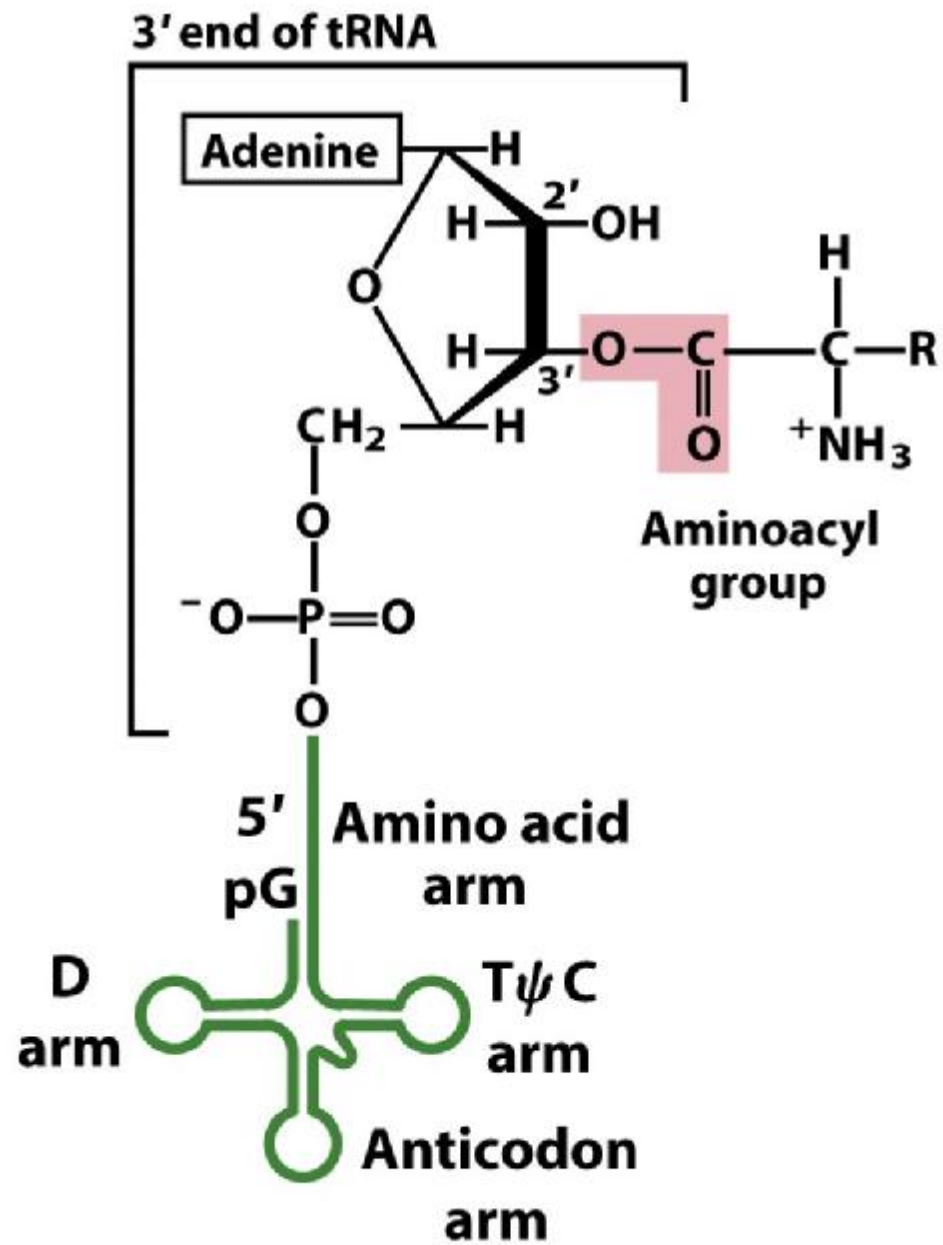


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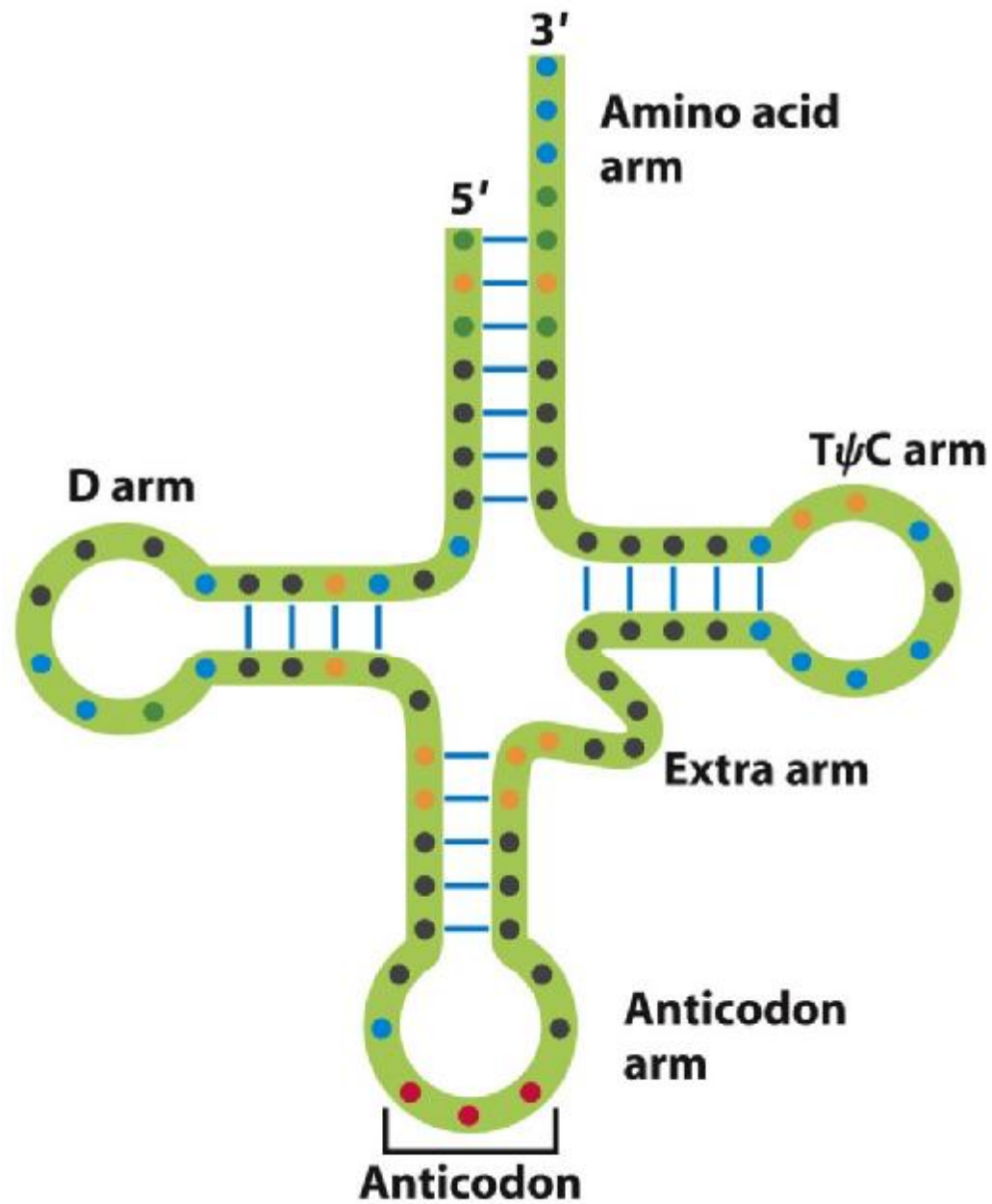


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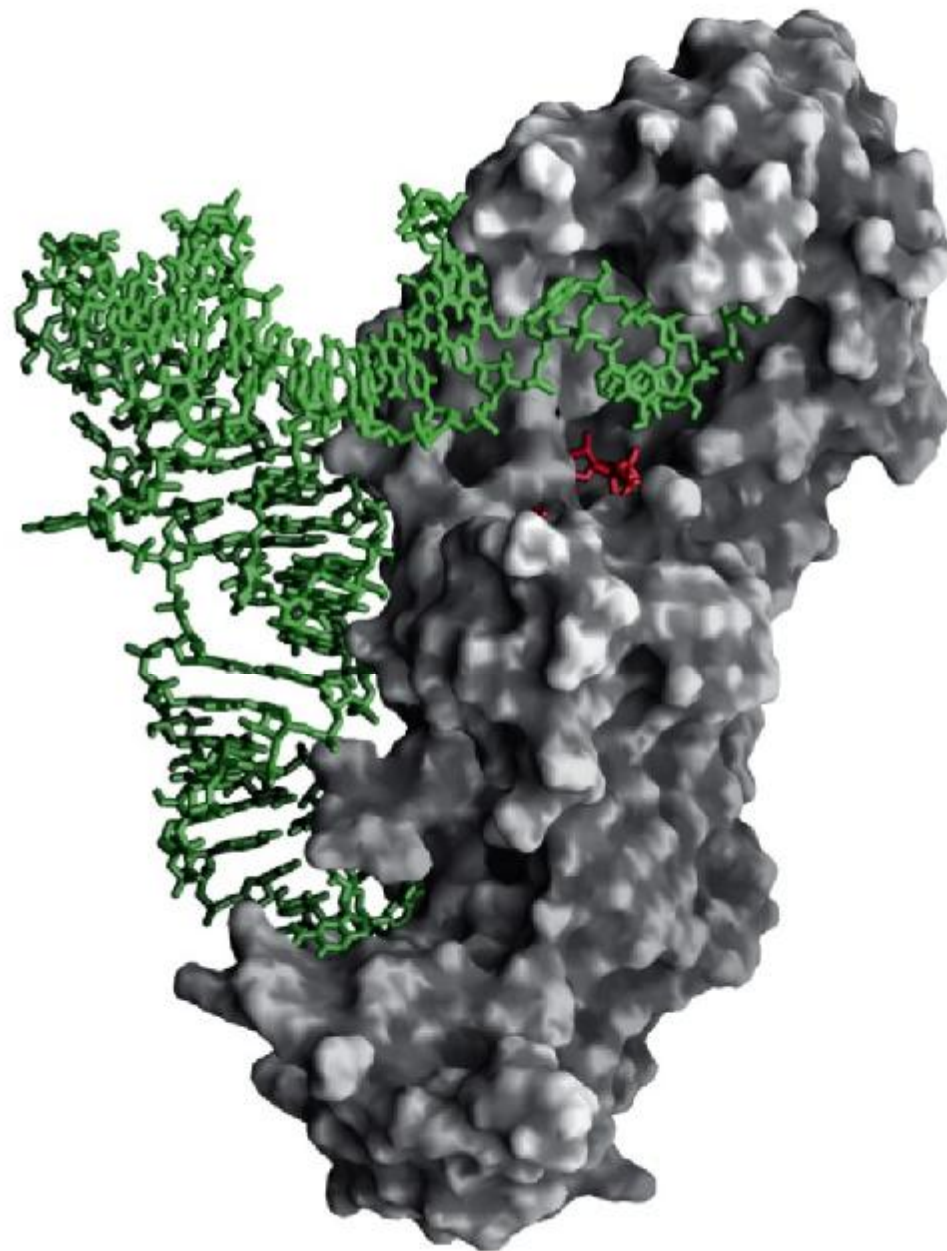


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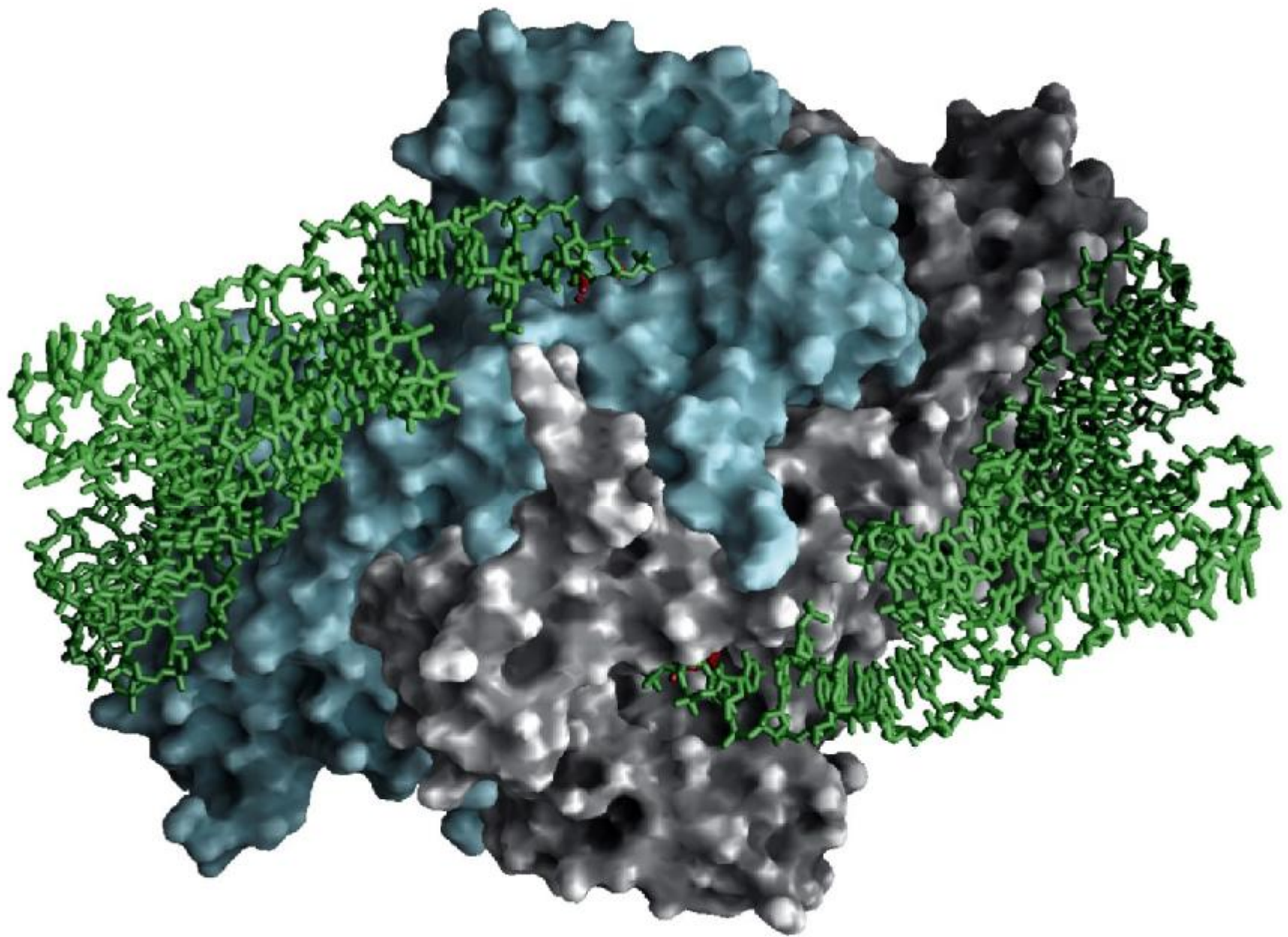


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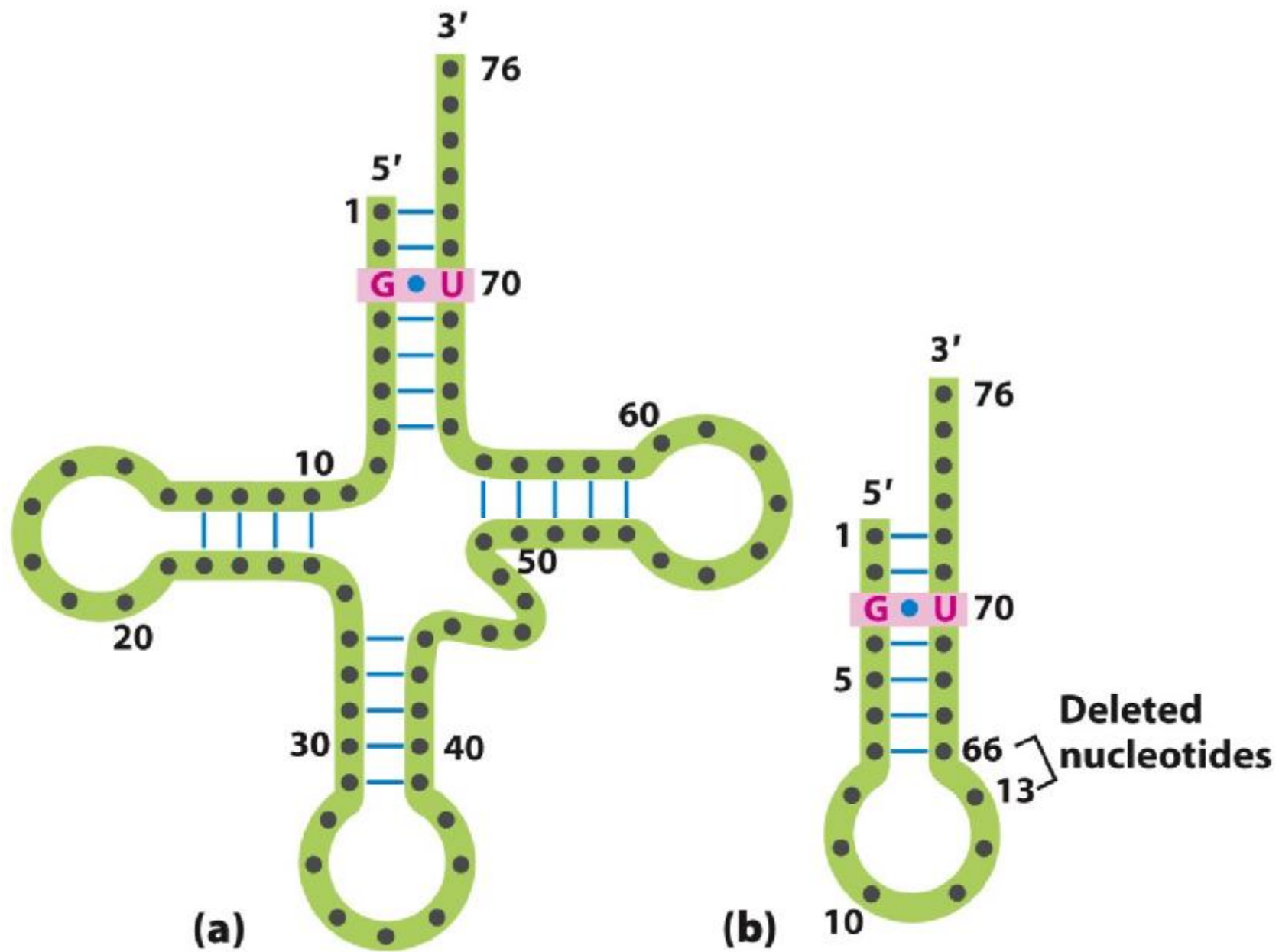
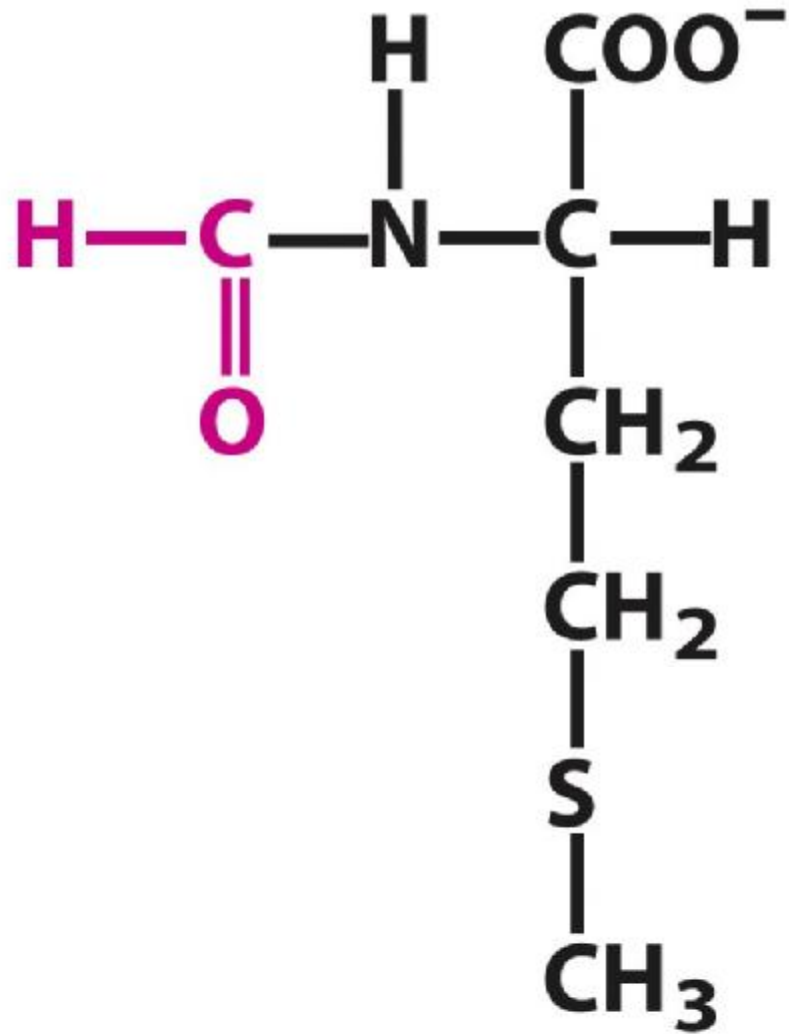


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N-Formylmethionine

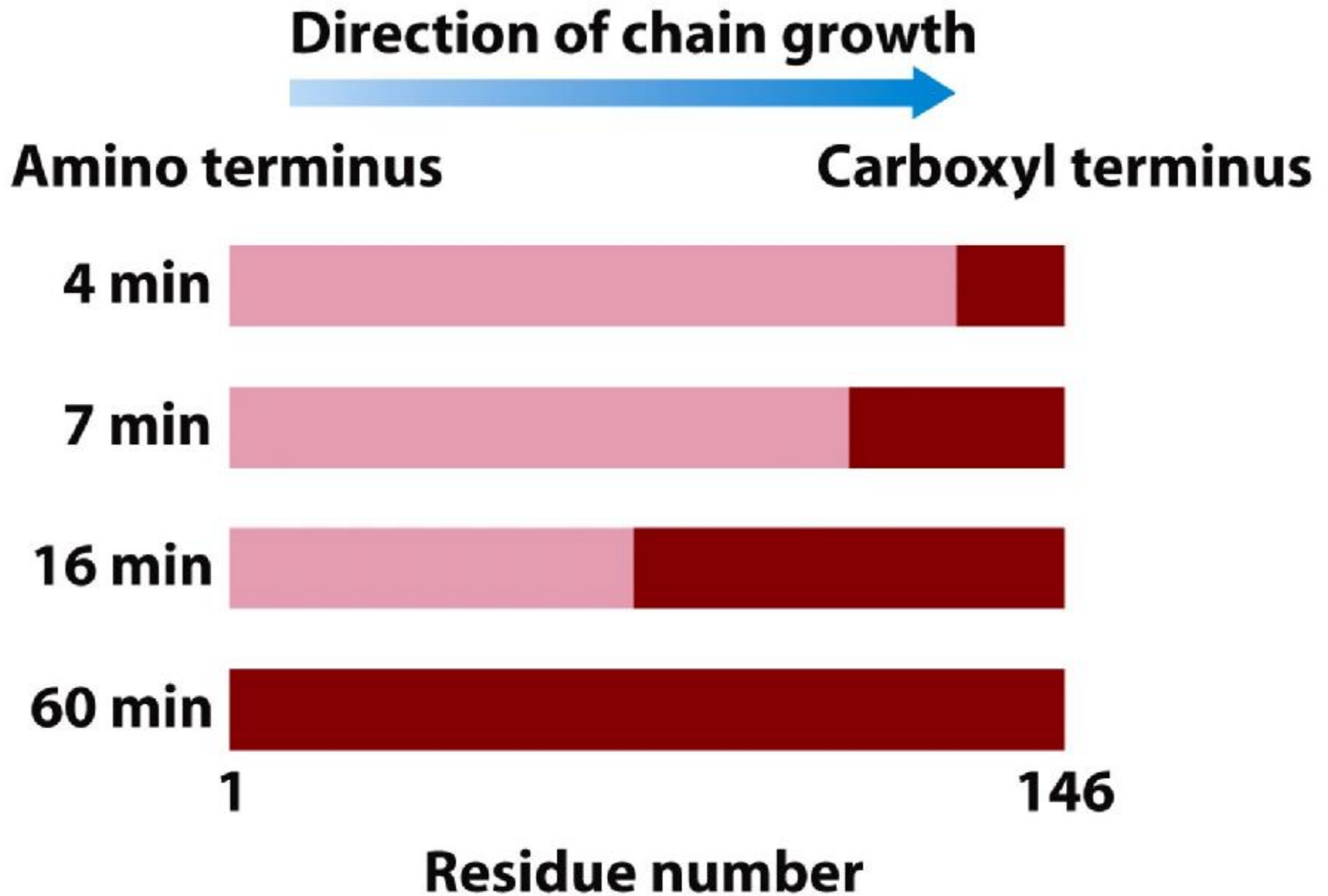


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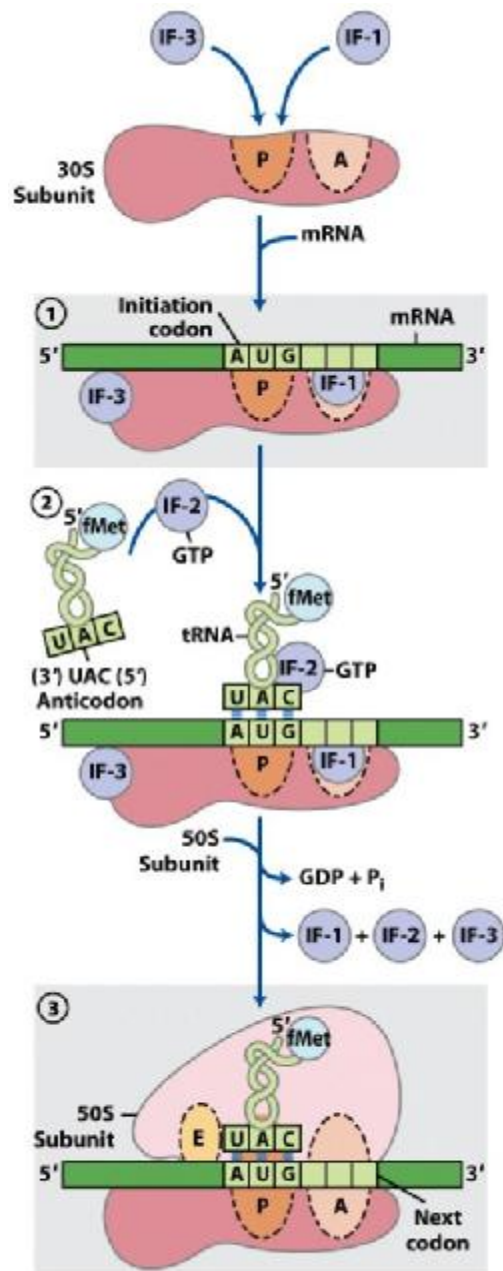


Figure 27-25

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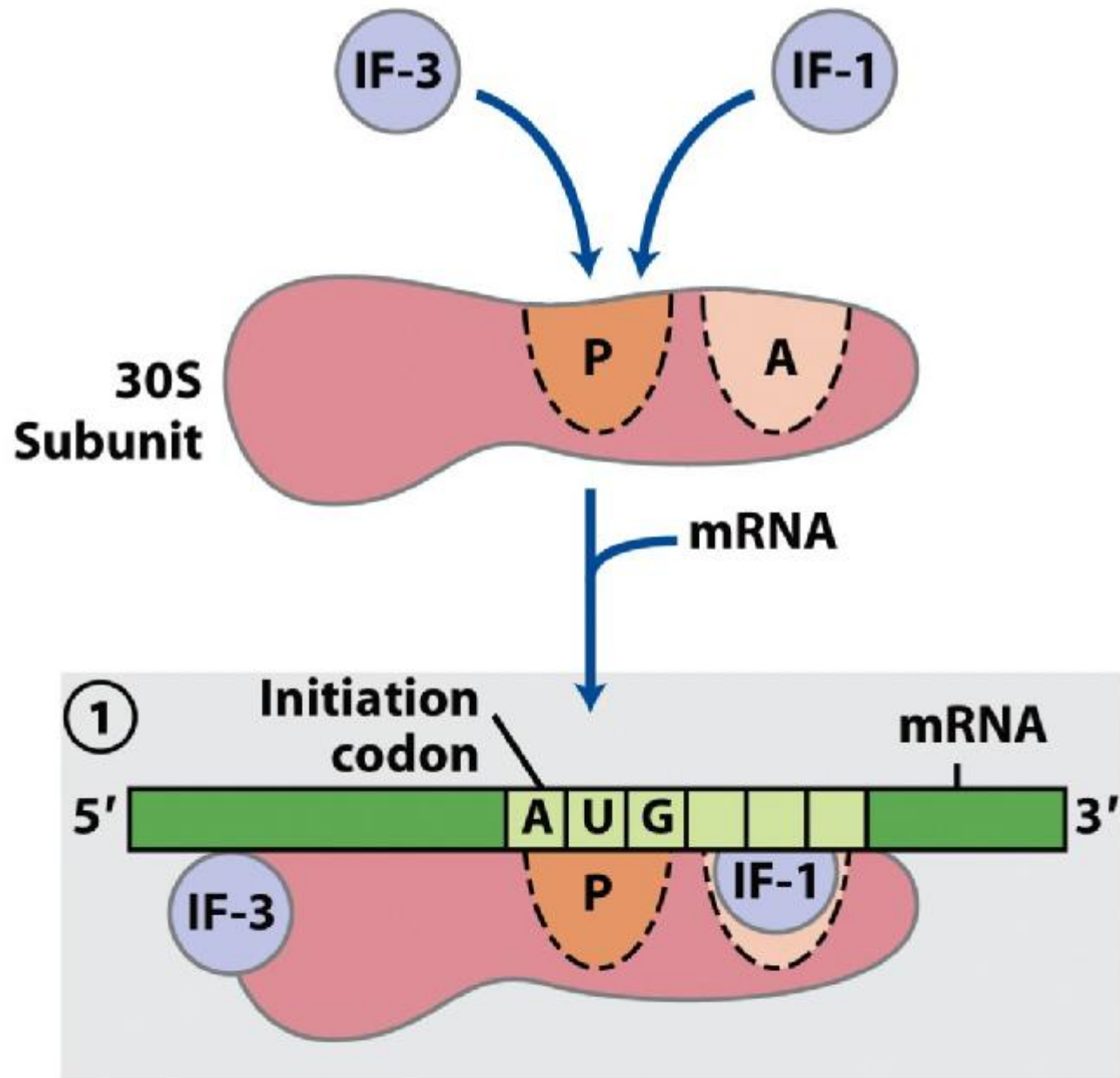


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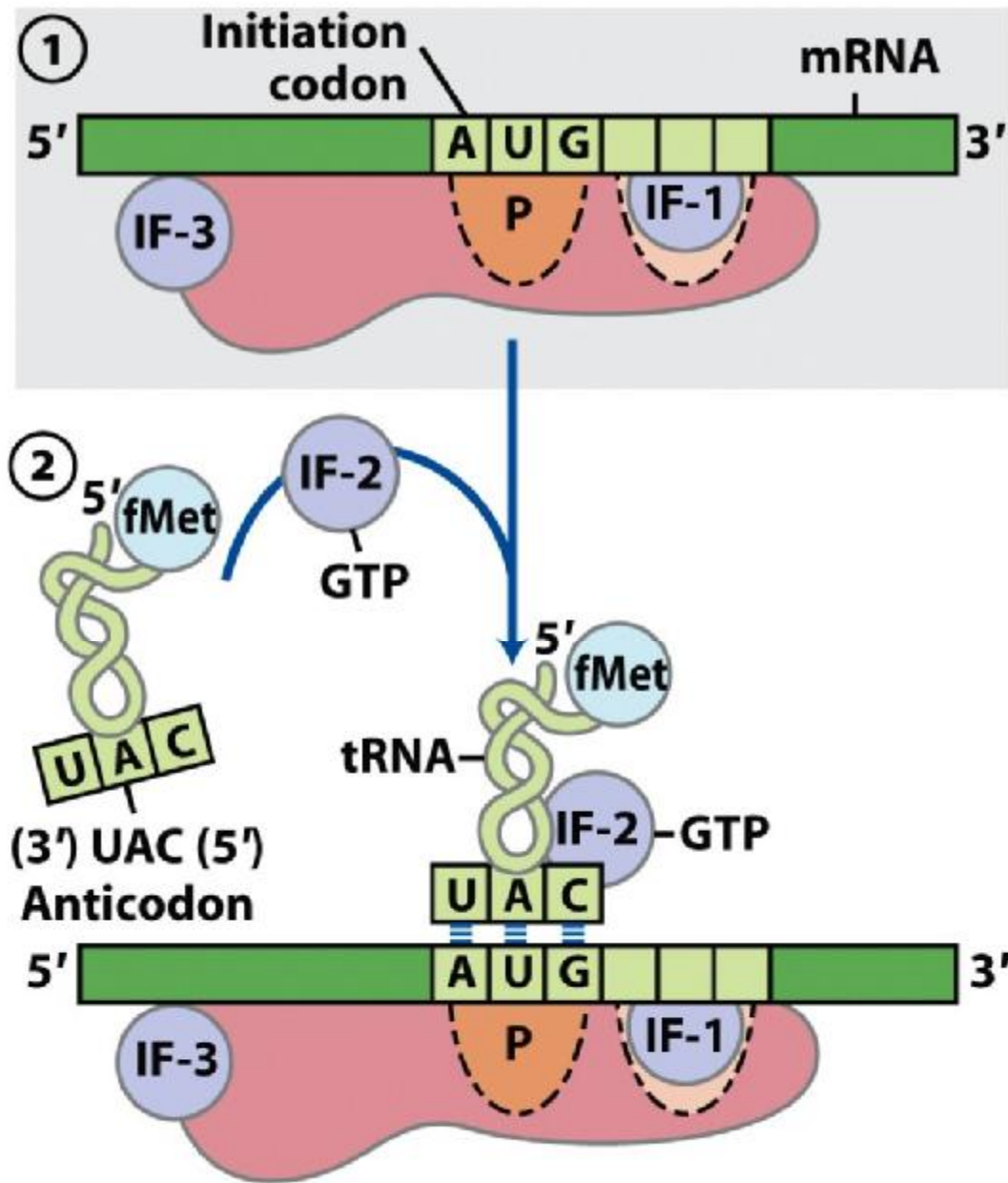


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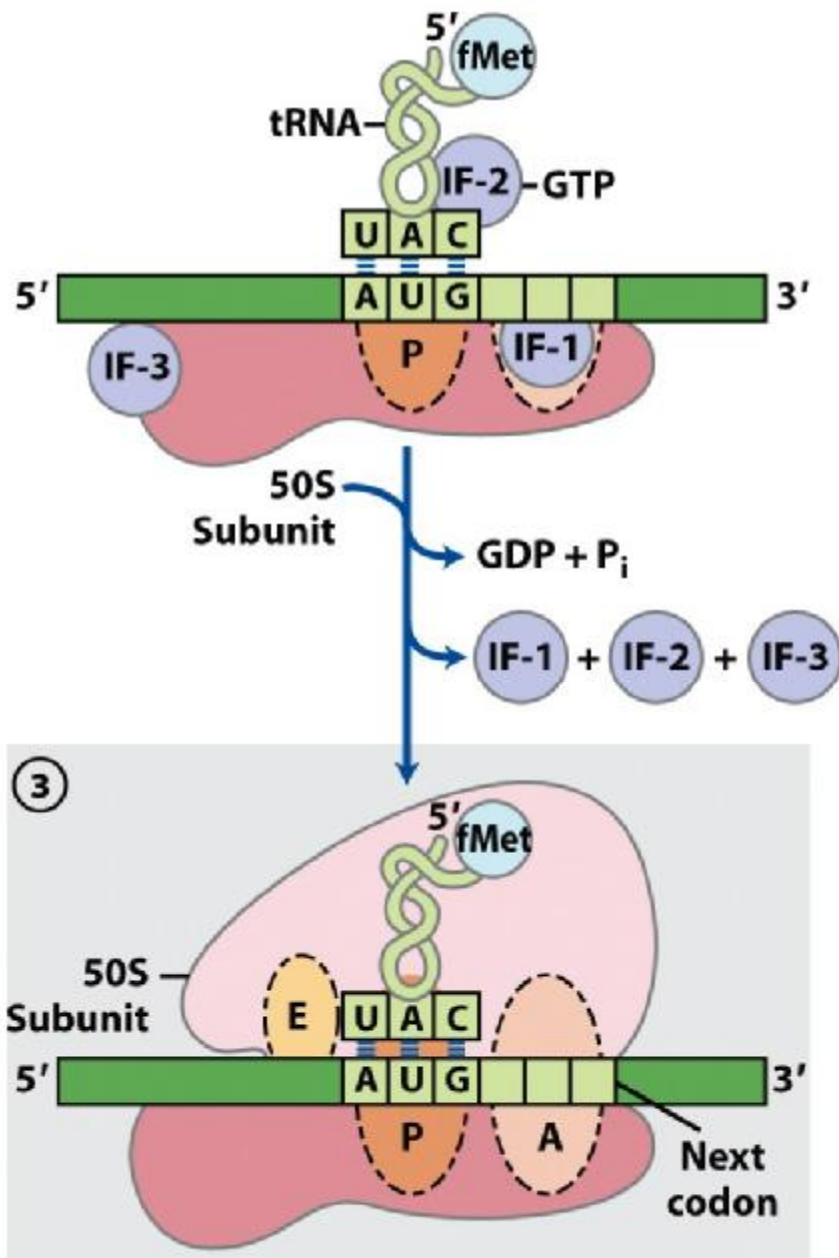
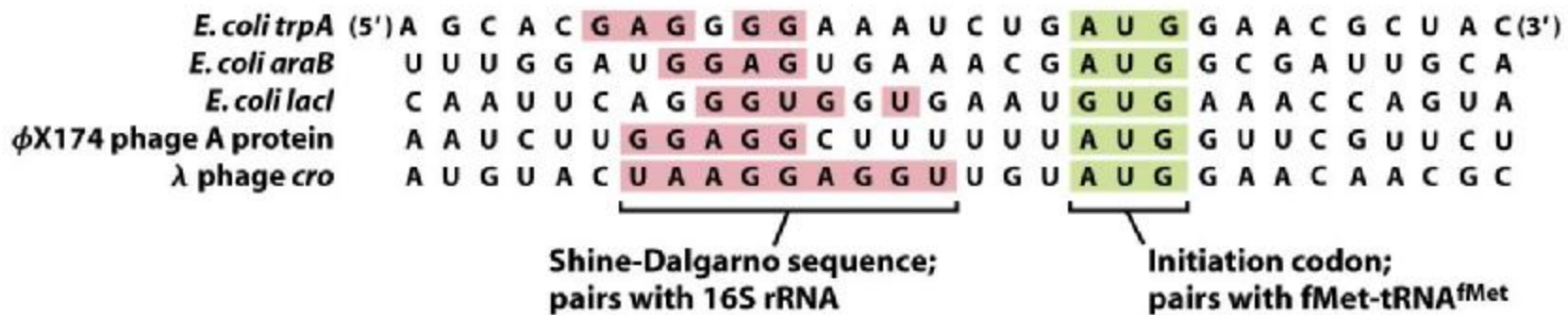
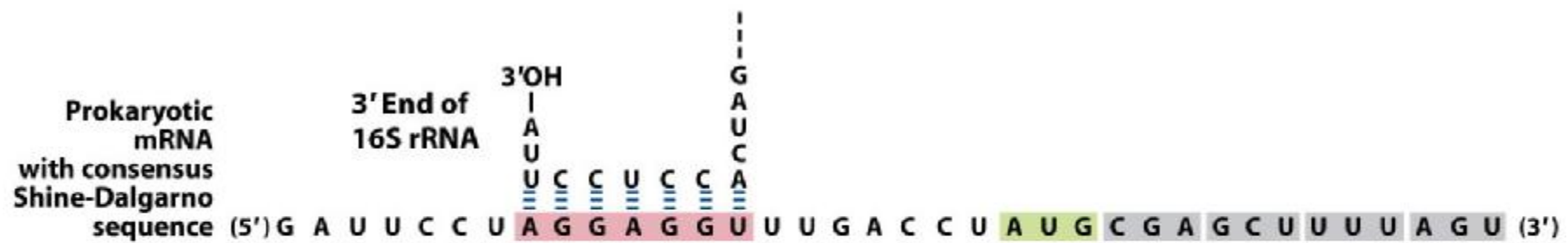


Figure 27-25 part 3
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(a)



(b)

Figure 27-26
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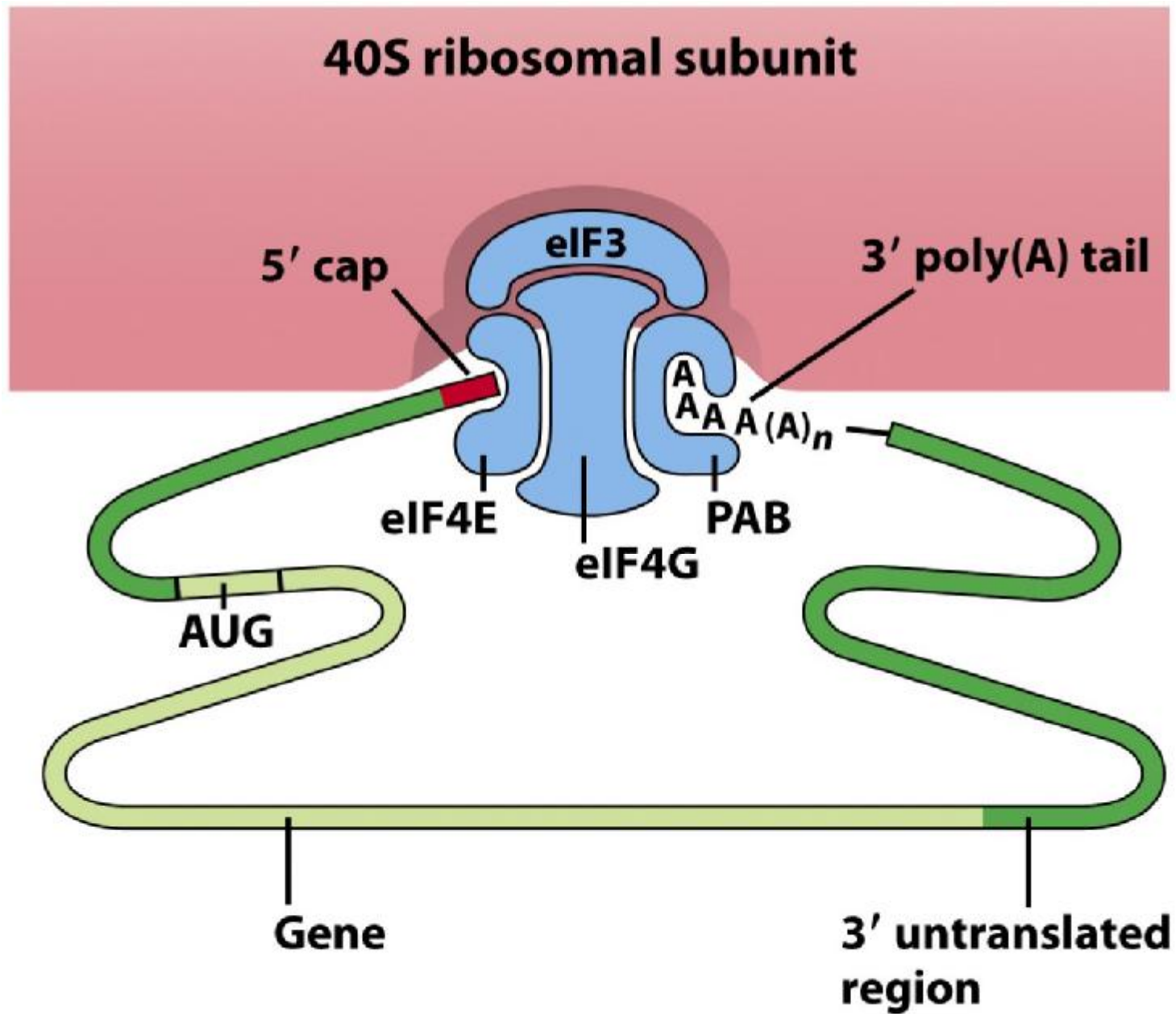


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TABLE 27-8 Protein Factors Required for Initiation of Translation in Bacterial and Eukaryotic Cells	
Factor	Function
Bacterial	
IF-1	Prevents premature binding of tRNAs to A site
IF-2	Facilitates binding of fMet-tRNA ^{fMet} to 30S ribosomal subunit
IF-3	Binds to 30S subunit; prevents premature association of 50S subunit; enhances specificity of P site for fMet-tRNA ^{fMet}
Eukaryotic	
eIF2	Facilitates binding of initiating Met-tRNA ^{Met} to 40S ribosomal subunit
eIF2B, eIF3	First factors to bind 40S subunit; facilitate subsequent steps
eIF4A	RNA helicase activity removes secondary structure in the mRNA to permit binding to 40S subunit; part of the eIF4F complex
eIF4B	Binds to mRNA; facilitates scanning of mRNA to locate the first AUG
eIF4E	Binds to the 5' cap of mRNA; part of the eIF4F complex
eIF4G	Binds to eIF4E and to poly(A) binding protein (PAB); part of the eIF4F complex
eIF5	Promotes dissociation of several other initiation factors from 40S subunit as a prelude to association of 60S subunit to form 80S initiation complex
eIF6	Facilitates dissociation of inactive 80S ribosome into 40S and 60S subunits

Table 27-8

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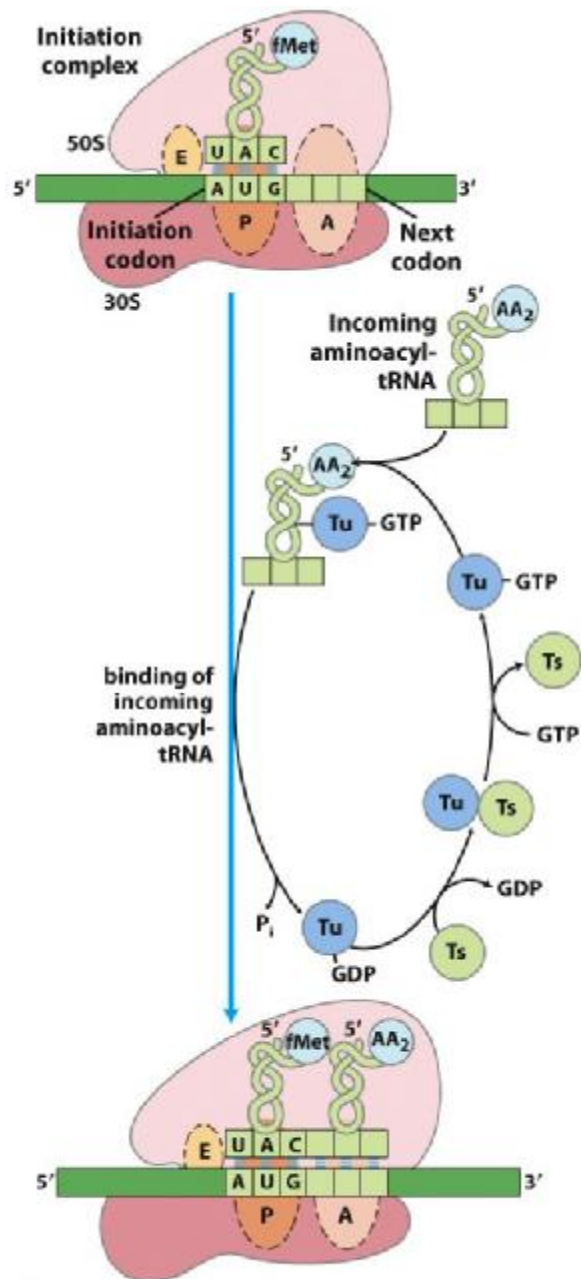


Figure 27-28

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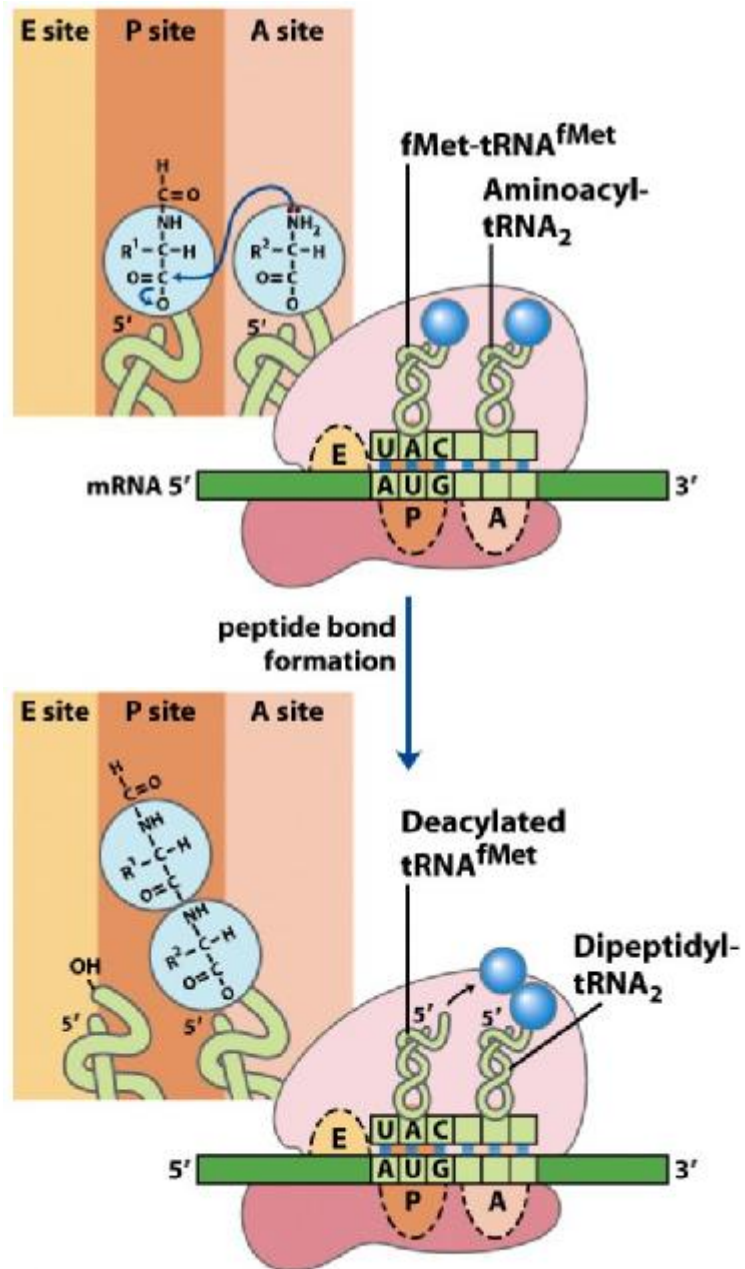


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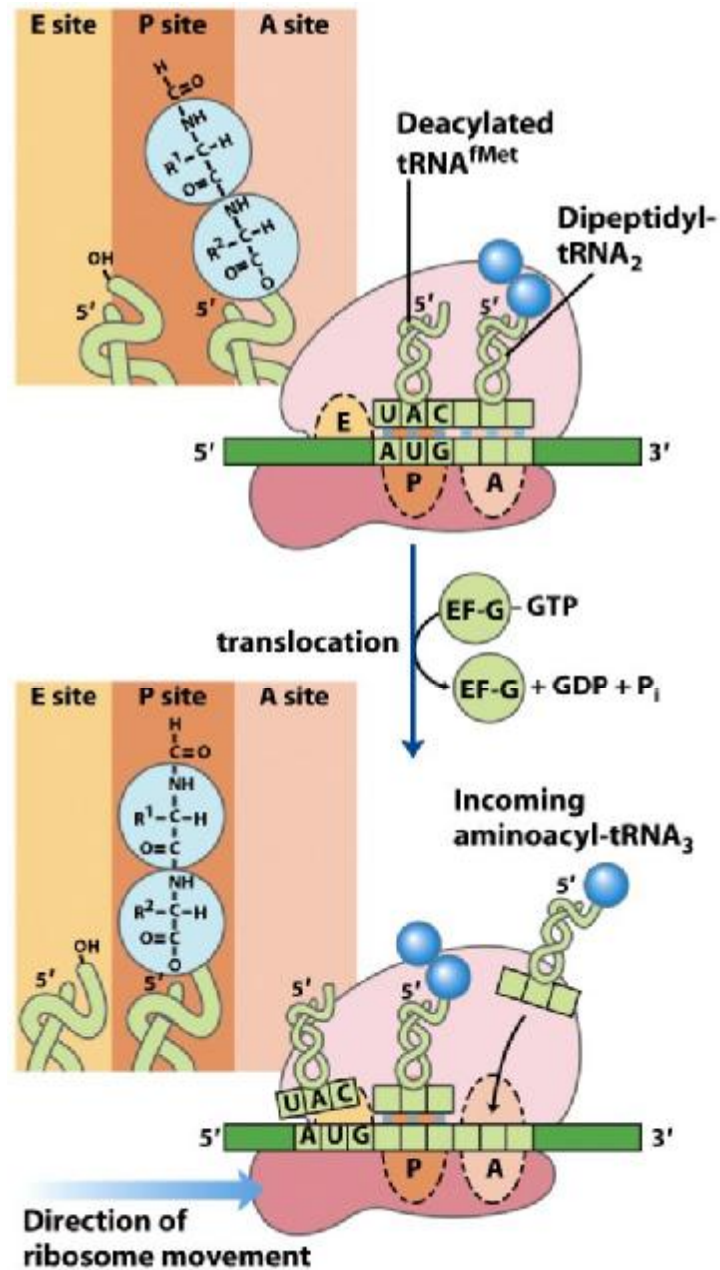


Figure 27-30a

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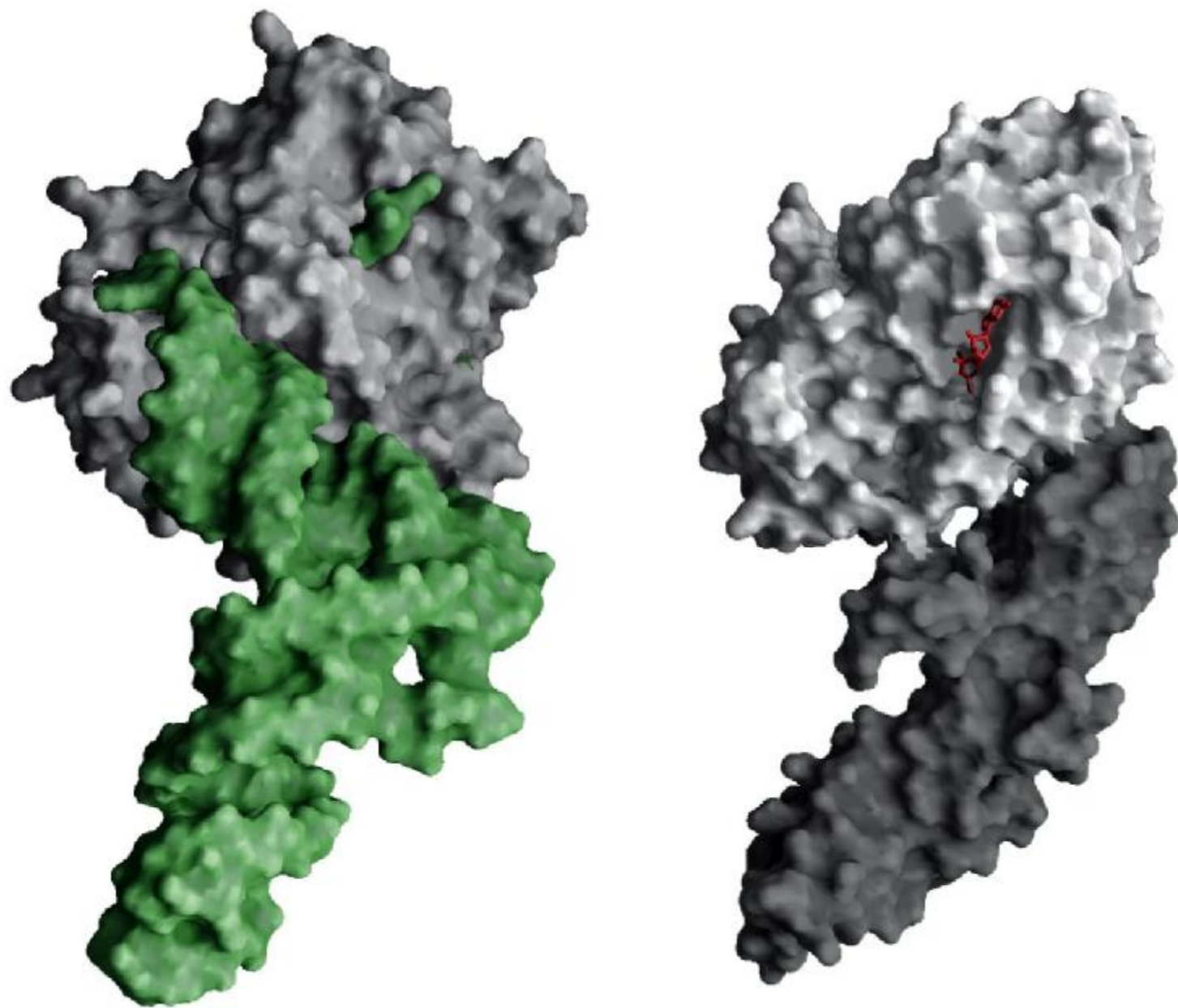
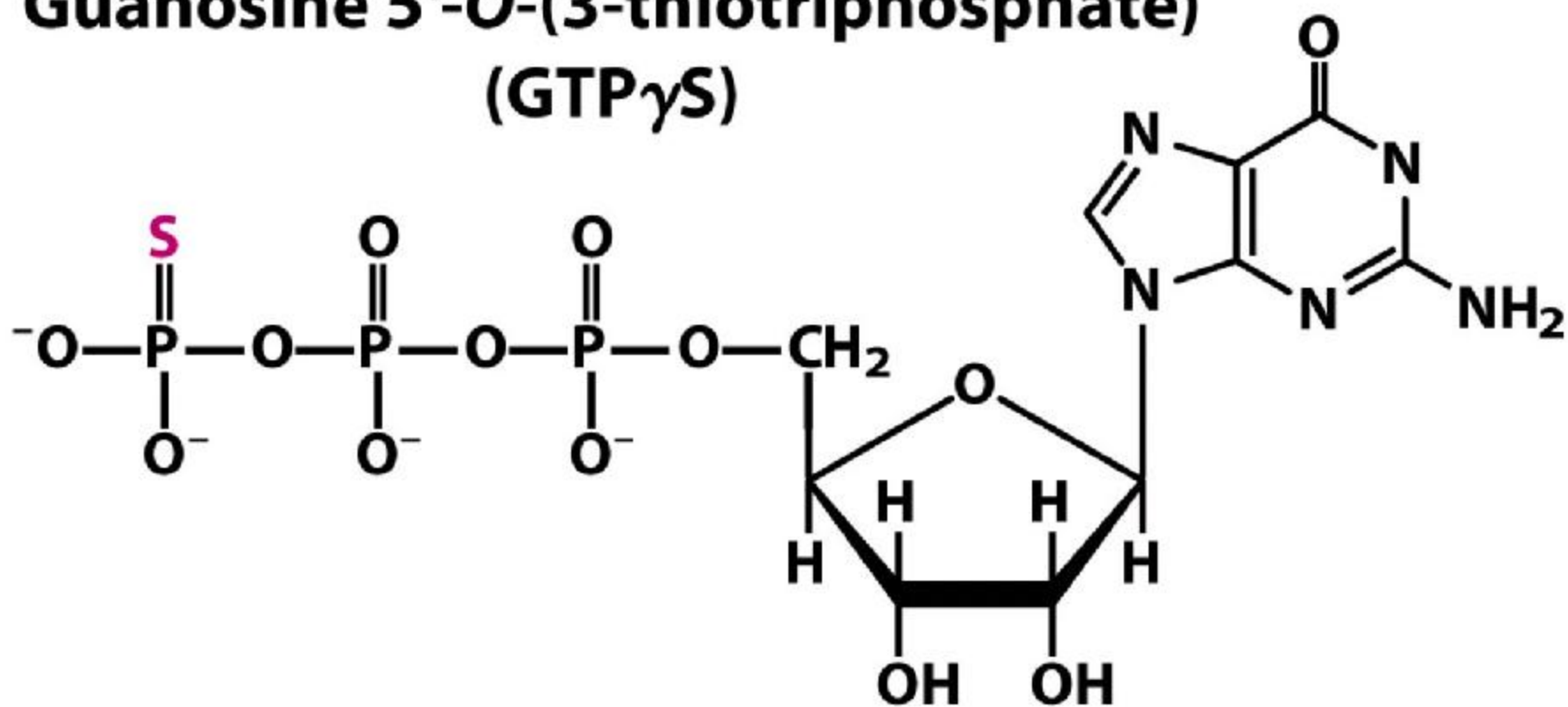


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Guanosine 5'-O-(3-thiotriphosphate) (GTP γ S)



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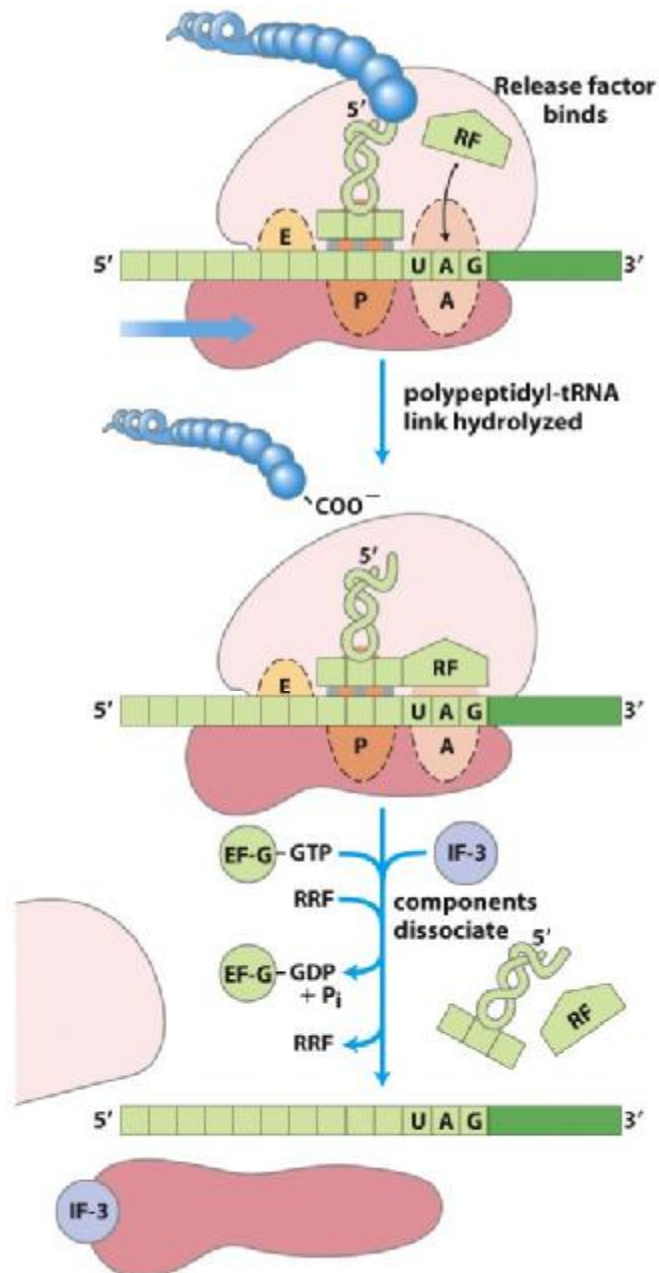


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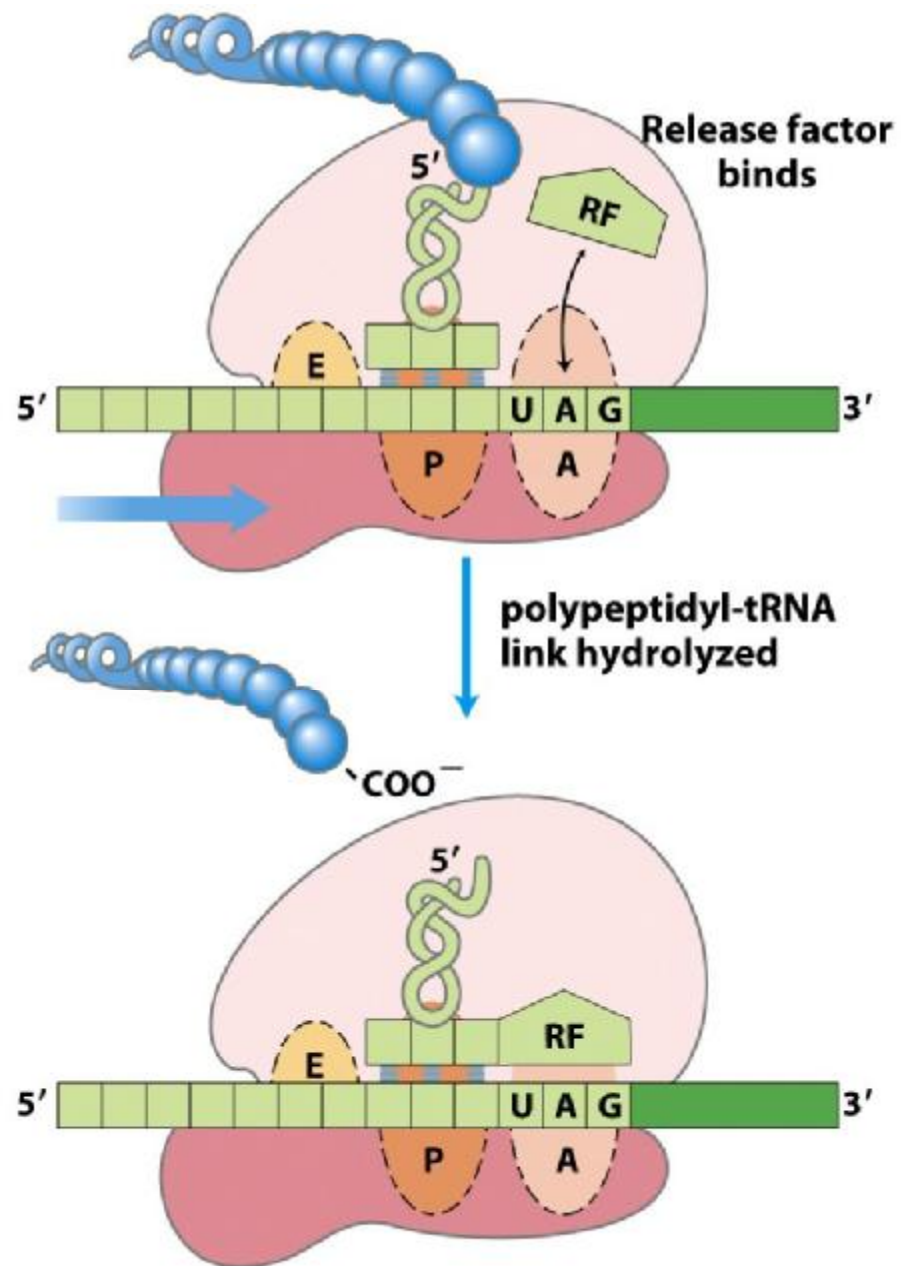


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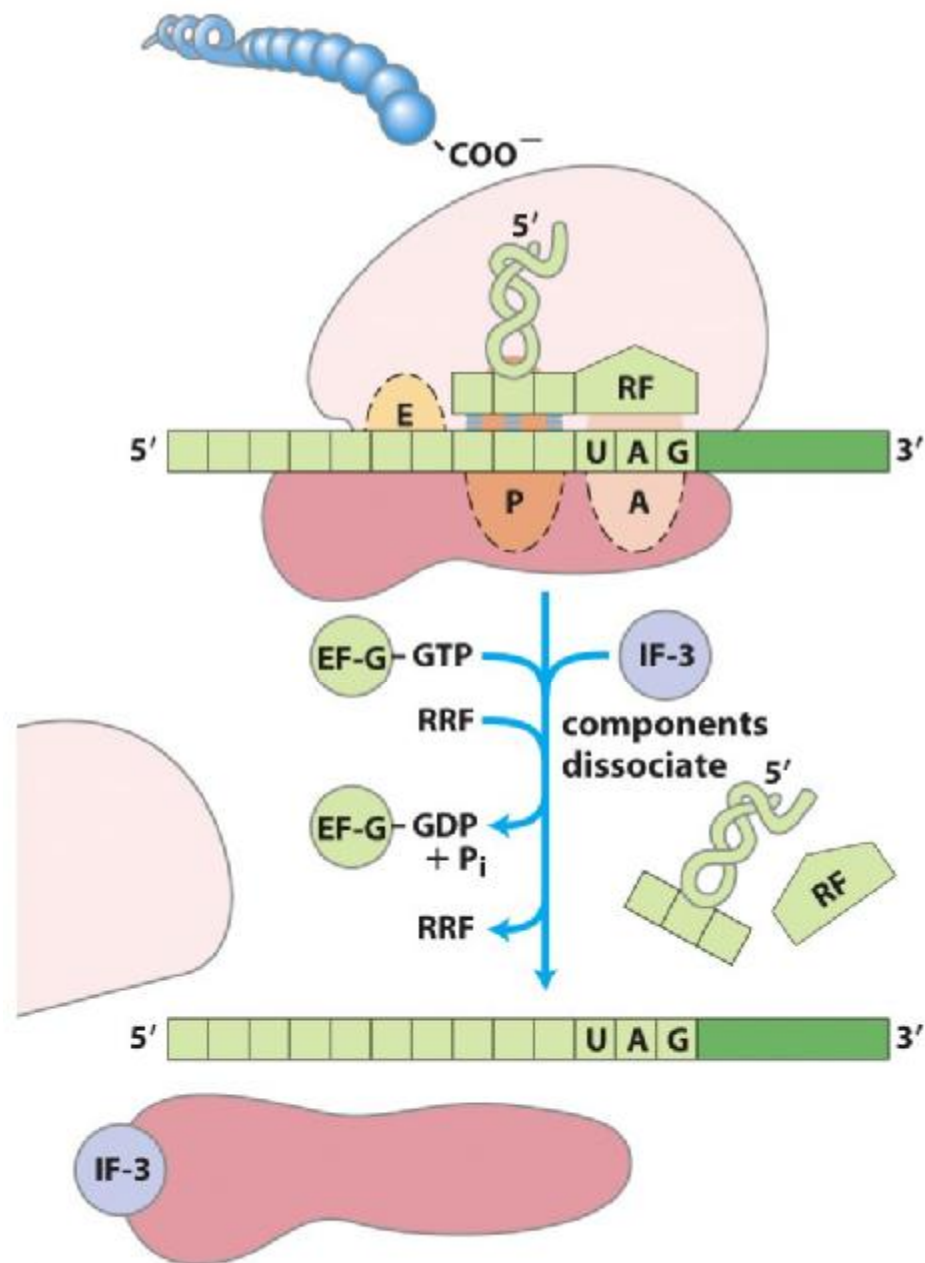


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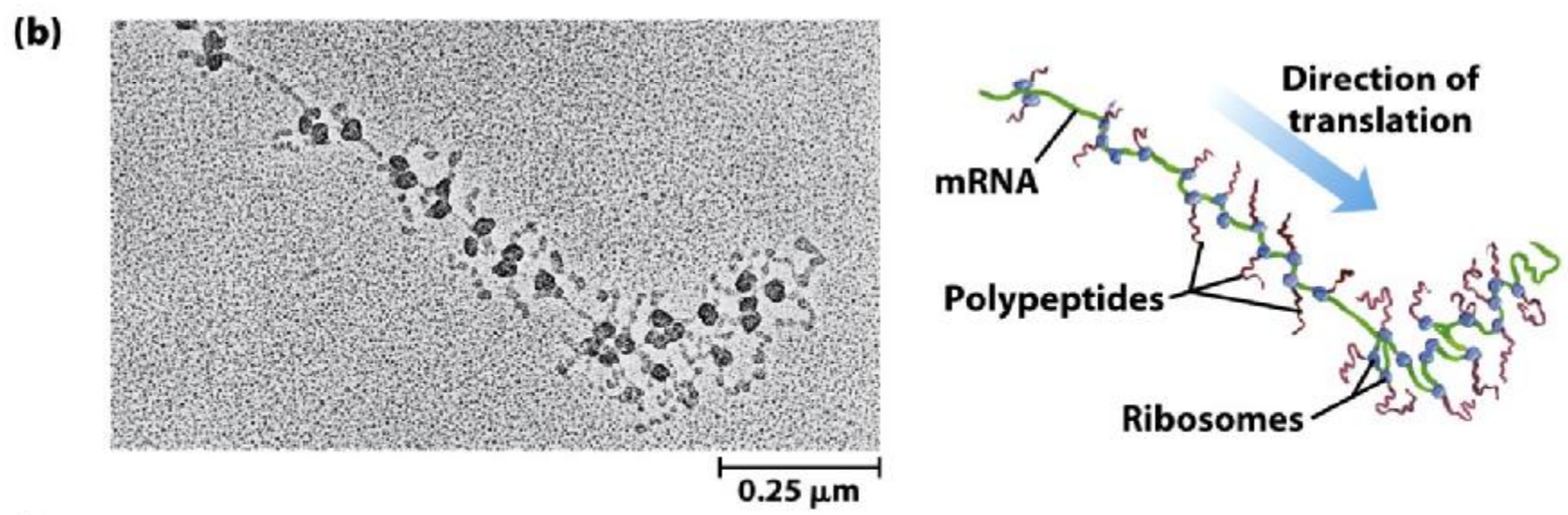
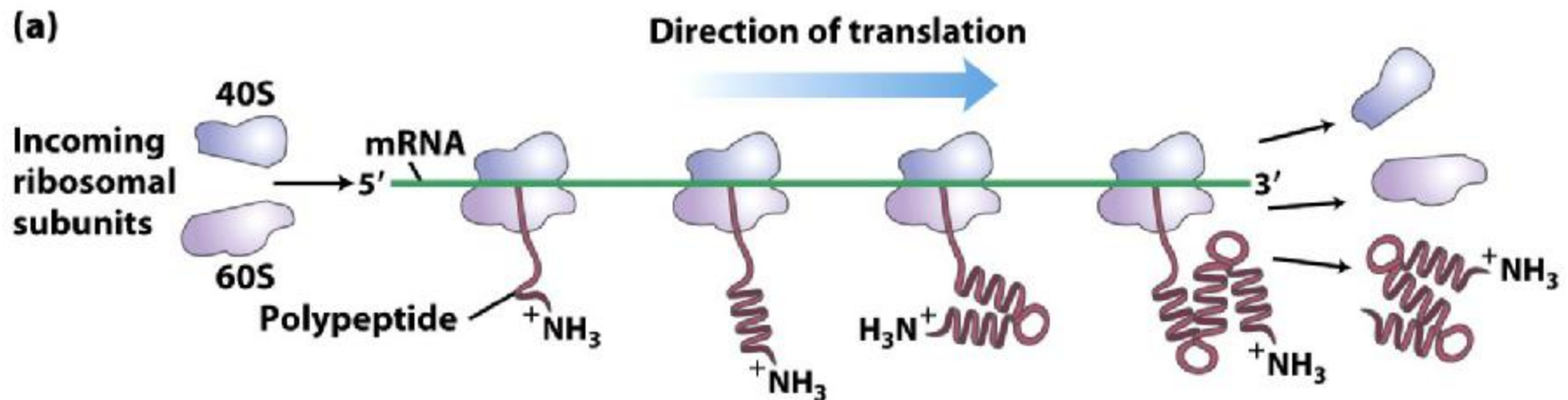


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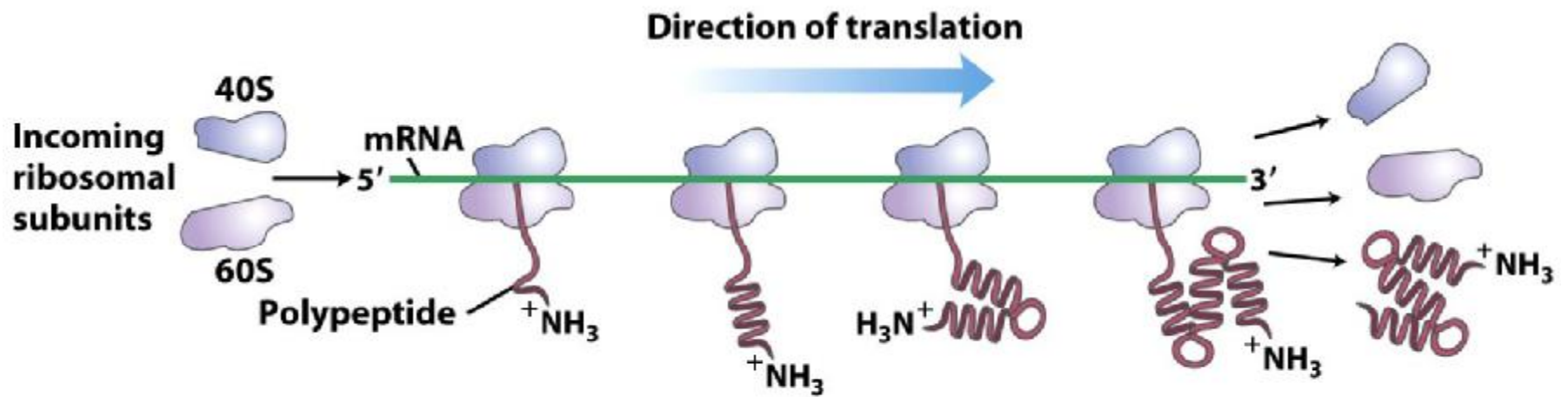
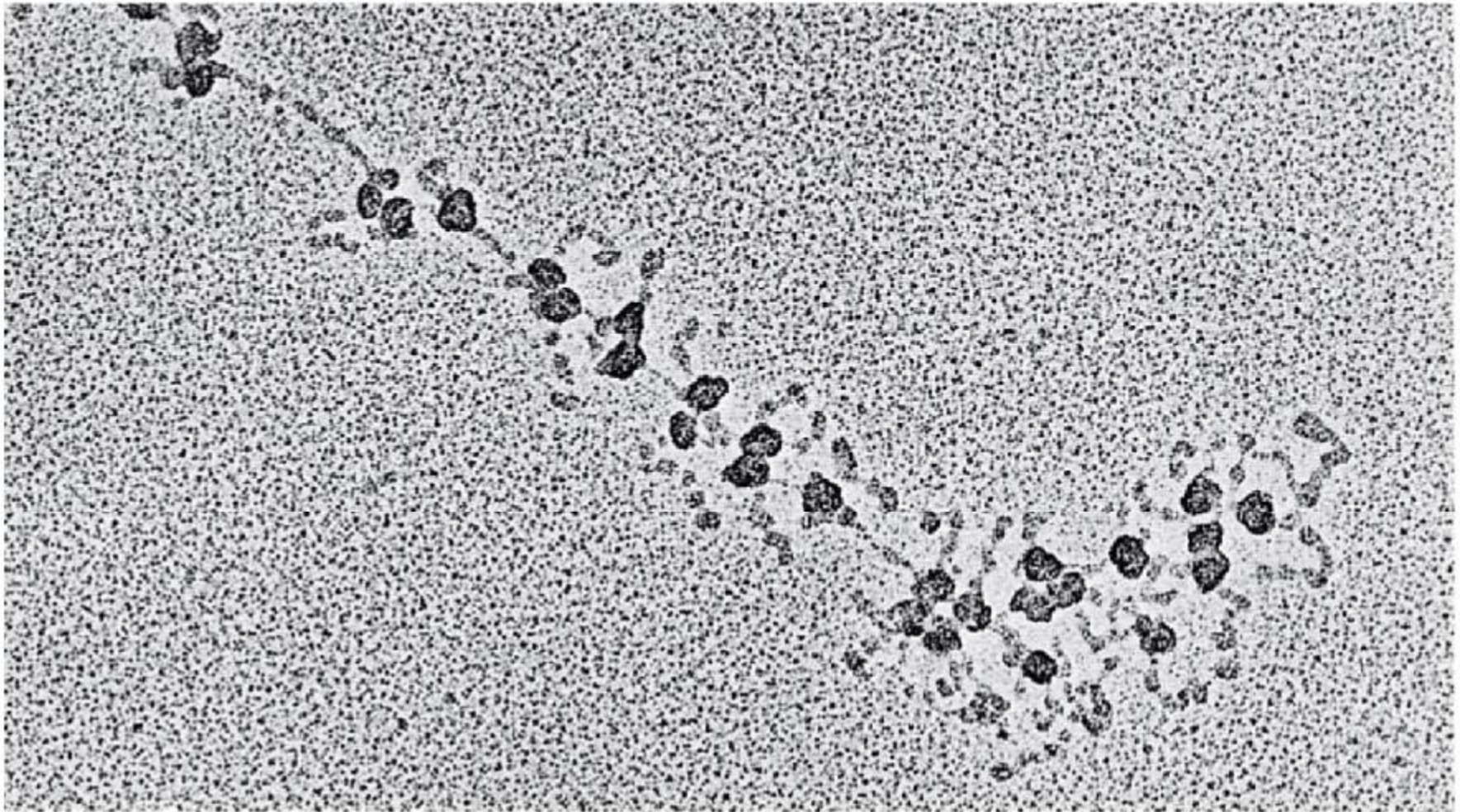


Figure 27-32a

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Figure 27-32b part 1

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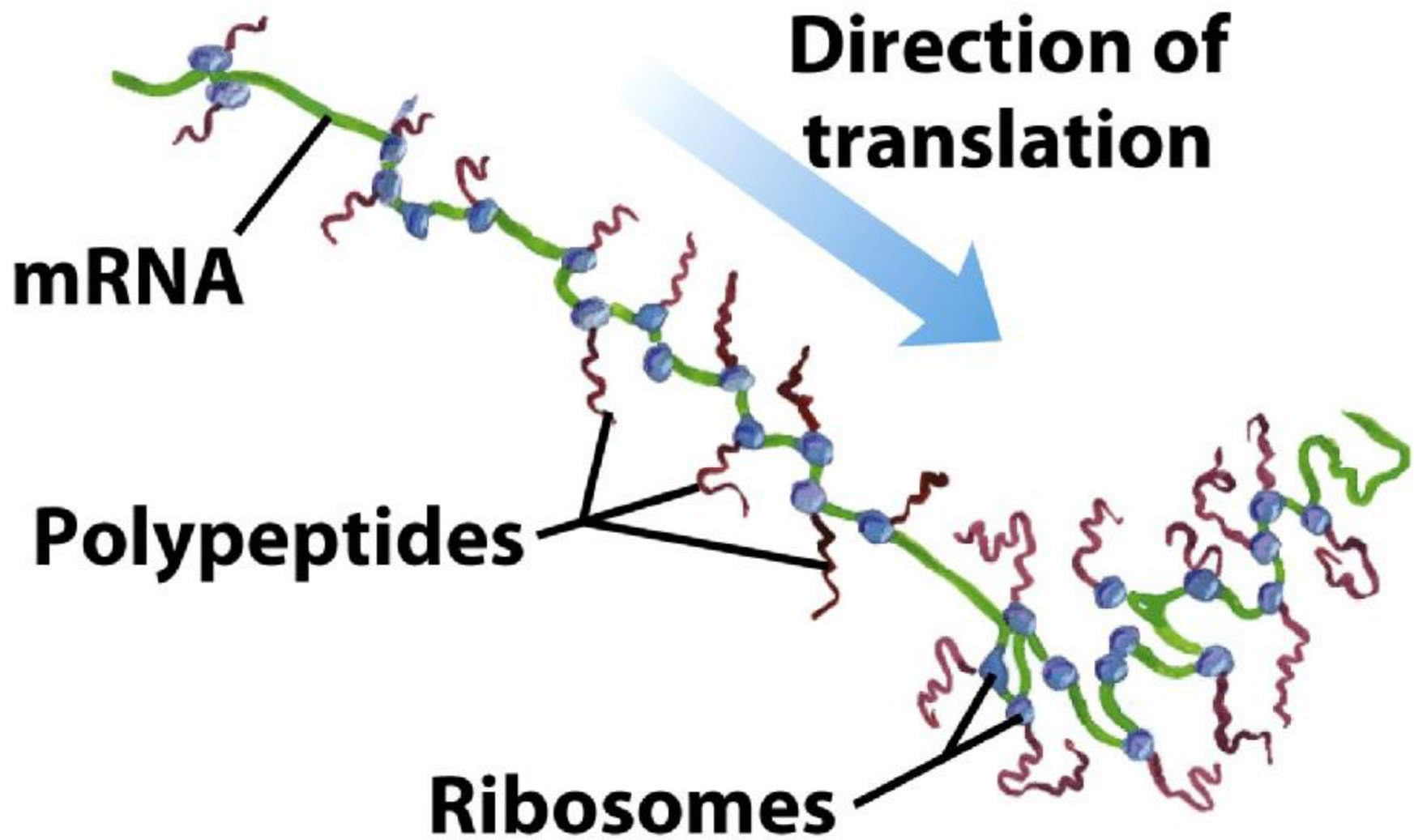


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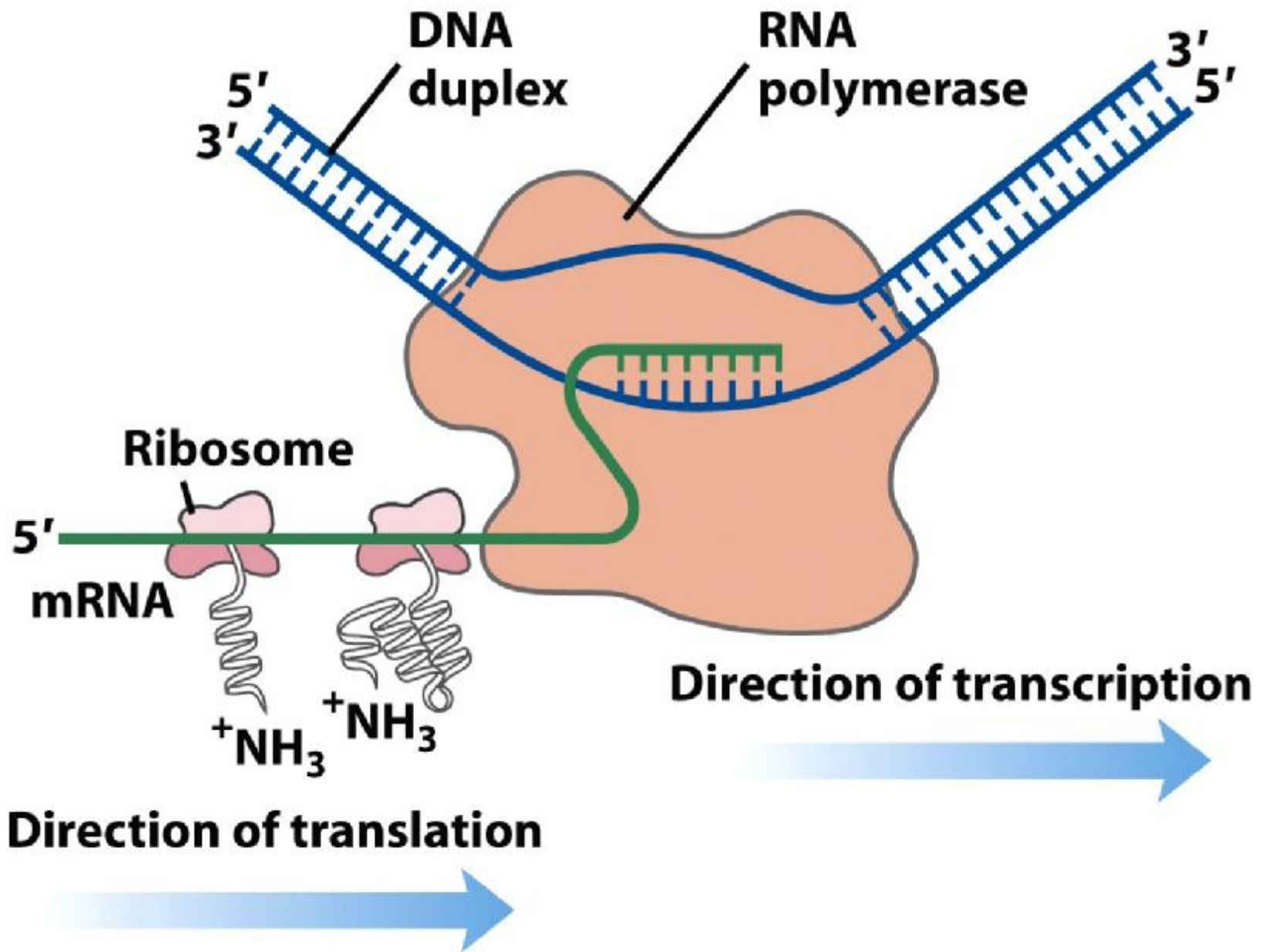
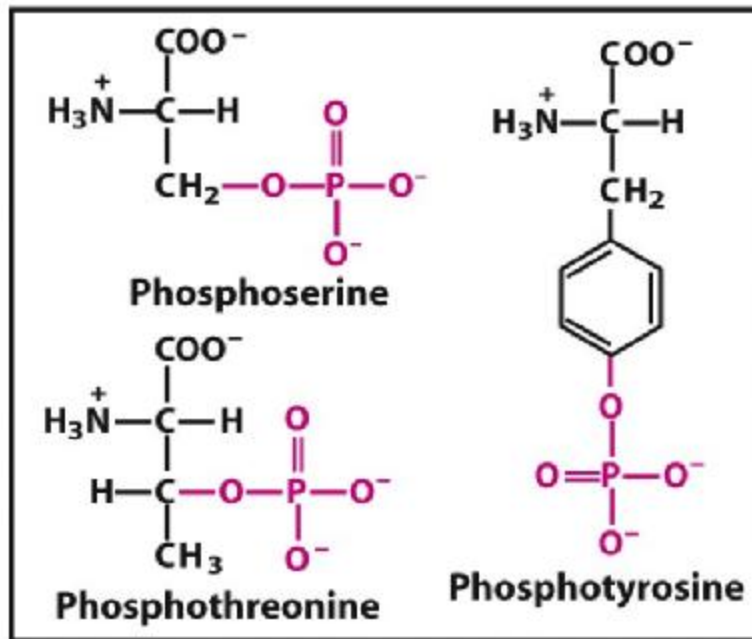
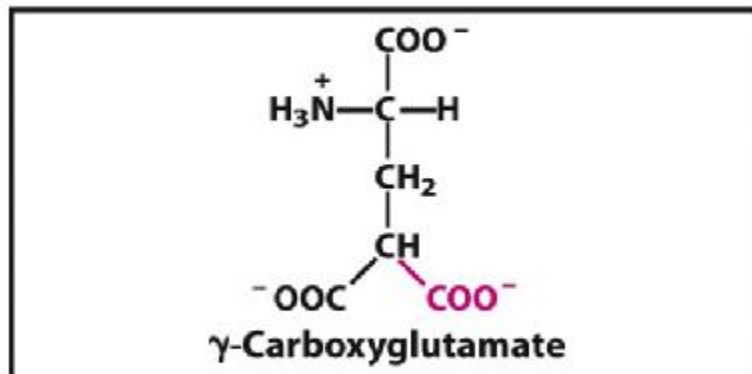


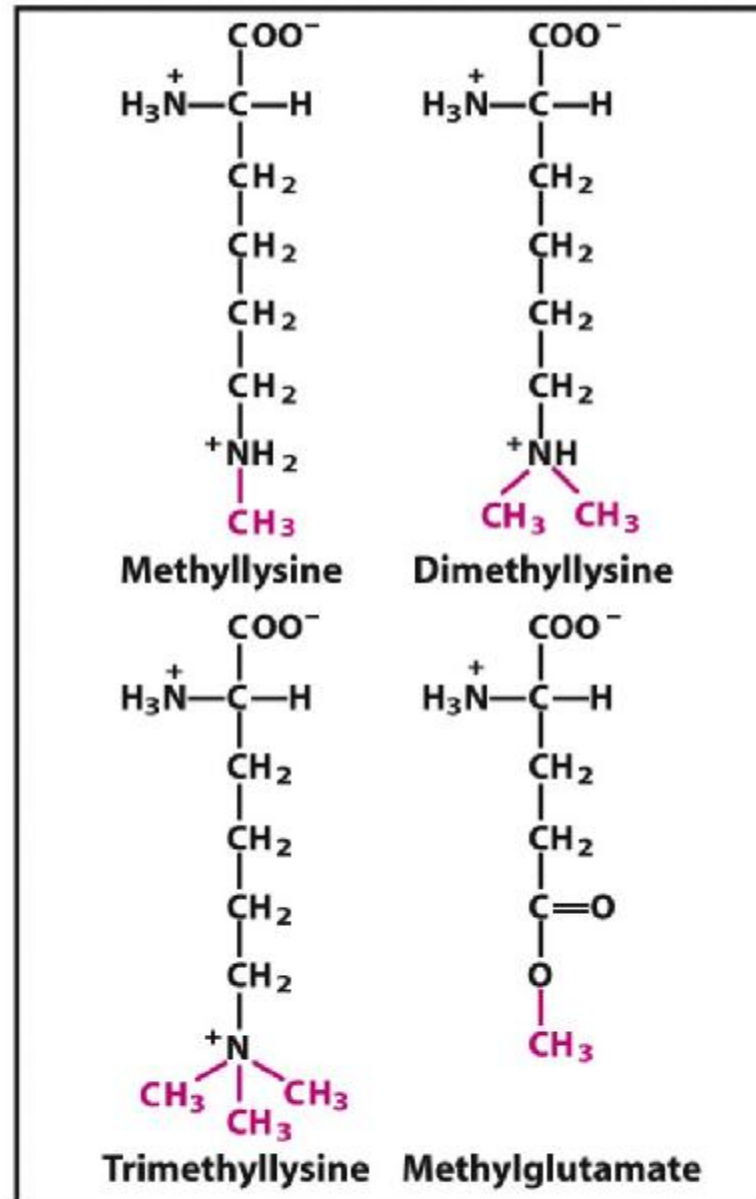
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(a)



(b)



(c)

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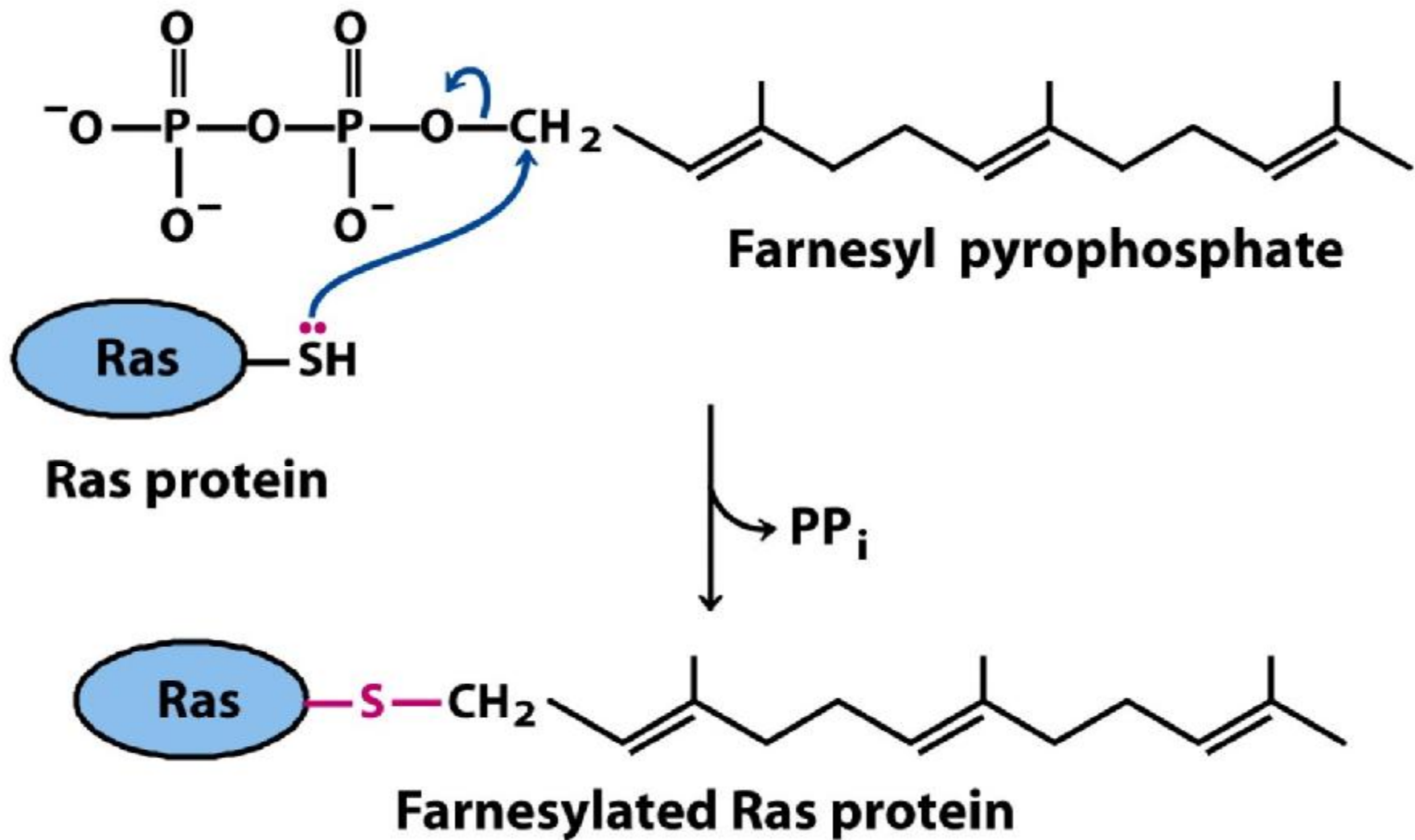
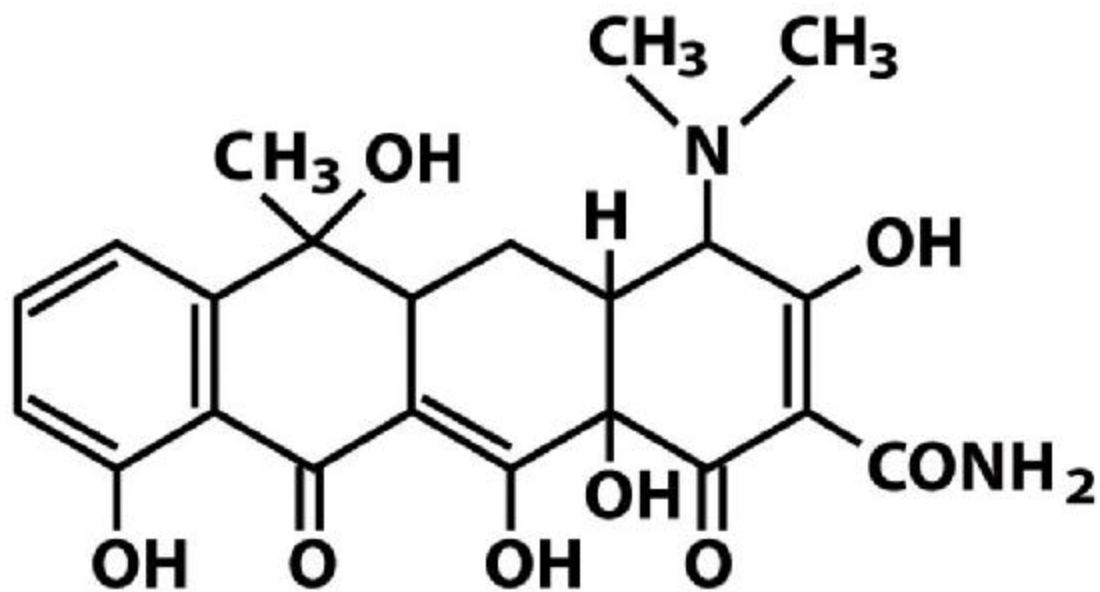
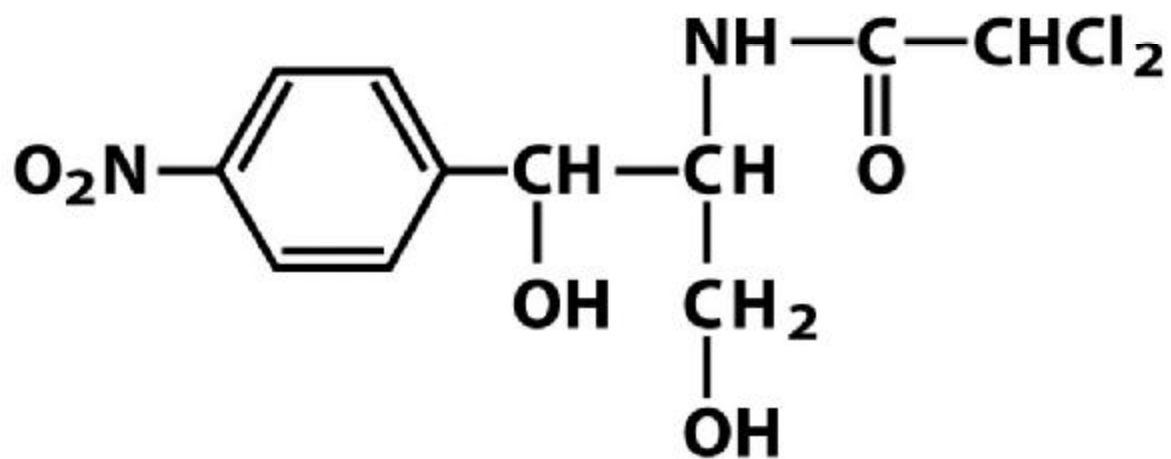


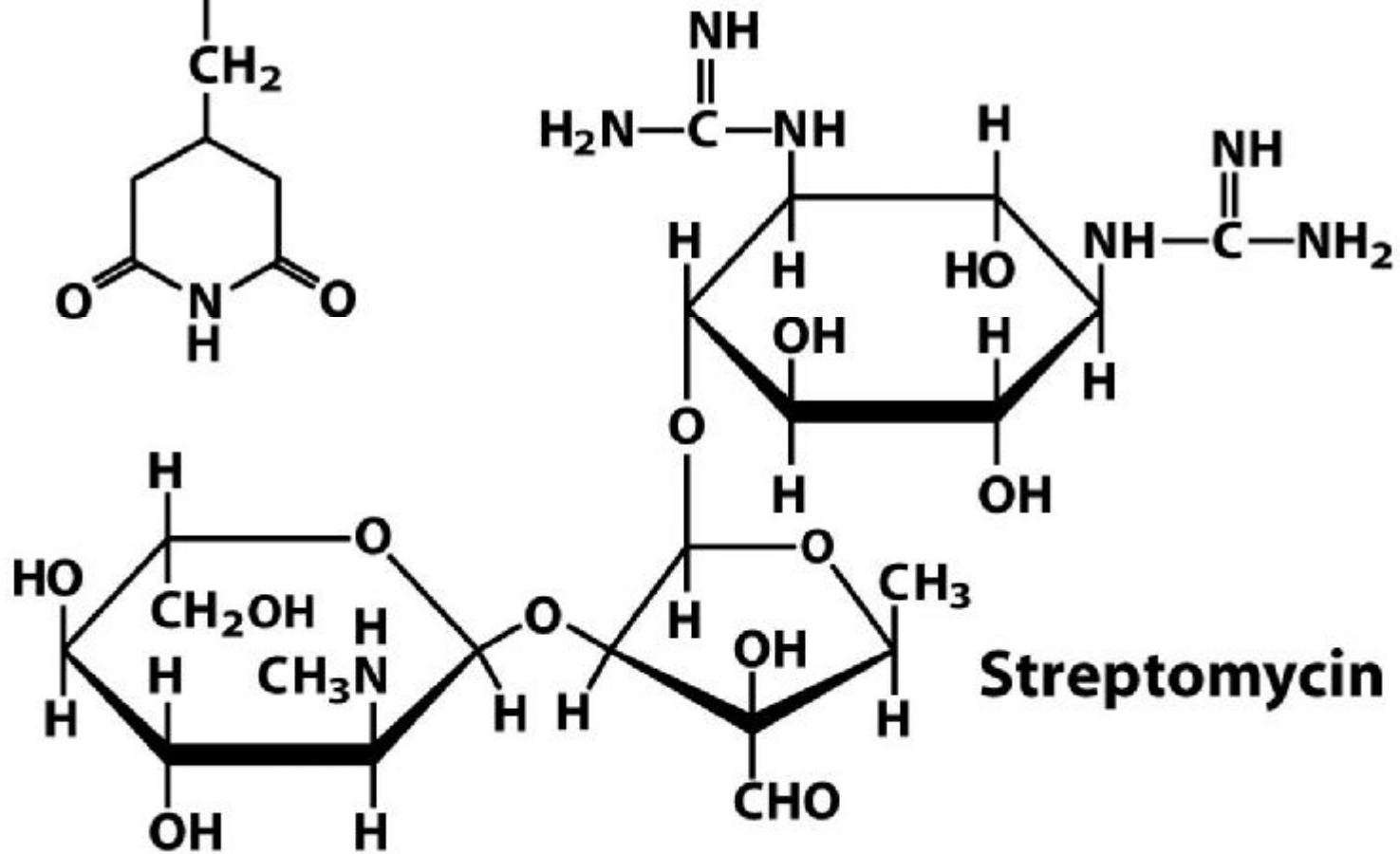
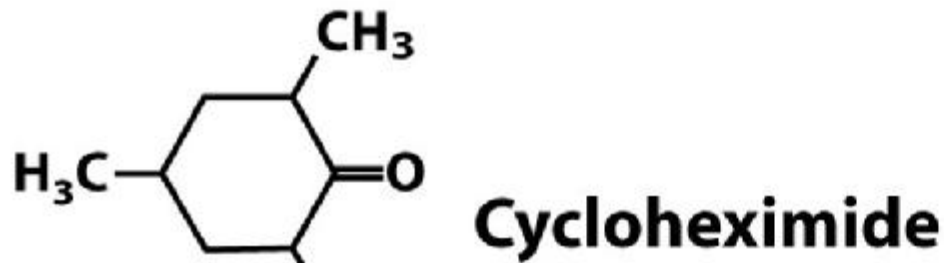
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Tetracycline



Chloramphenicol



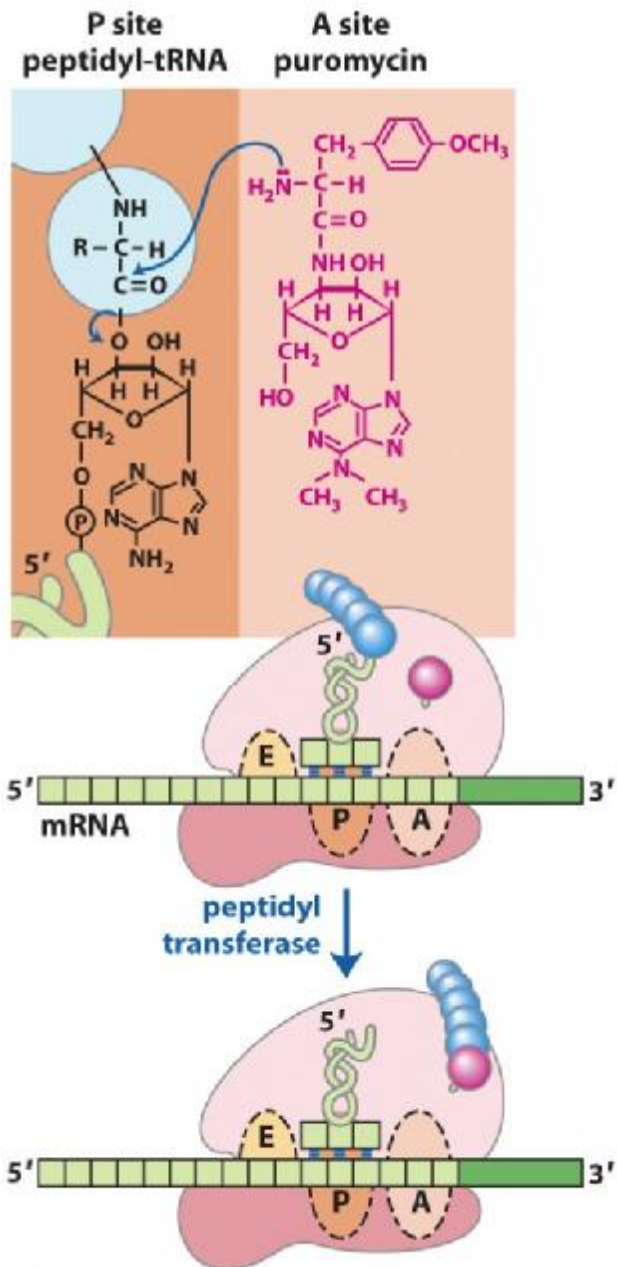


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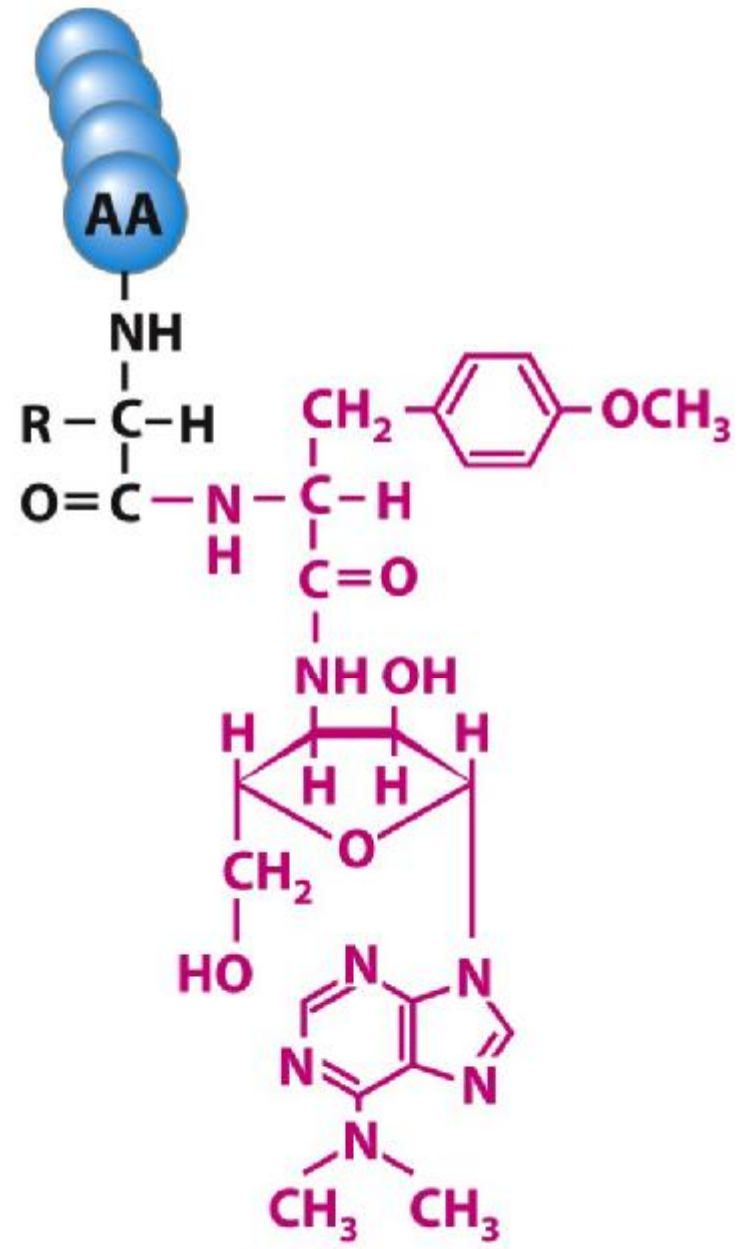


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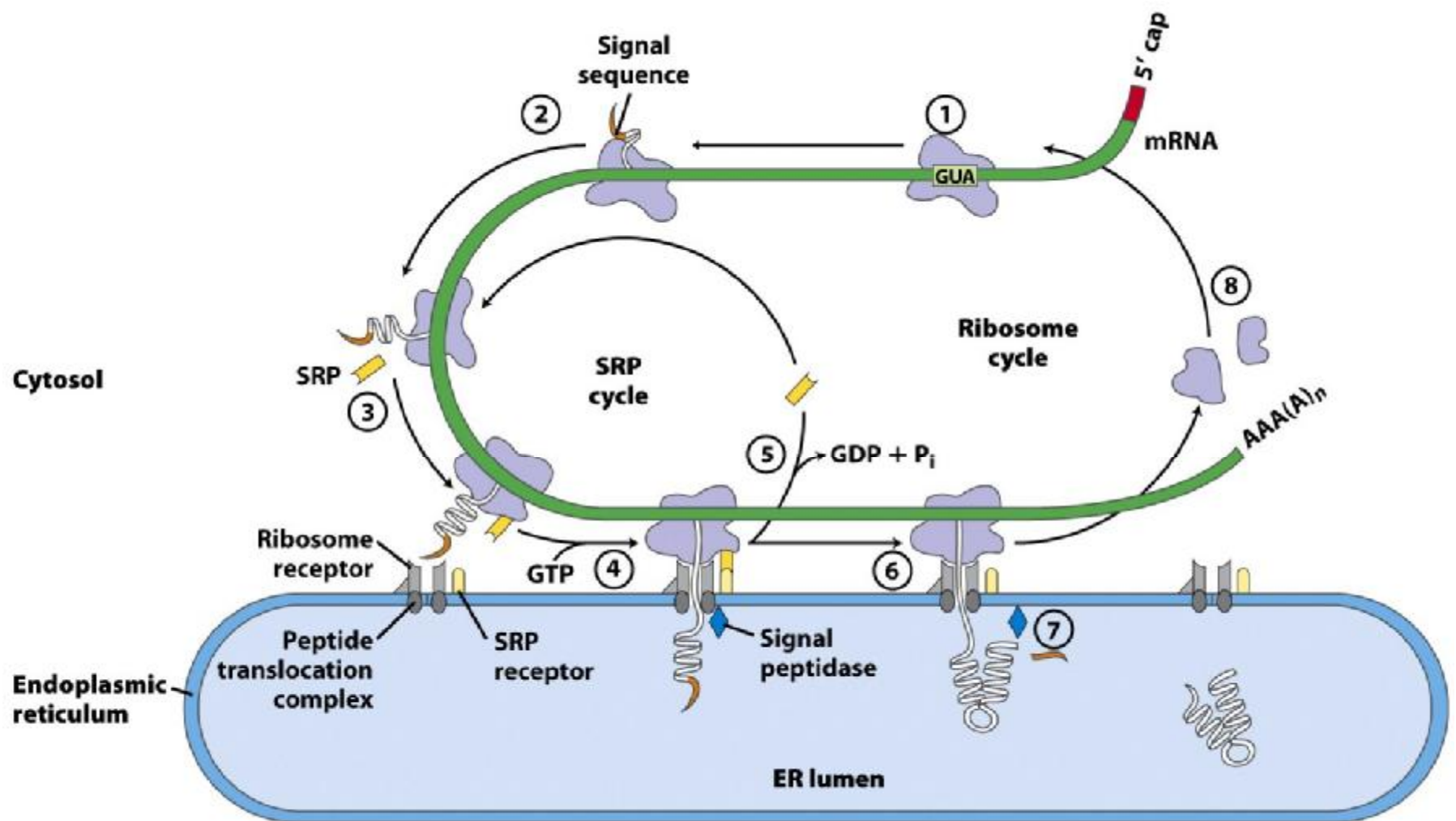
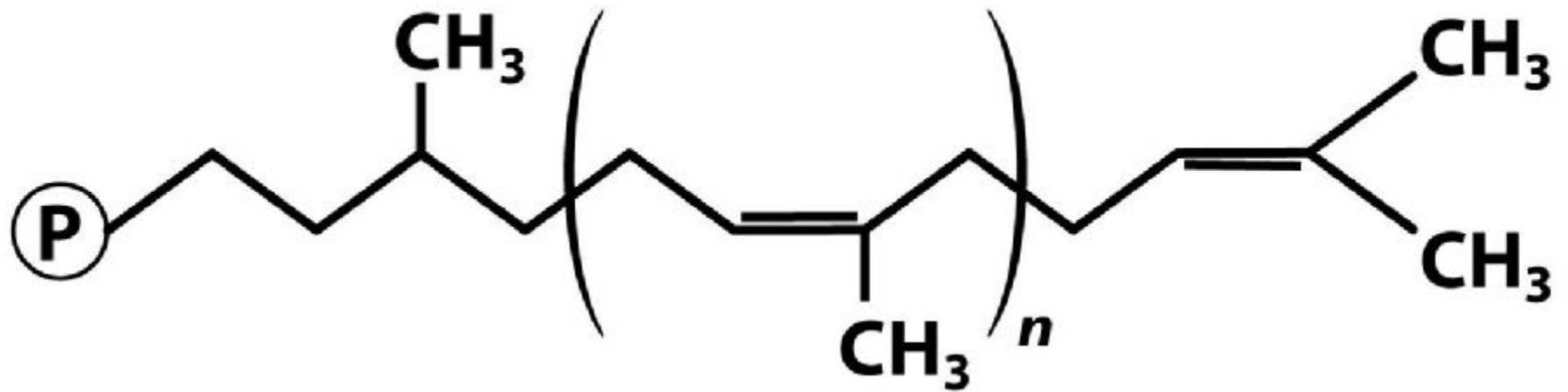


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Dolichol phosphate
($n = 9-22$)

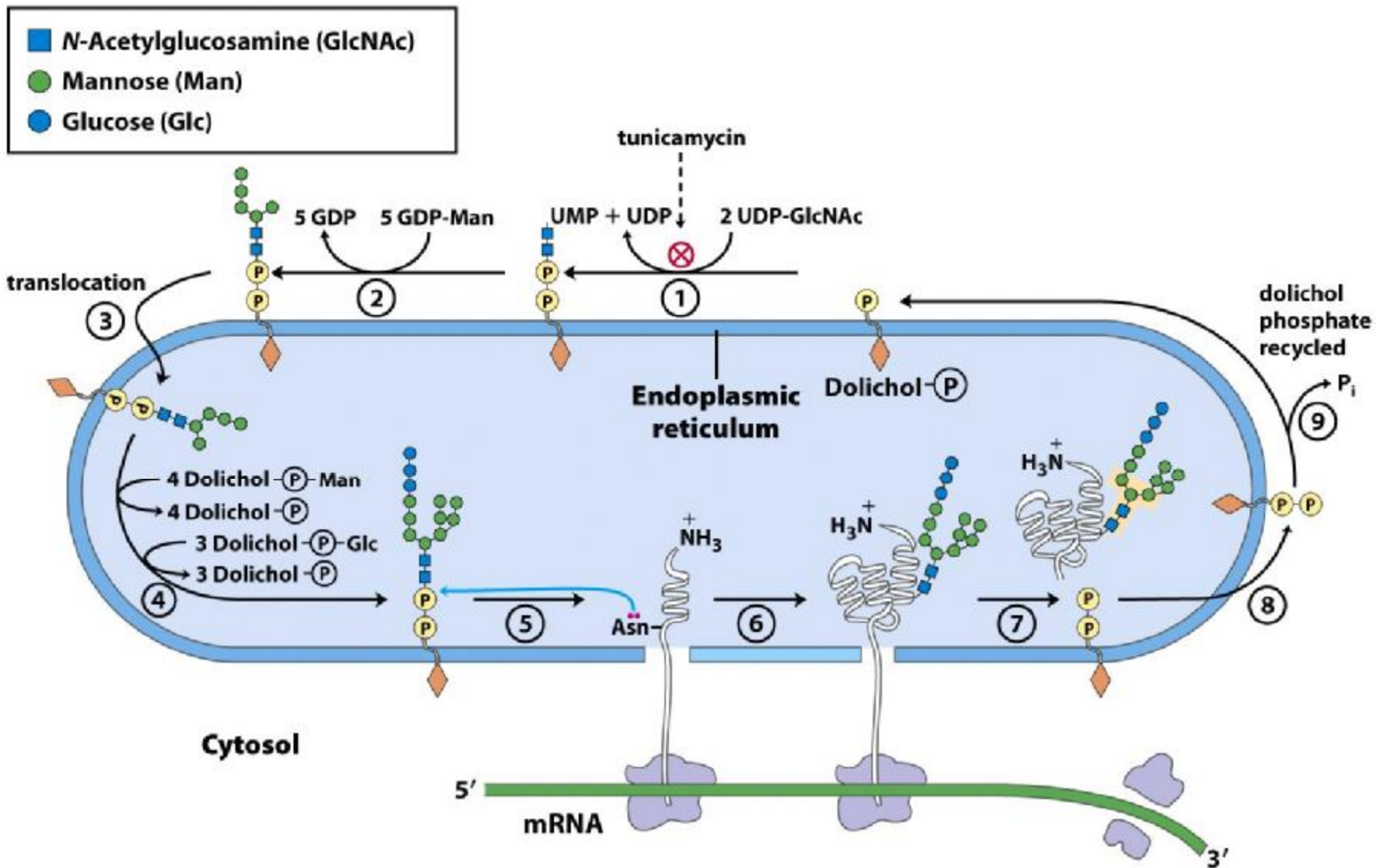
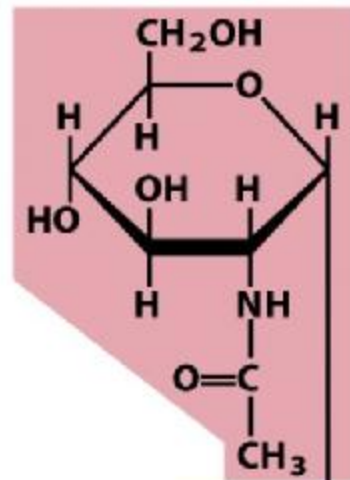


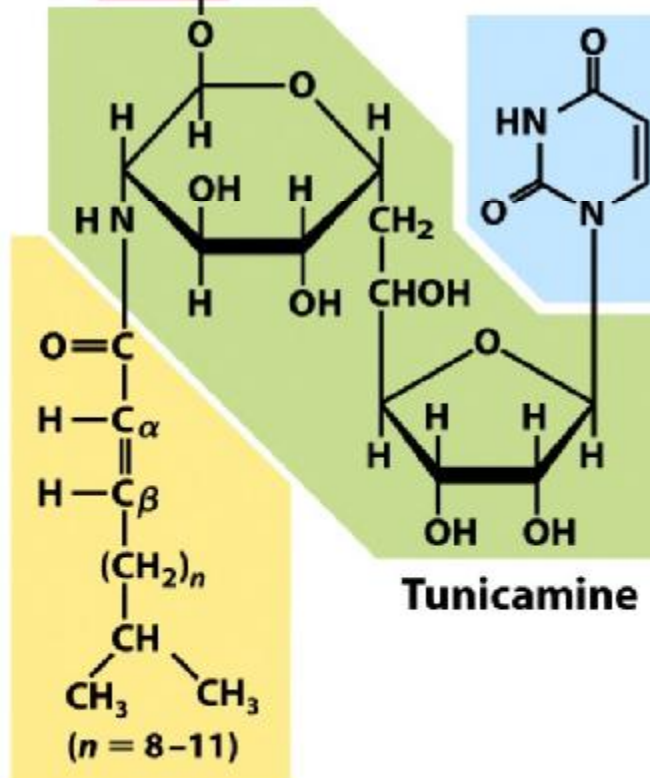
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Tunicamycin

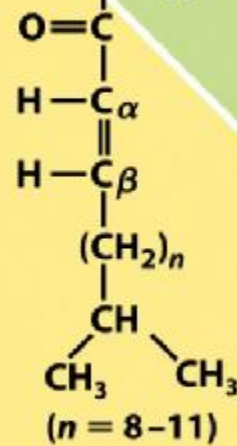
N-Acetylglucosamine



Uracil

Tunicamine

**Fatty acyl
side chain**



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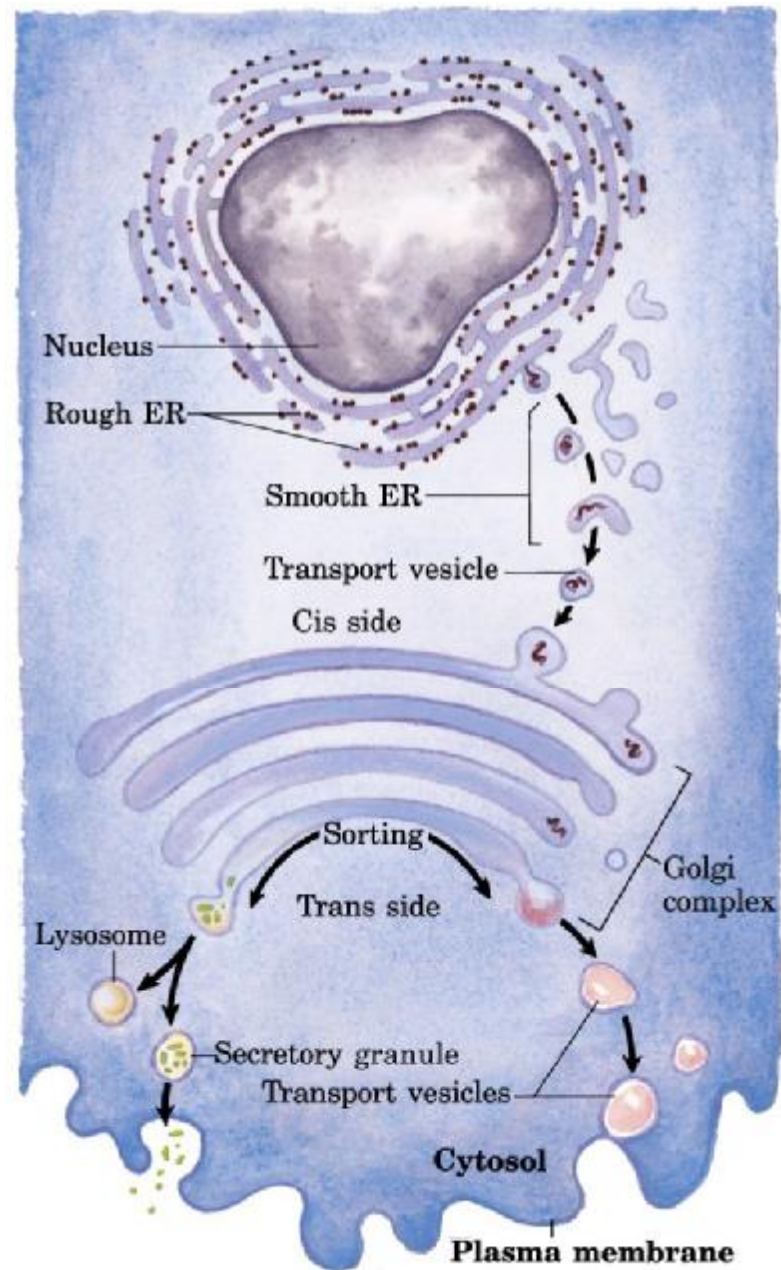


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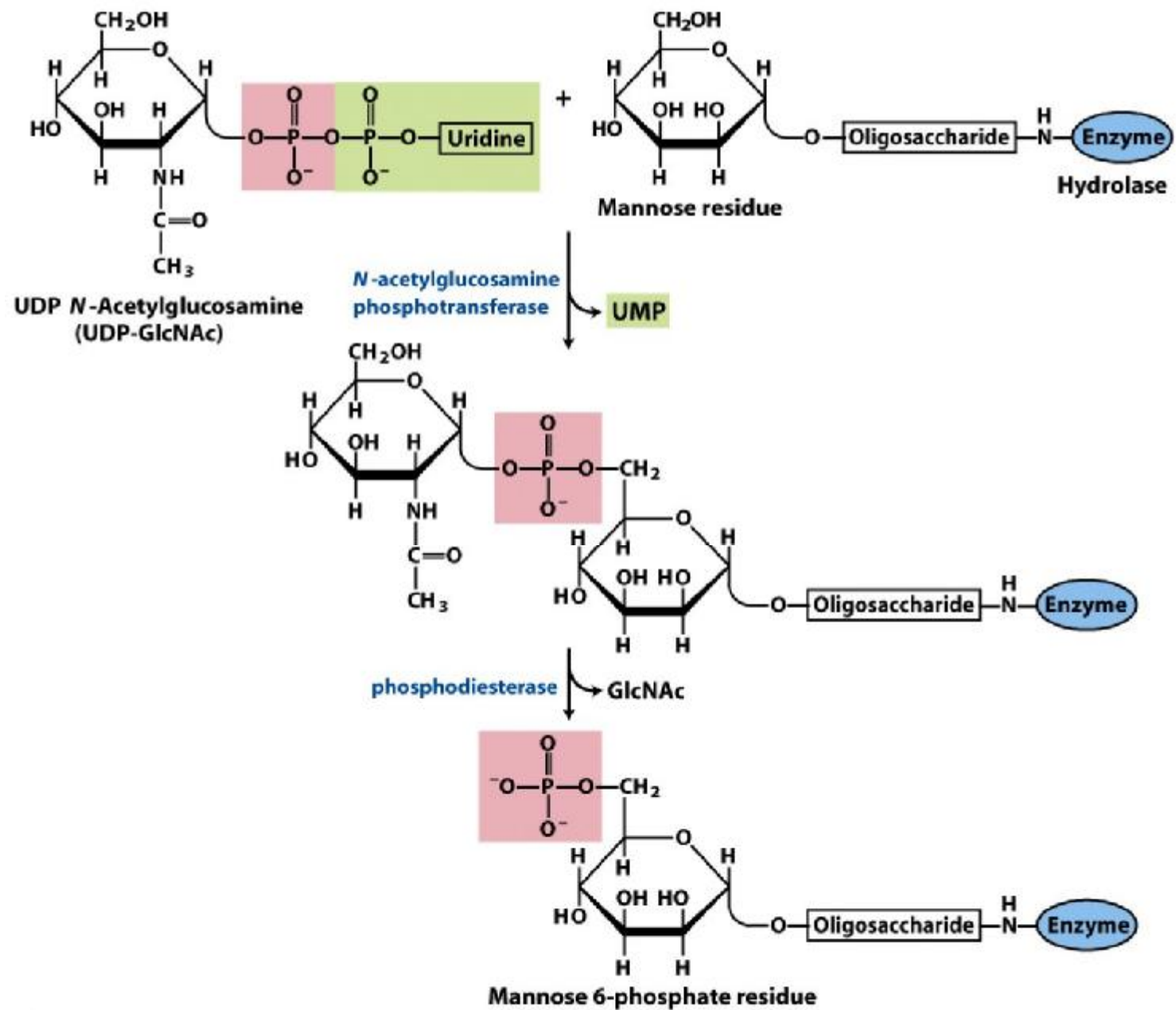


Figure 27-41

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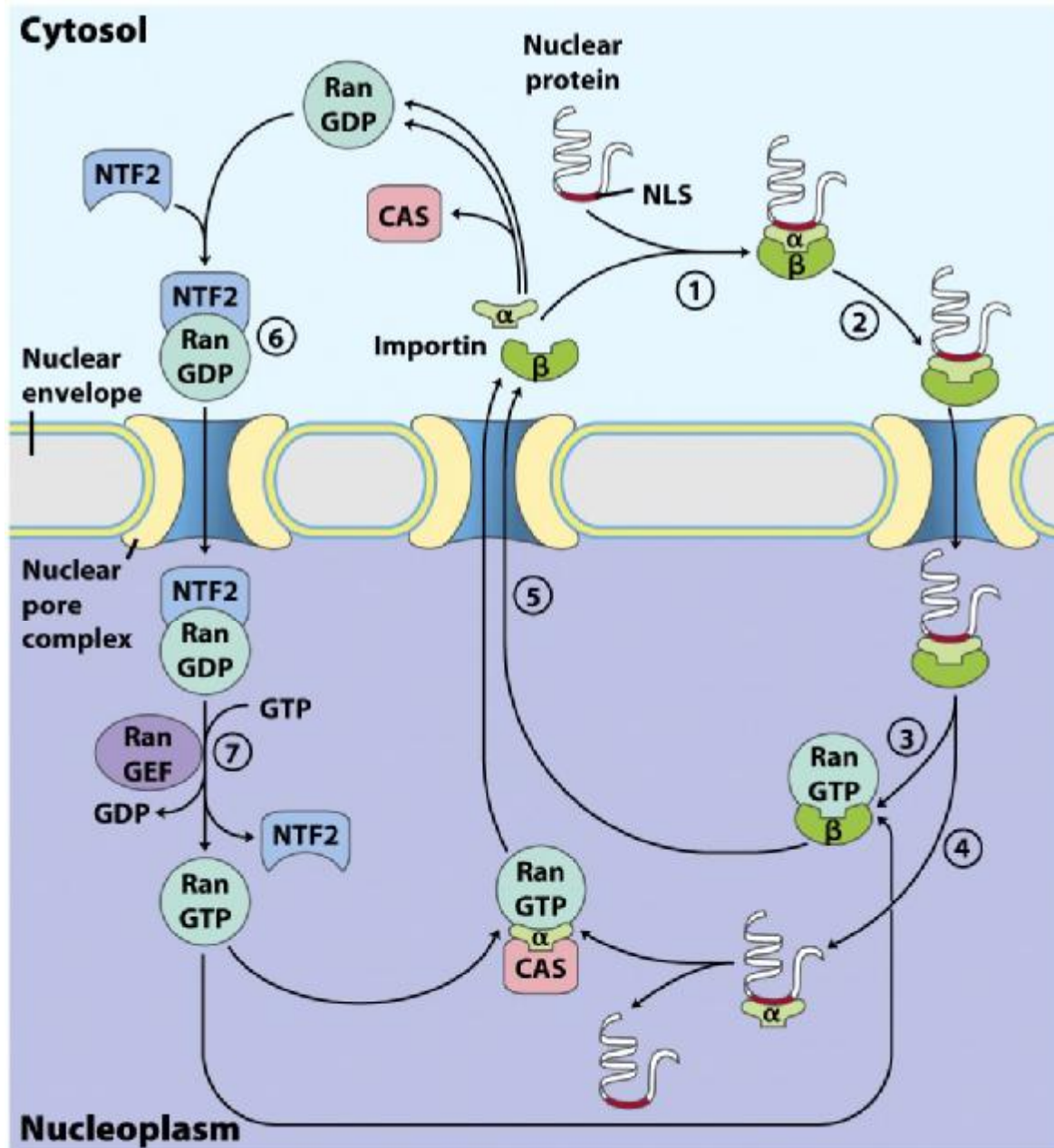
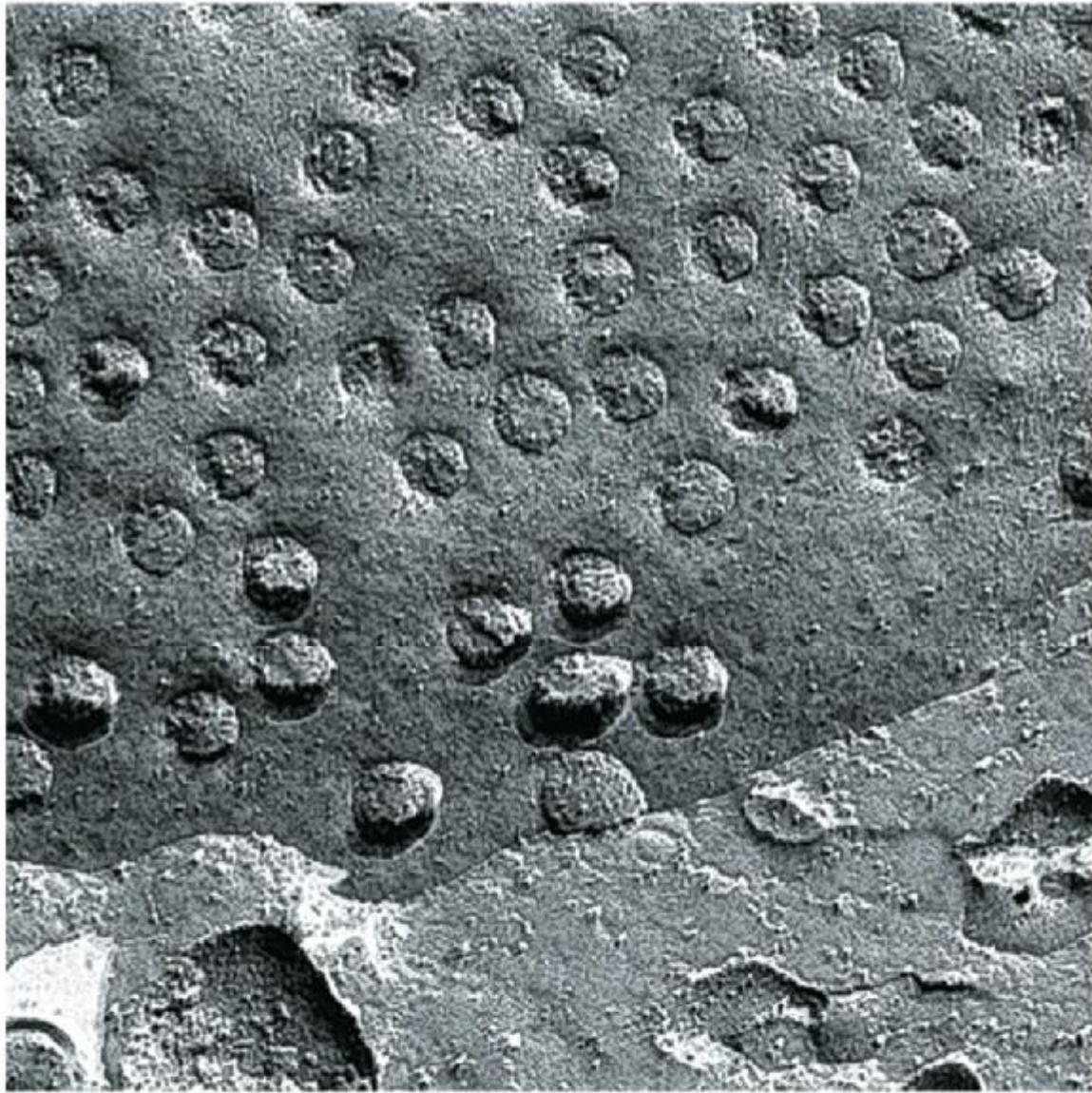


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0.2 μm

Figure 27-42b
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Inner membrane proteins

Phage fd, major coat protein

Met Lys Lys Ser Leu Val Leu Lys Ala Ser Val Ala Val Ala Thr Leu Val Pro Met Leu Ser Phe Ala Ala Glu --

Phage fd, minor coat protein

Met Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro Phe Tyr Ser His Ser Ala Glu --

Periplasmic proteins

Alkaline phosphatase

Met Lys Gln Ser Thr Ile Ala Leu Ala Leu Leu Pro Leu Leu Phe Thr Pro Val Thr Lys Ala Arg Thr --

Leucine-specific binding protein

Met Lys Ala Asn Ala Lys Thr Ile Ile Ala Gly Met Ile Ala Leu Ala Ile Ser His Thr Ala Met Ala Asp Asp --

β -Lactamase of pBR322

Met Ser Ile Gln His Phe Arg Val Ala Leu Ile Pro Phe Phe Ala Ala Phe Cys Leu Pro Val Phe Ala His Pro --

Outer membrane proteins

Lipoprotein

Met Lys Ala Thr Lys Leu Val Leu Gly Ala Val Ile Leu Gly Ser Thr Leu Leu Ala Gly Cys Ser --

LamB

Leu Arg Lys Leu Pro Leu Ala Val Ala Val Ala Ala Gly Val Met Ser Ala Gln Ala Met Ala Val Asp --

OmpA

Met Met Ile Thr Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Ala Pro --

Figure 27-43

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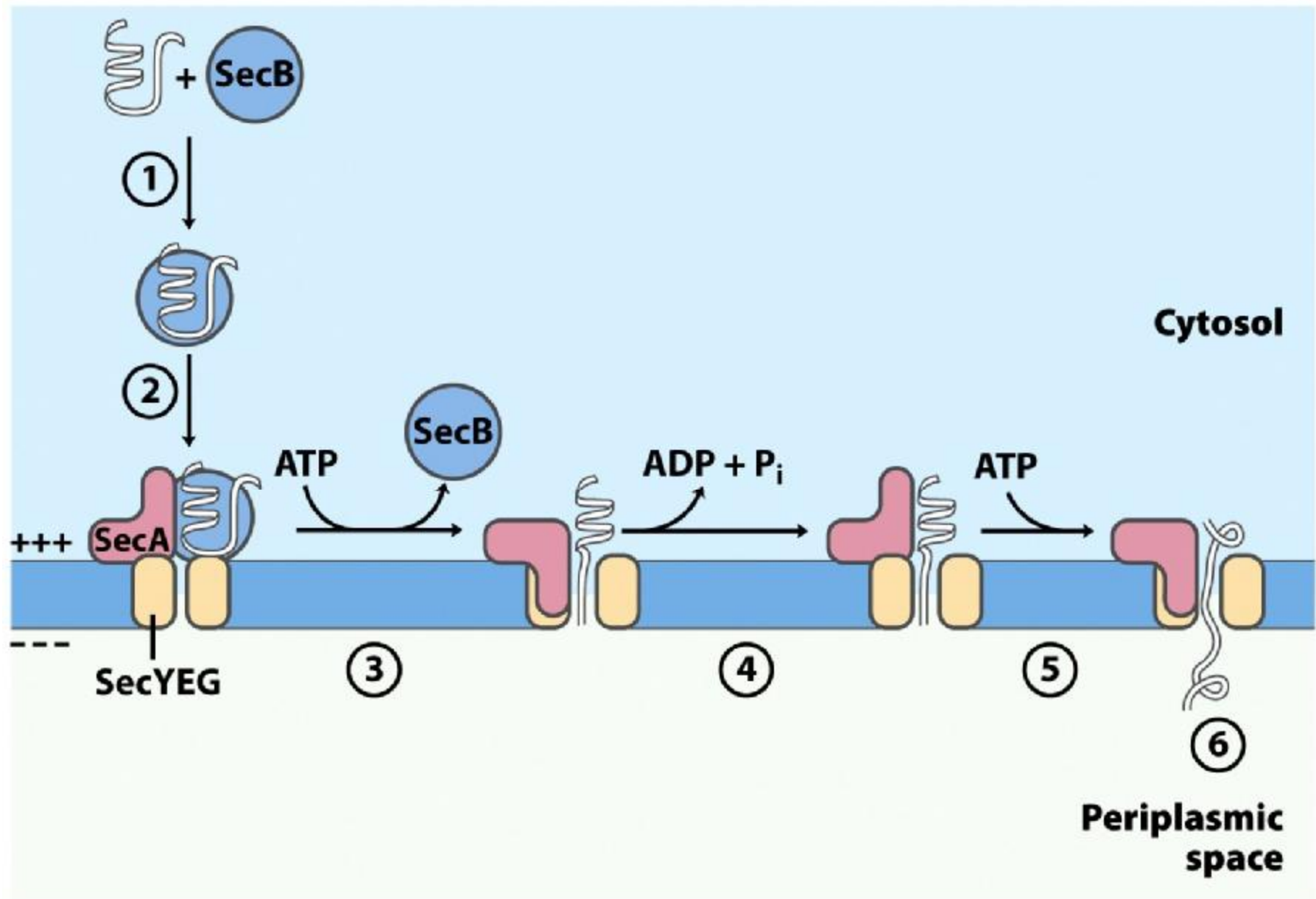


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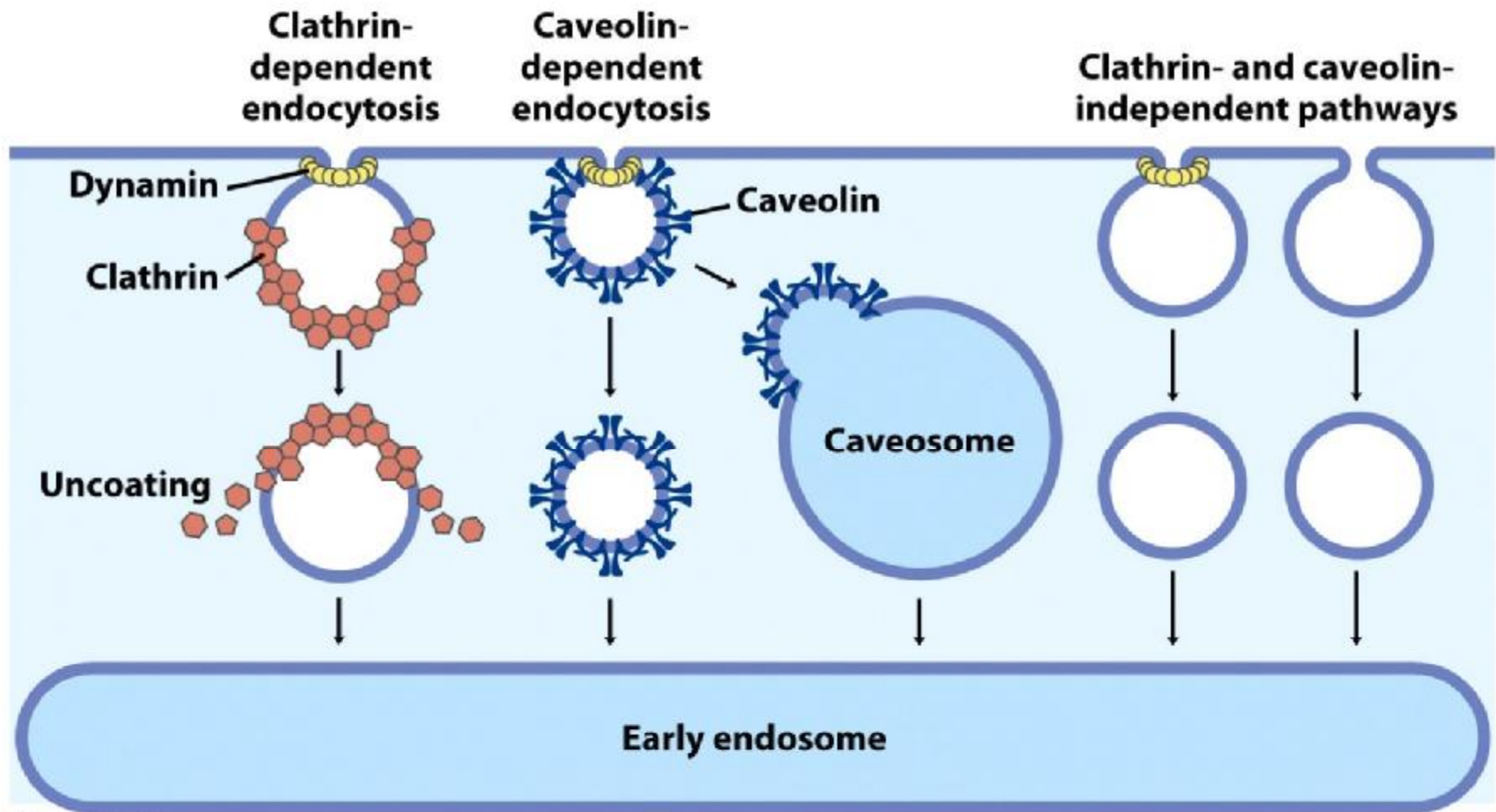


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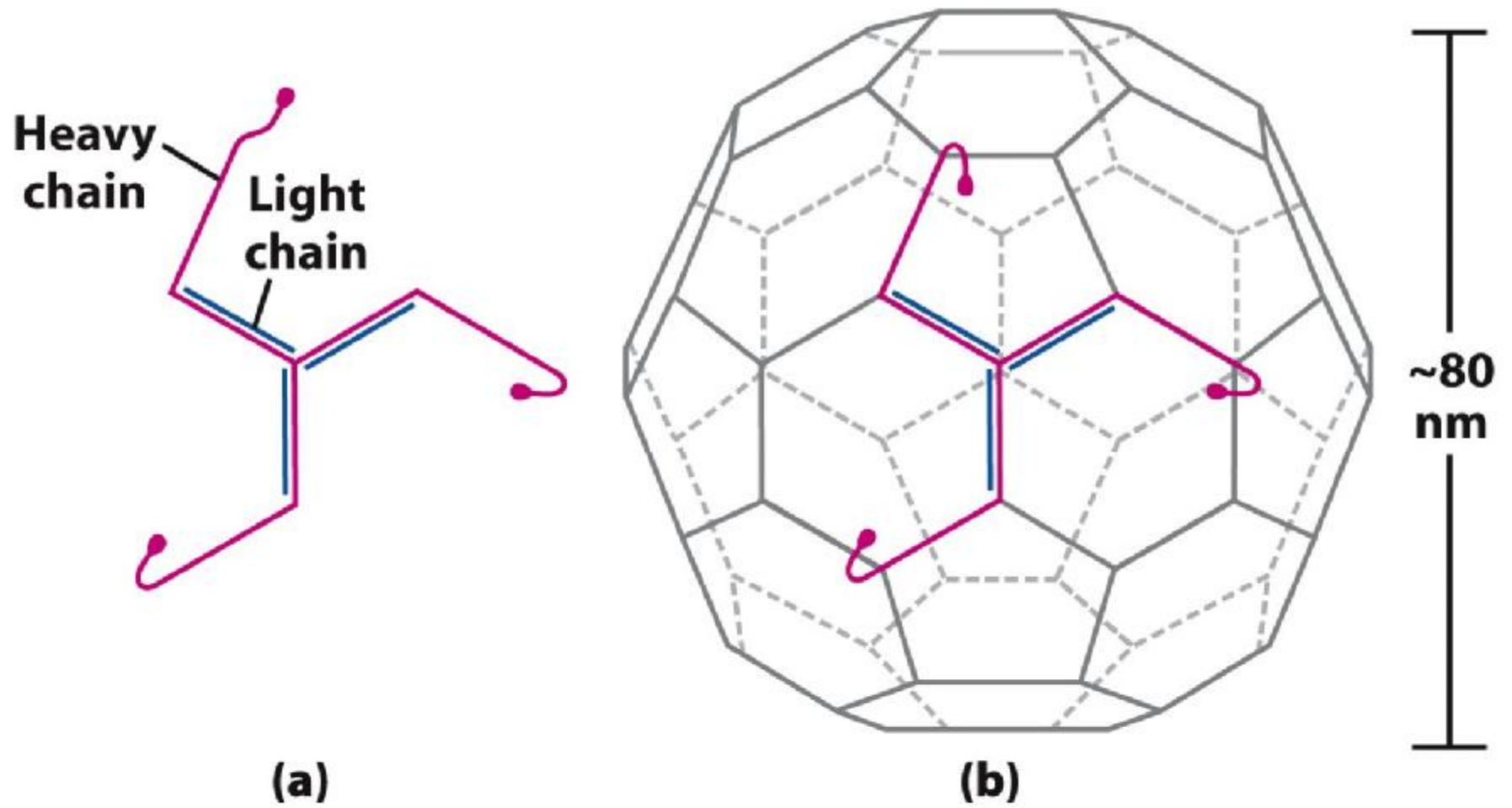
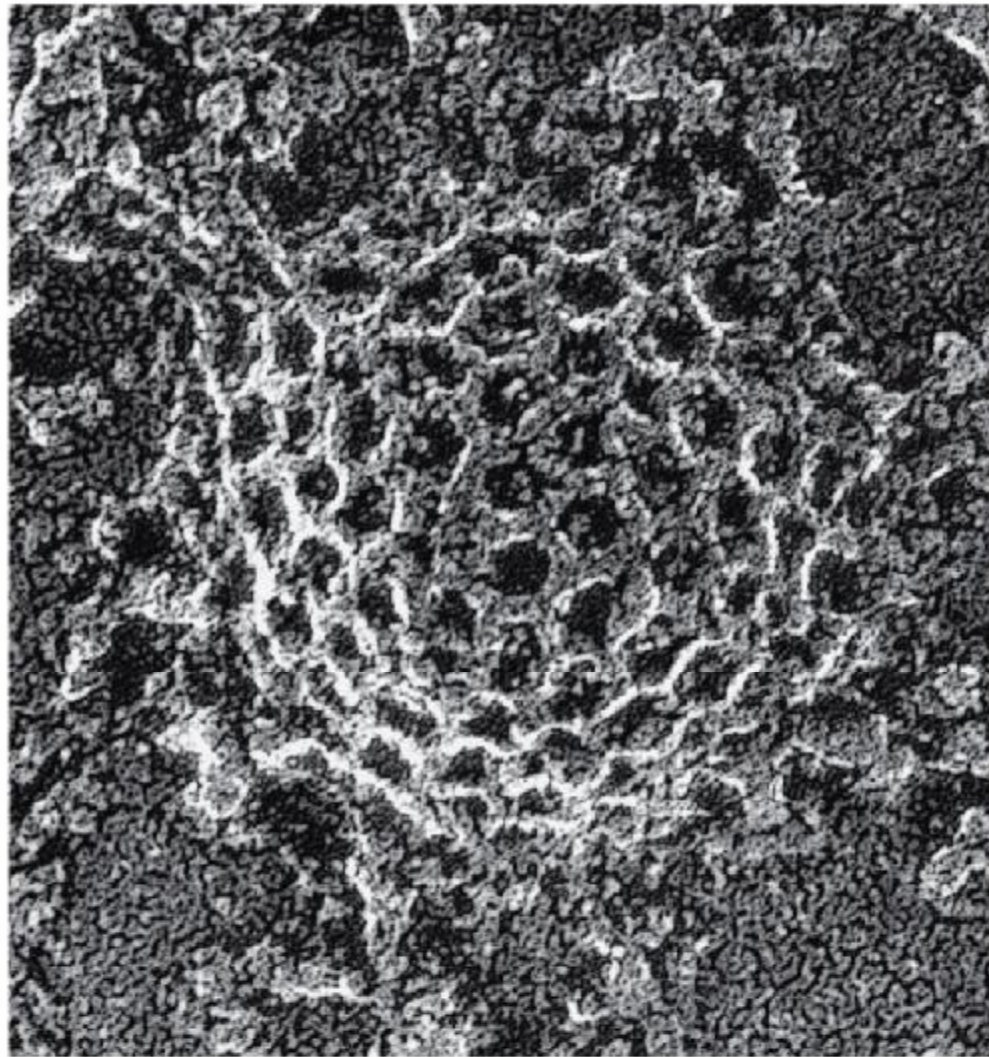


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Figure 27-46c
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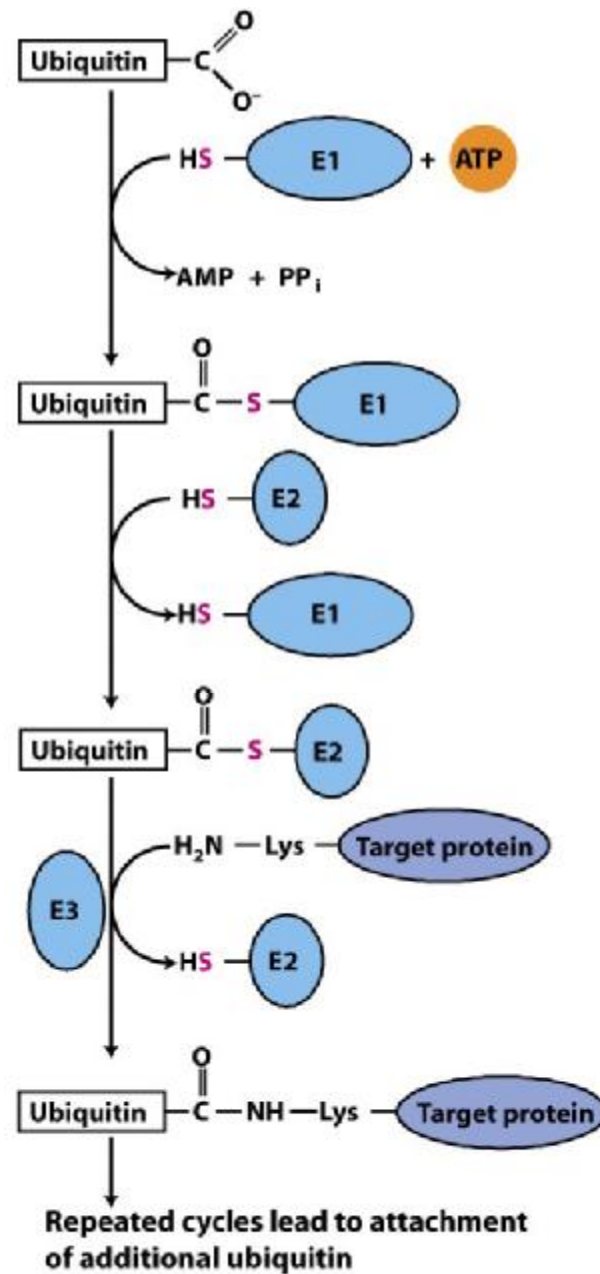


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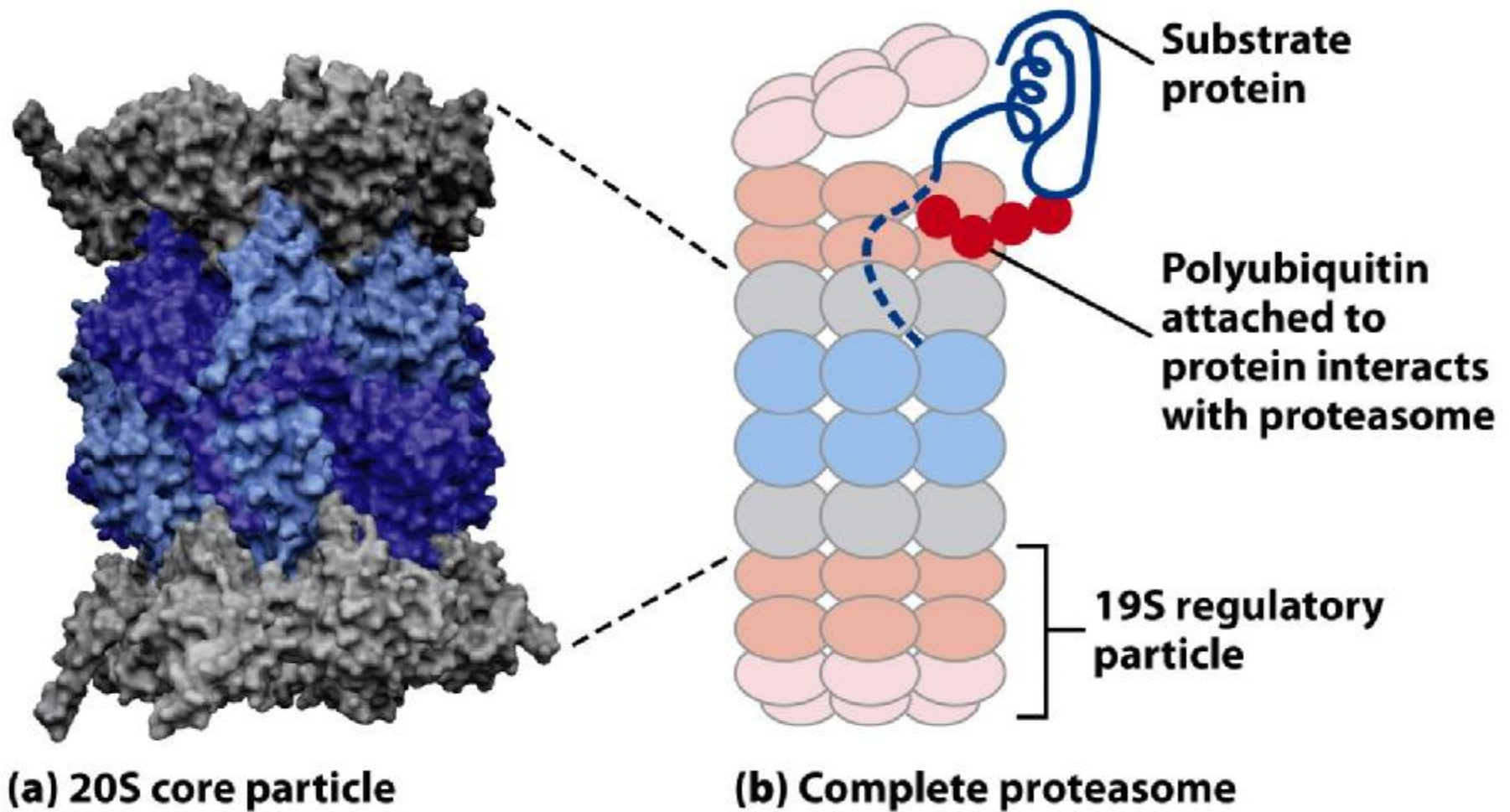


Figure 27-48

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TABLE 27-9**Relationship between Protein Half-Life and Amino-Terminal Amino Acid Residue**

Amino-terminal residue	Half-life*
Stabilizing	
Met, Gly, Ala, Ser, Thr, Val	>20 h
Destabilizing	
Ile, Gln	~30 min
Tyr, Glu	~10 min
Pro	~7 min
Leu, Phe, Asp, Lys	~3 min
Arg	~2 min

Source: Modified from Bachmair, A., Finley, D., & Varshavsky, A. (1986) In vivo half-life of a protein is a function of its amino-terminal residue. *Science* 234, 179—186.

*Half-lives were measured in yeast for the β -galactosidase protein modified so that in each experiment it had a different amino-terminal residue. Half-lives may vary for different proteins and in different organisms, but this general pattern appears to hold for all organisms.

Table 27-9

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