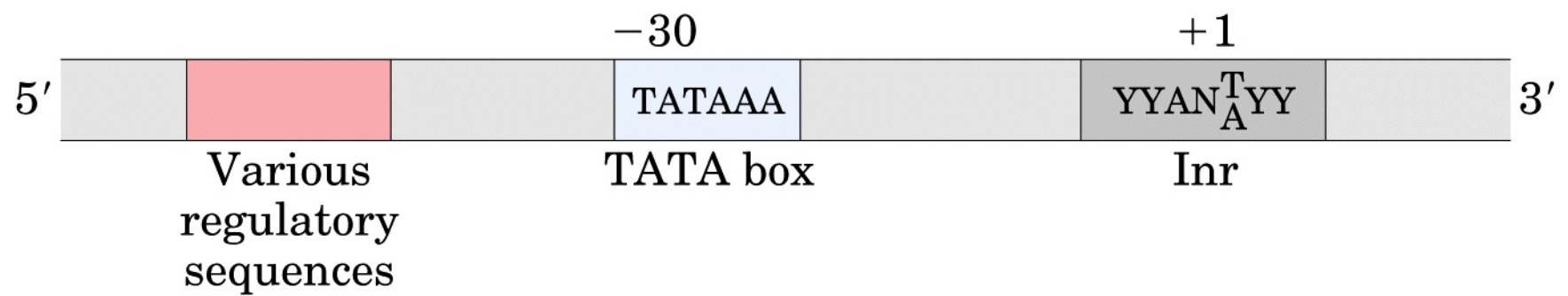


# TRANSCRIPCIÓN EN EUCARIONTES



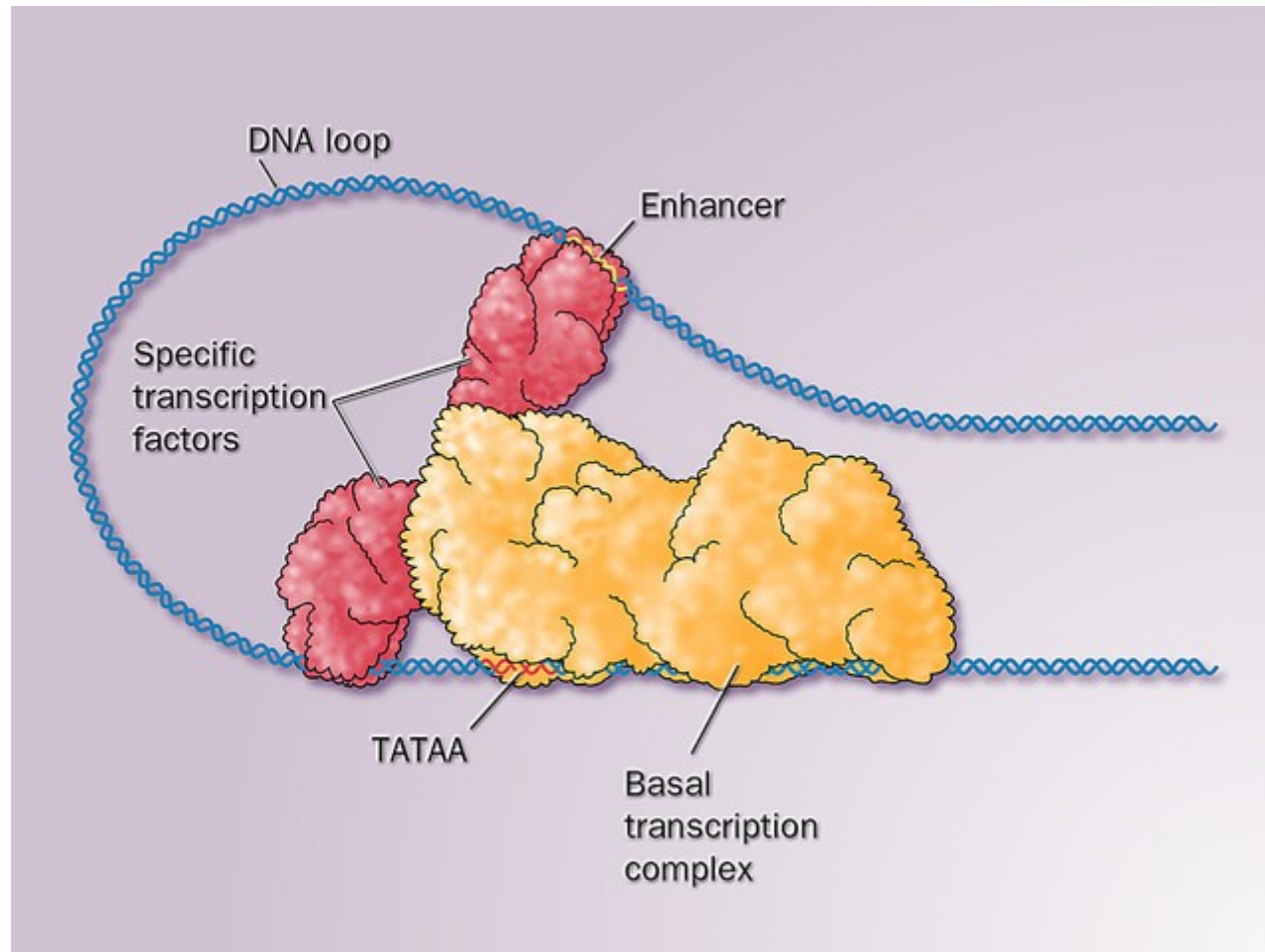
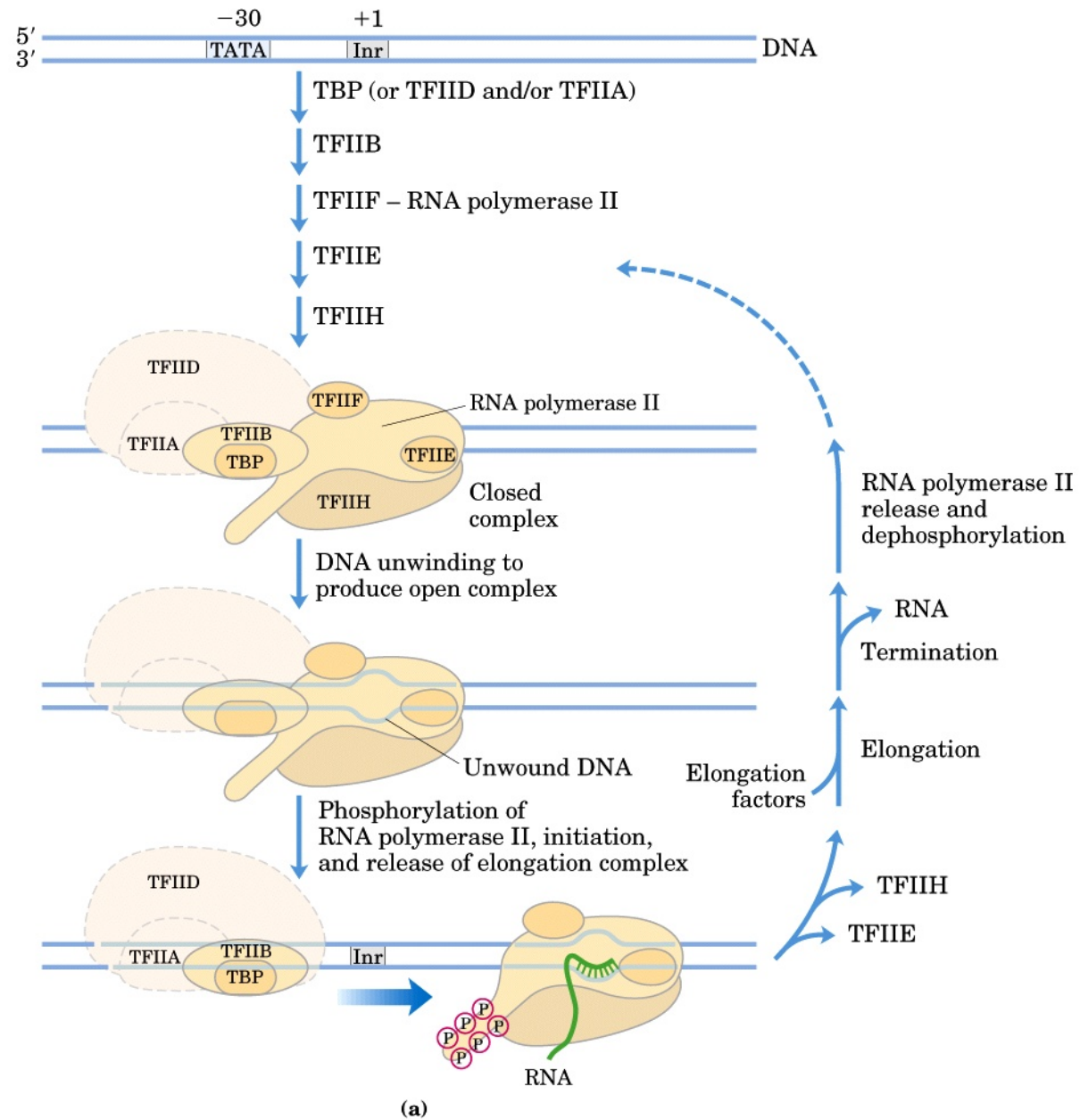


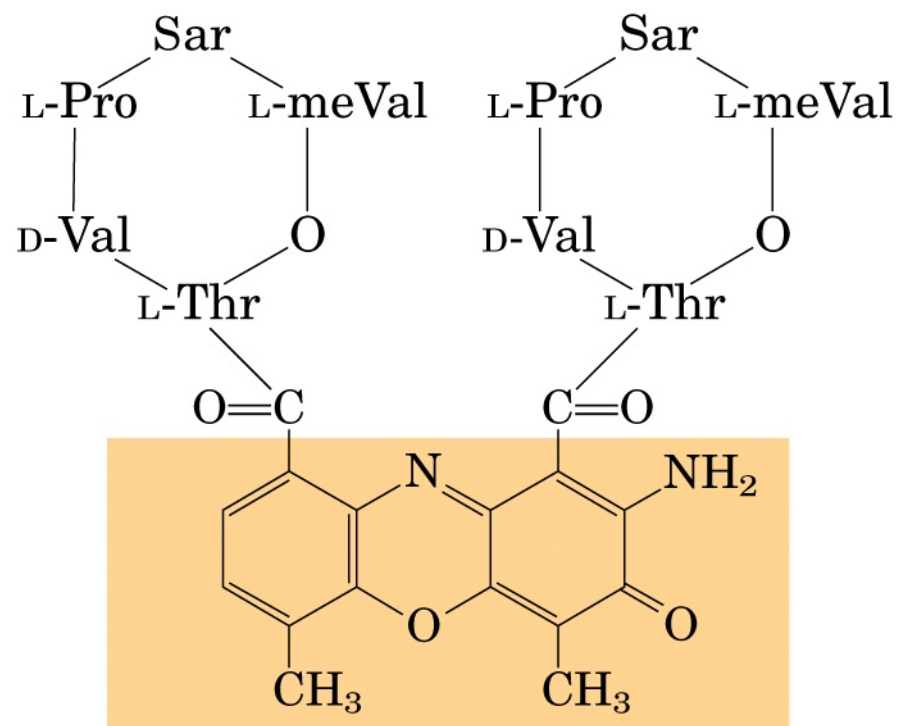
table 26–1

Proteins Required for Transcription at the RNA Polymerase II Promoters of Eukaryotes			
Transcription factor	Number of subunits	Subunit $M_r$	Functions
<b>Initiation</b>			
RNA polymerase II	12	10,000–220,000	Catalyzes RNA synthesis
TBP (TATA-binding protein)	1	38,000	Specifically recognizes the TATA box
TFIIA	3	12,000, 19,000, 35,000	Stabilizes binding of TFIIB and TBP to the promoter
TFIIB	1	35,000	Binds to TBP; recruits RNA polymerase–TFIIF complex
TFIID	12	15,000–250,000	Interacts with positive and negative regulatory proteins
TFIIE	2	34,000, 57,000	Recruits TFIIH; ATPase and helicase activities
TFIIF	2	30,000, 74,000	Binds tightly to RNA polymerase II; binds to TFIIB and prevents binding of RNA polymerase to nonspecific DNA sequences
TFIIH	12	35,000–89,000	Unwinds DNA at promoter; phosphorylates RNA polymerase; recruits nucleotide-excision repair complex
<b>Elongation*</b>			
ELL <sup>†</sup>	1	80,000	
P-TEFb	2	43,000, 124,000	
SII (TFIIS)	1	38,000	
Elongin (SIID)	3	15,000, 18,000, 110,000	

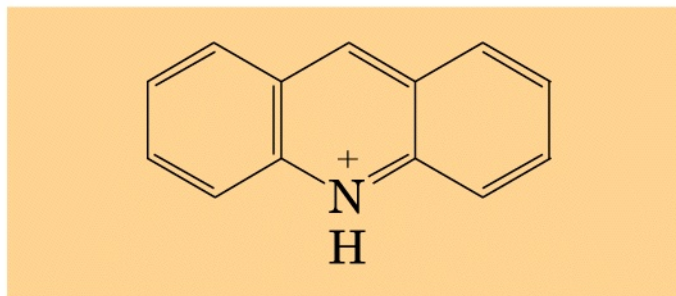
\*All elongation factors suppress the pausing or arrest of transcription by the RNA polymerase II – TFIIF complex.

<sup>†</sup>The name is derived from the term *eleven-nineteen lysine-rich leukemia*. The gene for the factor ELL is the site of chromosomal recombination events frequently associated with the cancerous condition known as acute myeloid leukemia.

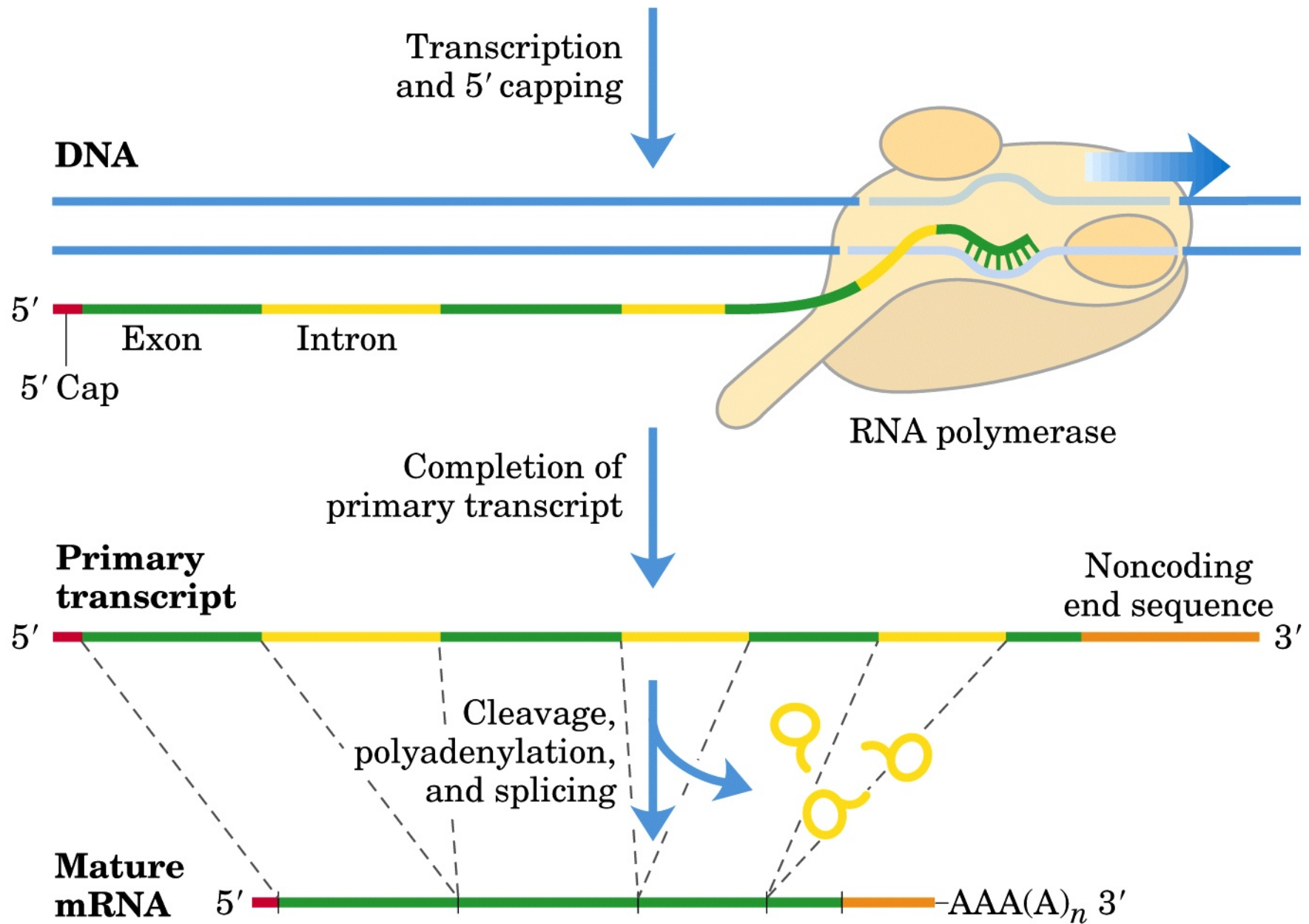


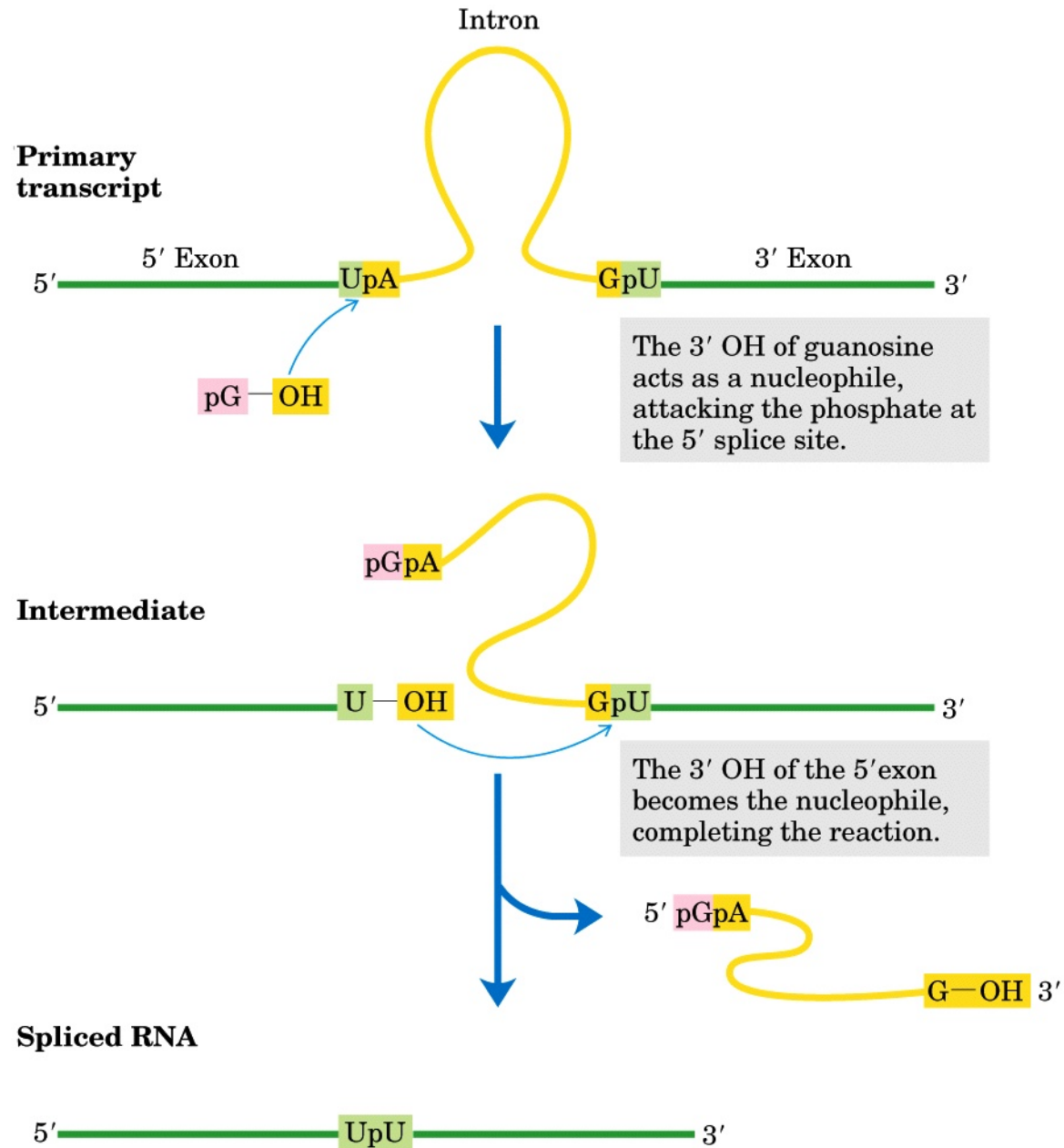


Actinomycin D

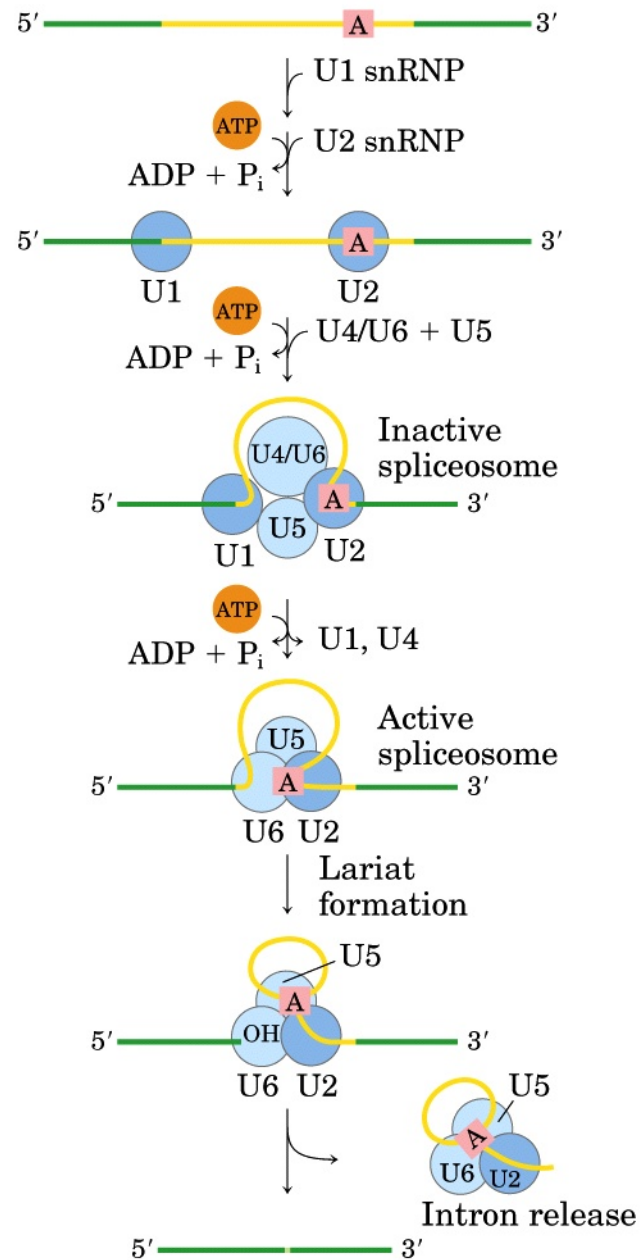


Acridine

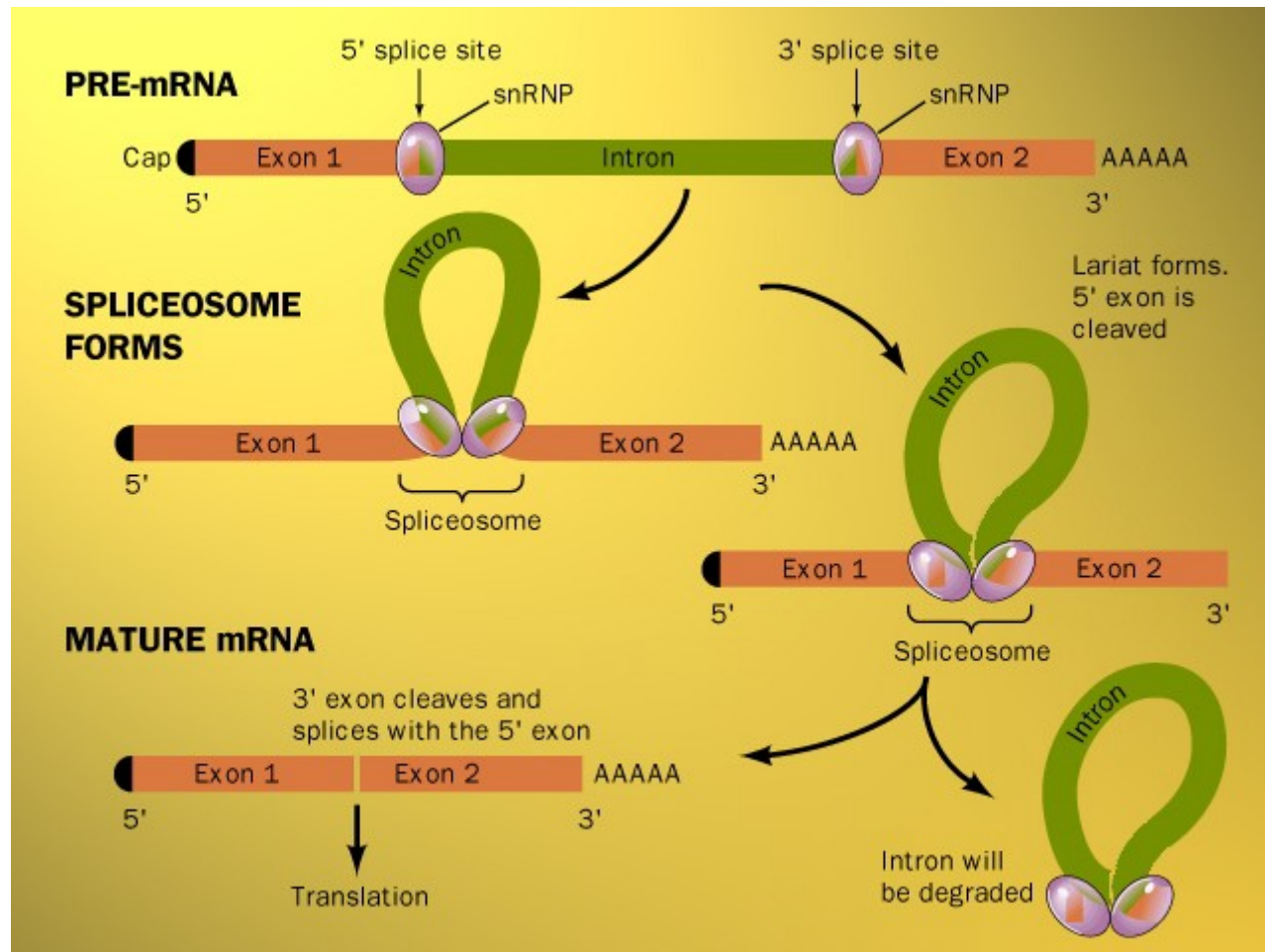


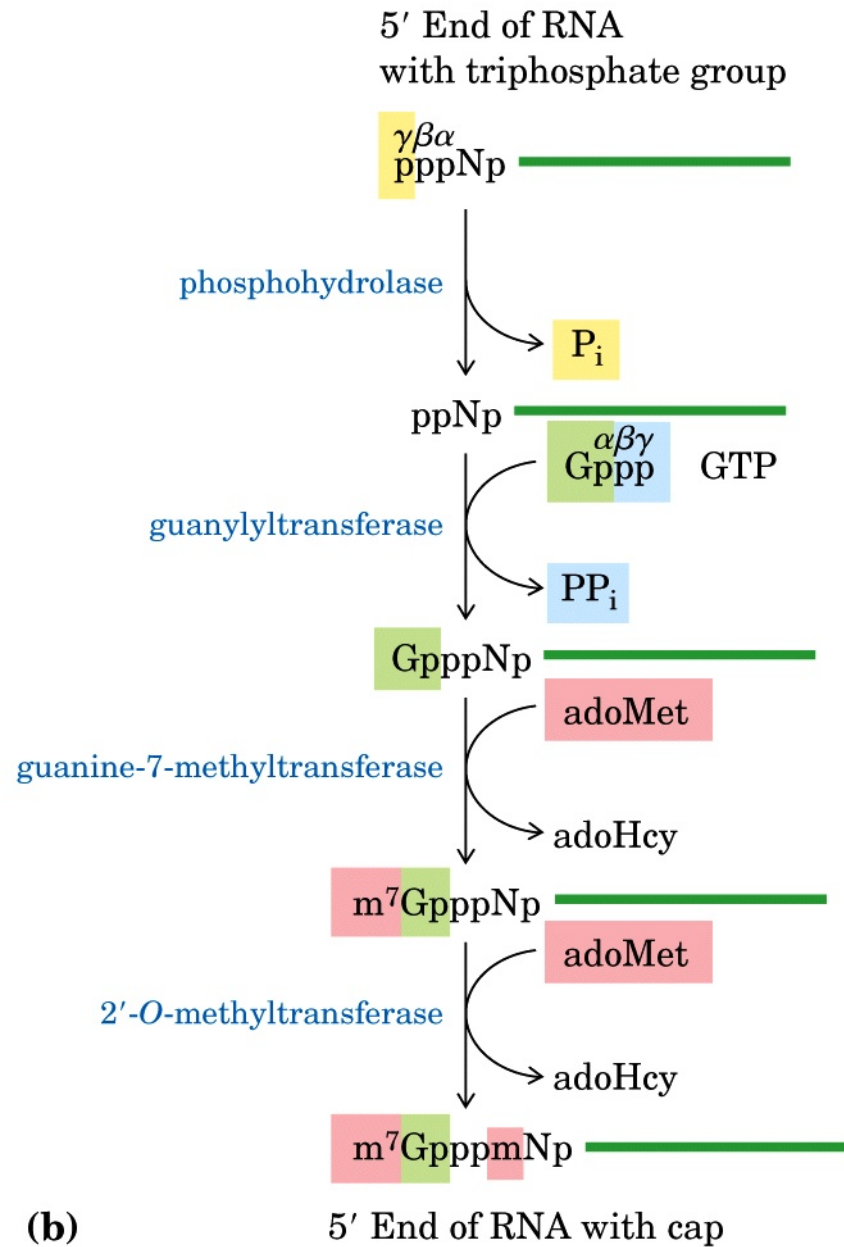


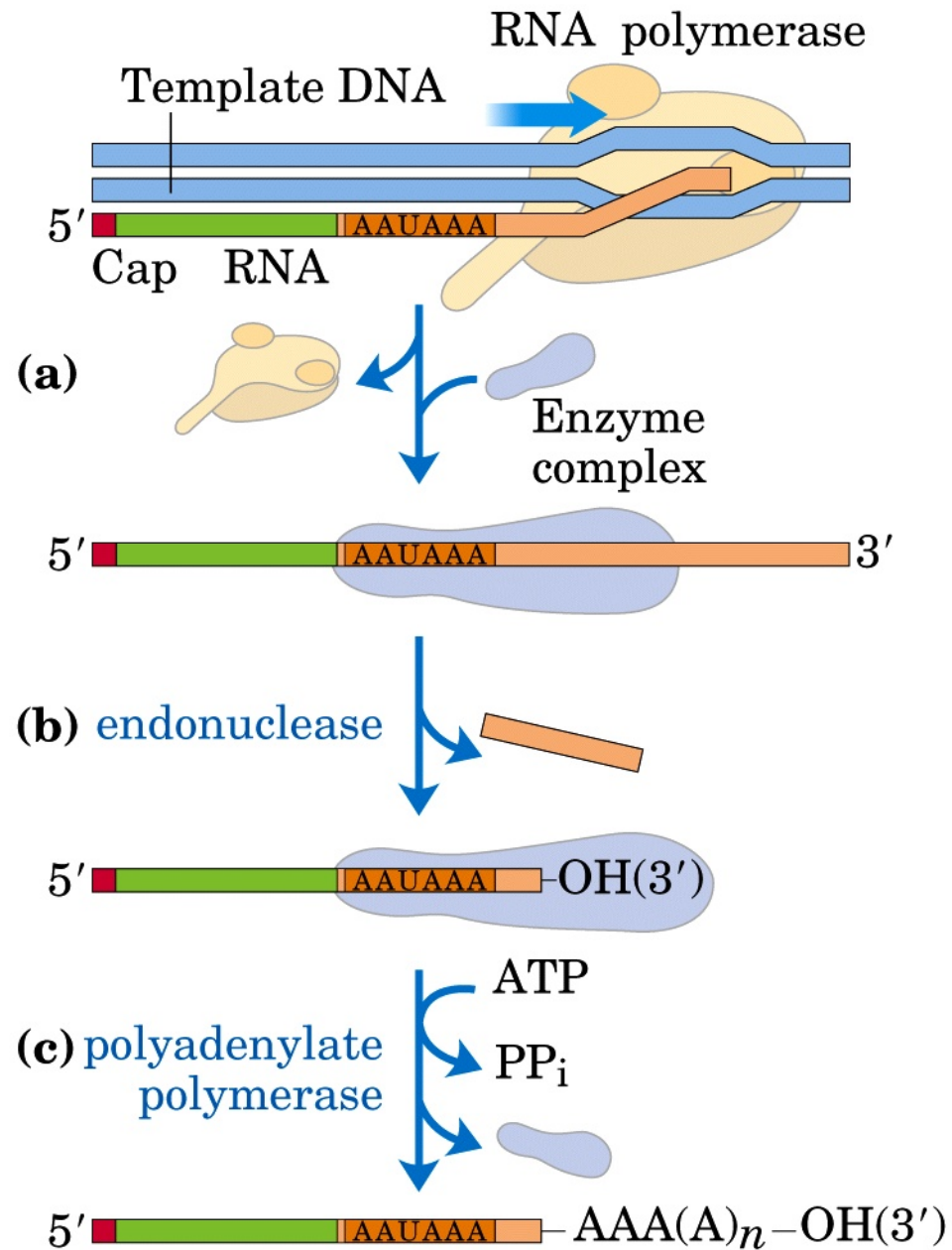


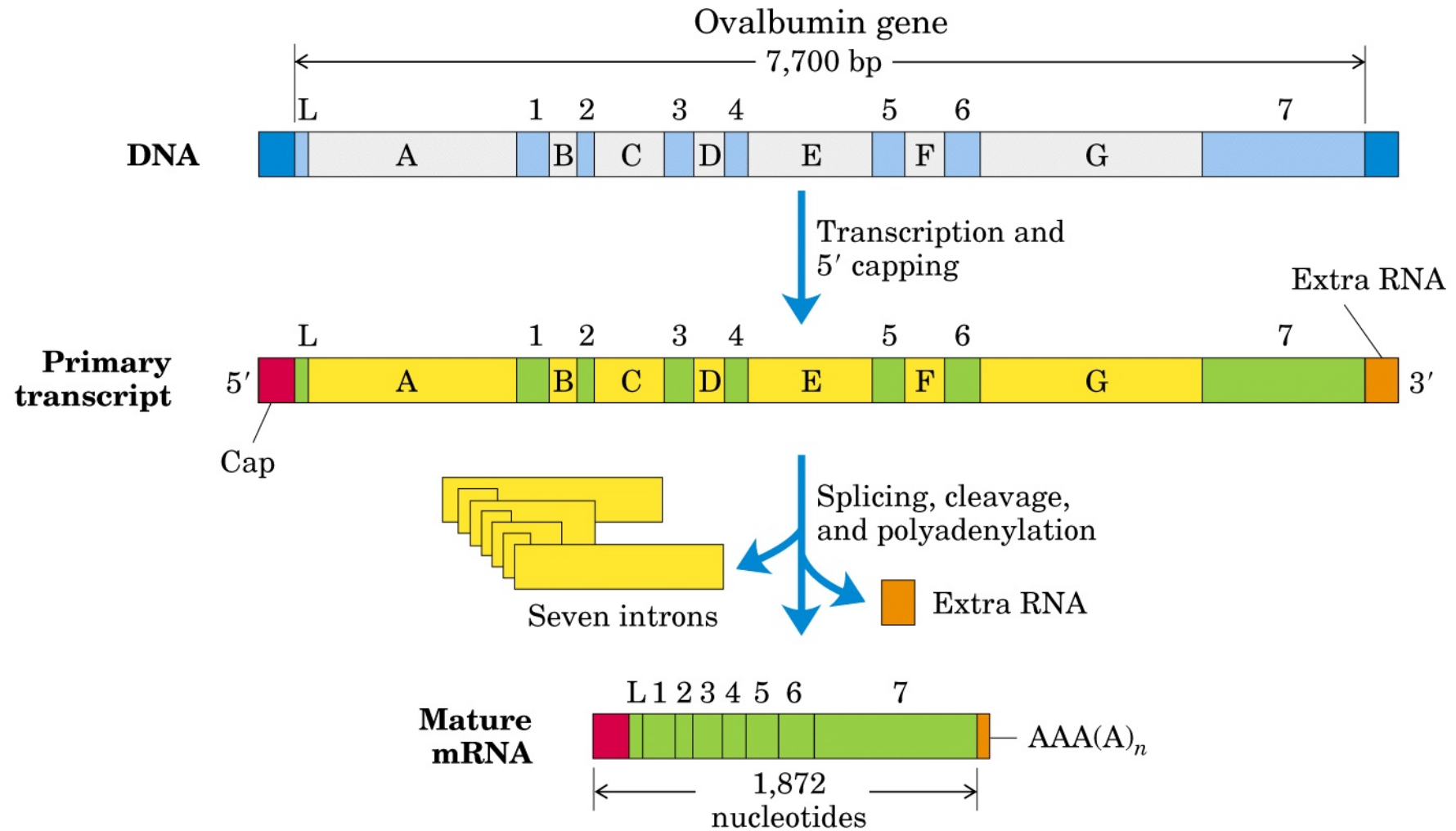


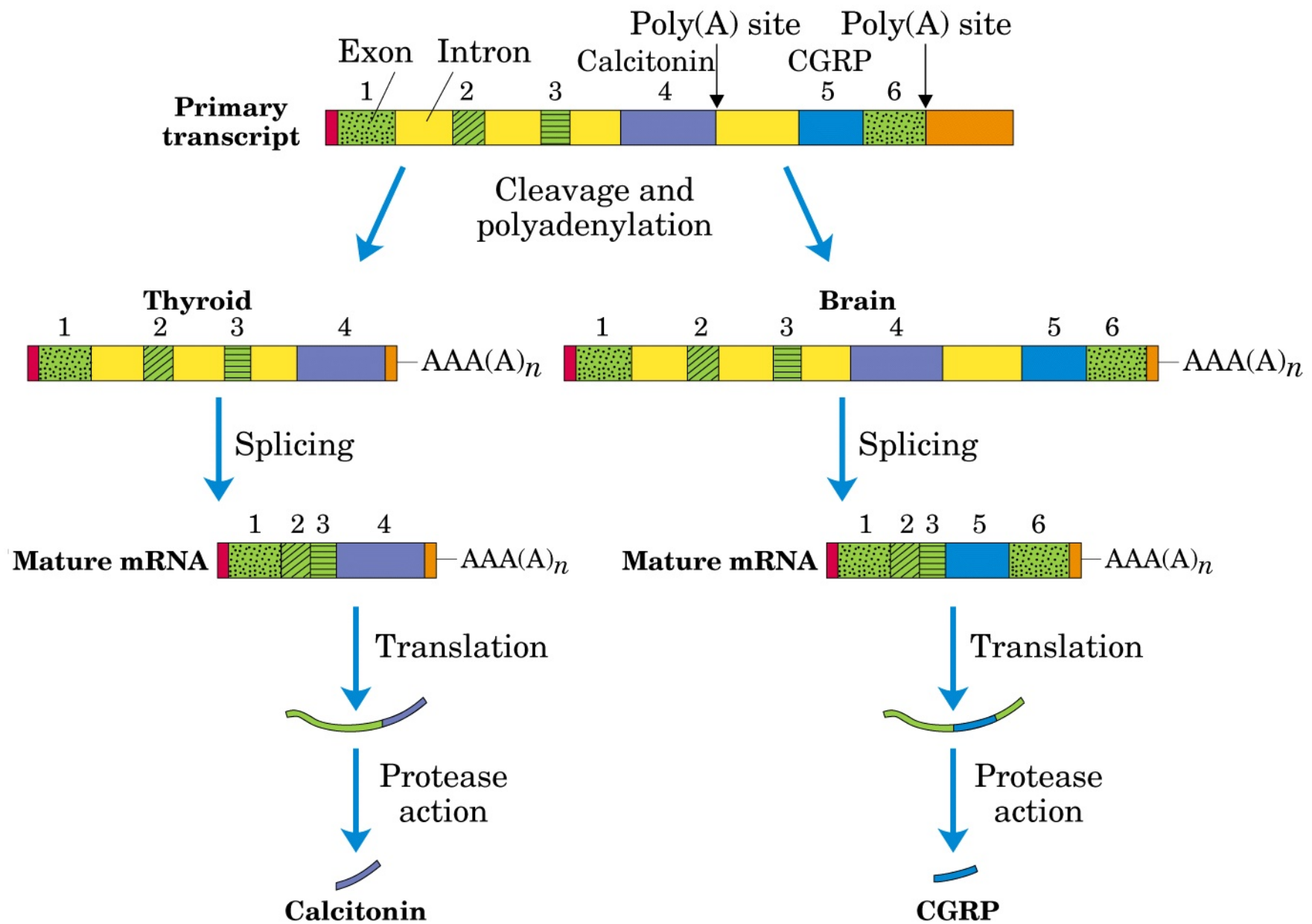
# pre-RNA<sub>m</sub> → RNA<sub>m</sub>

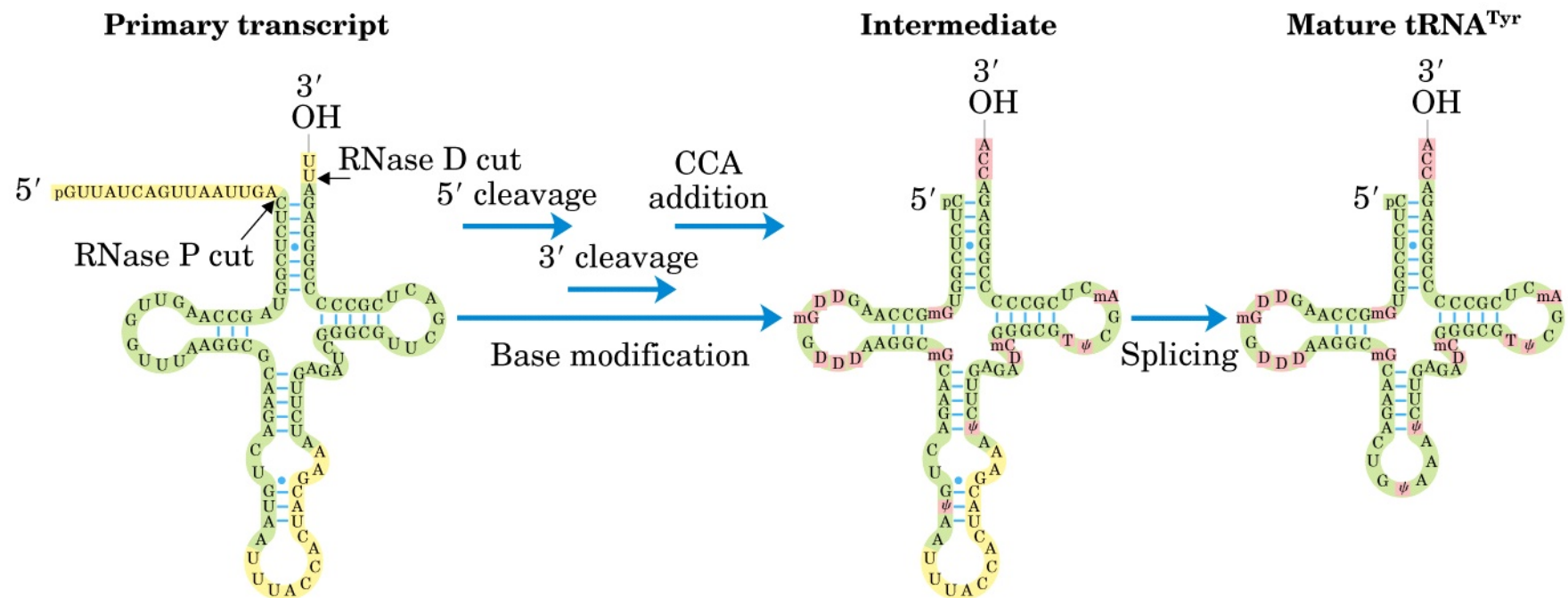













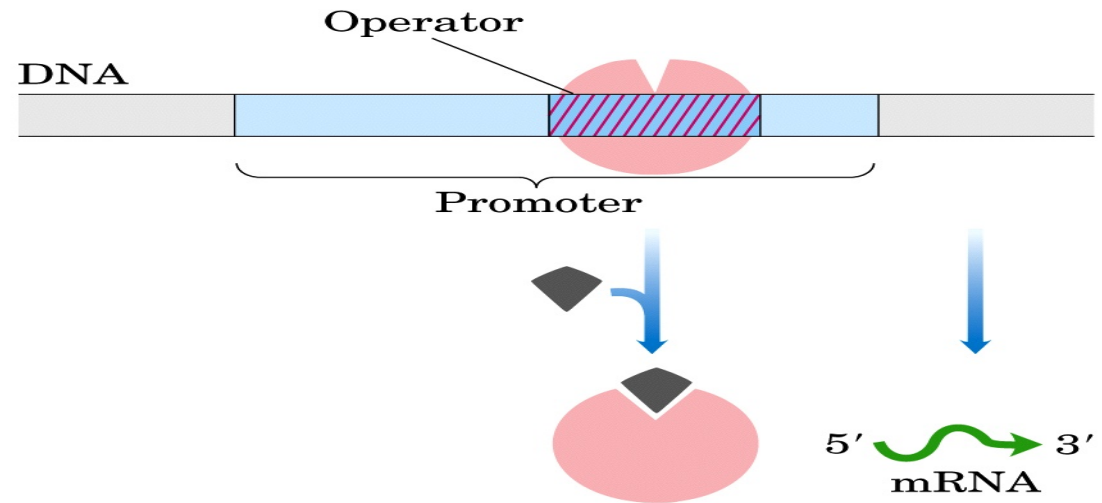
# REGULACION GENICA



**Negative regulation**  
(bound repressor inhibits transcription)


(a)

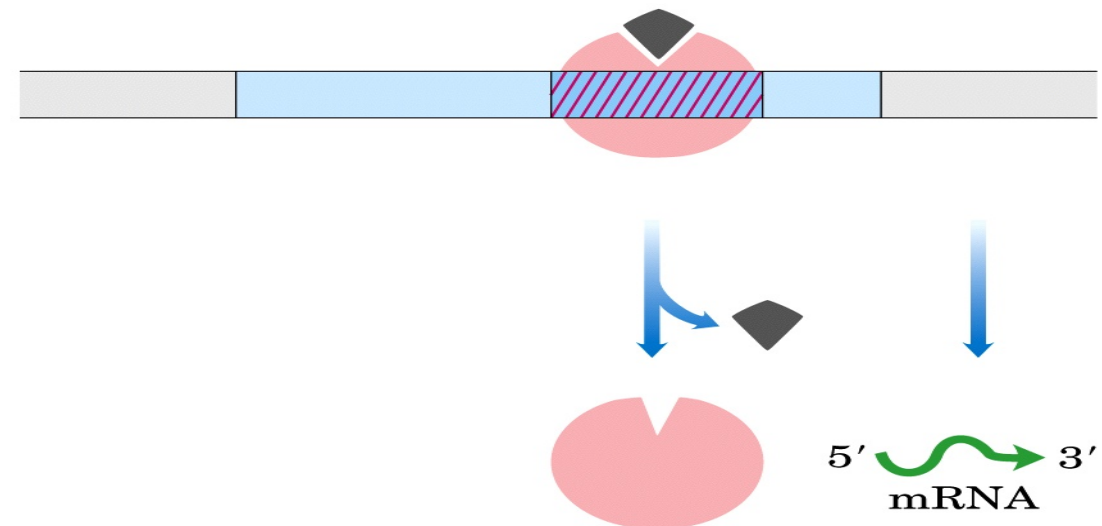
Molecular signal  
() causes *dissociation*  
of regulatory protein  
from DNA




**Negative regulation**  
(bound repressor inhibits transcription)

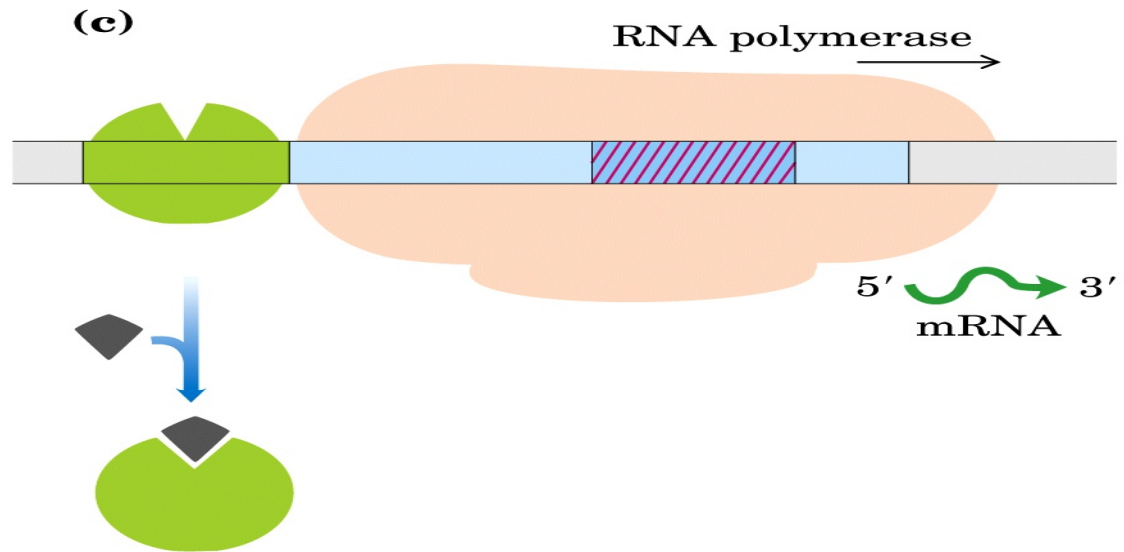
(b)

Molecular signal  
() causes *binding*  
of regulatory protein  
to DNA



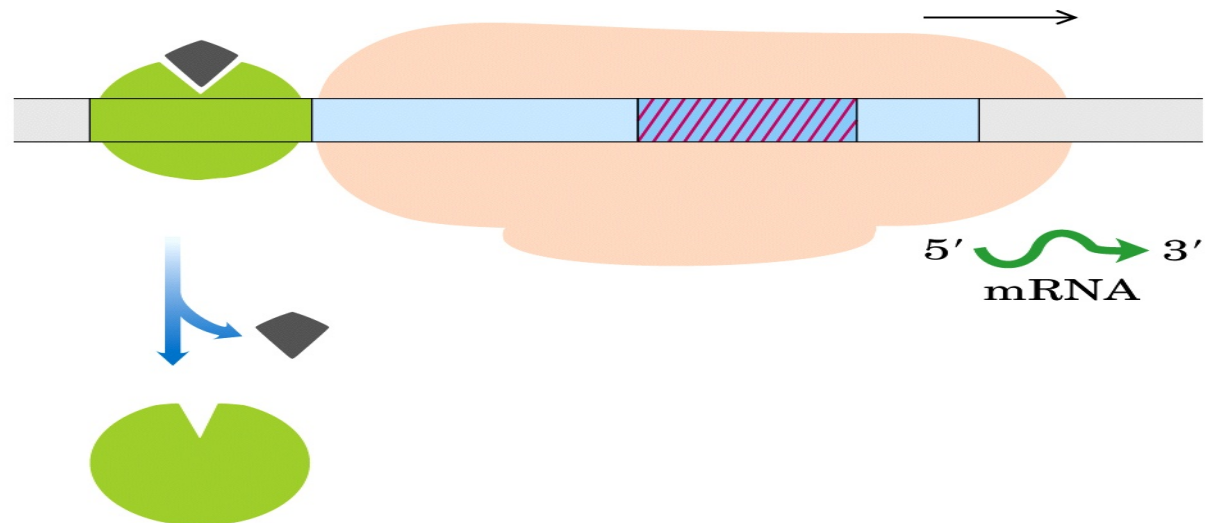
**Positive regulation**  
(bound activator facilitates transcription)

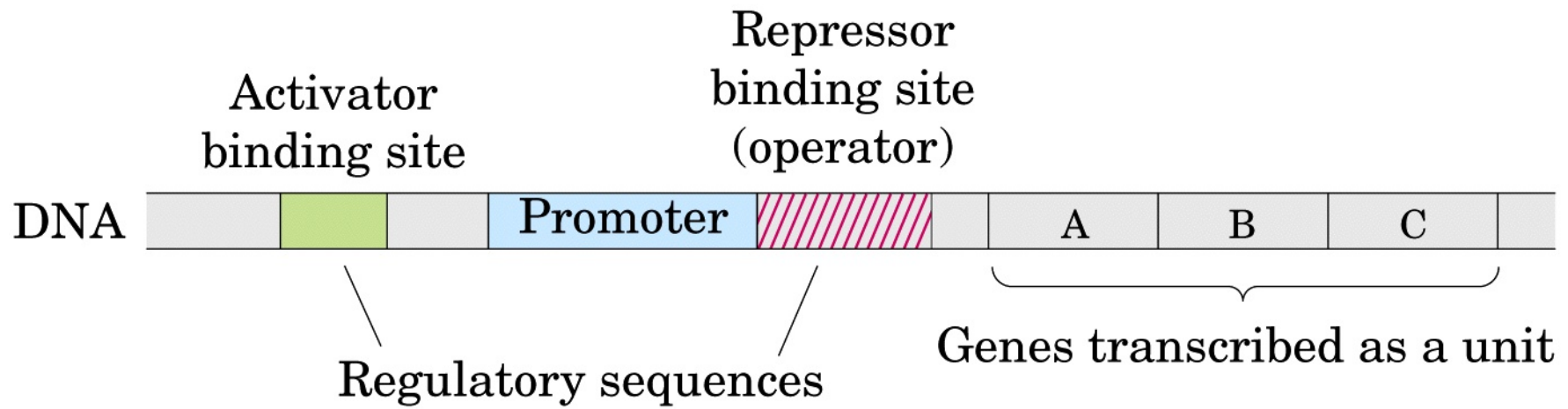
Molecular signal  
() causes *dissociation*  
of regulatory protein  
from DNA

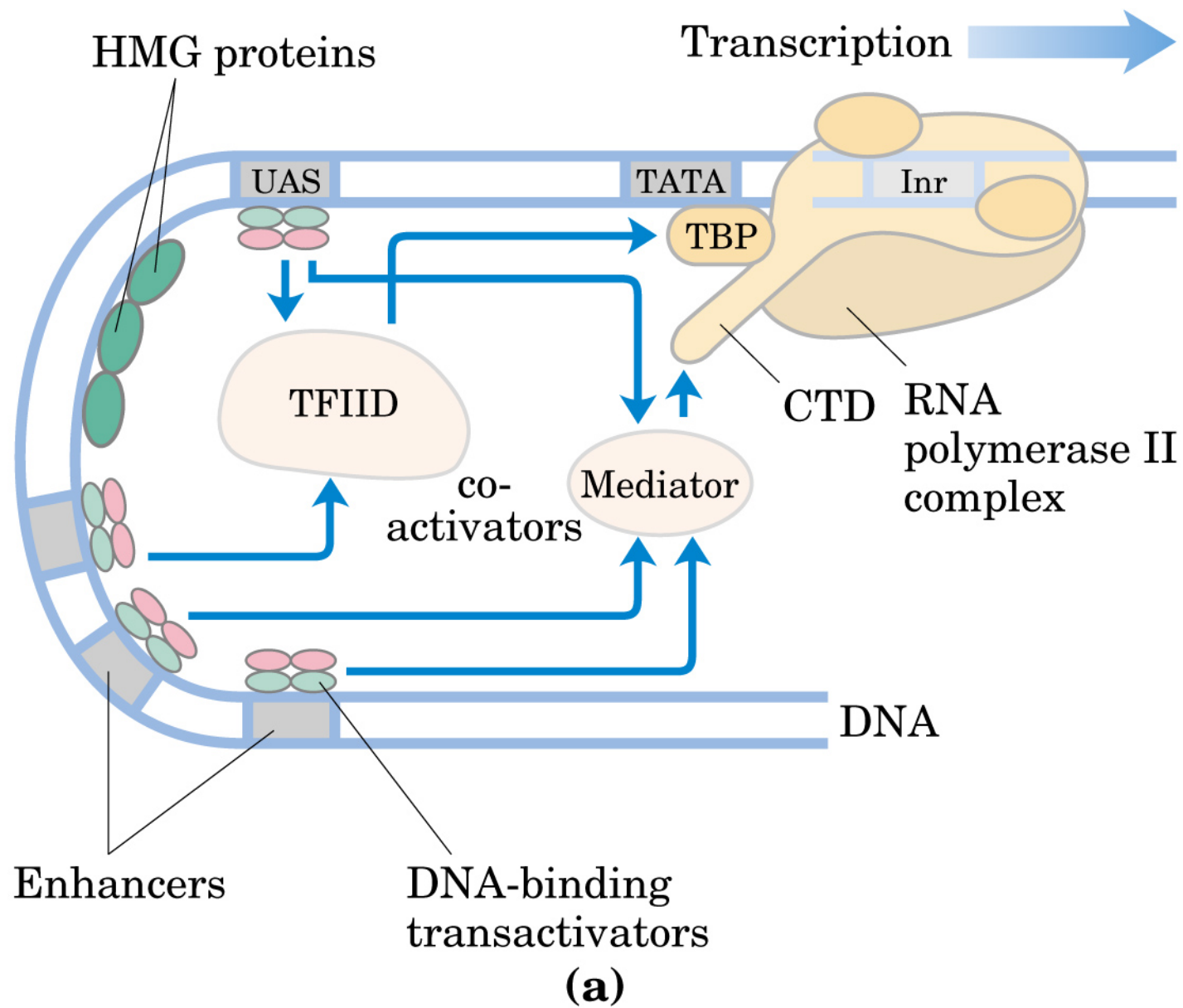


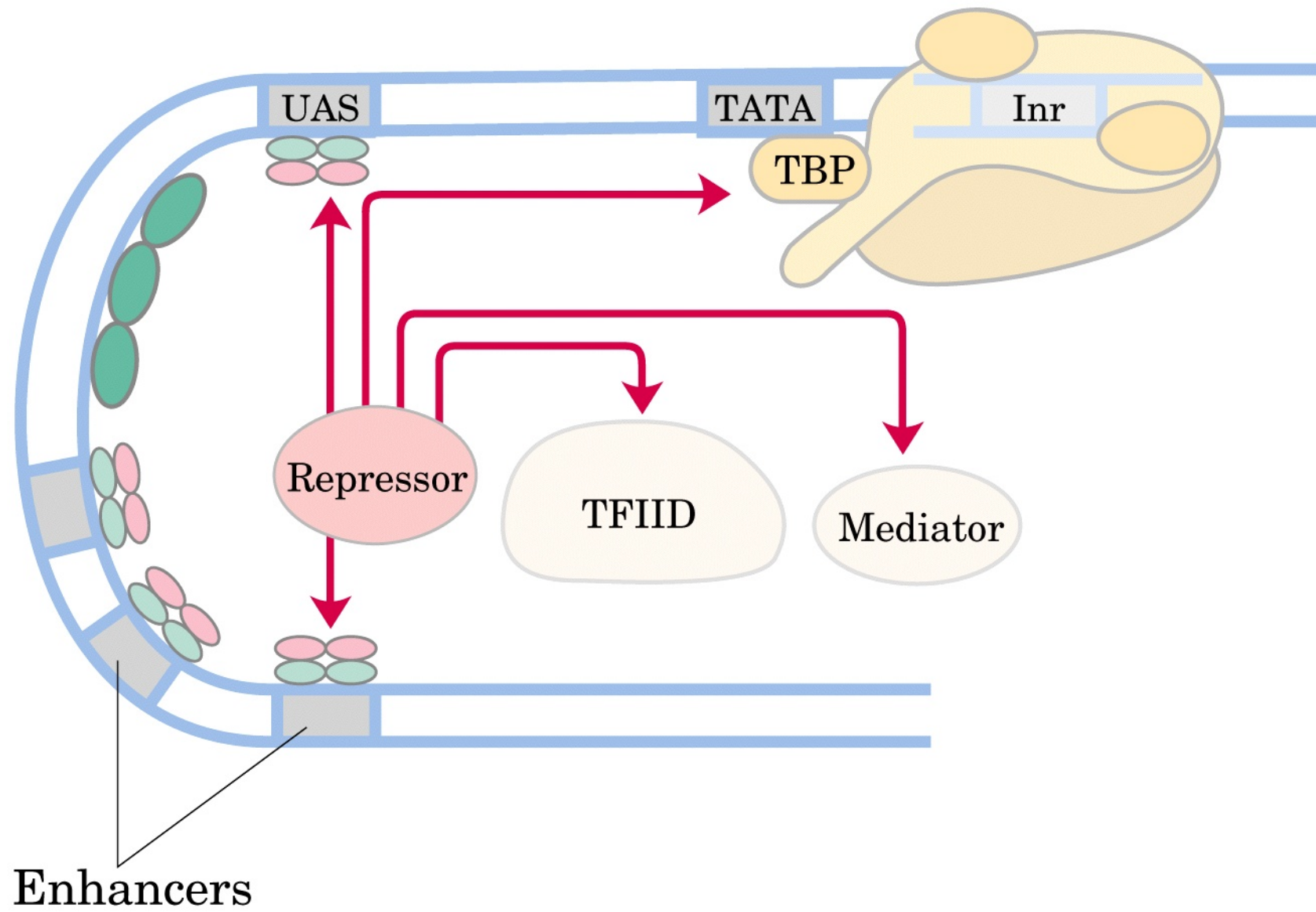
**Positive regulation**  
(bound activator facilitates transcription)

Molecular signal  
() causes *binding*  
of regulatory protein  
to DNA





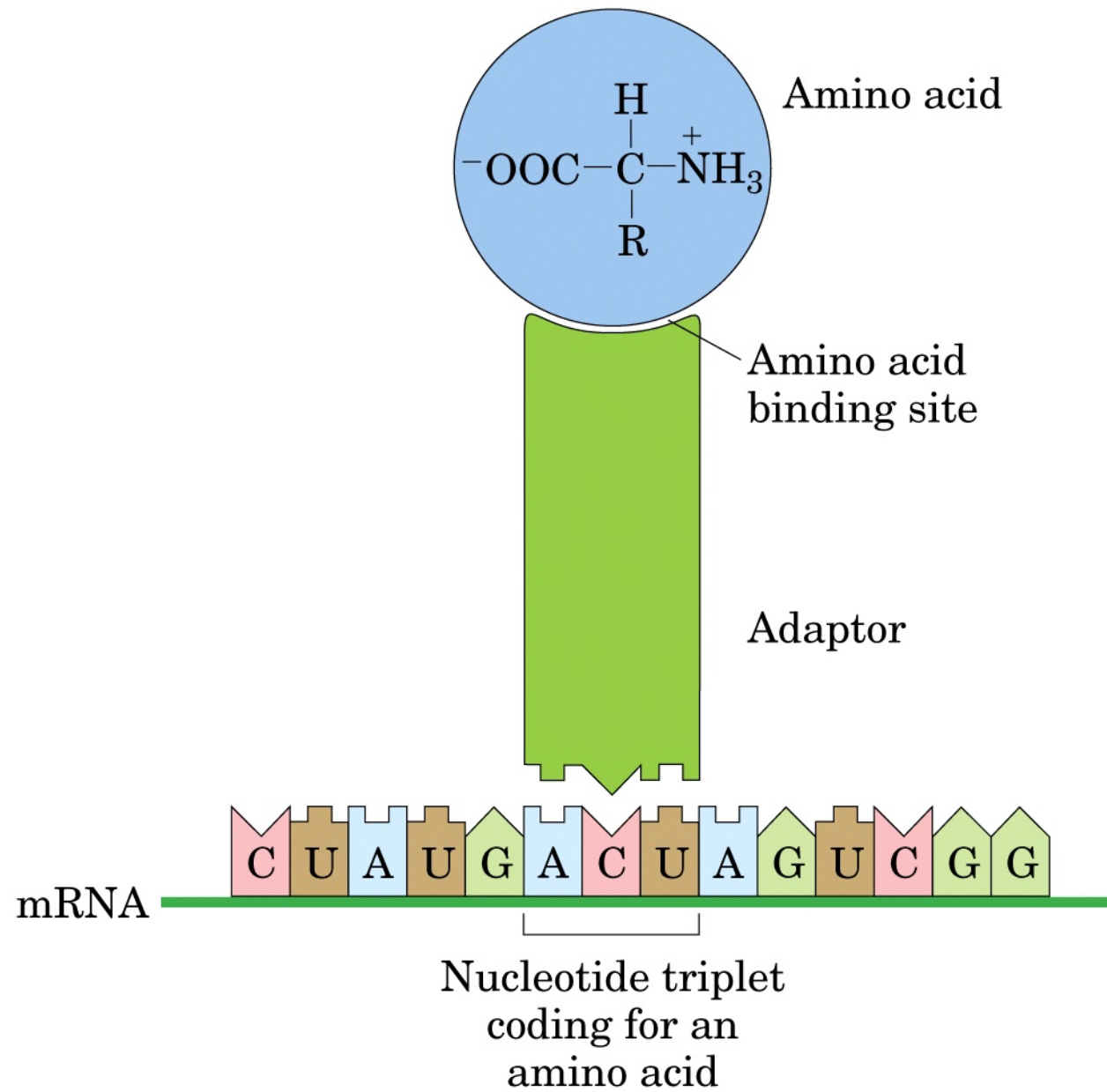




(b)

FIN

# BIOSINTESIS DE PROTEINAS

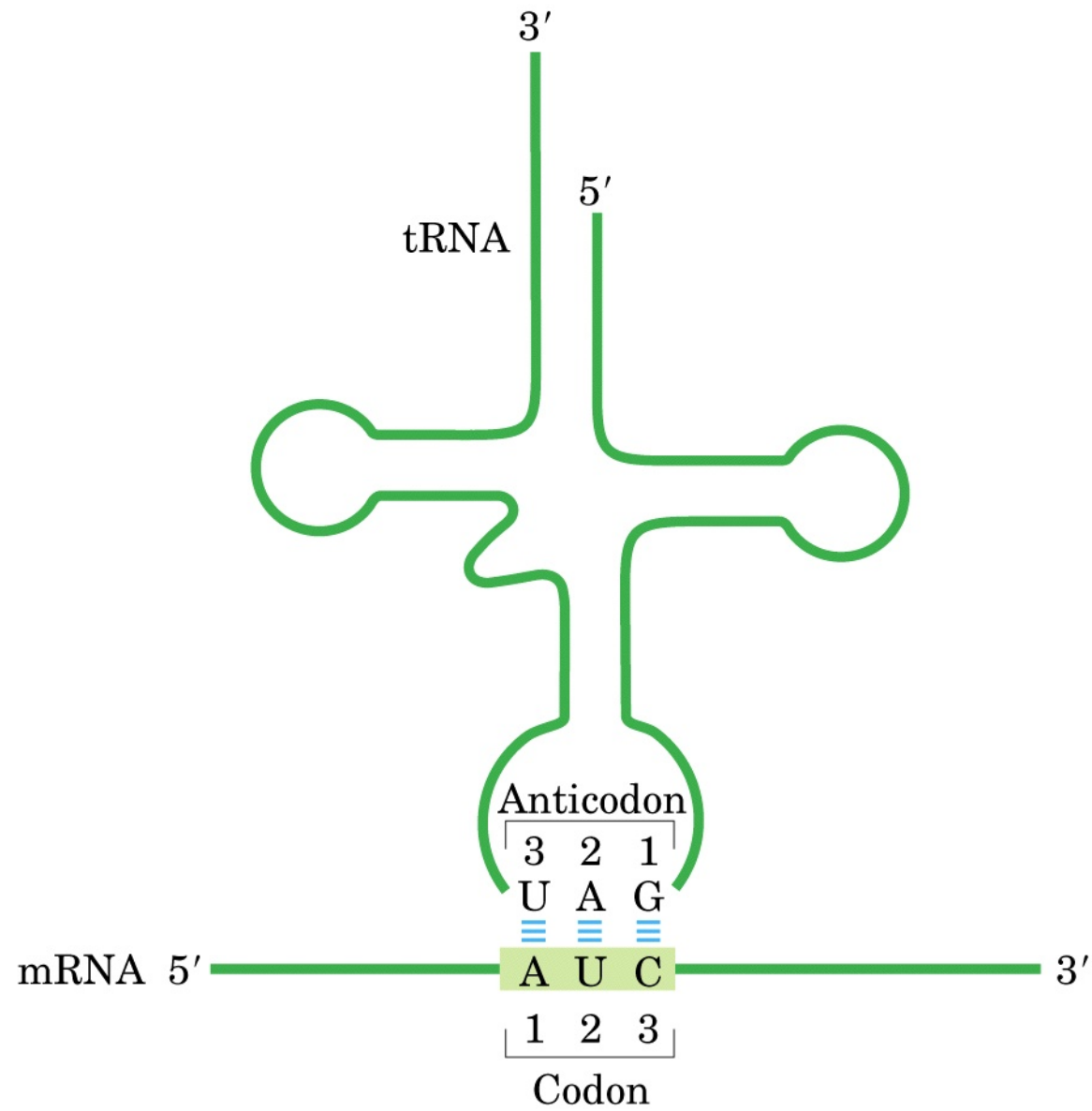




		Second letter of codon							
		U		C		A		G	
		U	C	U	C	U	C	U	C
First letter of codon (5' end)	U	UUU	Phe	UCU	Ser	UAU	Tyr	UGU	Cys
		UUC	Phe	UCC	Ser	UAC	Tyr	UGC	Cys
		UUA	Leu	UCA	Ser	UAA	Stop	UGA	Stop
		UUG	Leu	UCG	Ser	UAG	Stop	UGG	Trp
	C	CUU	Leu	CCU	Pro	CAU	His	CGU	Arg
		CUC	Leu	CCC	Pro	CAC	His	CGC	Arg
		CUA	Leu	CCA	Pro	CAA	Gln	CGA	Arg
		CUG	Leu	CCG	Pro	CAG	Gln	CGG	Arg
	A	AUU	Ile	ACU	Thr	AAU	Asn	AGU	Ser
		AUC	Ile	ACC	Thr	AAC	Asn	AGC	Ser
		AUA	Ile	ACA	Thr	AAA	Lys	AGA	Arg
		AUG	Met	ACG	Thr	AAG	Lys	AGG	Arg
	G	GUU	Val	GCU	Ala	GAU	Asp	GGU	Gly
		GUC	Val	GCC	Ala	GAC	Asp	GGC	Gly
		GUA	Val	GCA	Ala	GAA	Glu	GGA	Gly
		GUG	Val	GCG	Ala	GAG	Glu	GGG	Gly

table 27-4

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

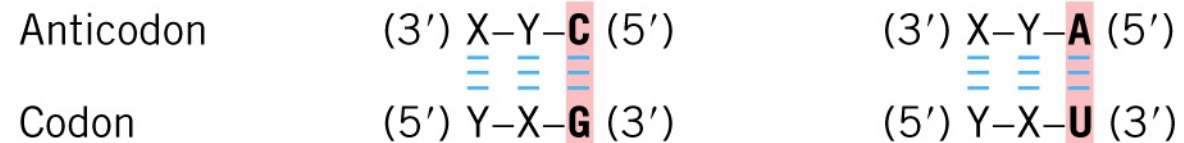


(a)

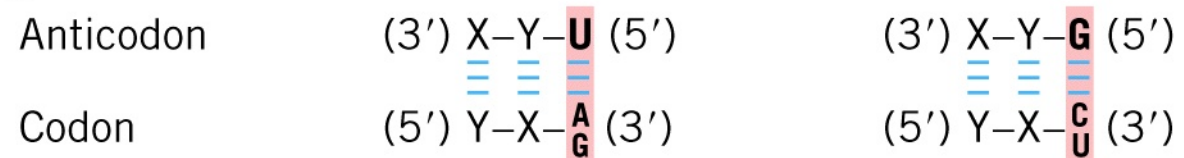
## table 27–5

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

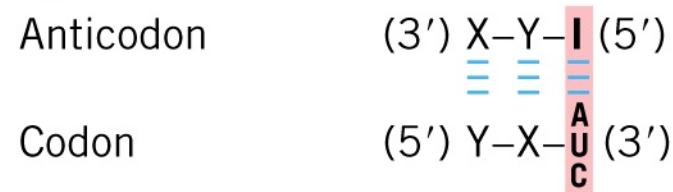
1. One codon recognized:



2. Two codons recognized:



3. Three codons recognized:



\*X and Y denote complementary bases capable of strong Watson-Crick base pairing with each other. The bases in the wobble positions—the 3' position of codons and 5' position of anticodons—are shaded in red.

table 1

Known Variant Codon Assignments in Mitochondria					
	Codons*				
	UGA	AUA	AGA AGG	CUN	CGG
<b>Normal code assignment</b>	<b>Stop</b>	<b>Ile</b>	<b>Arg</b>	<b>Leu</b>	<b>Arg</b>
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>	?	+	+	+	?

\*A question mark Indicates that the codon has not been observed in the indicated mitochondrial genome; N, any nucleotide; +, the codon has the same meaning as in the normal code.

table 27–6

**Components Required for the Five Major Stages of Protein Synthesis in *E. coli***

Stage	Essential components
1. Activation of amino acids	20 amino acids 20 aminoacyl-tRNA synthetases 20 or more tRNAs ATP $Mg^{2+}$
2. Initiation	mRNA <i>N</i> -Formylmethionyl-tRNA 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 release	Termination codon in mRNA Polypeptide release factors (RF <sub>1</sub> , RF <sub>2</sub> , RF <sub>3</sub> ) ATP
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 phosphate, methyl, carboxyl, carbohydrate, or prosthetic groups

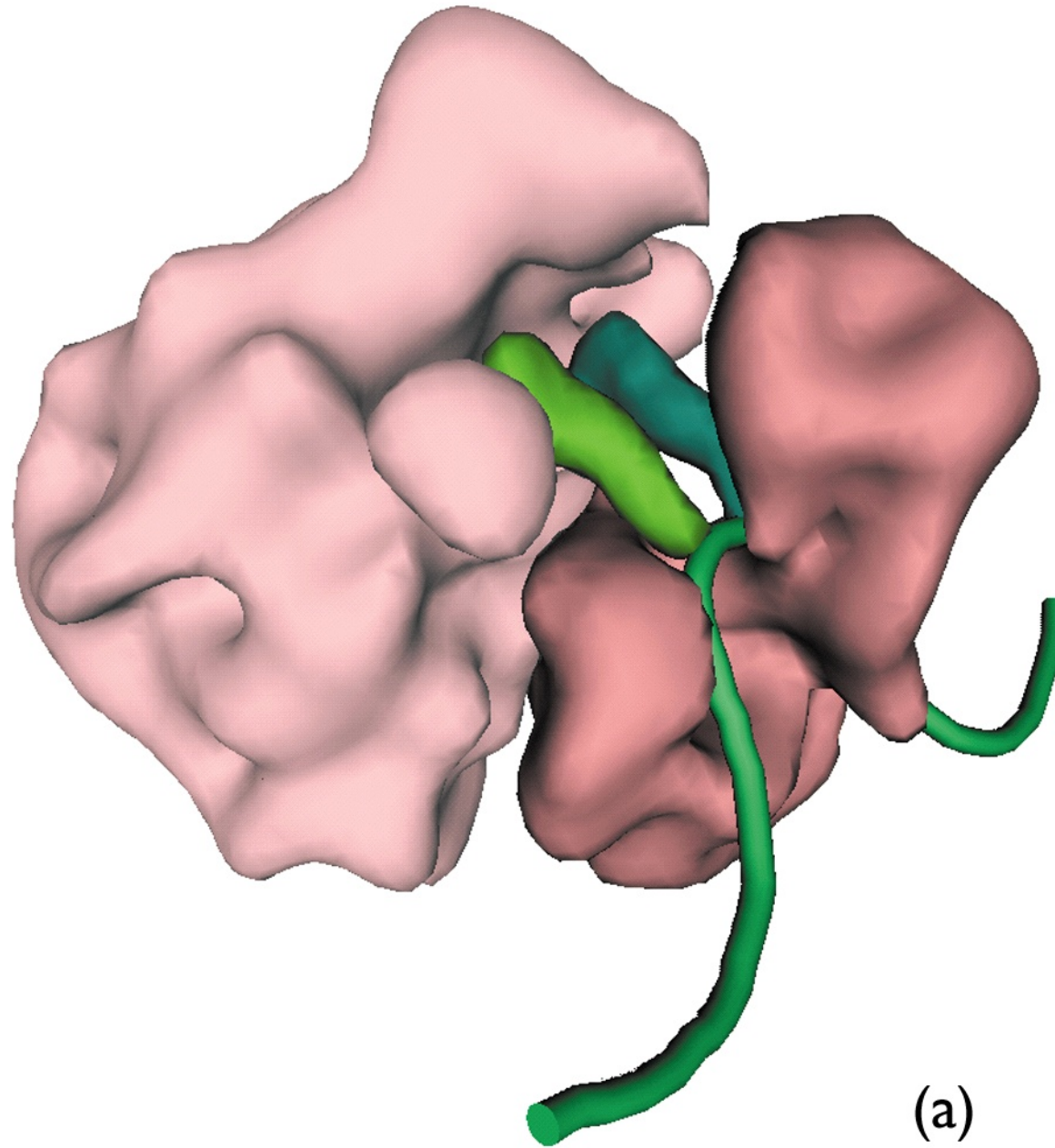
table 27–7

### RNA and Protein Components of the *E. coli* 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)

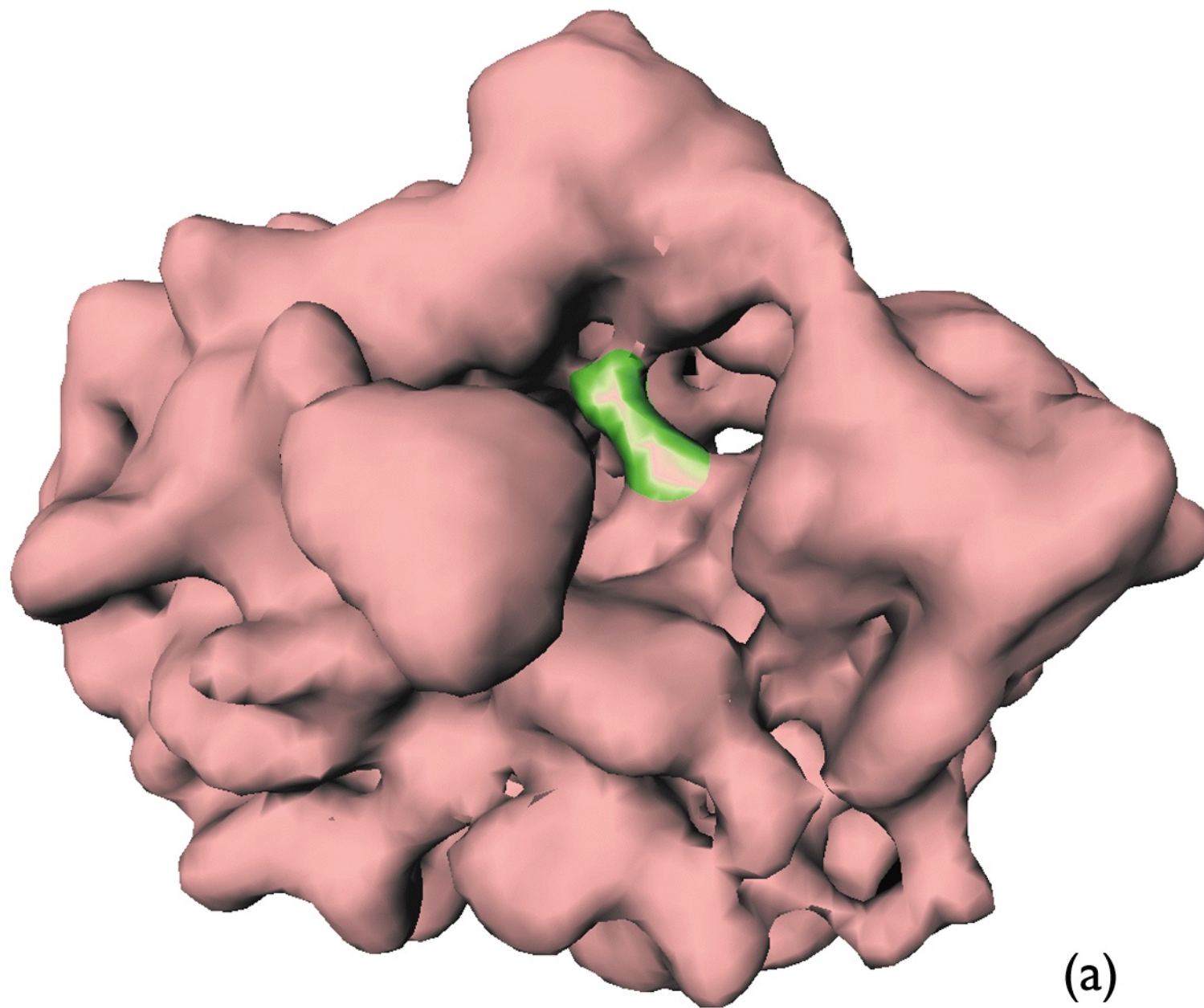
\*The L1 to L36 protein designations do not correspond to 36 different proteins. The protein originally designated L7 is in fact a modified form of L12, and L8 is a complex of three other proteins. Also, L26 proved to be the same protein as S20 (and not part of the 50S subunit). This gives 33 different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



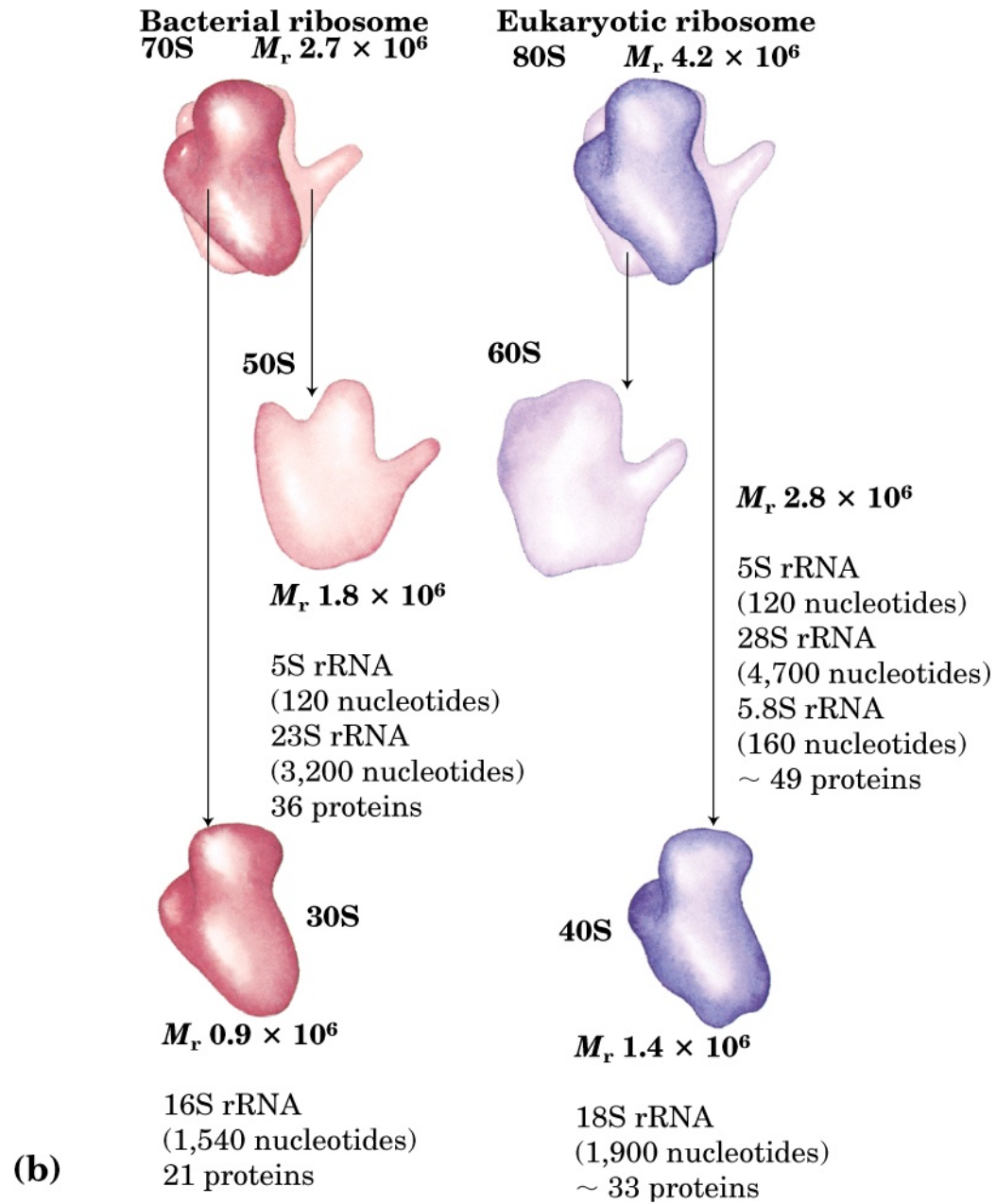


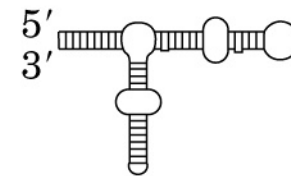
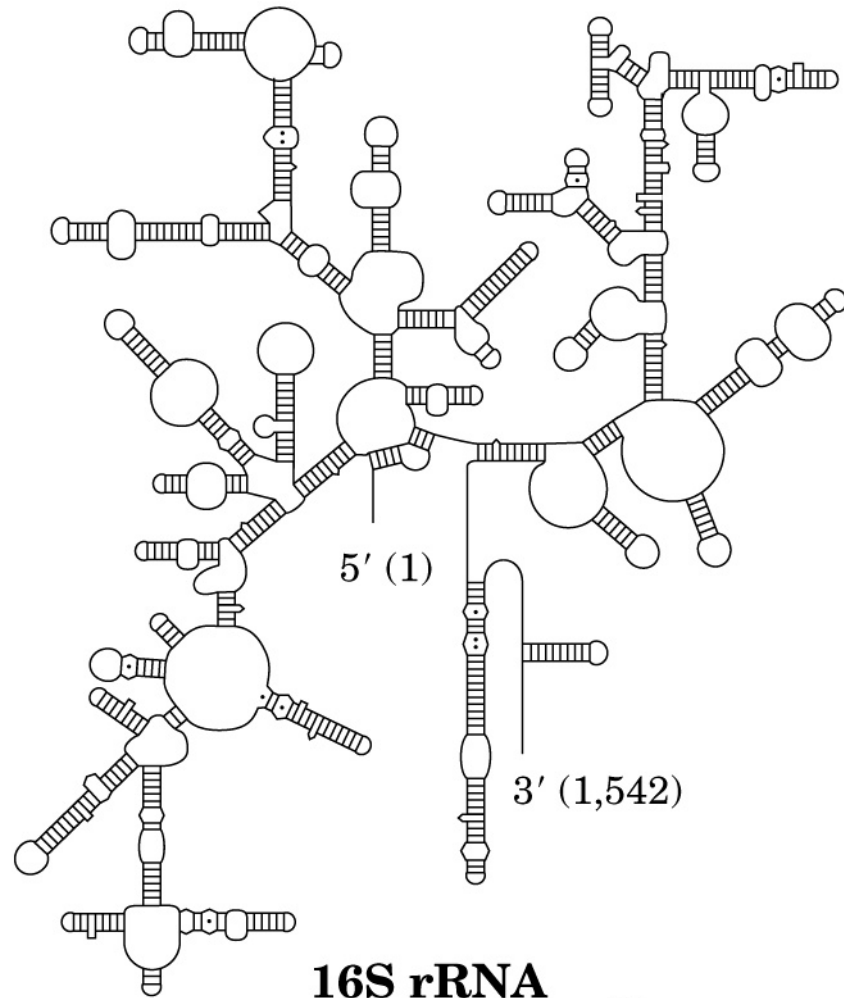
(a)



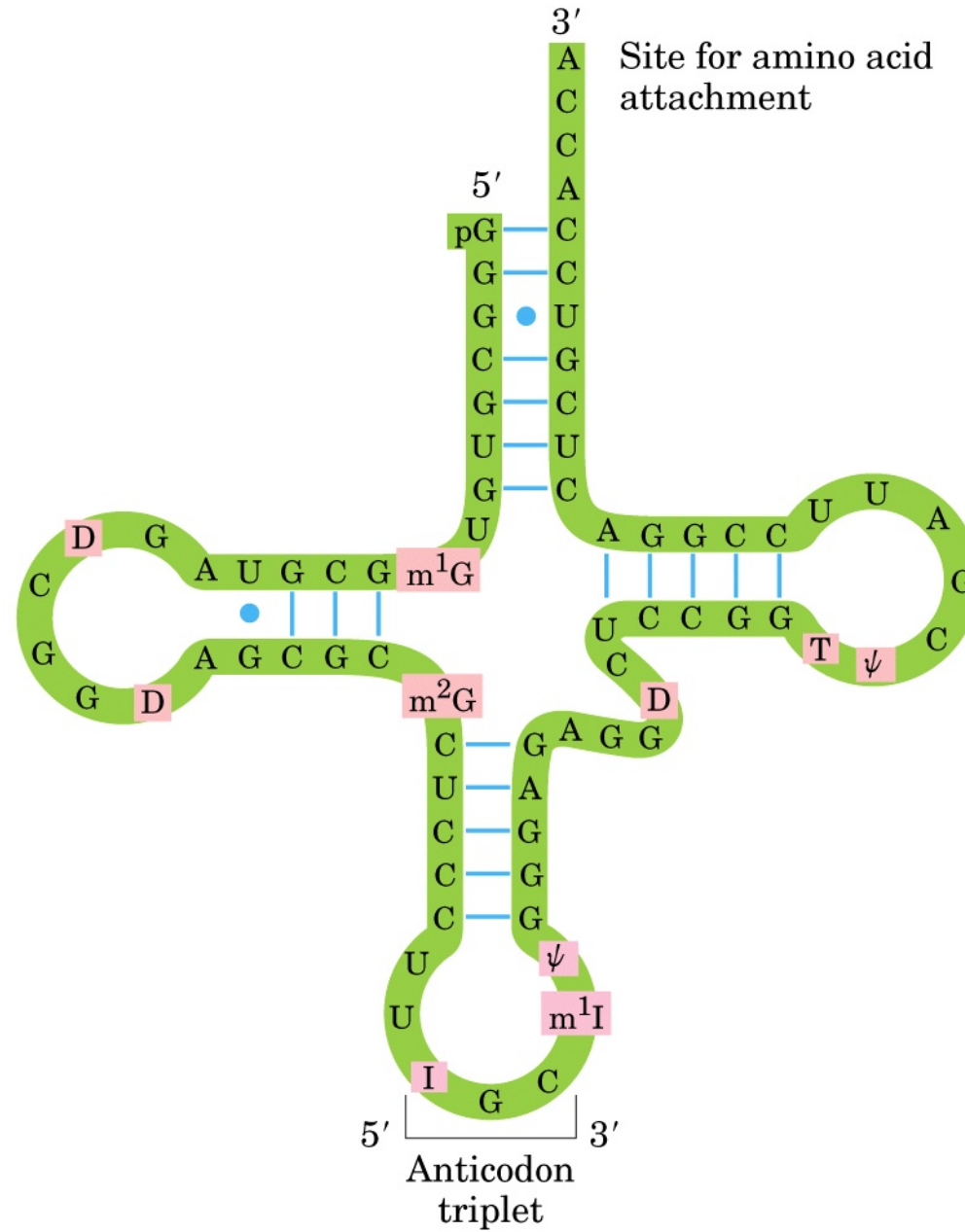


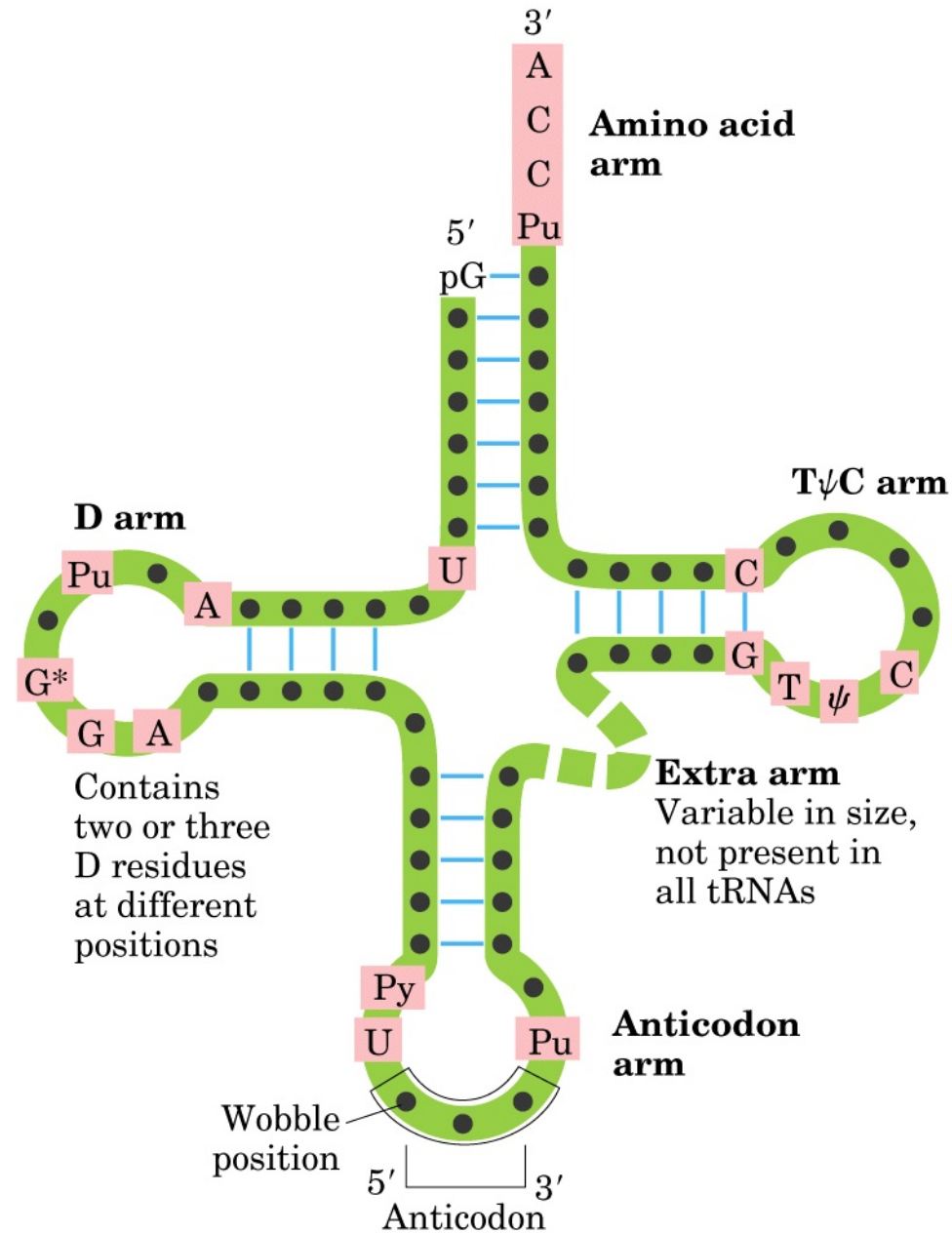
(a)

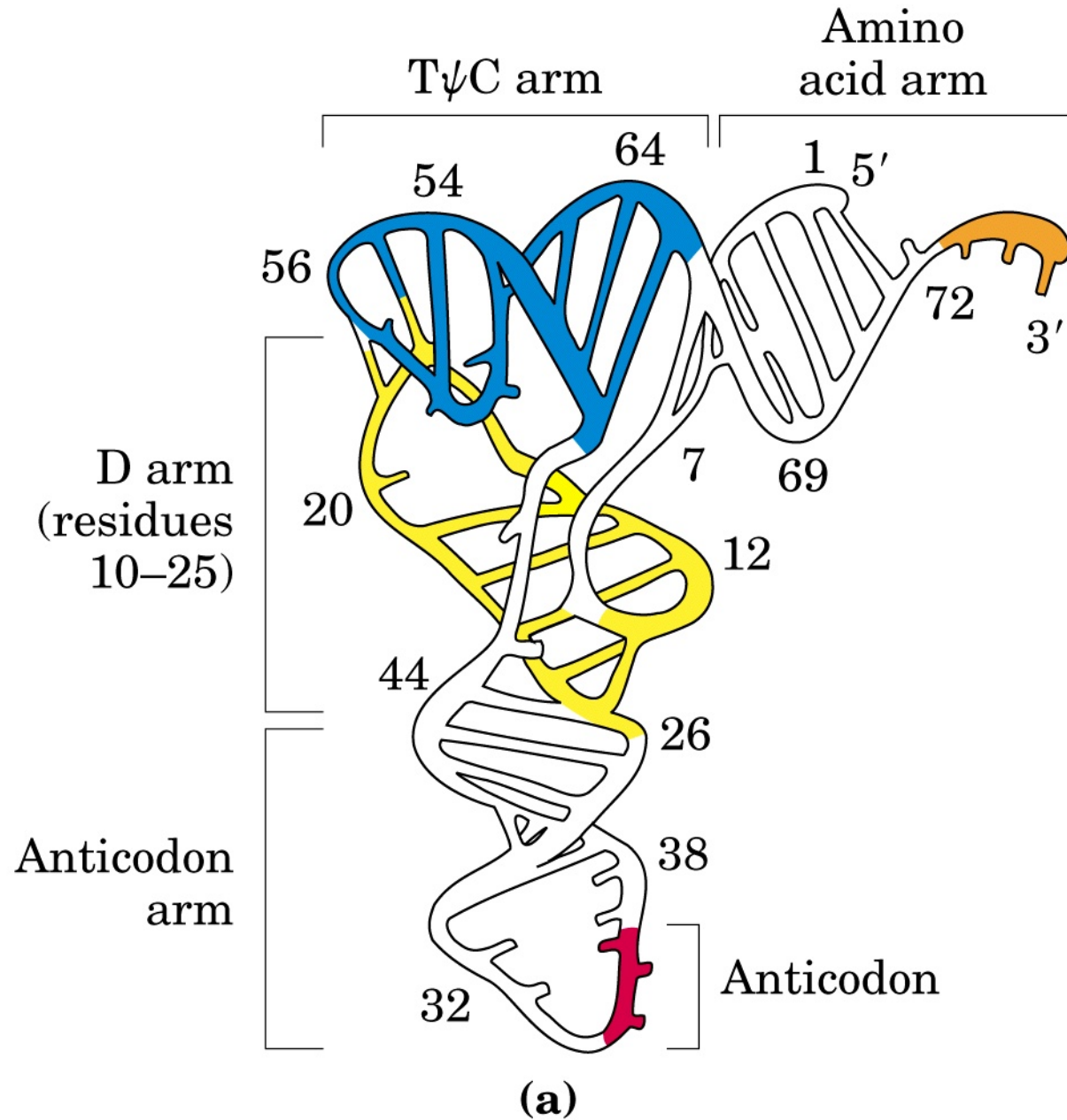




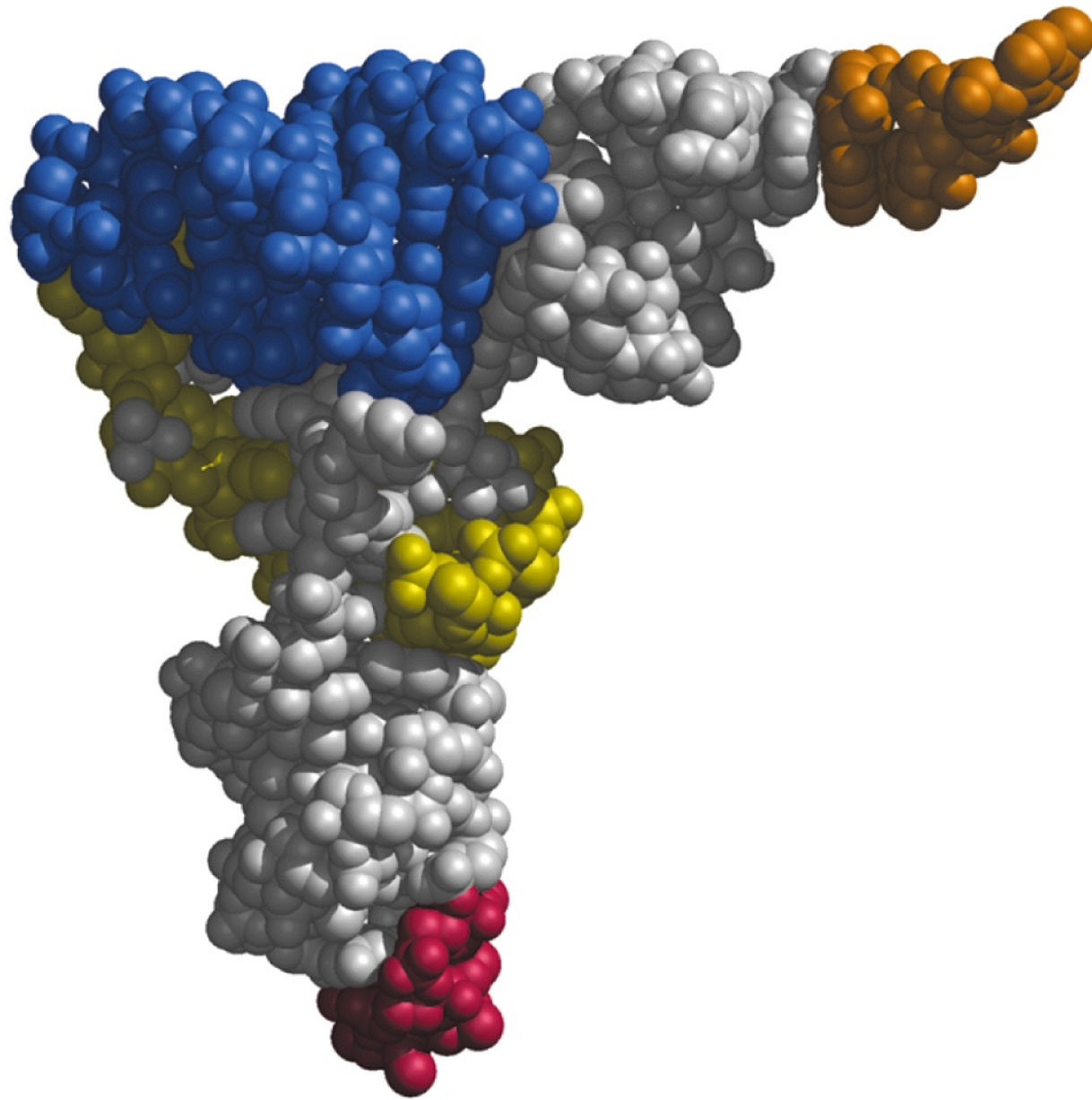
**5S rRNA**

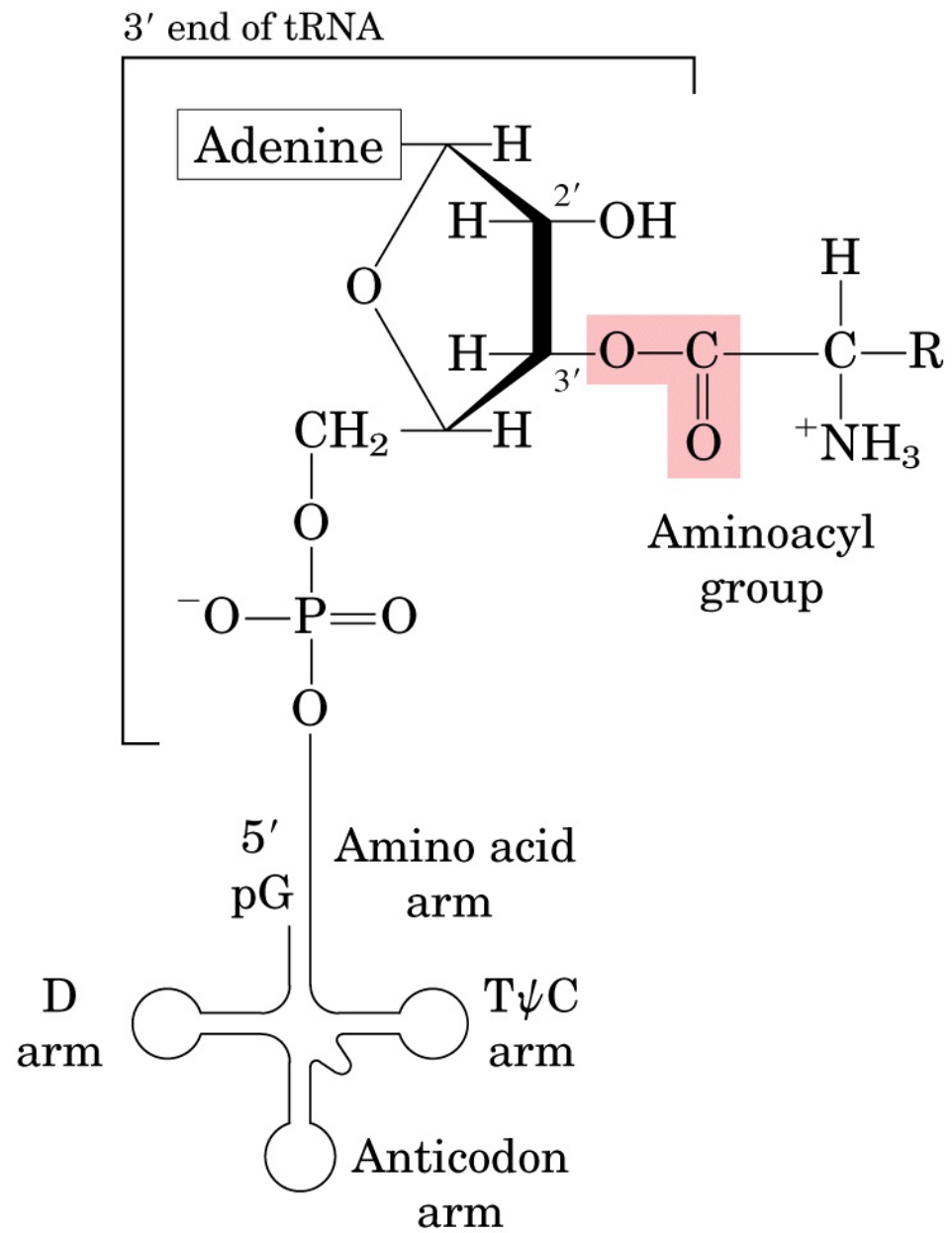




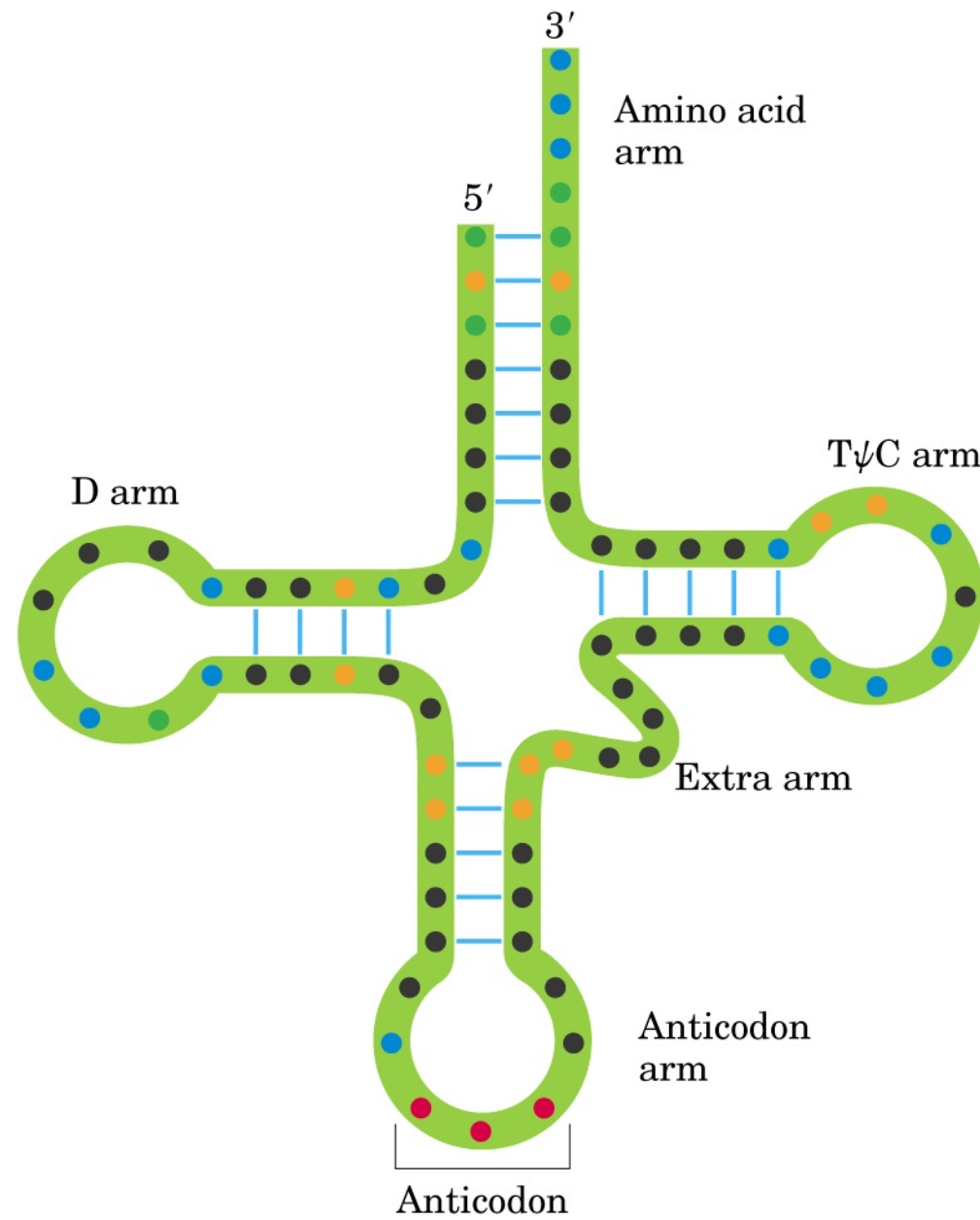


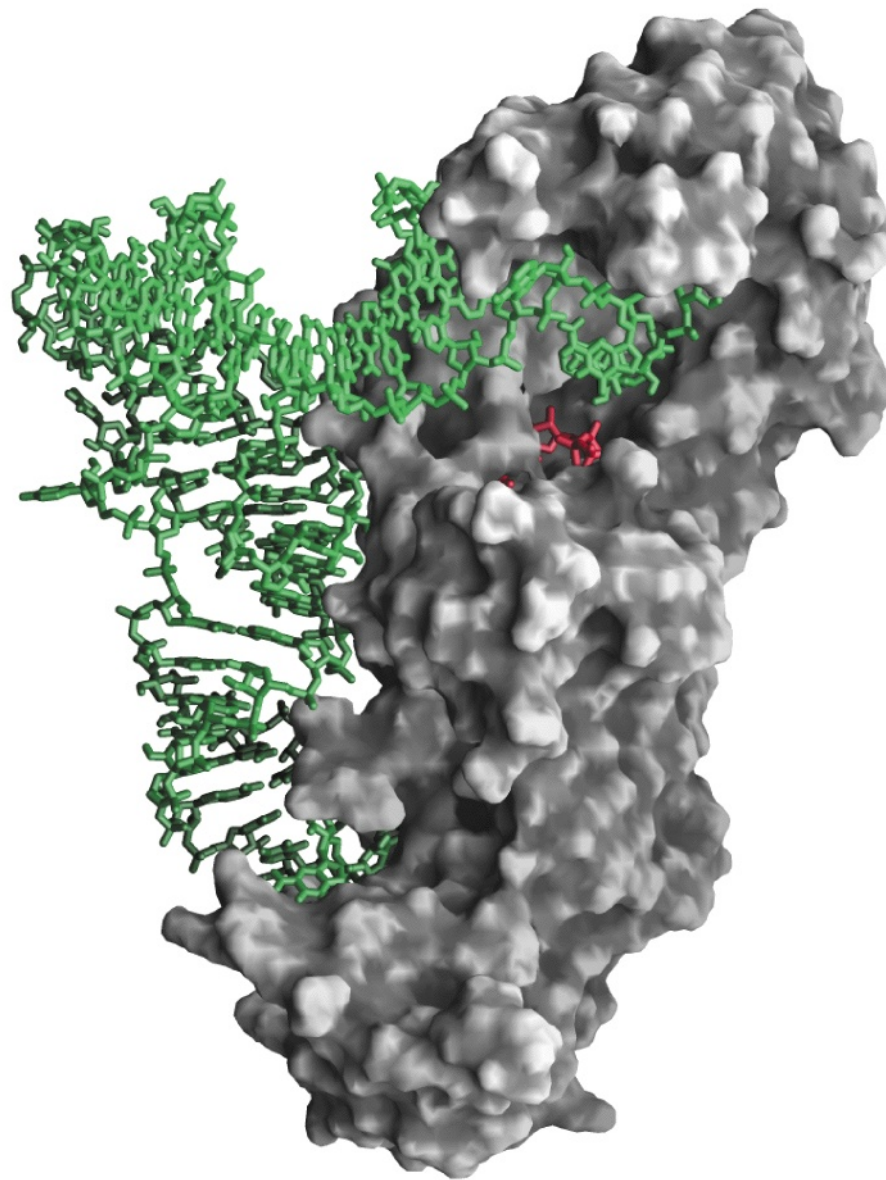




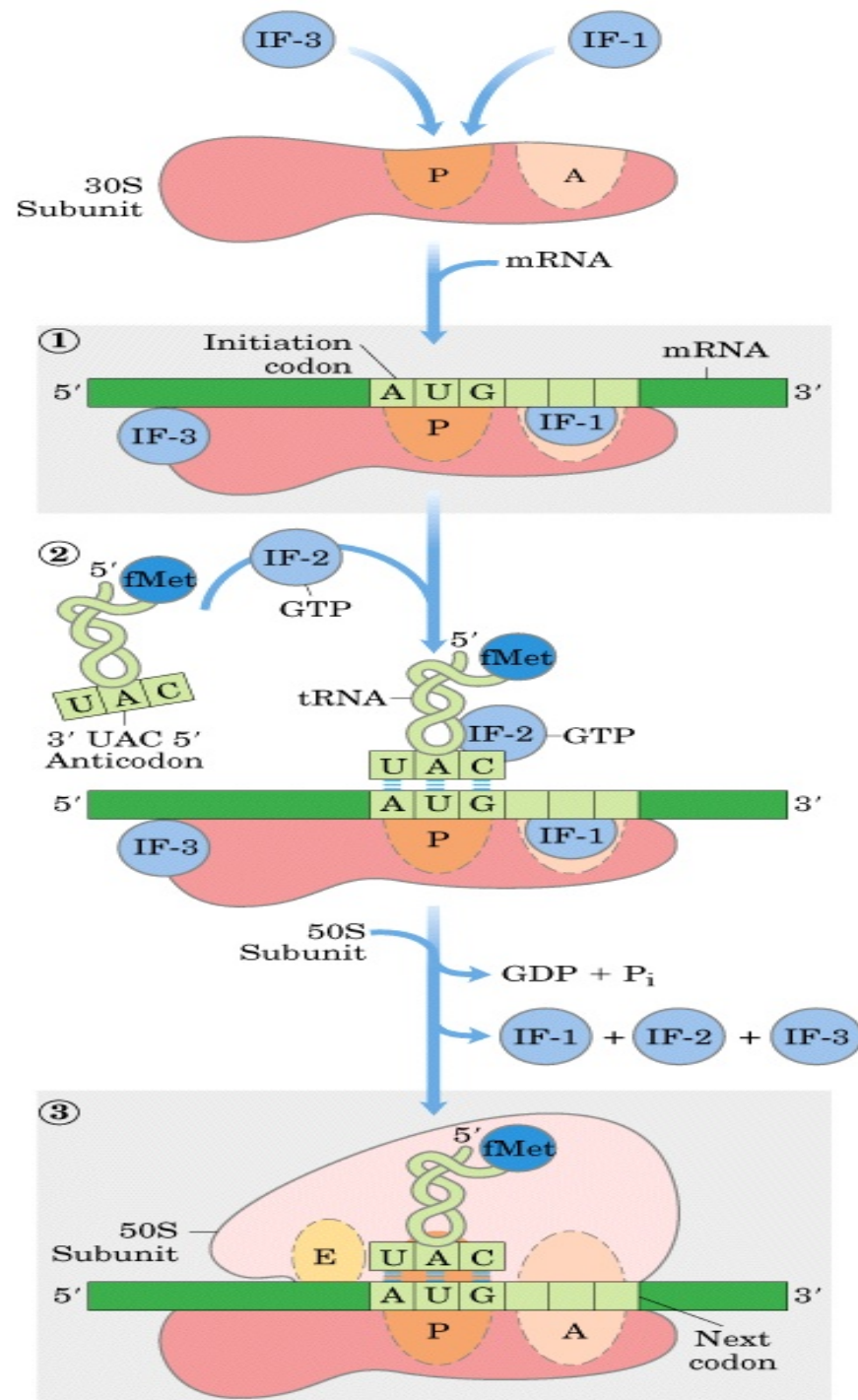


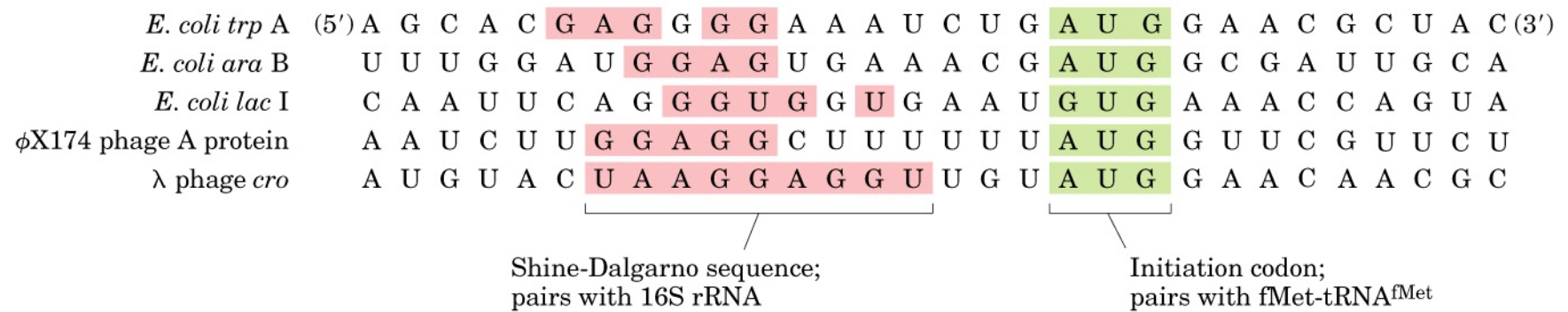




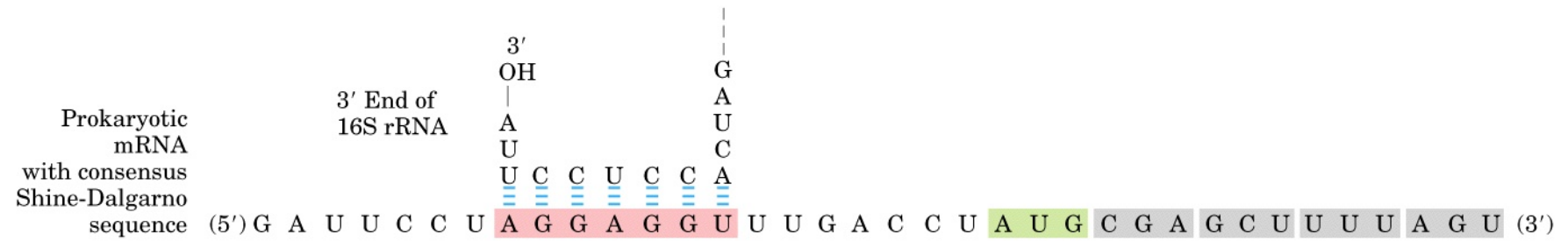


**(a)**





(a)



(b)

## Secuencia Kozak

Muchos mRNA eucarióticos contienen una secuencia de reconocimiento corta, que facilita la unión inicial del mRNA a la subunidad pequeña del ribosoma. La secuencia consenso para la iniciación de la traducción en vertebrados (denominada secuencia Kozak) es:

ACCATGG

Más general:

(GCC)RCCATGG

Donde R es una purina.

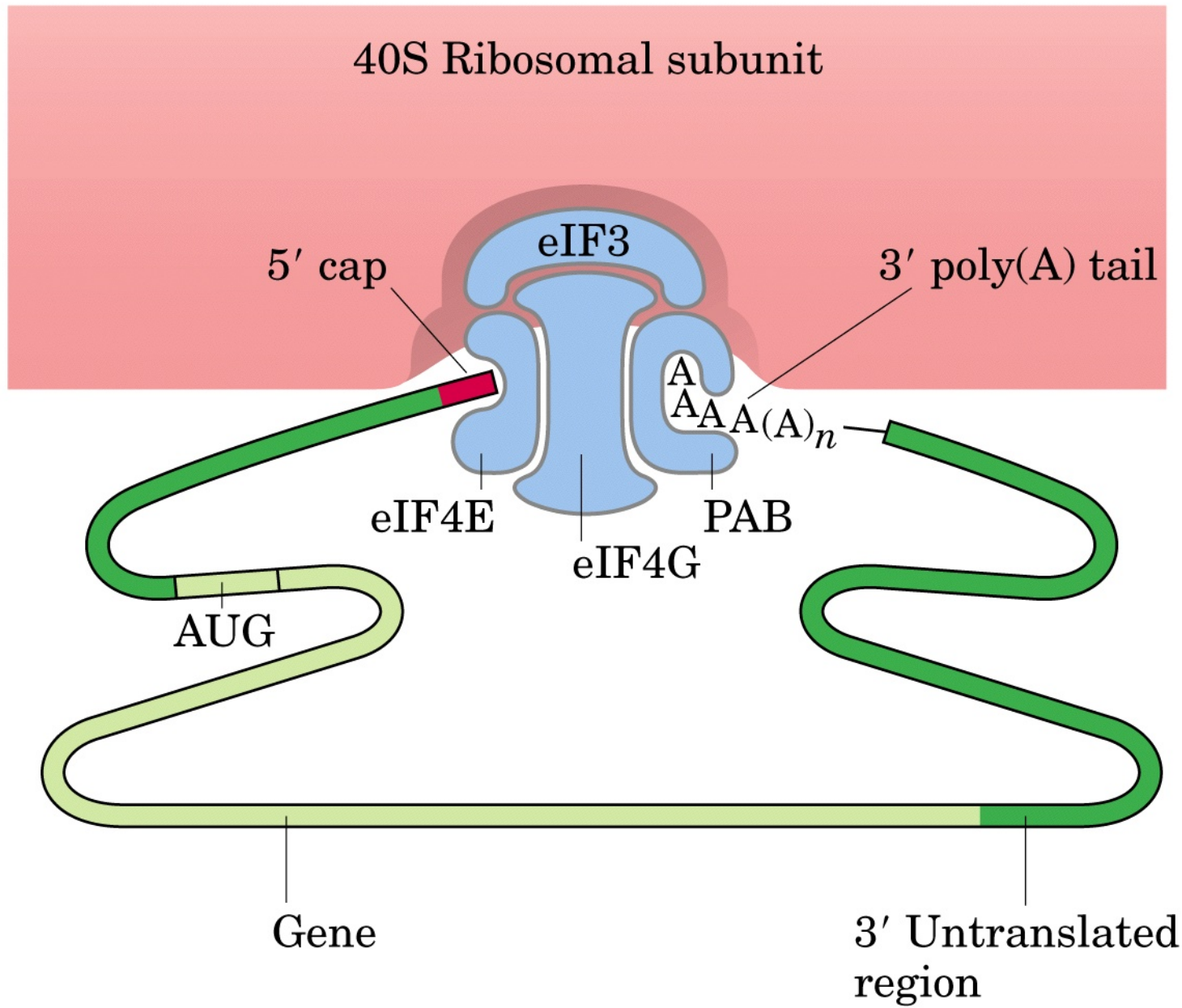




table 27-9

**Protein Factors Required for Initiation of Translation in Bacterial and Eukaryotic Cells**

**Bacterial**

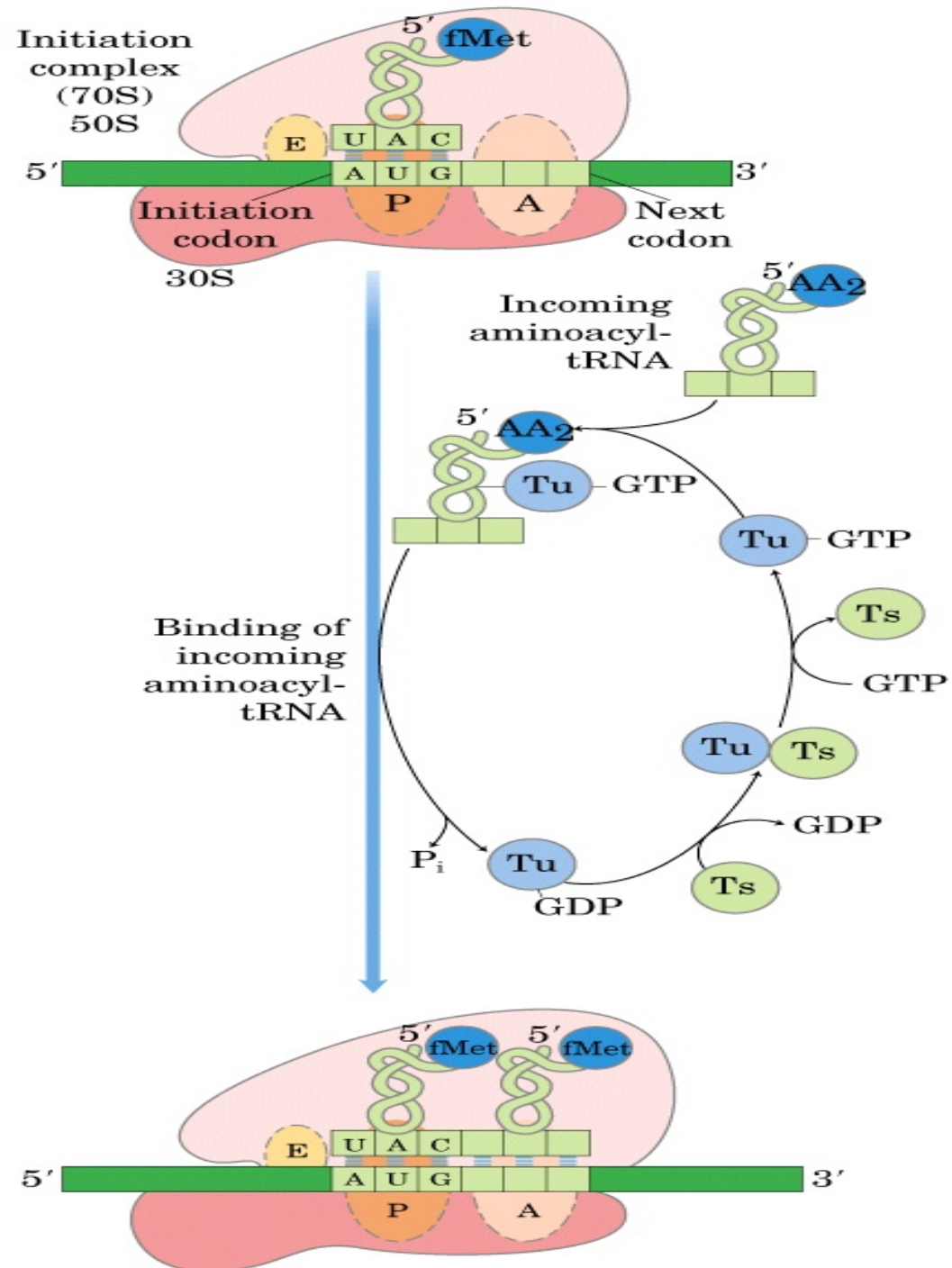
Factor	Function
IF-1	Prevents premature binding of tRNAs to A site
IF-2	Facilitates binding of fMet-tRNA <sup>fMet</sup> to 30S ribosomal subunit
IF-3	Binds to 30S subunit; prevents premature association of 50S subunit; enhances specificity of P site for fMet-tRNA <sup>fMet</sup>

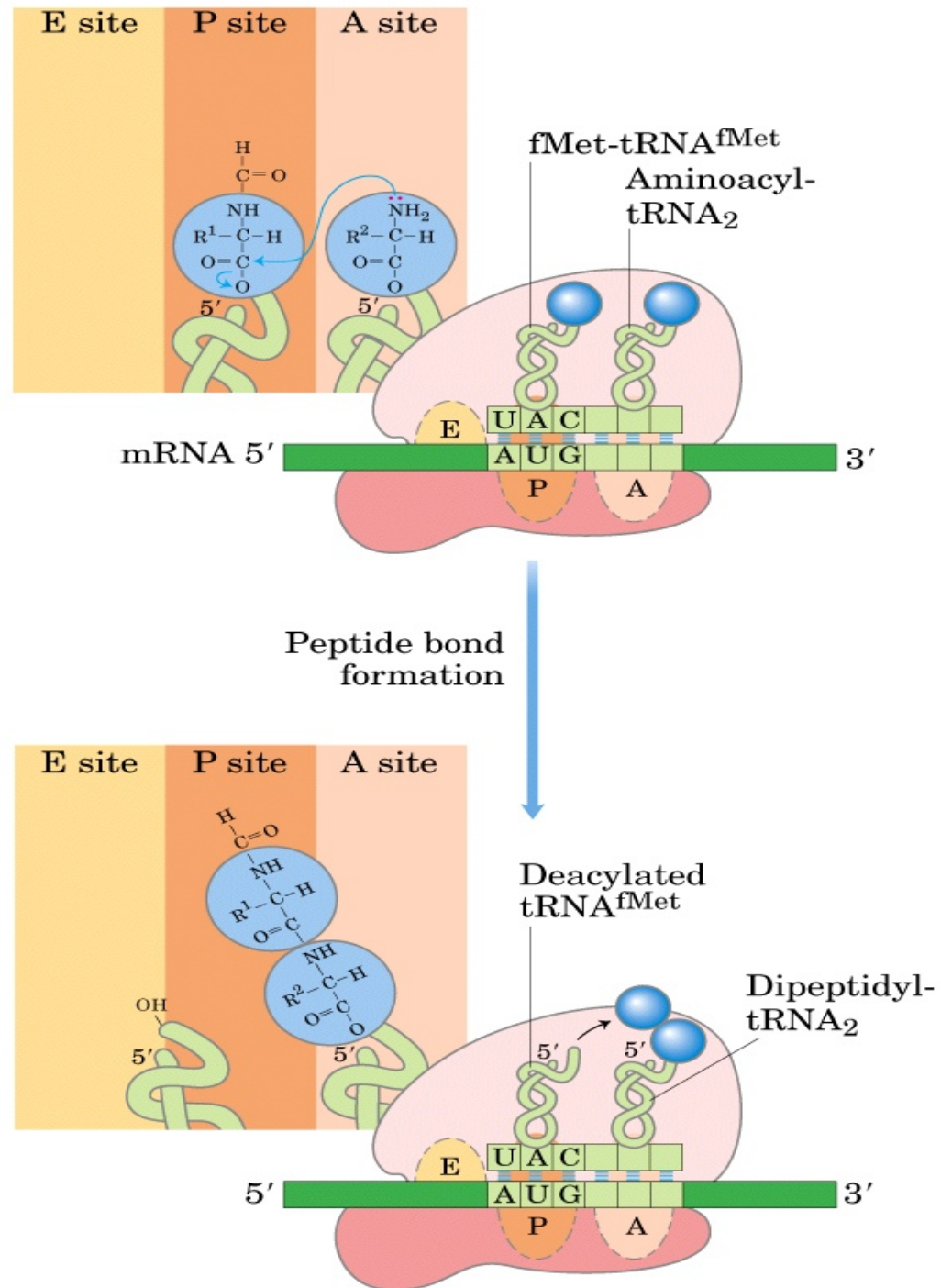
**Eukaryotic**

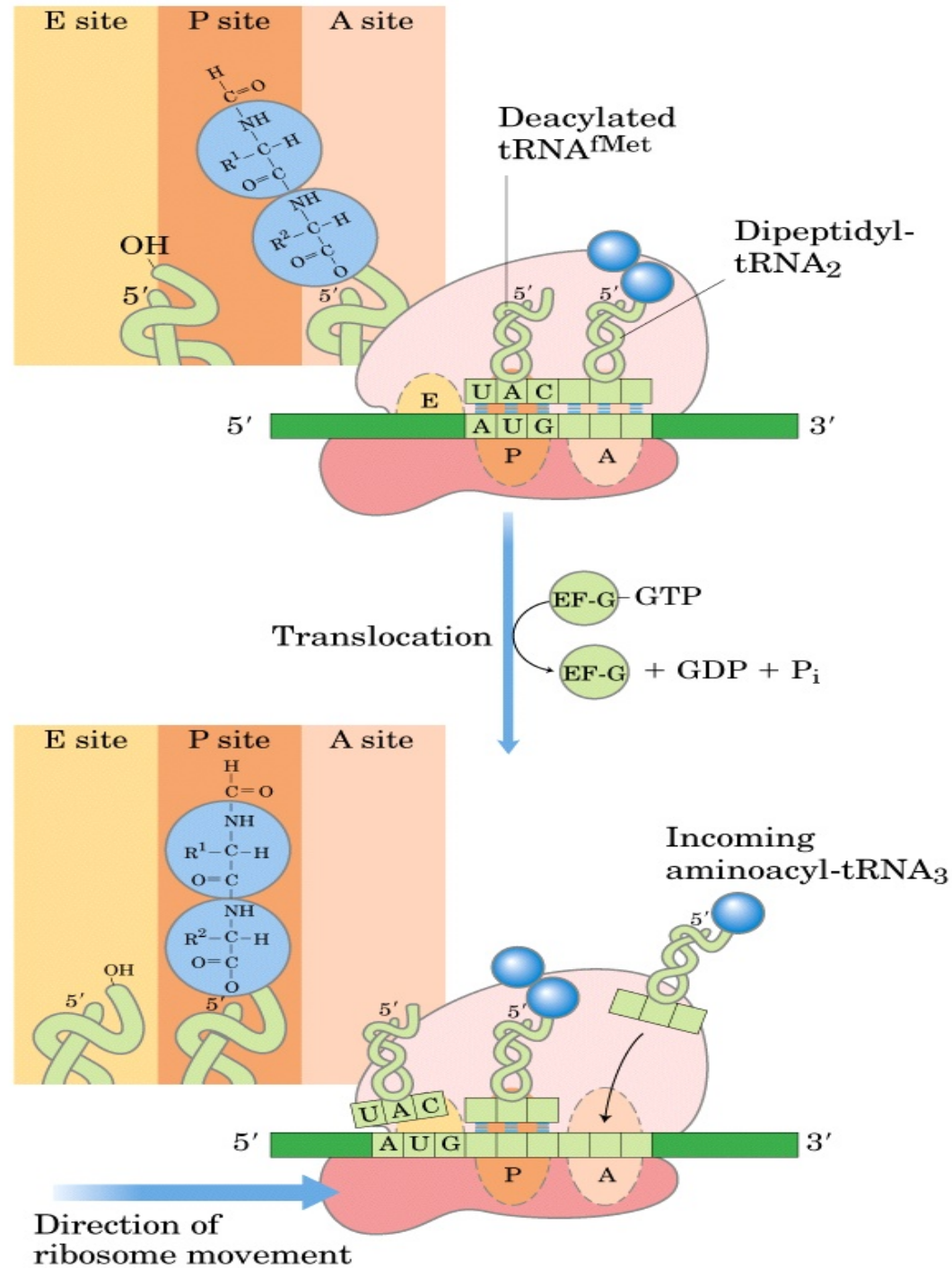
Factor*	Function
eIF2	Facilitates binding of initiating Met-tRNA <sup>Met</sup> to 40S ribosomal subunit
eIF2B, eIF3	First factors to bind 40S subunit; facilitate subsequent steps
eIF4A	RNA helicase activity removes secondary structure in the mRNA to permit binding to 40S subunit; part of the eIF4F complex
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

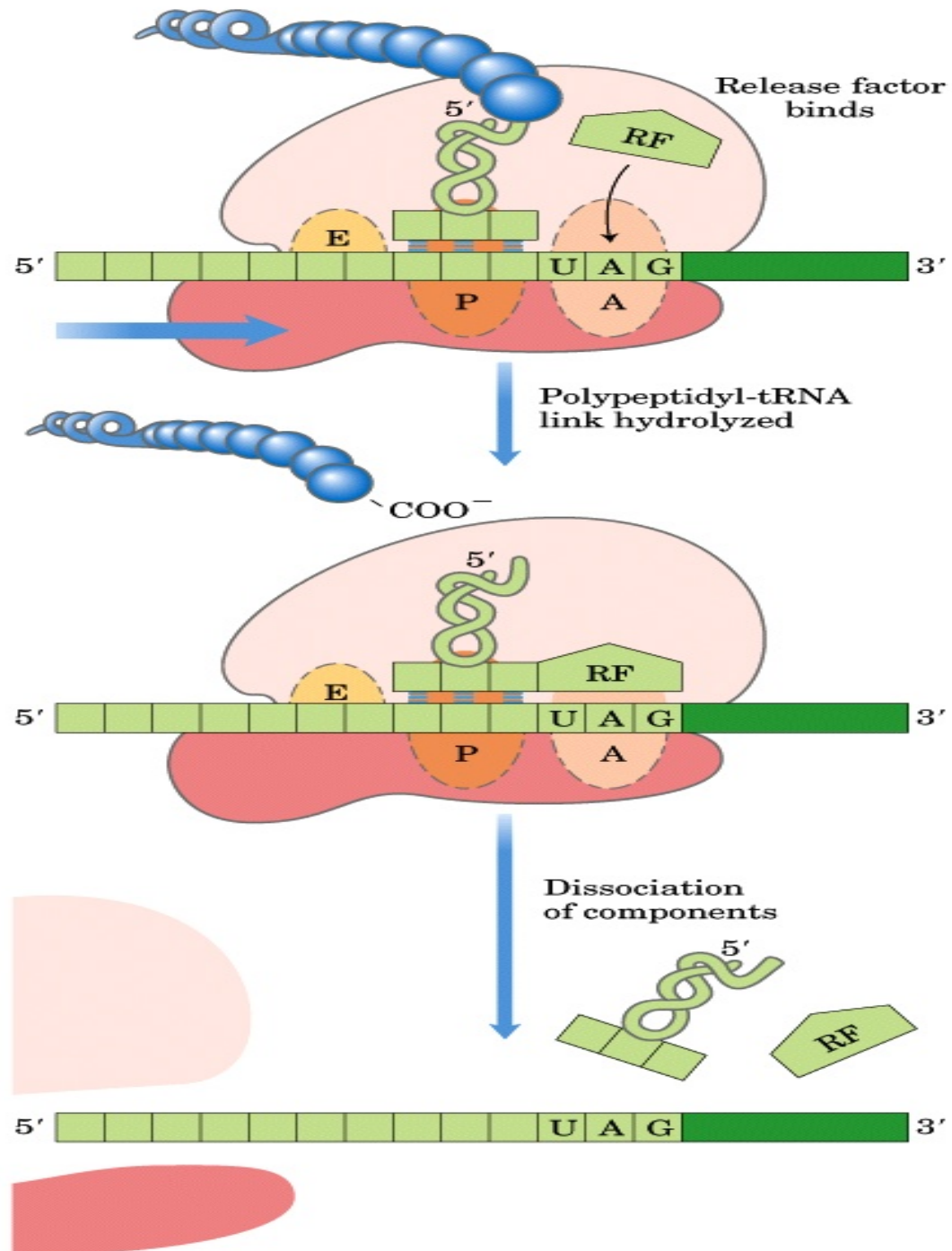
\*The prefix "e" identifies these as eukaryotic factors.

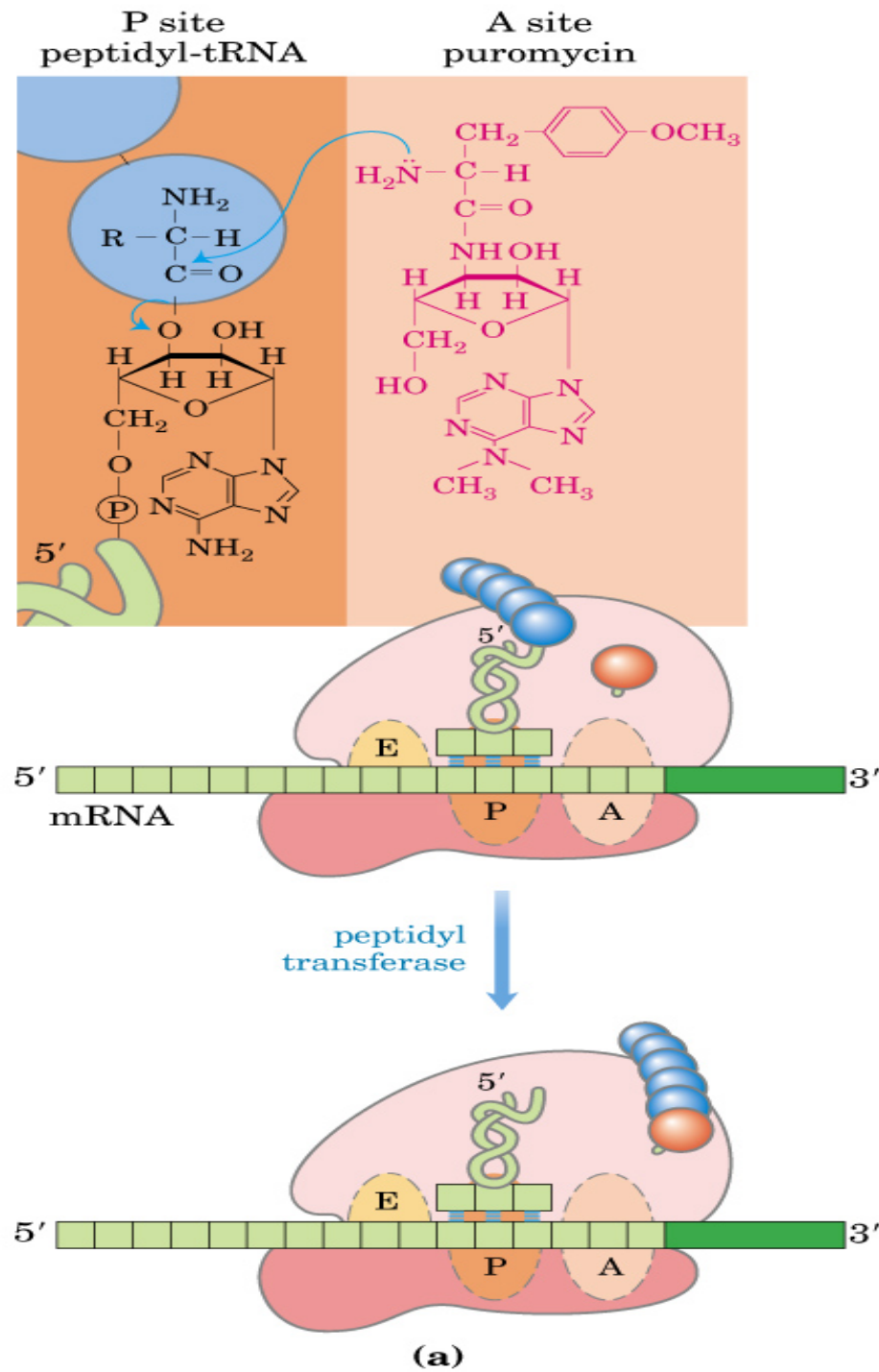


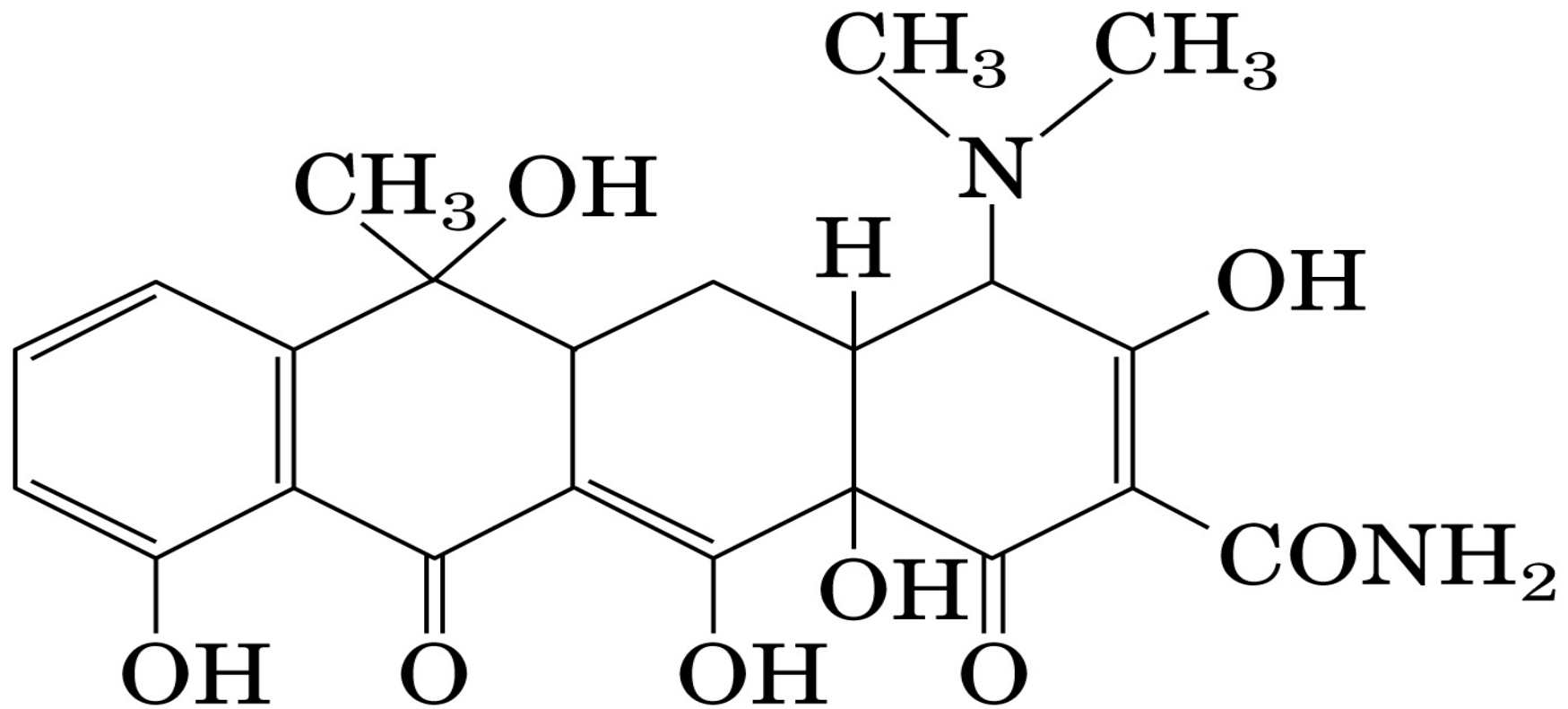






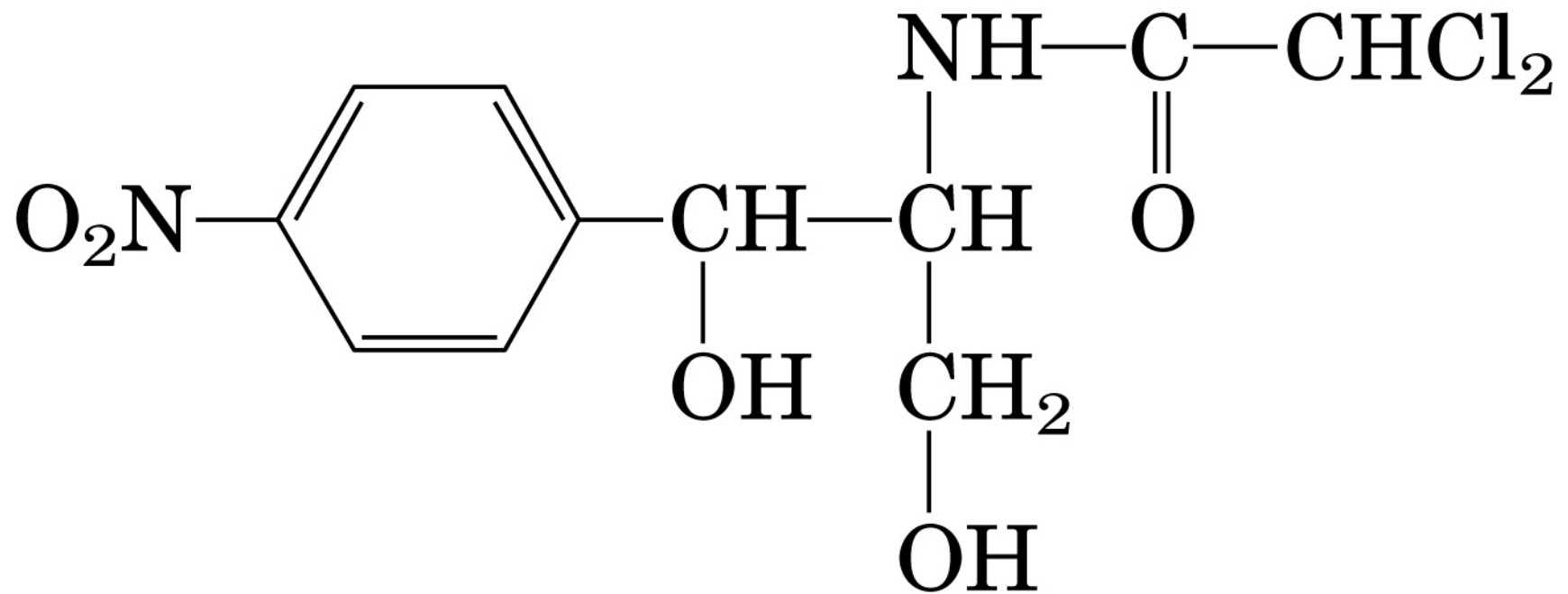






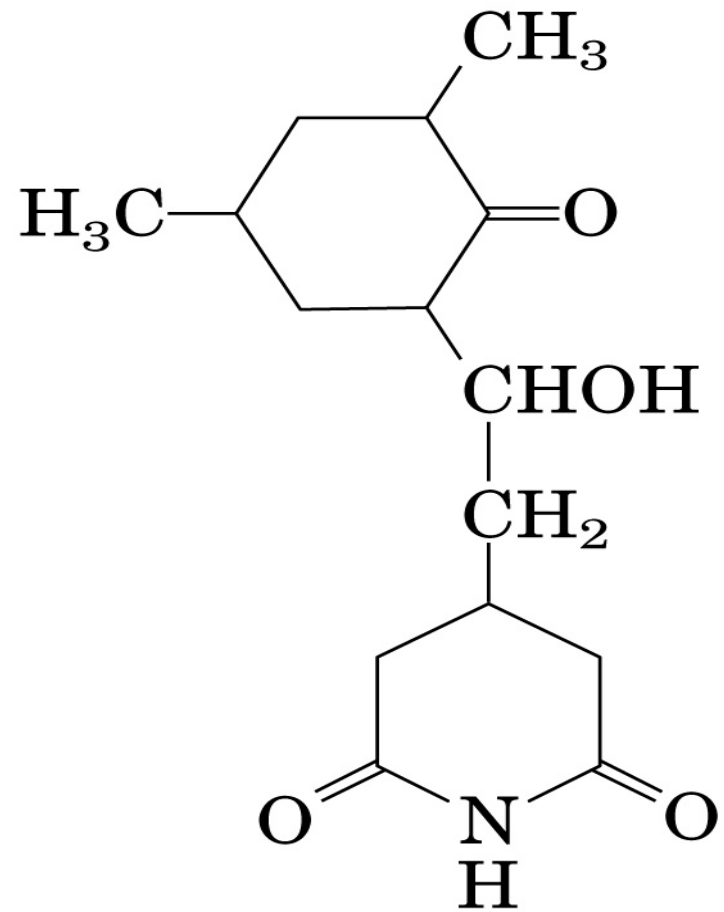
Tetracycline

Bloquea el sitio A en los ribosomas bacterianos.



## Chloramphenicol

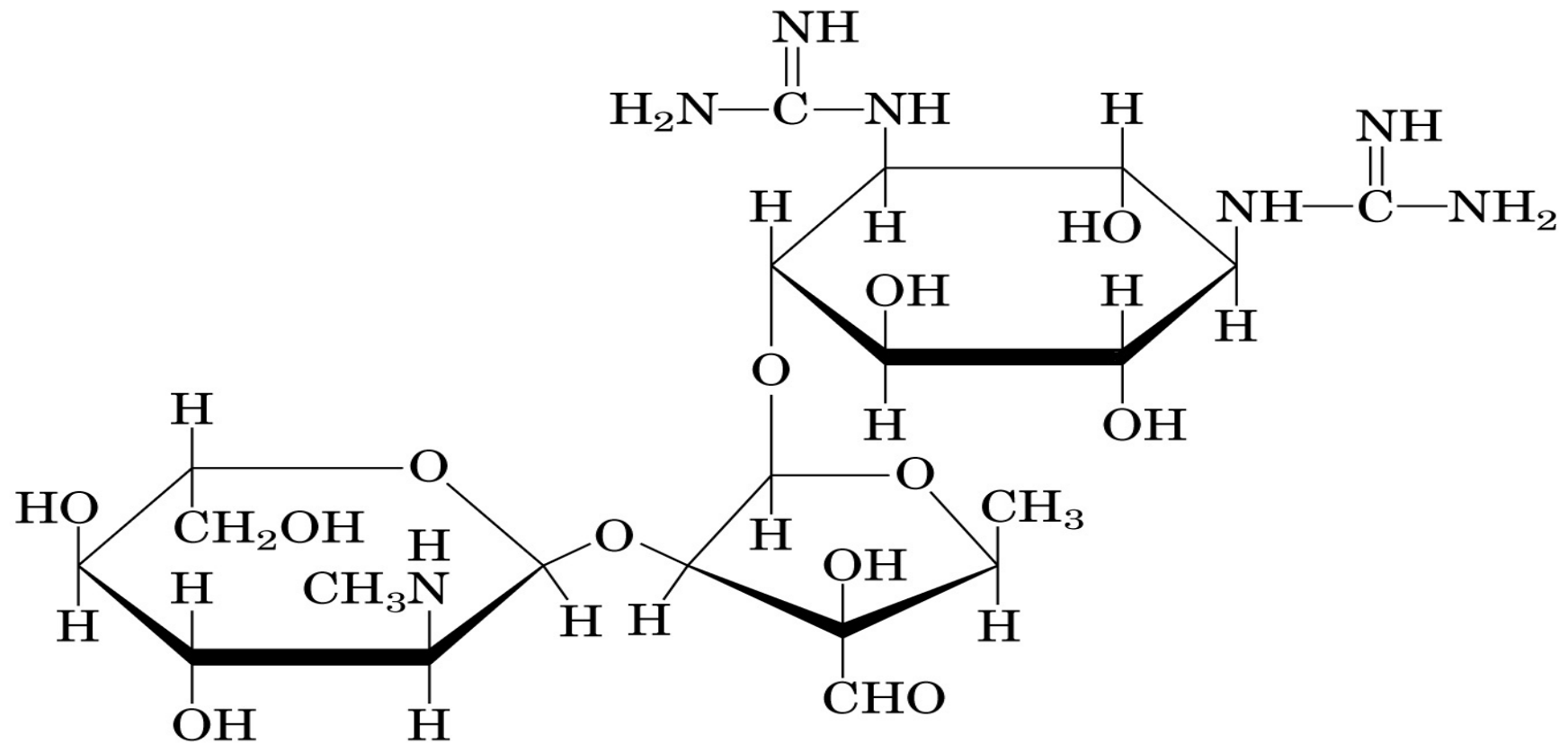
Bloquea la transfencia del peptido en ribosomas bacterianos.



Cycloheximide

Bloquea la peptidil transferasa en eucariontes.





Streptomycin

Inhibe el inicio de la traducción en altas concentraciones, en bacterias.

Produce lectura errónea del código genético en bacterias, en bajas concentraciones.

**FIN**