

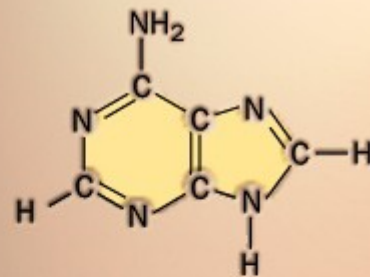
REPLICACION DEL DNA

Introducción

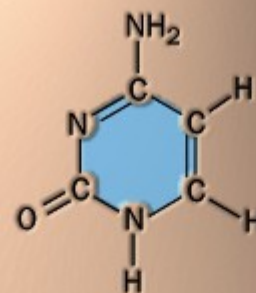


La molécula de ADN (ácido desoxirribonucleico) es el modelo genético de cada célula y, en última instancia, lo que determina todos los aspectos de un ser vivo. La molécula de ADN fue descubierta en 1951 por James Watson, Francis Crick y Maurice Wilkins empleando la técnica de difracción de los rayos X. En 1953, Watson (izquierda) y Francis Crick (derecha) describieron la estructura en doble hélice de la molécula de ADN como una especie de escalera de caracol con muchos escalones. En 1962 ambos recibieron el Premio Nobel de Medicina por su trabajo.

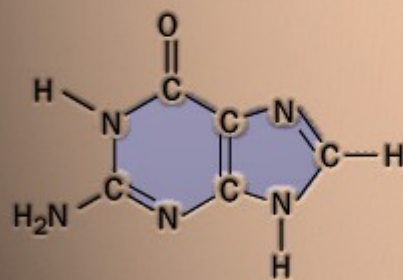
Bases nitrogenadas



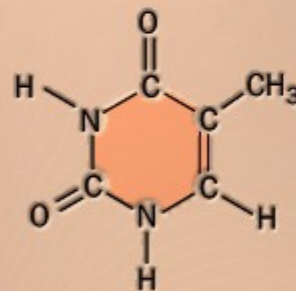
Adenine (A)



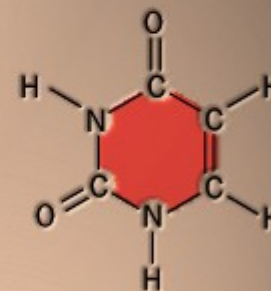
Cytosine (C)



Guanine (G)

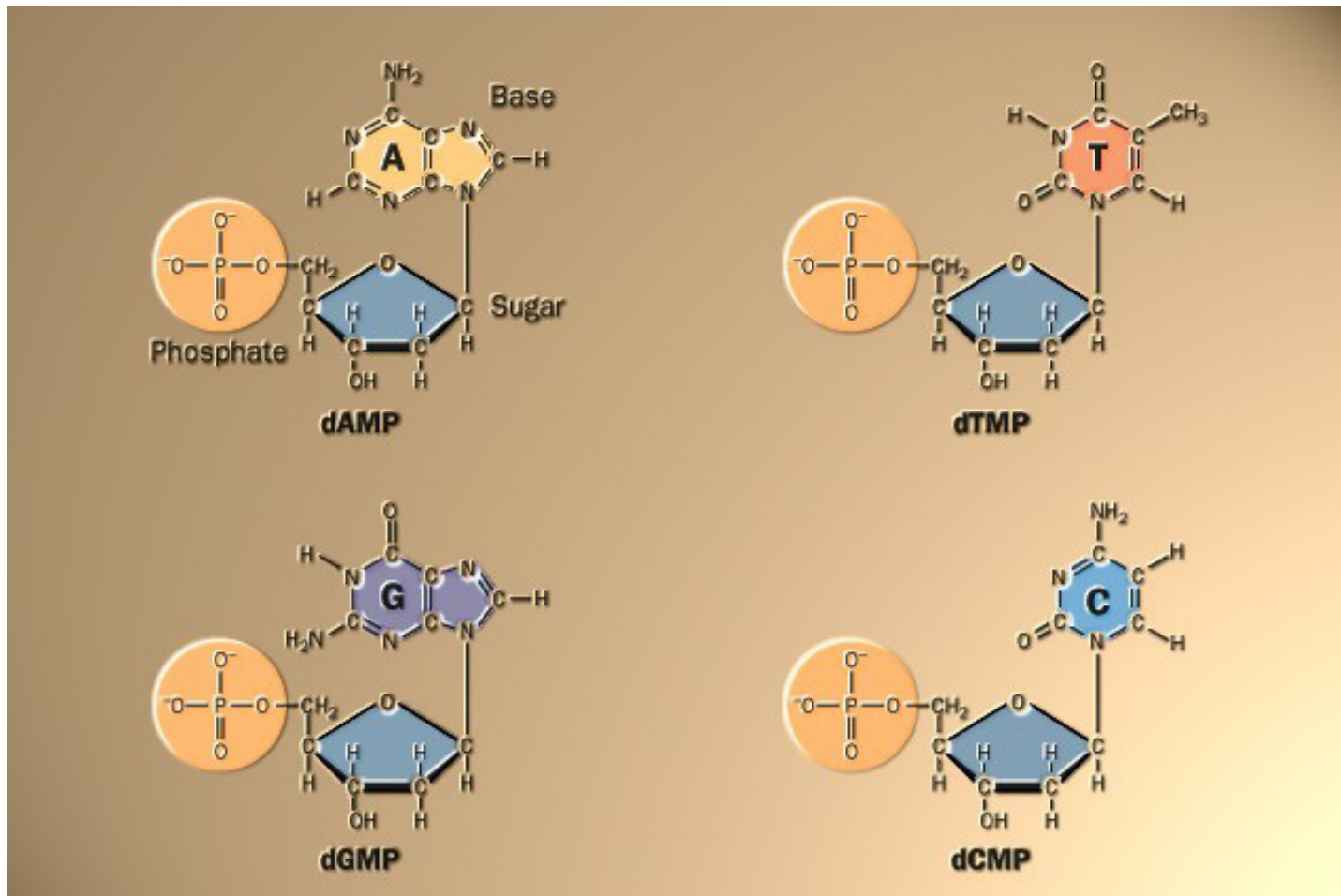


Thymine (T)

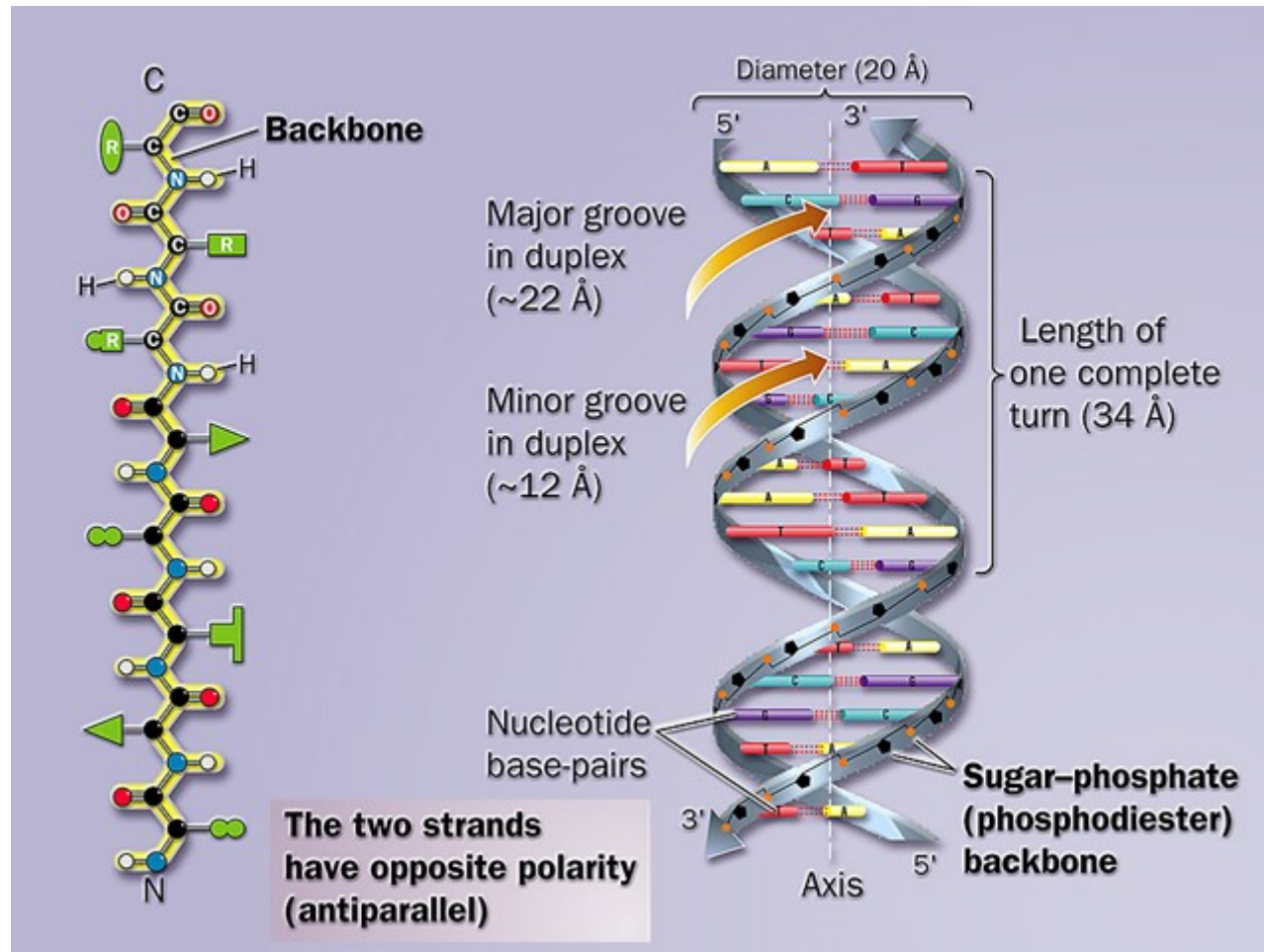


Uracil (U)

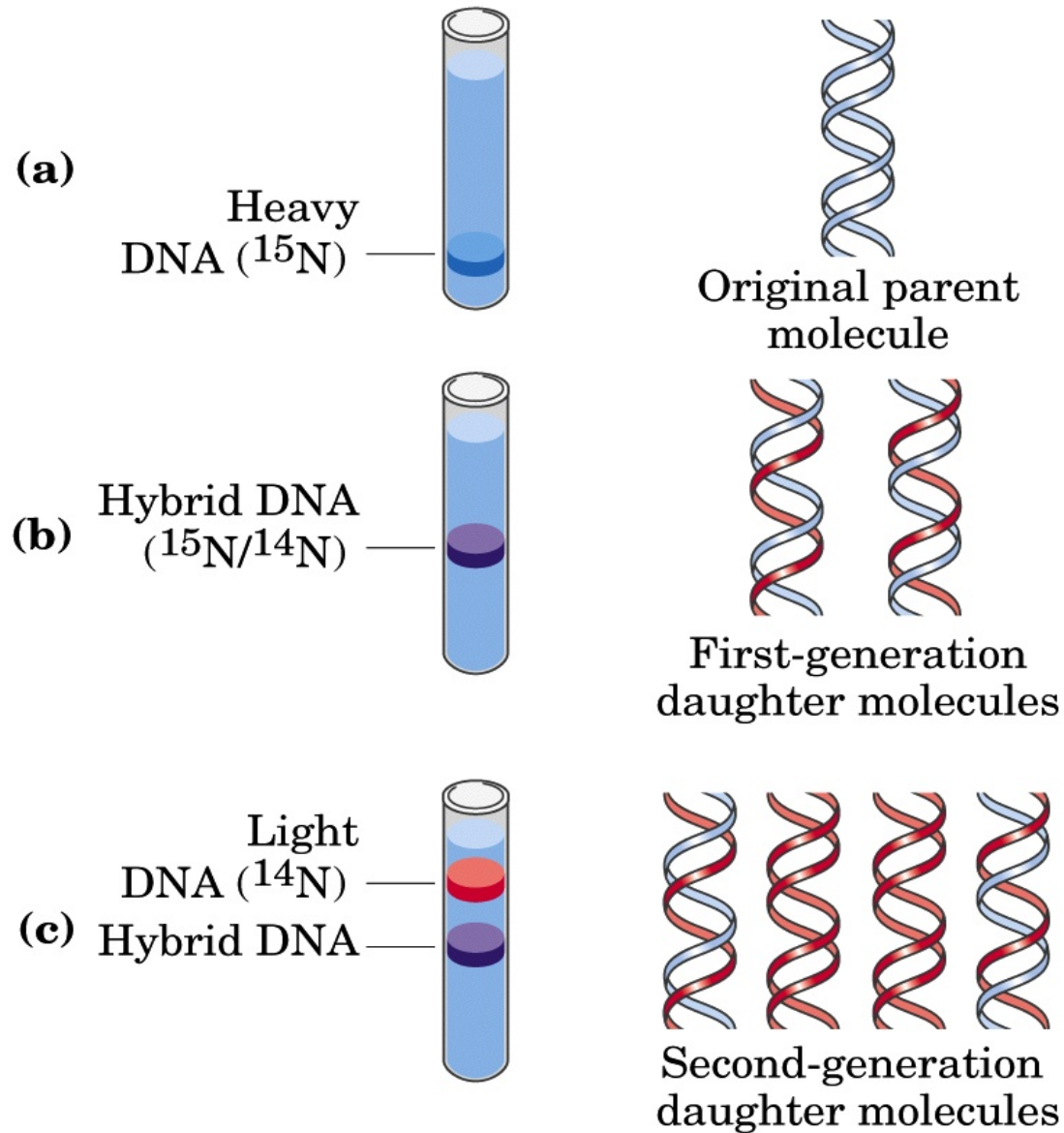
Ácido desoxirribonucleico



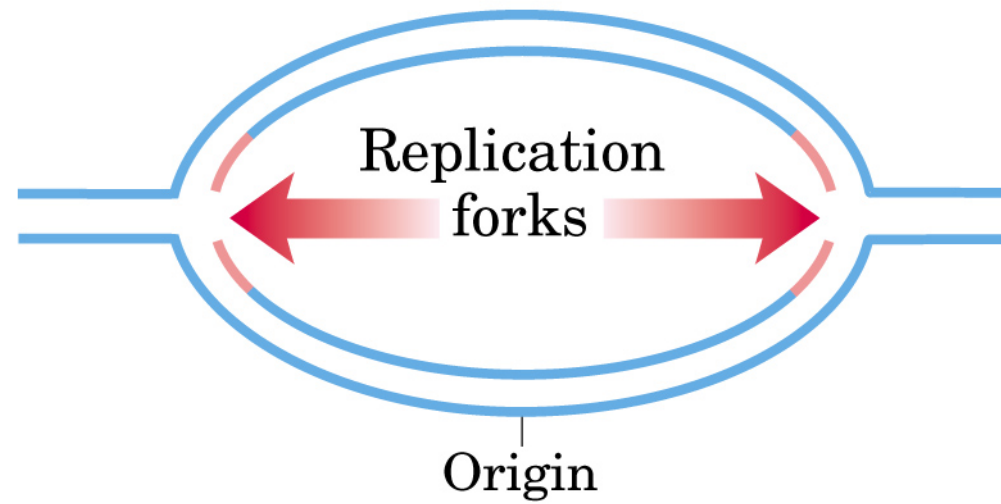
DNA: doble hebra antiparalela



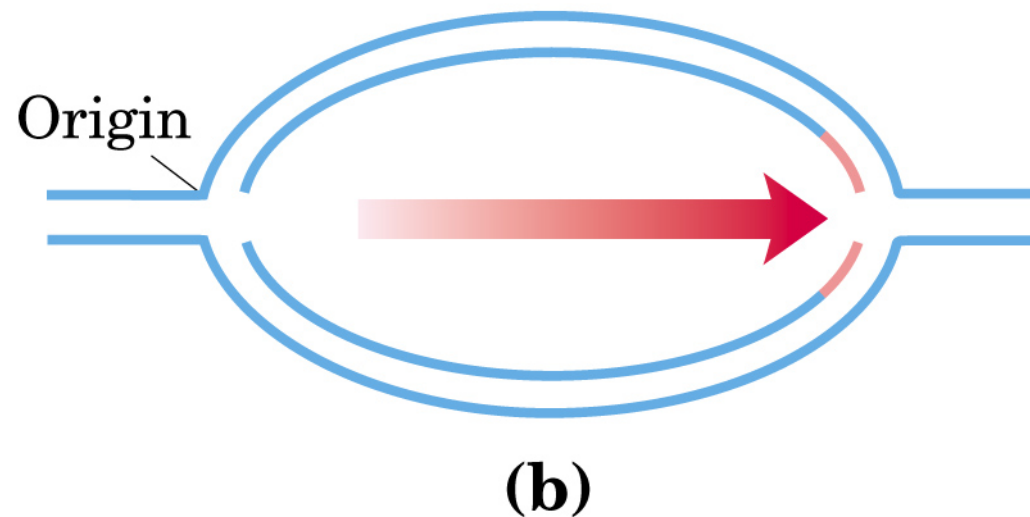
DNA extracted and centrifuged
to equilibrium in CsCl
density gradient

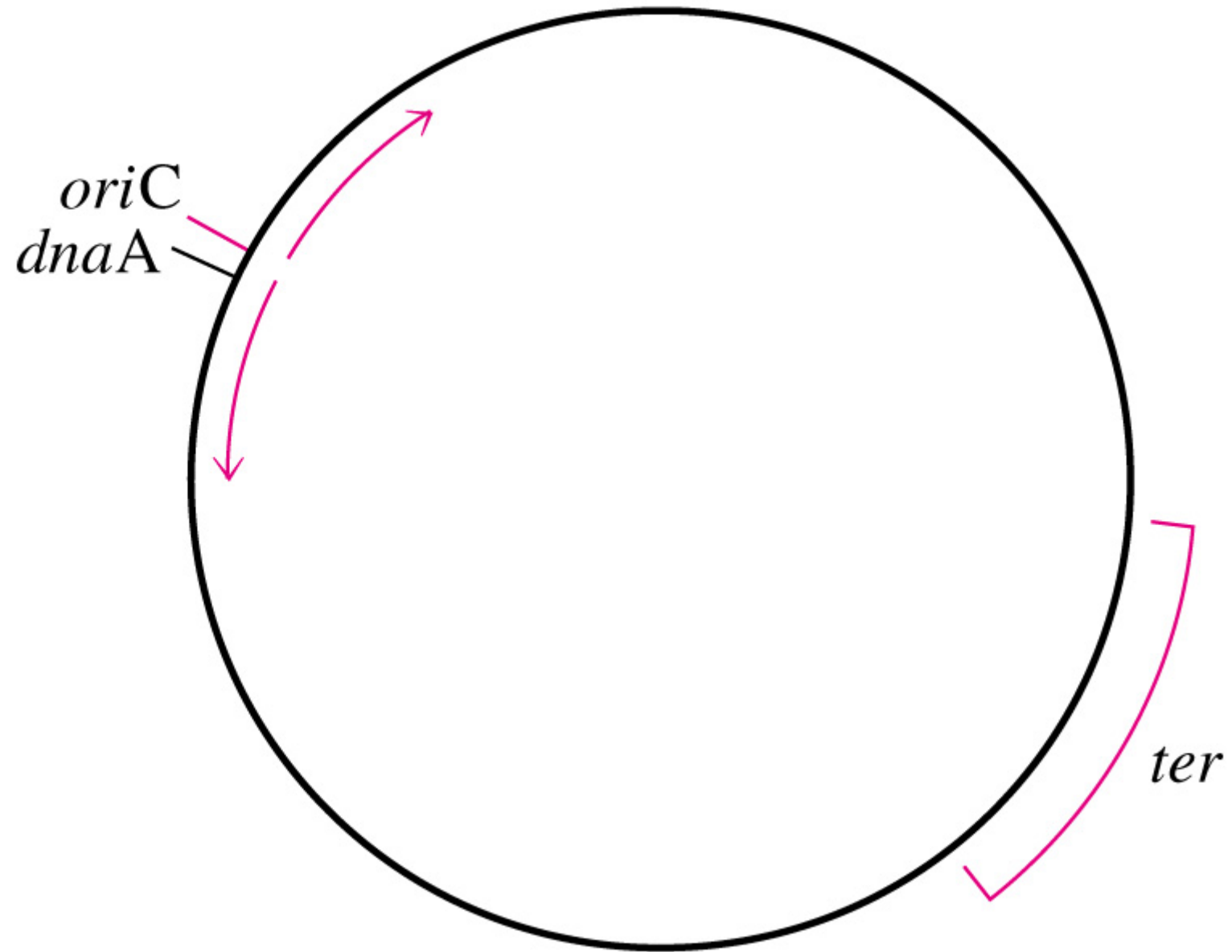


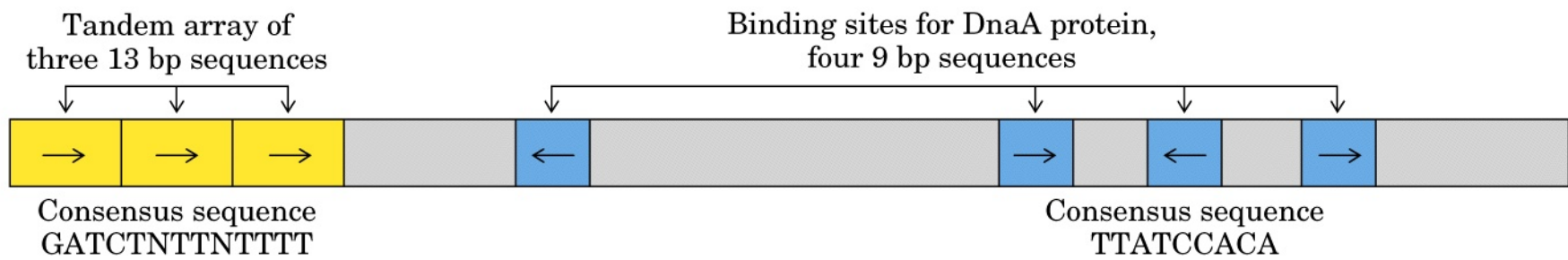
Bidirectional

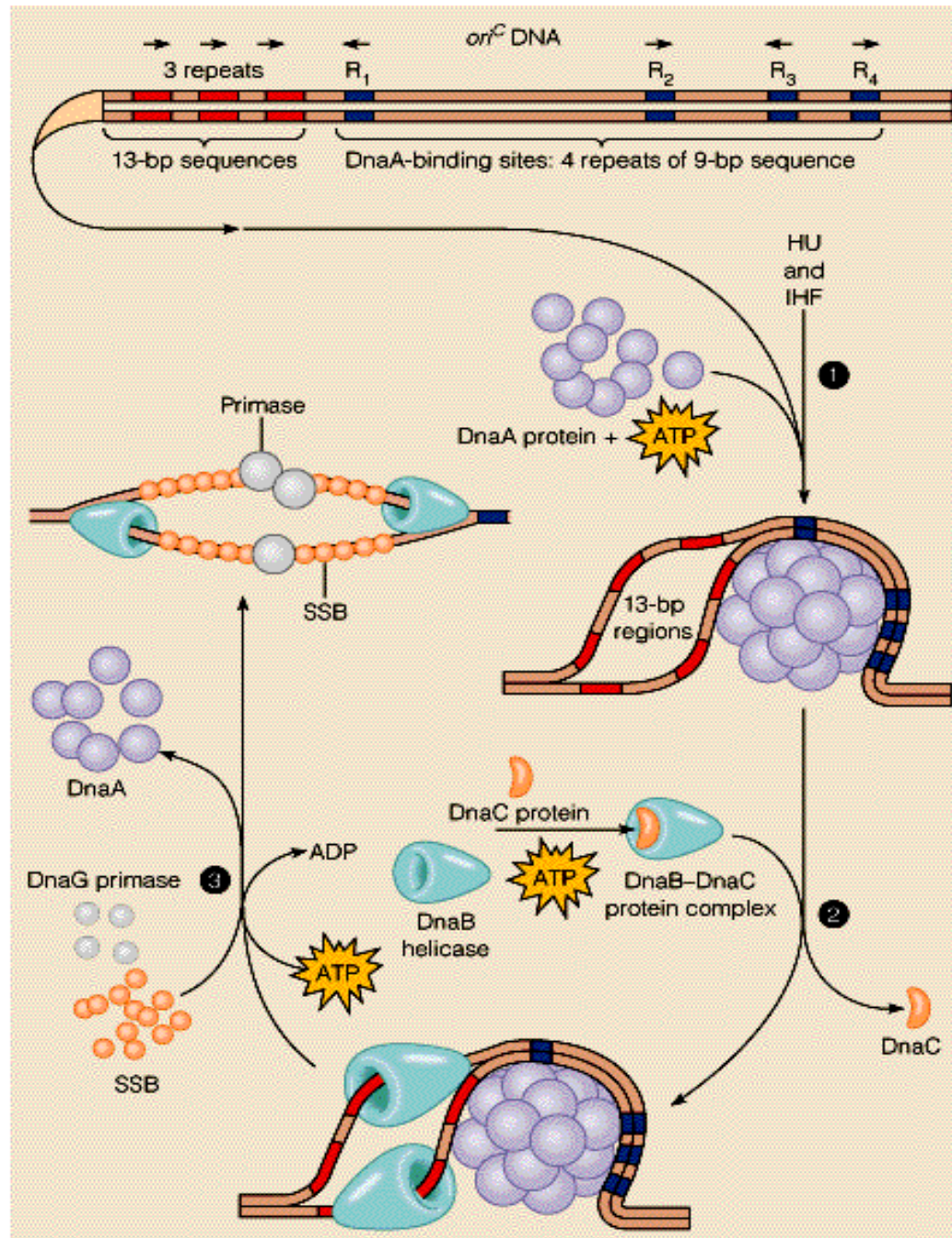


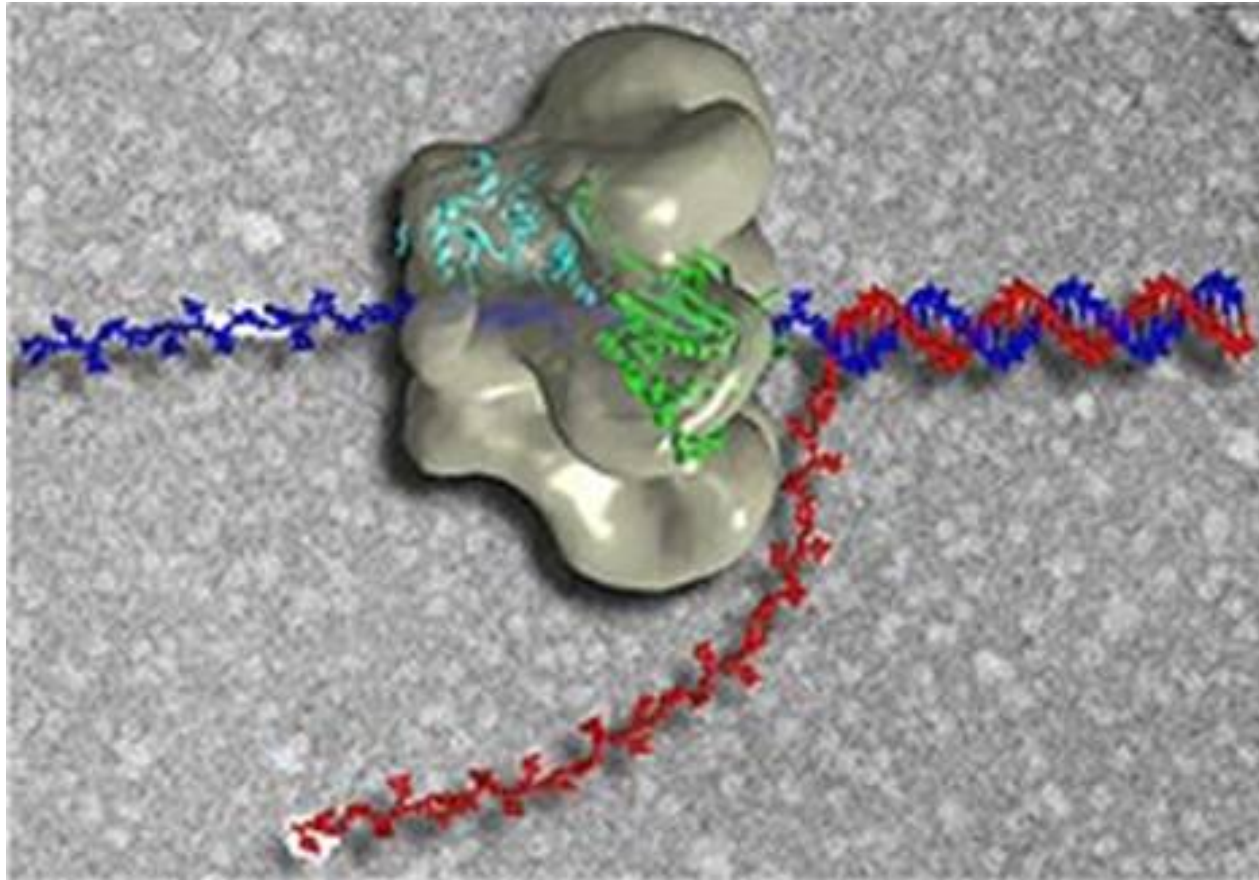
Unidirectional

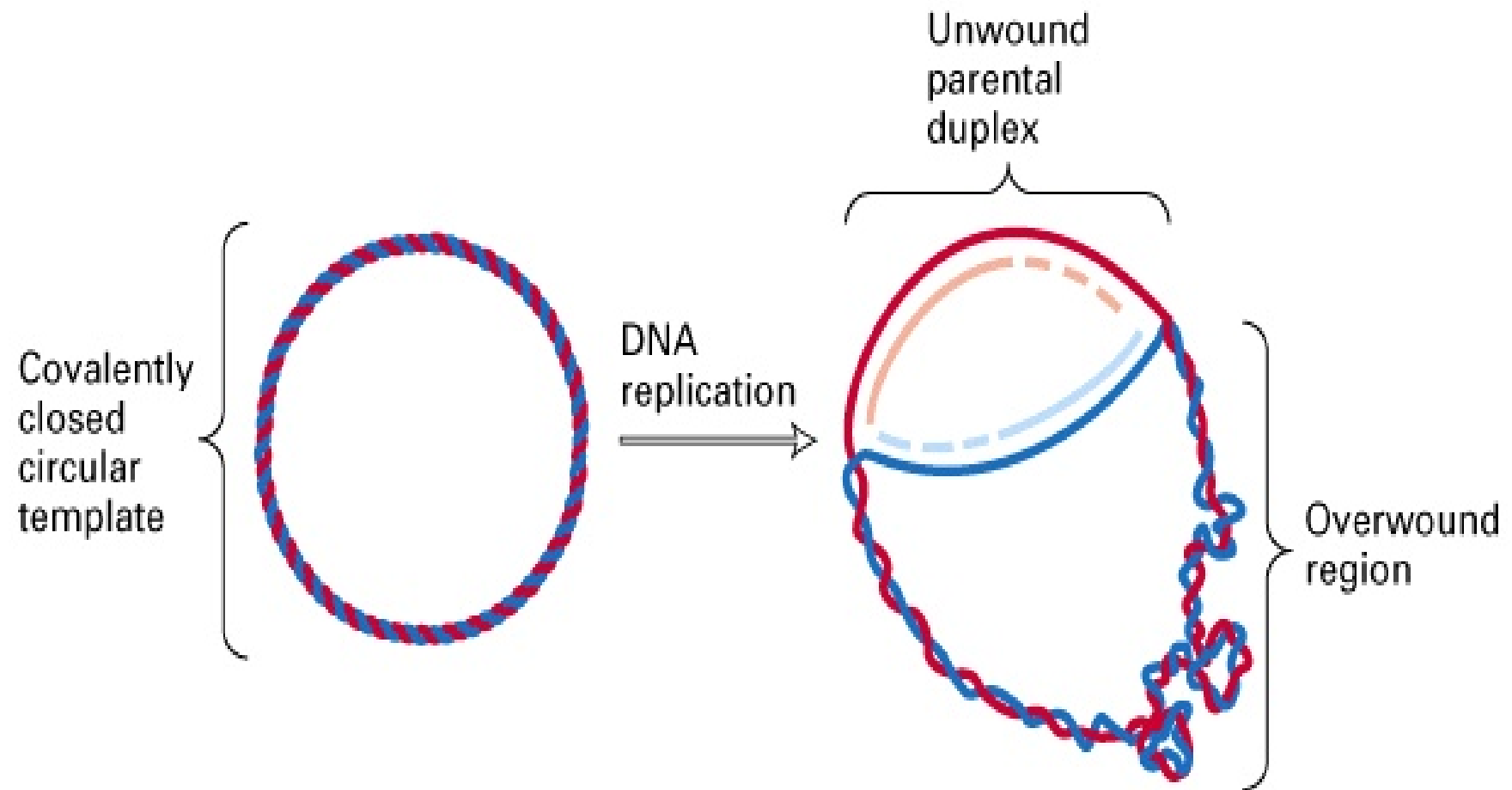


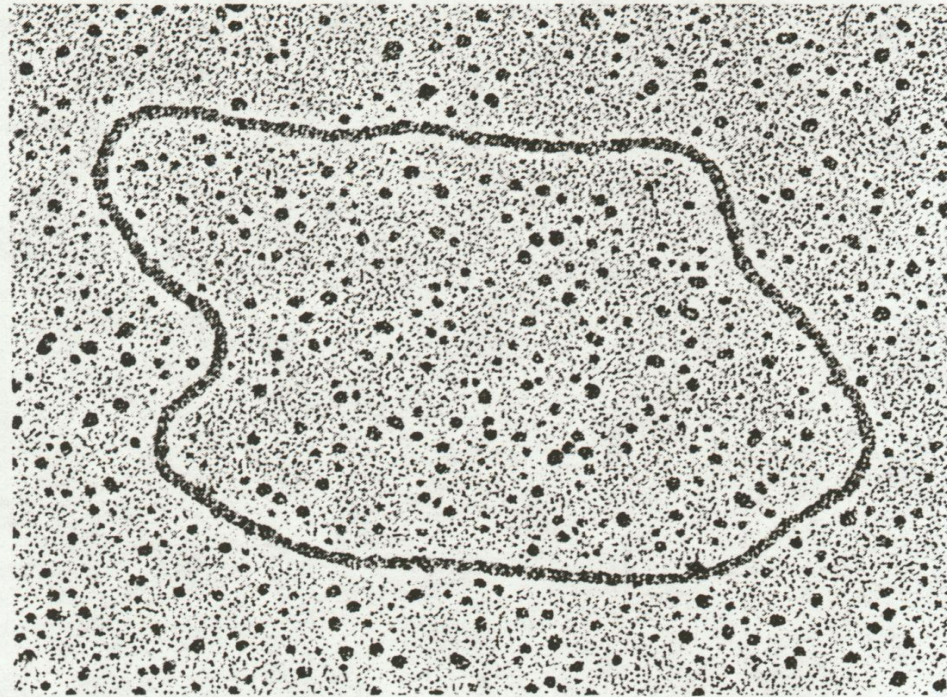




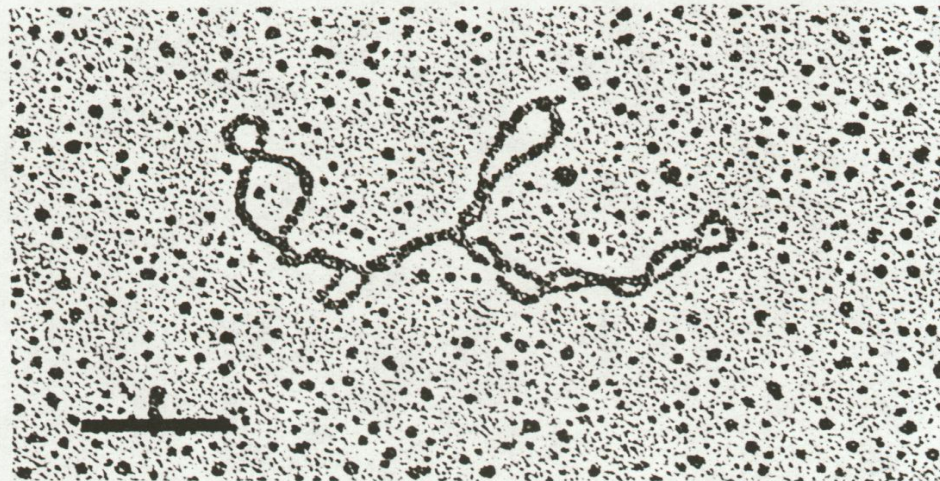




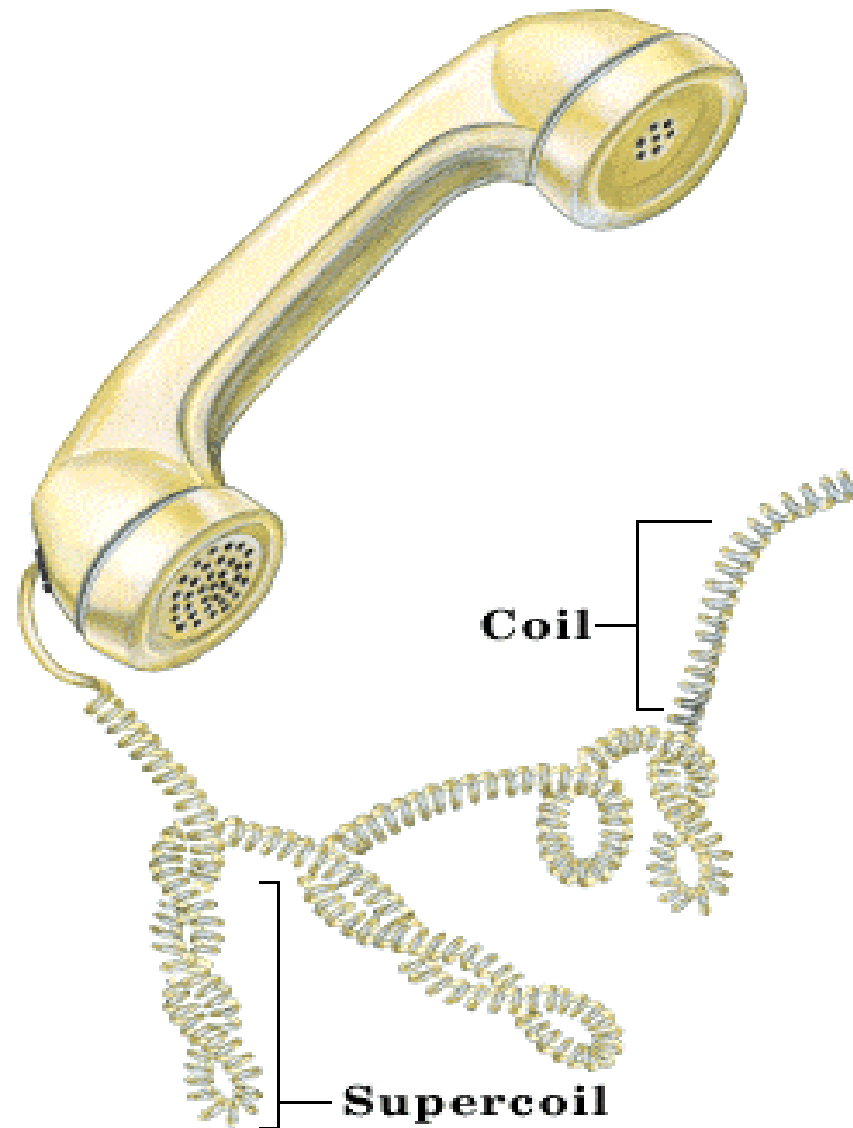


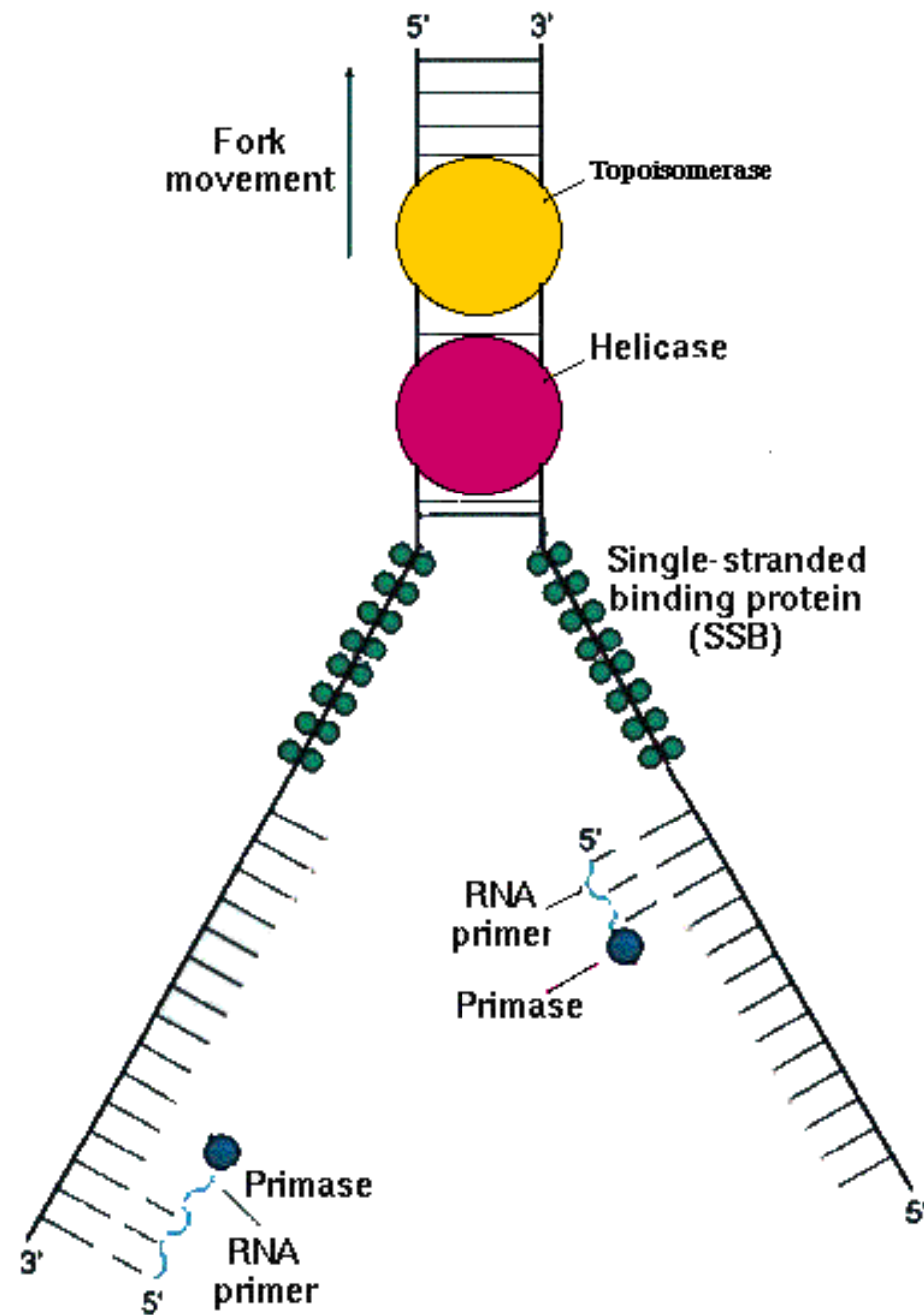


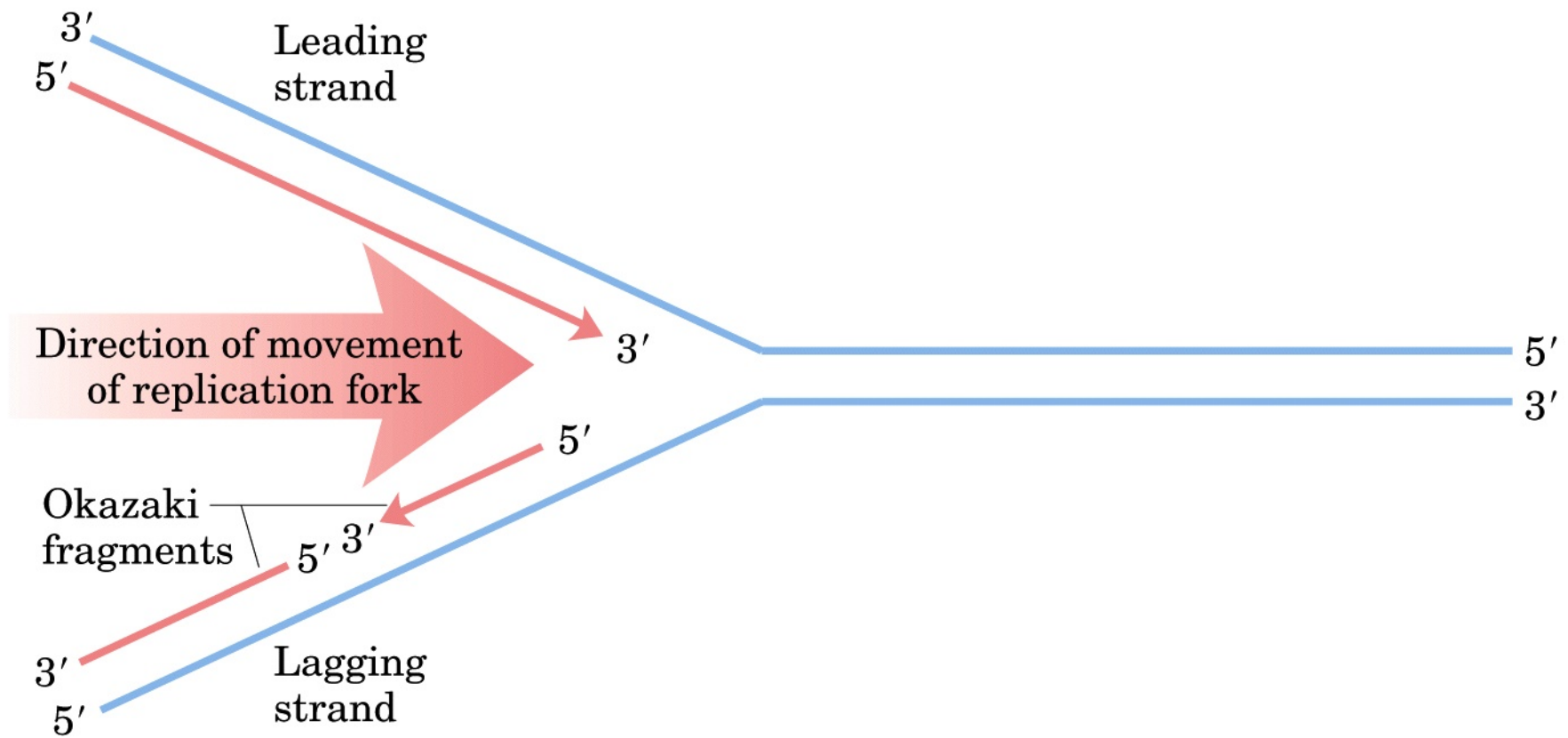
(a)



(b)

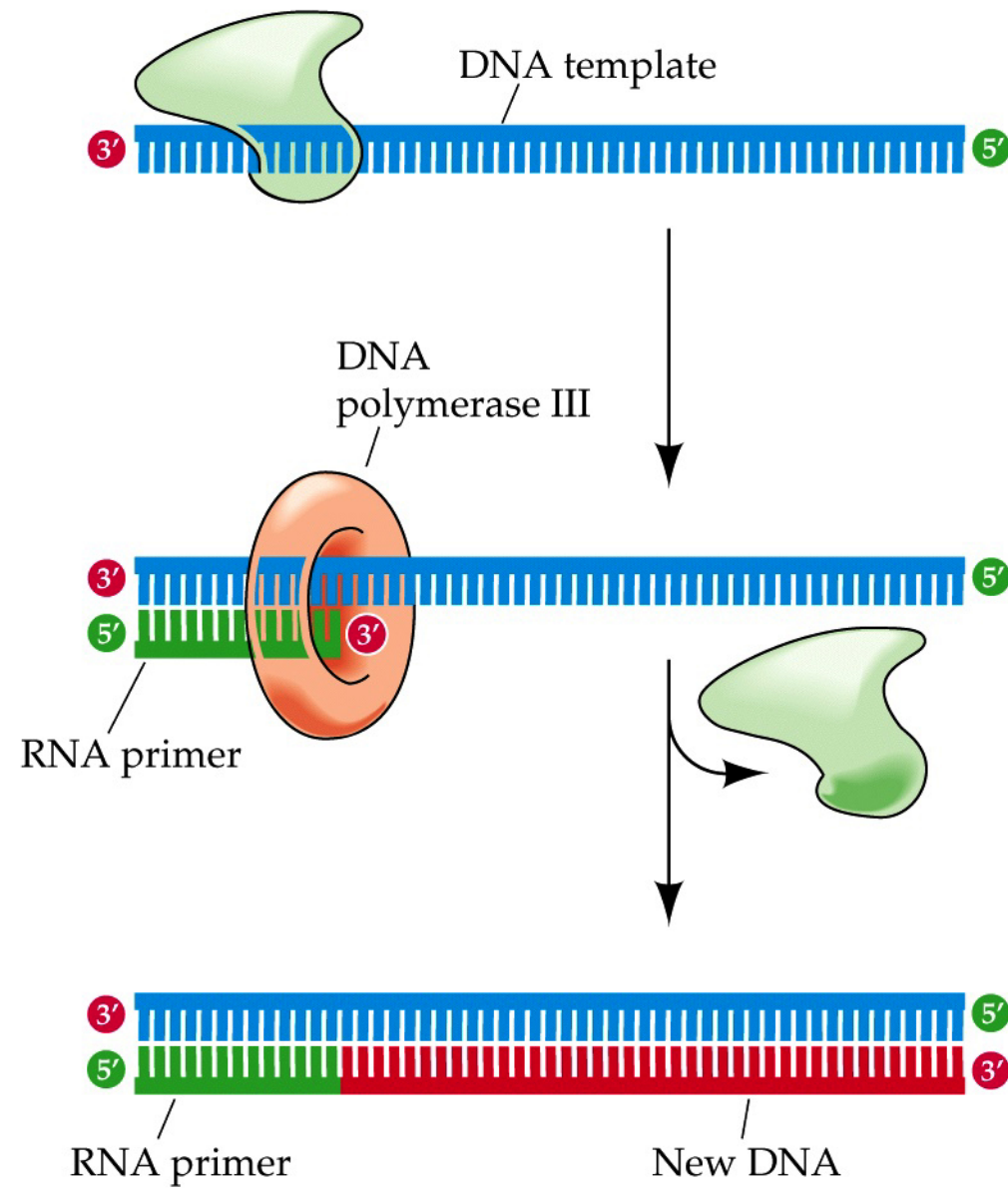




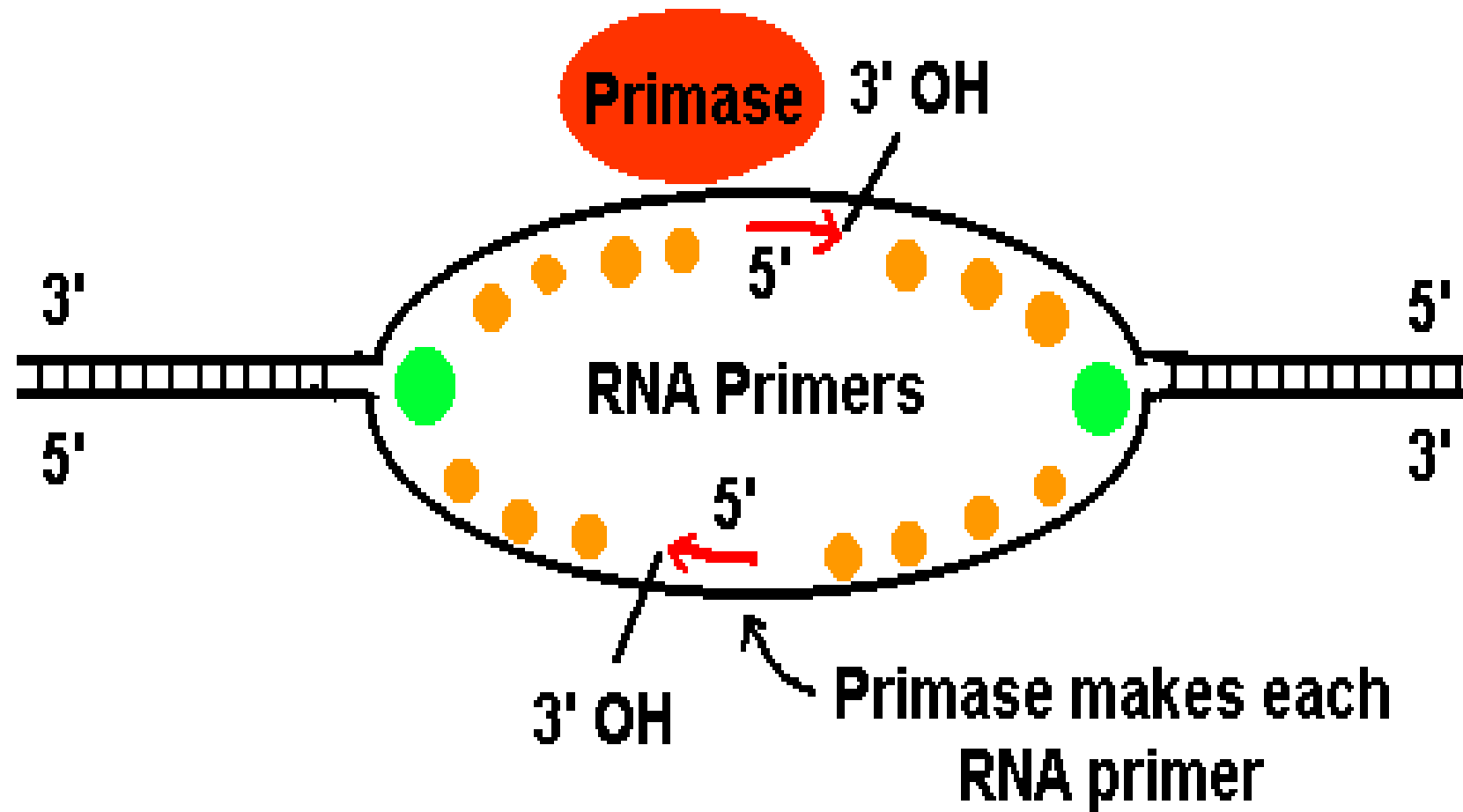


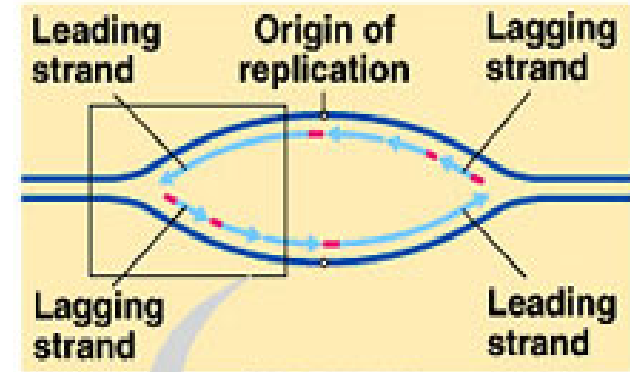
DNA polimerasas

- 1. Requieren una hebra de DNA molde (templado)**
- 2. Necesitan un partidor (primer)**
- 3. Utilizan d-ATP, d-GTP, d-CTP y d-TTP**
- 4. Polimerizan en sentido 5' a 3',
adicionando nucleótidos al extremo 3'
libre**



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OVERVIEW

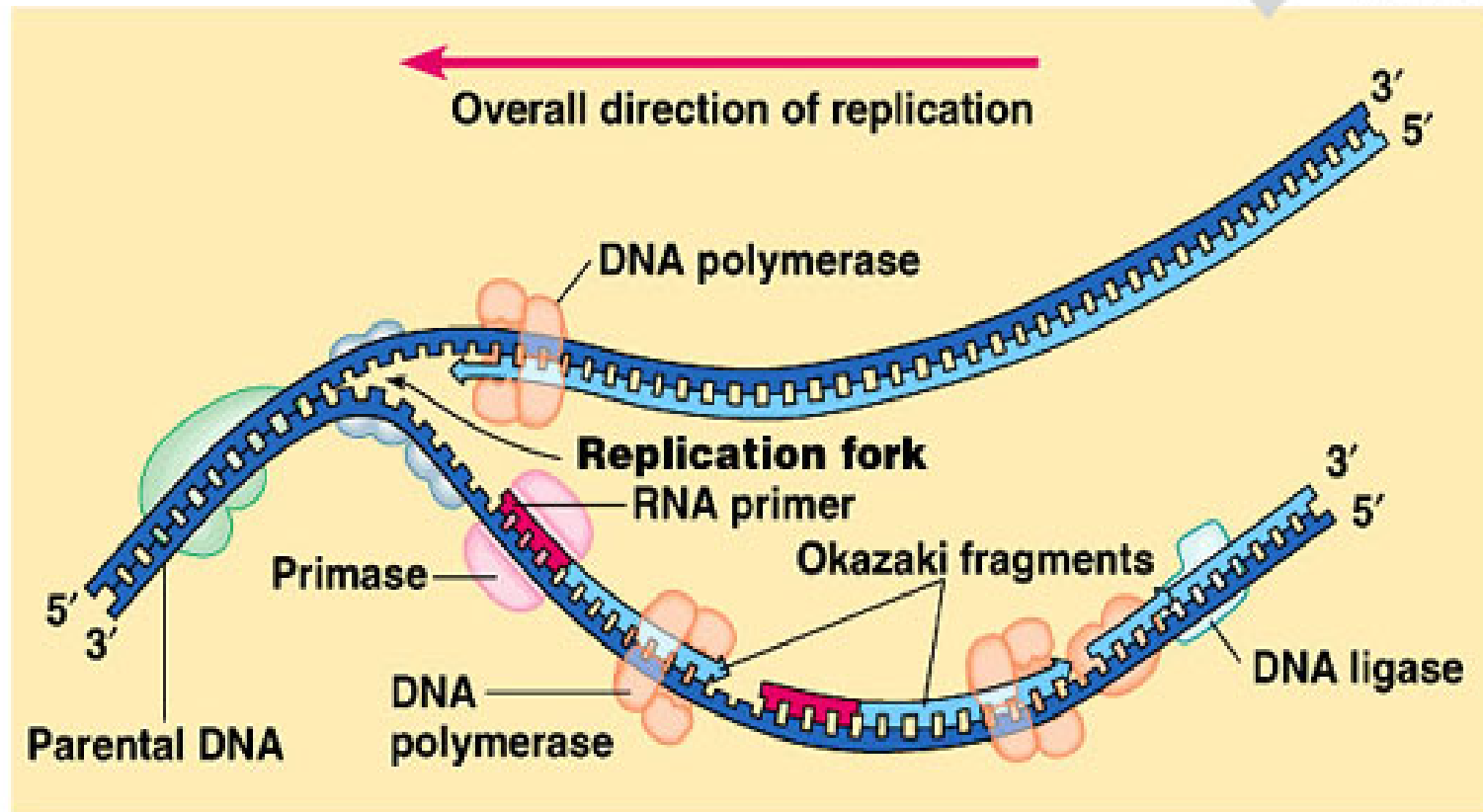


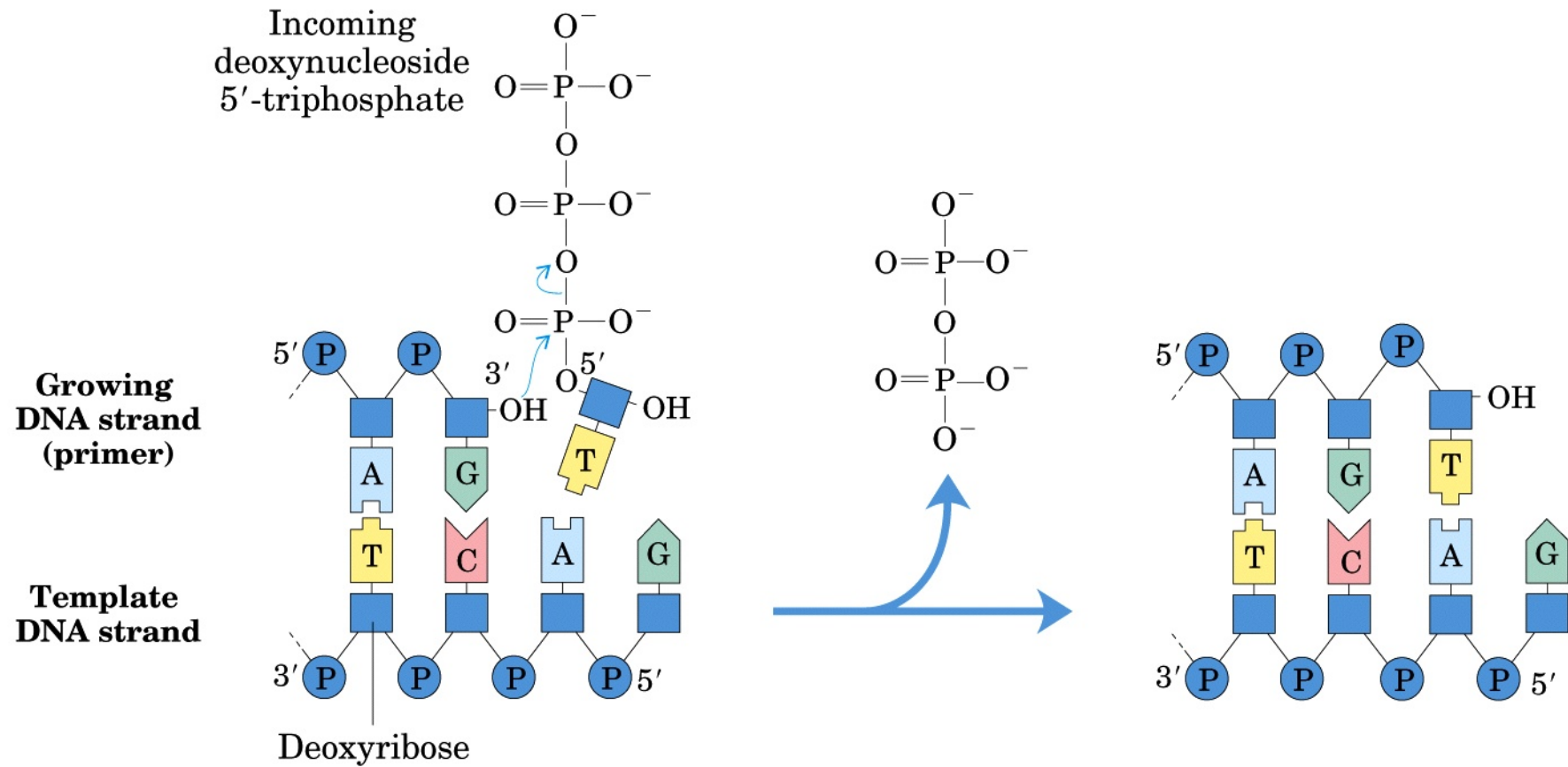
table 25–1

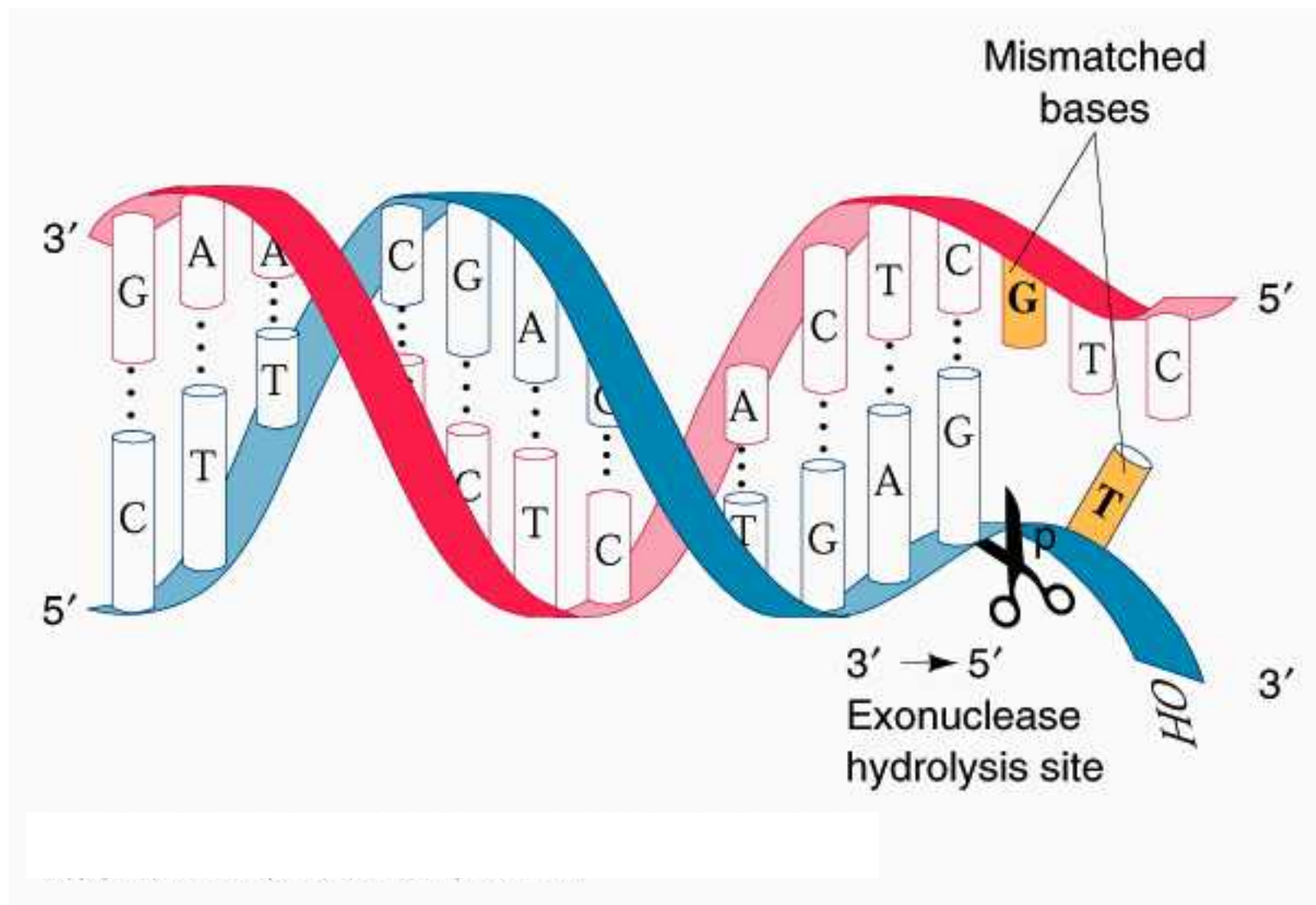
Comparison of DNA Polymerases of *E. coli*

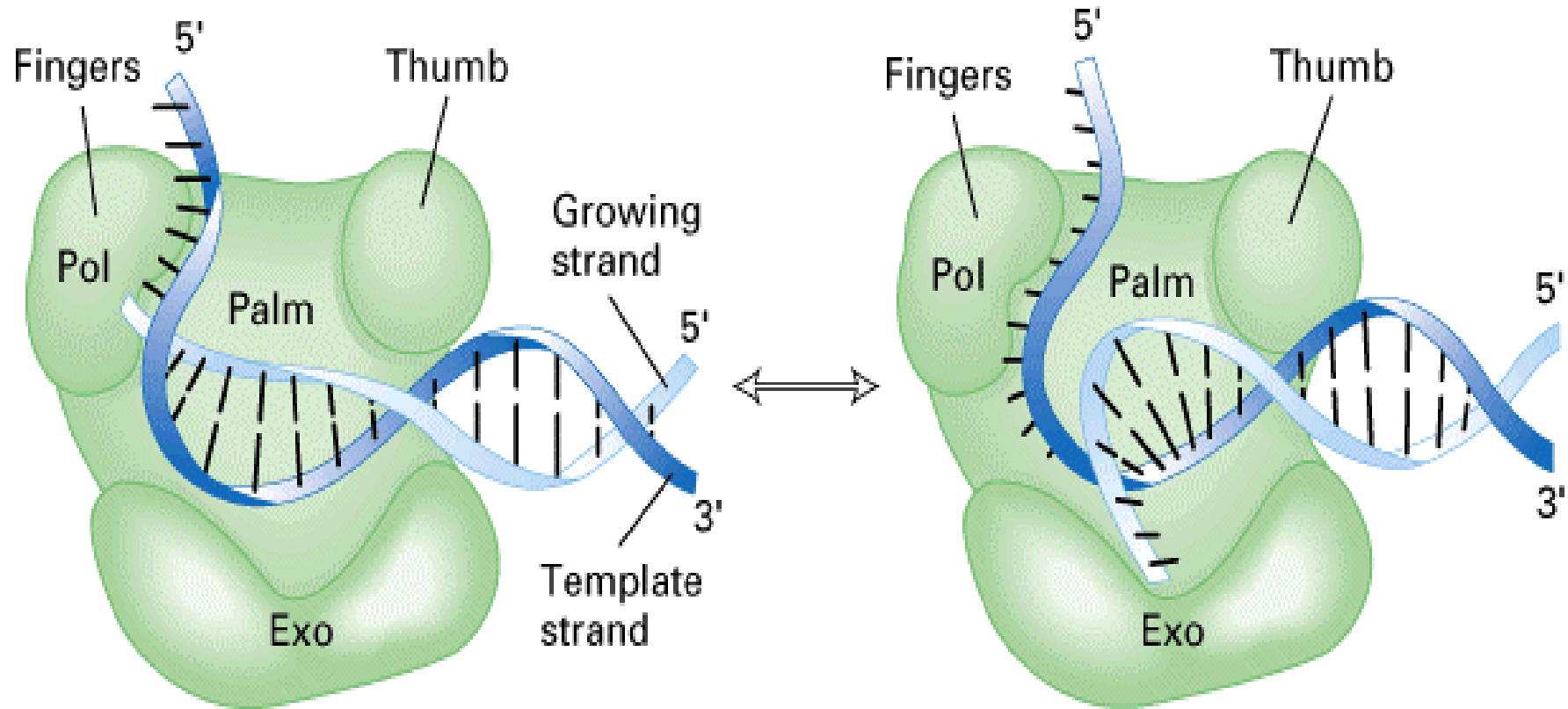
	DNA polymerase		
	I	II	III
Structural gene*	<i>polA</i>	<i>polB</i>	<i>polC</i> (<i>dnaE</i>)
Subunits (number of different types)	1	≥4	≥10
M_r	103,000	88,000 [†]	830,000
3'→5' Exonuclease (proofreading)	Yes	Yes	Yes
5'→3' Exonuclease	Yes	No	No
Polymerization rate (nucleotides/sec)	16–20	40	250–1,000
Processivity (nucleotides added before polymerase dissociates)	3–200	1,500	≥500,000

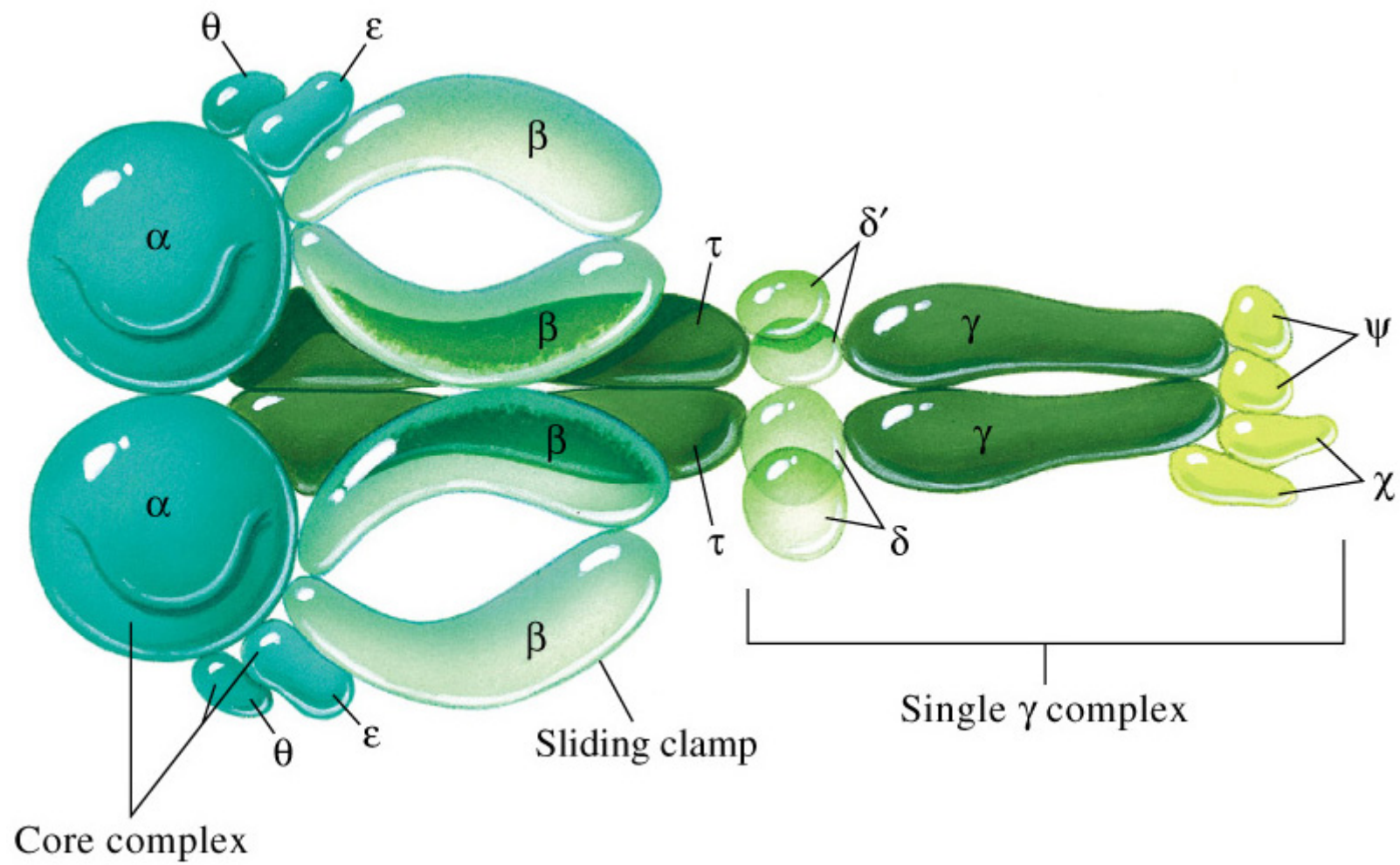
*For enzymes with more than one subunit, the gene listed here encodes the subunit with polymerization activity. Note that *dnaE* is an earlier designation of the gene now referred to as *polC*.

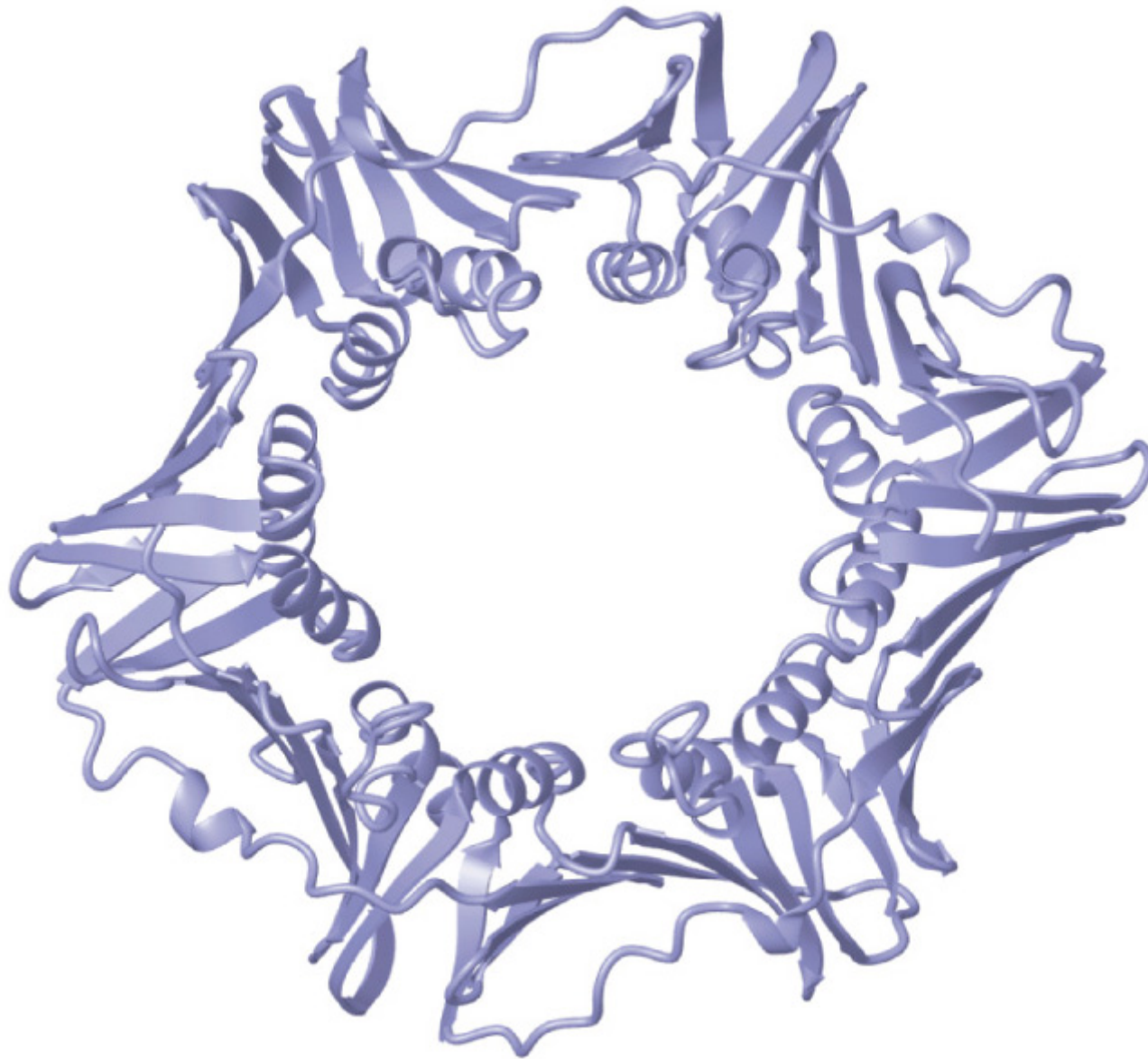
[†]Polymerization subunit only. DNA polymerase II shares several subunits with DNA polymerase III, including the β , γ , δ , δ' , χ , and ψ subunits (see Table 25–2).

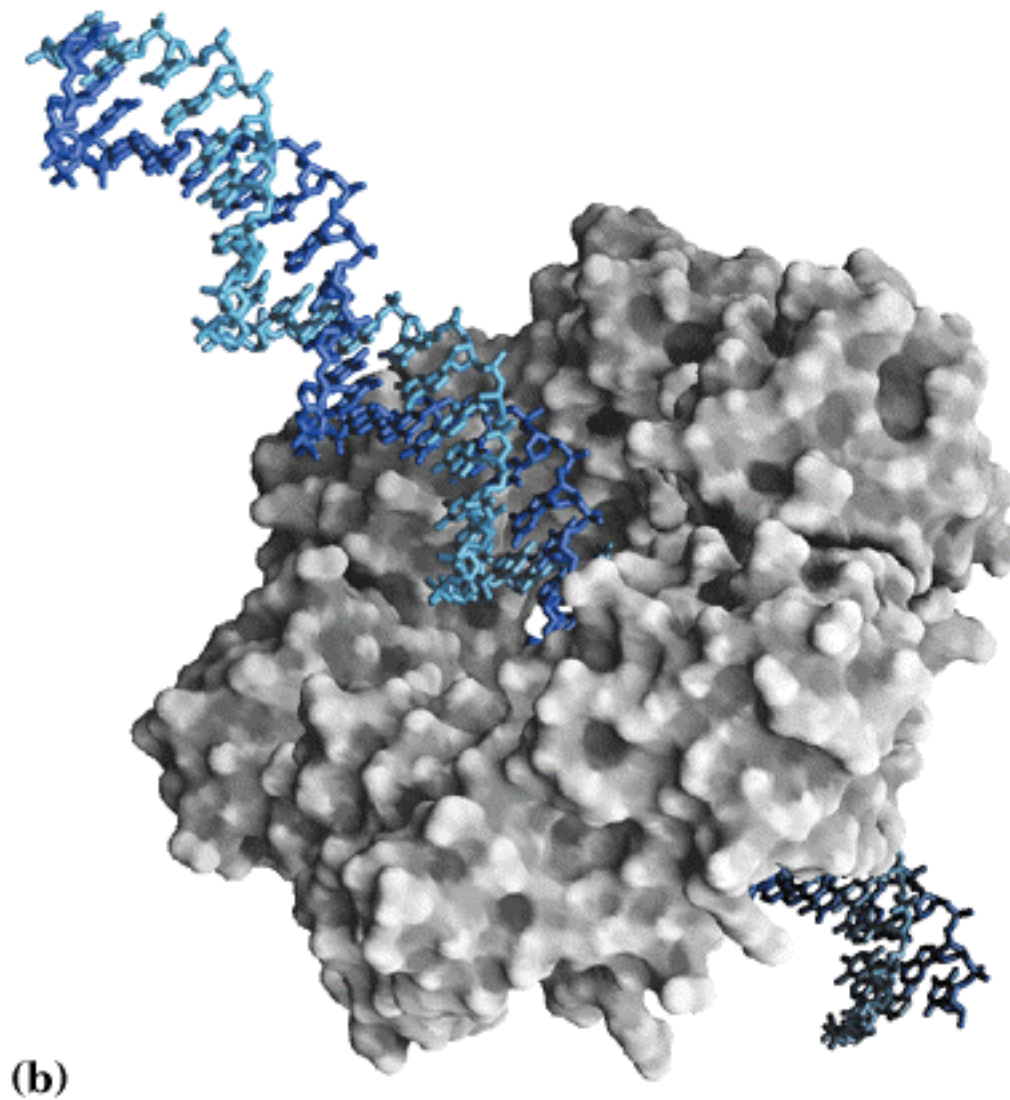




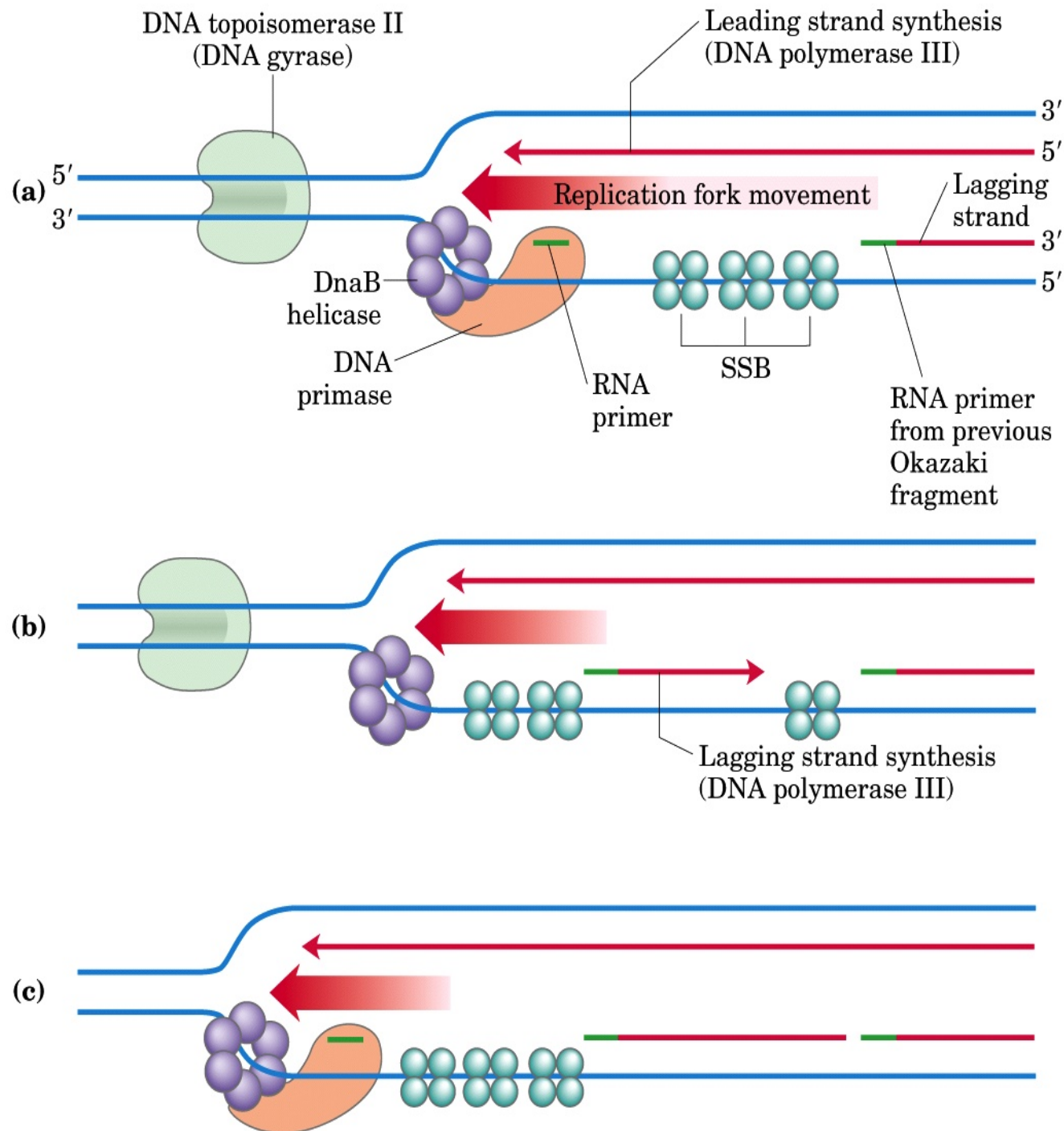


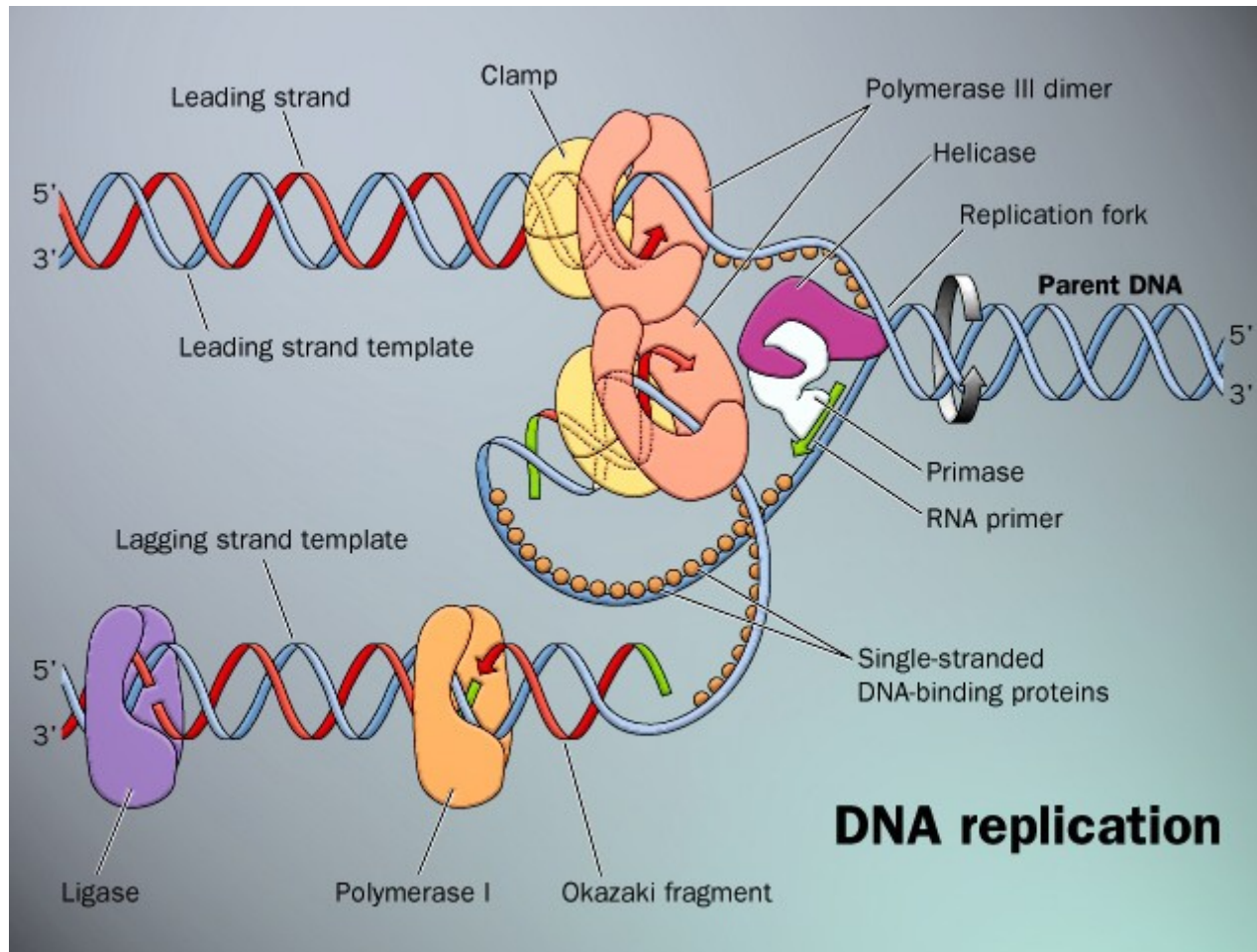


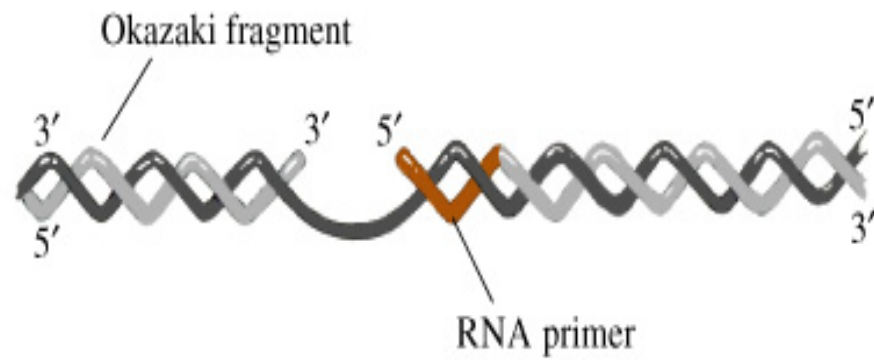
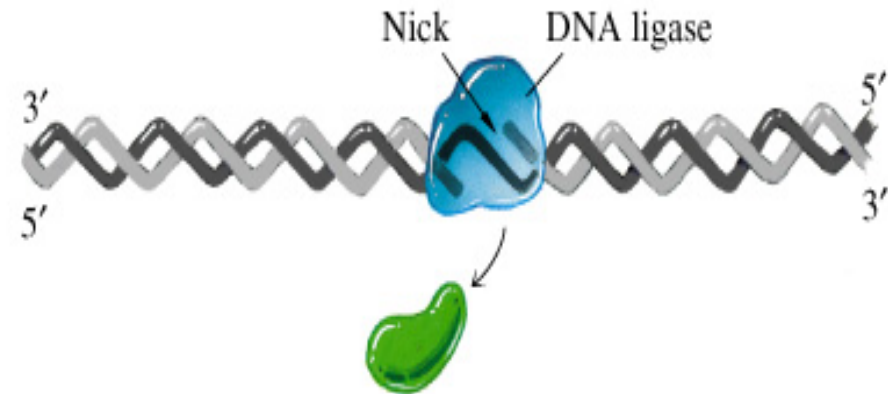
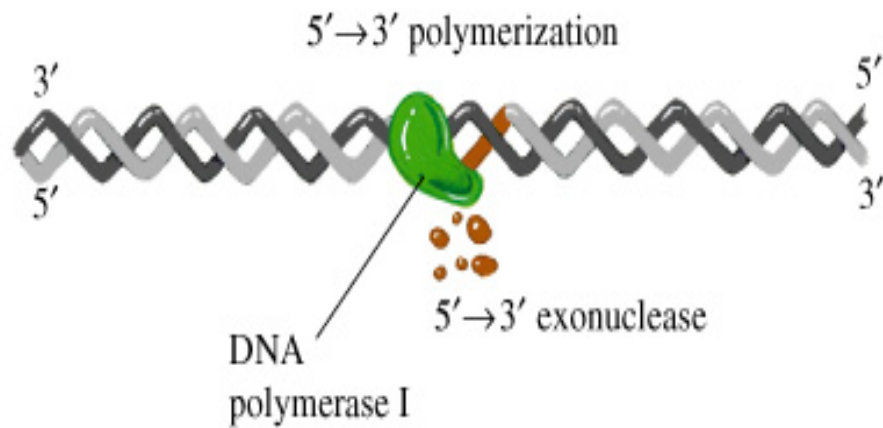
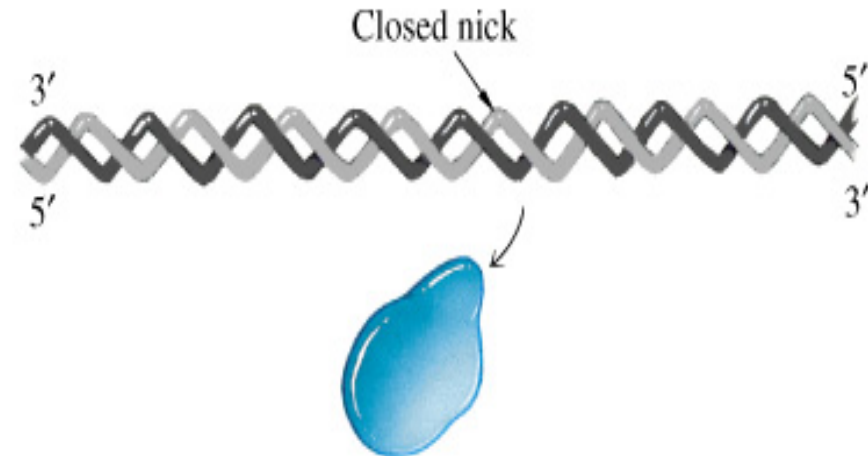


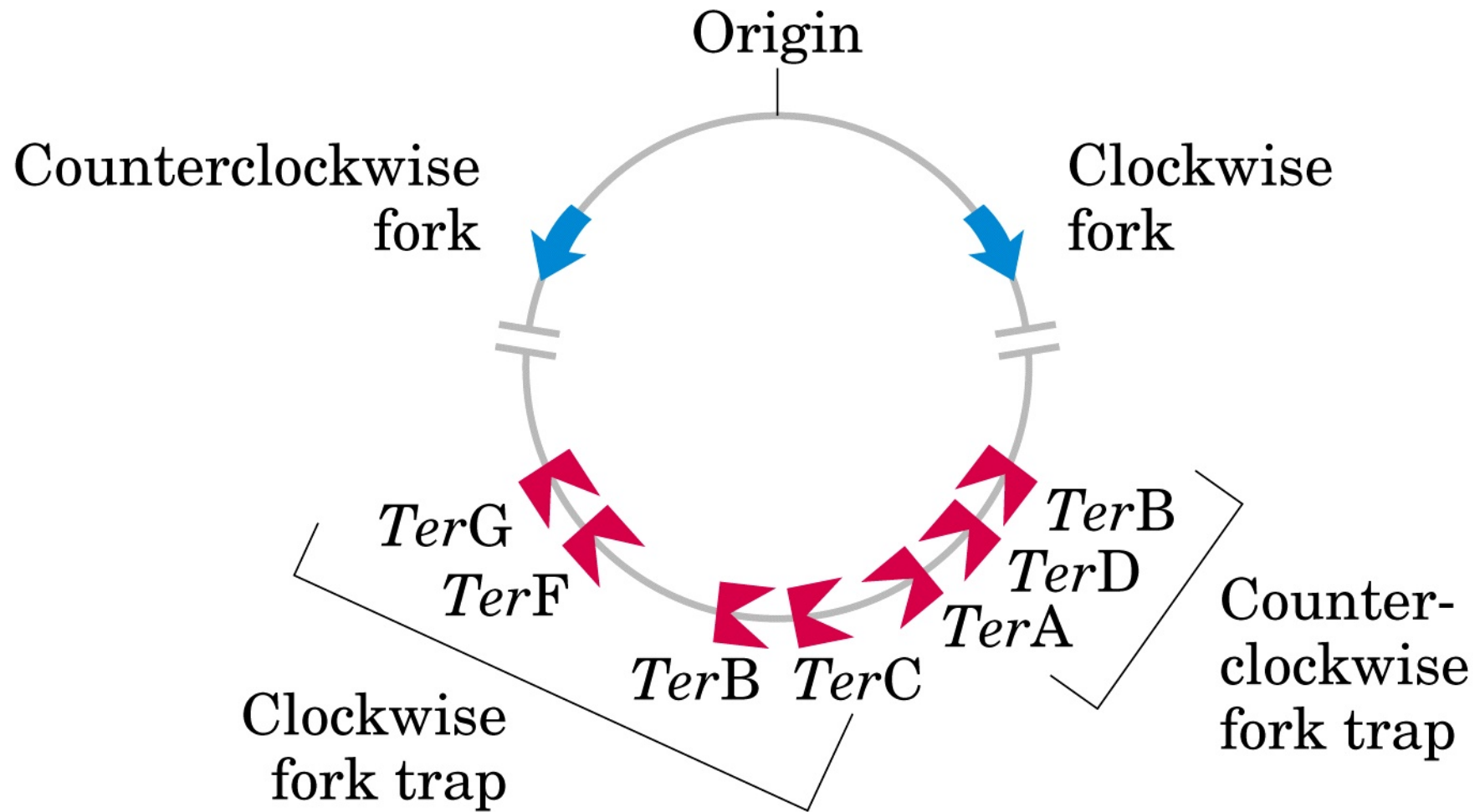


(b)

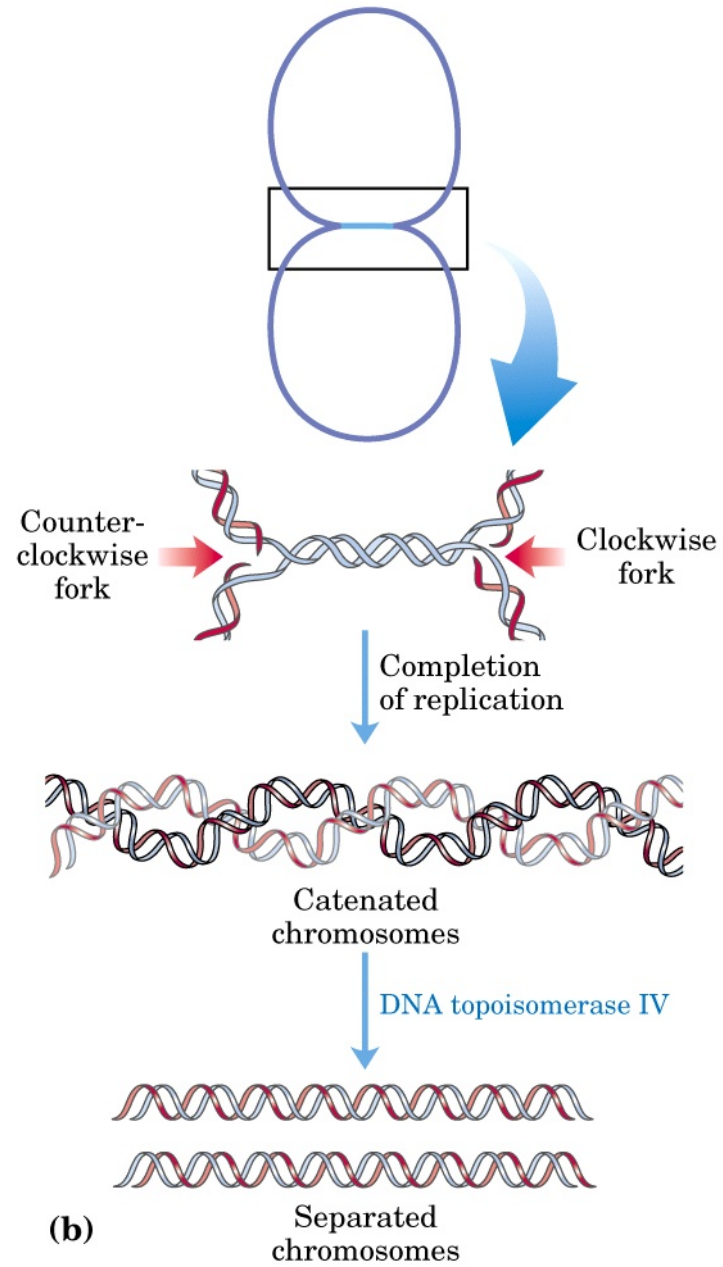


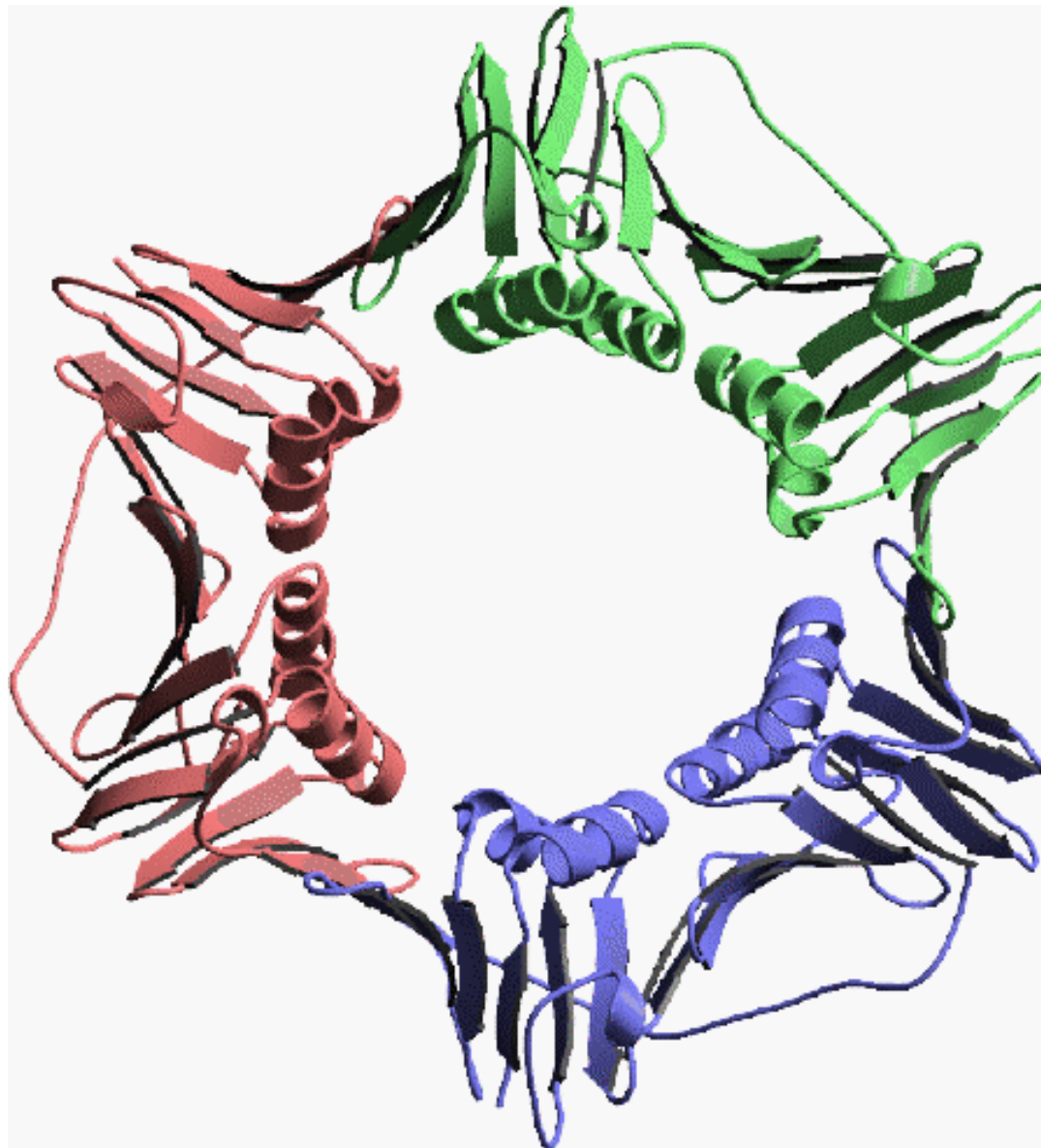


A**C****B****D**



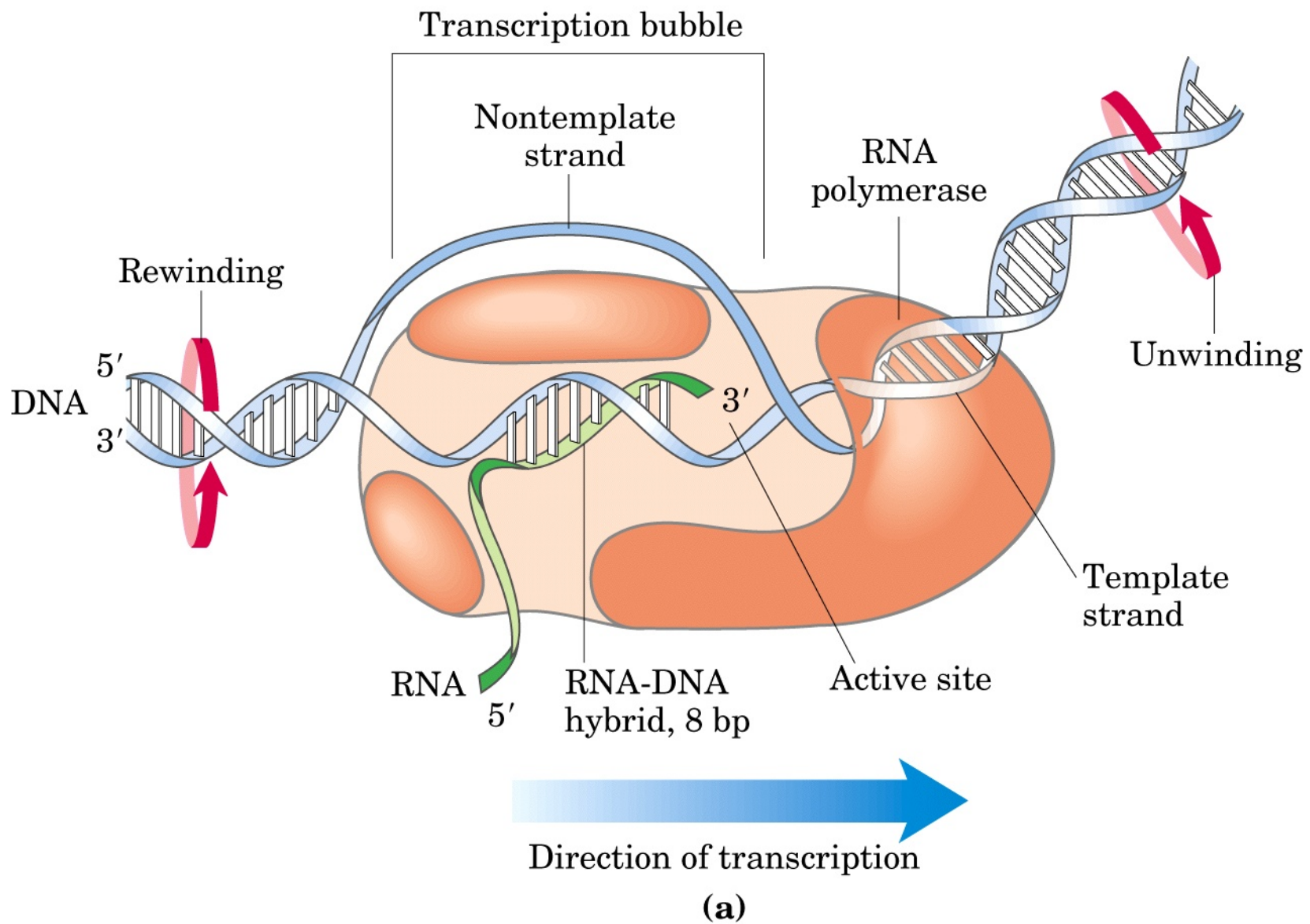
(a)

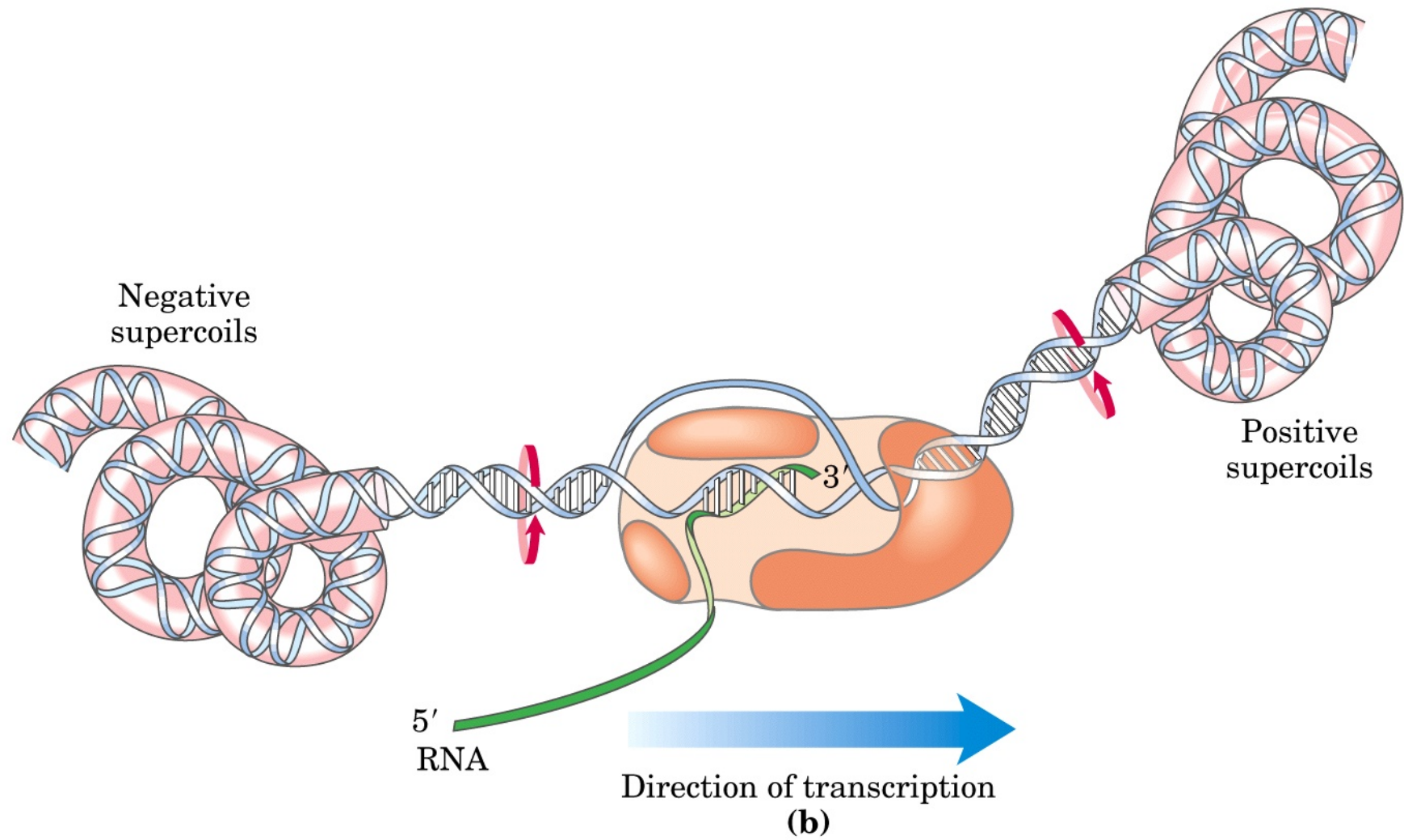




FIN

TRANSCRIPCION





(5') CGCTATAGCGTTT(3')

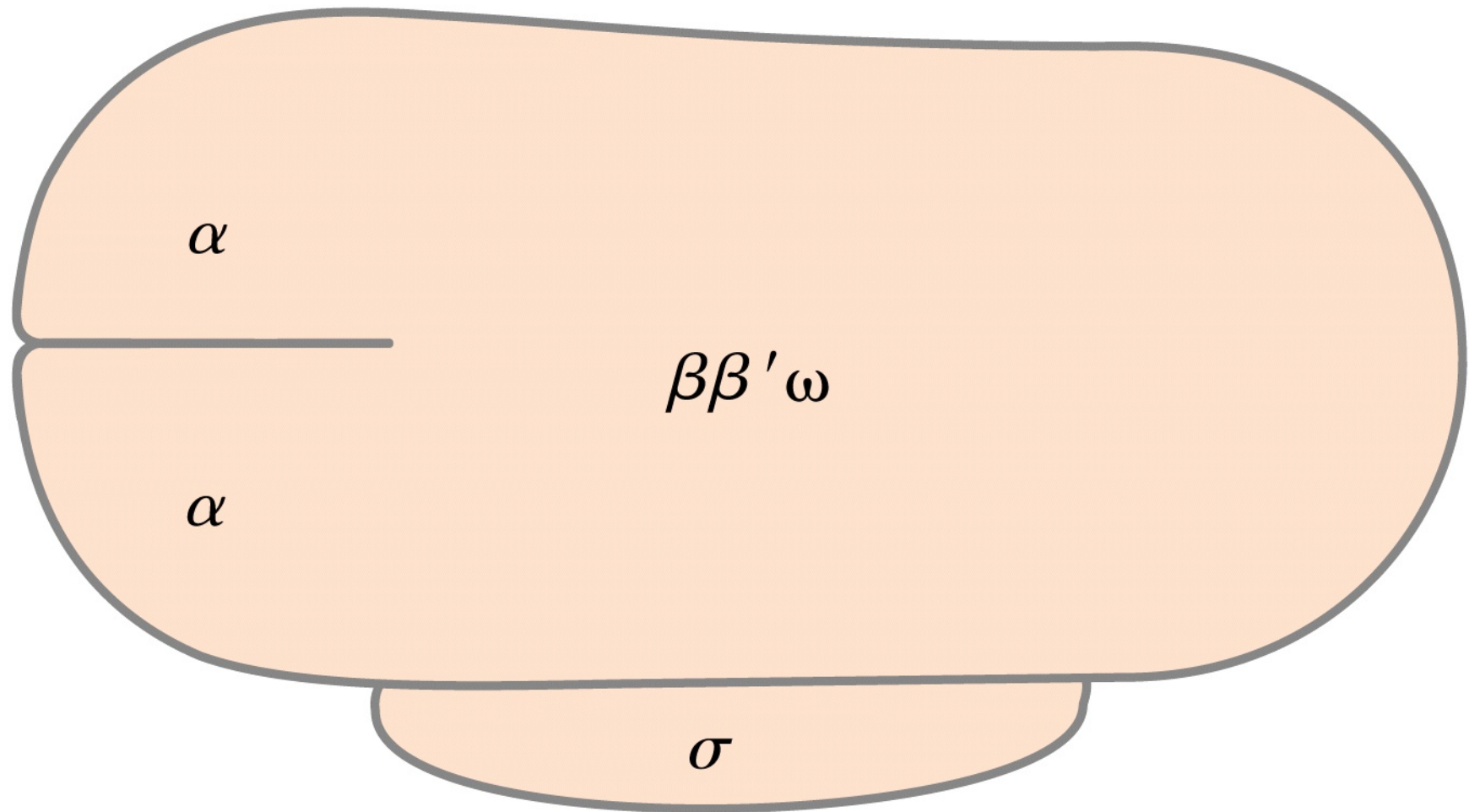
DNA nontemplate (coding) strand

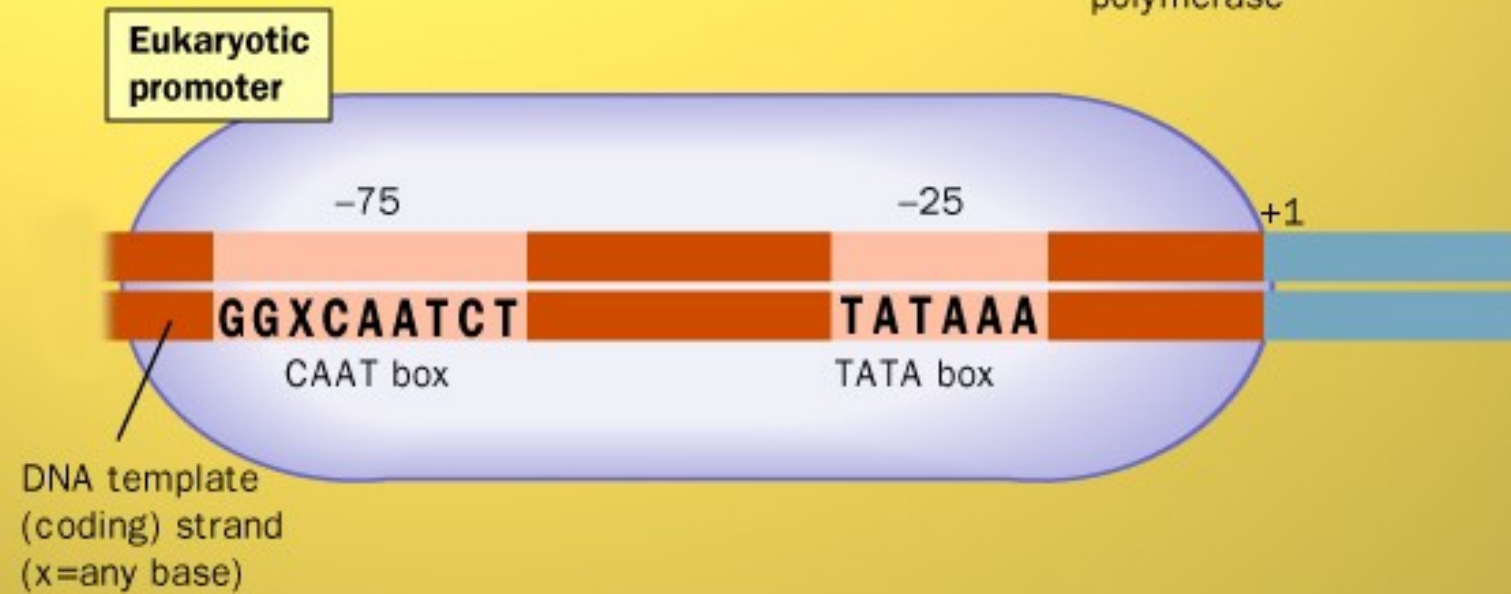
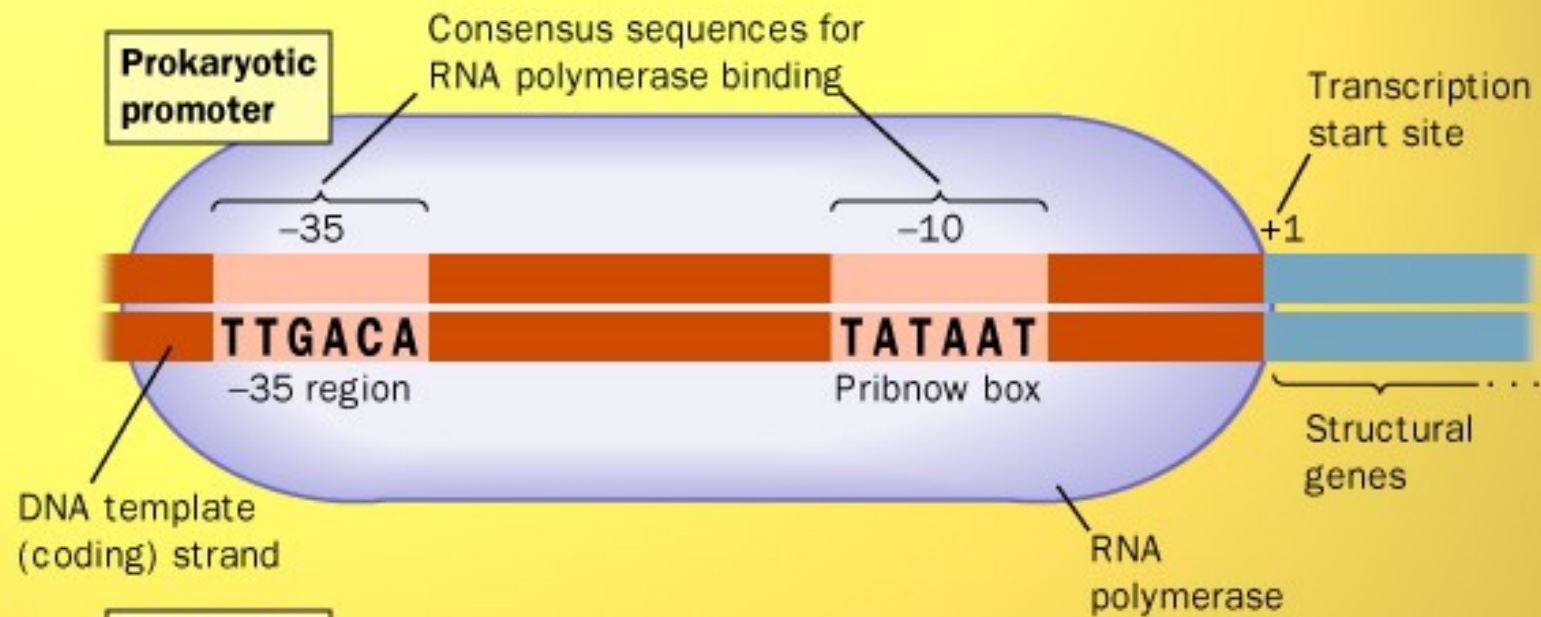
(3') GCGATATCGCAAA(5')

DNA template strand

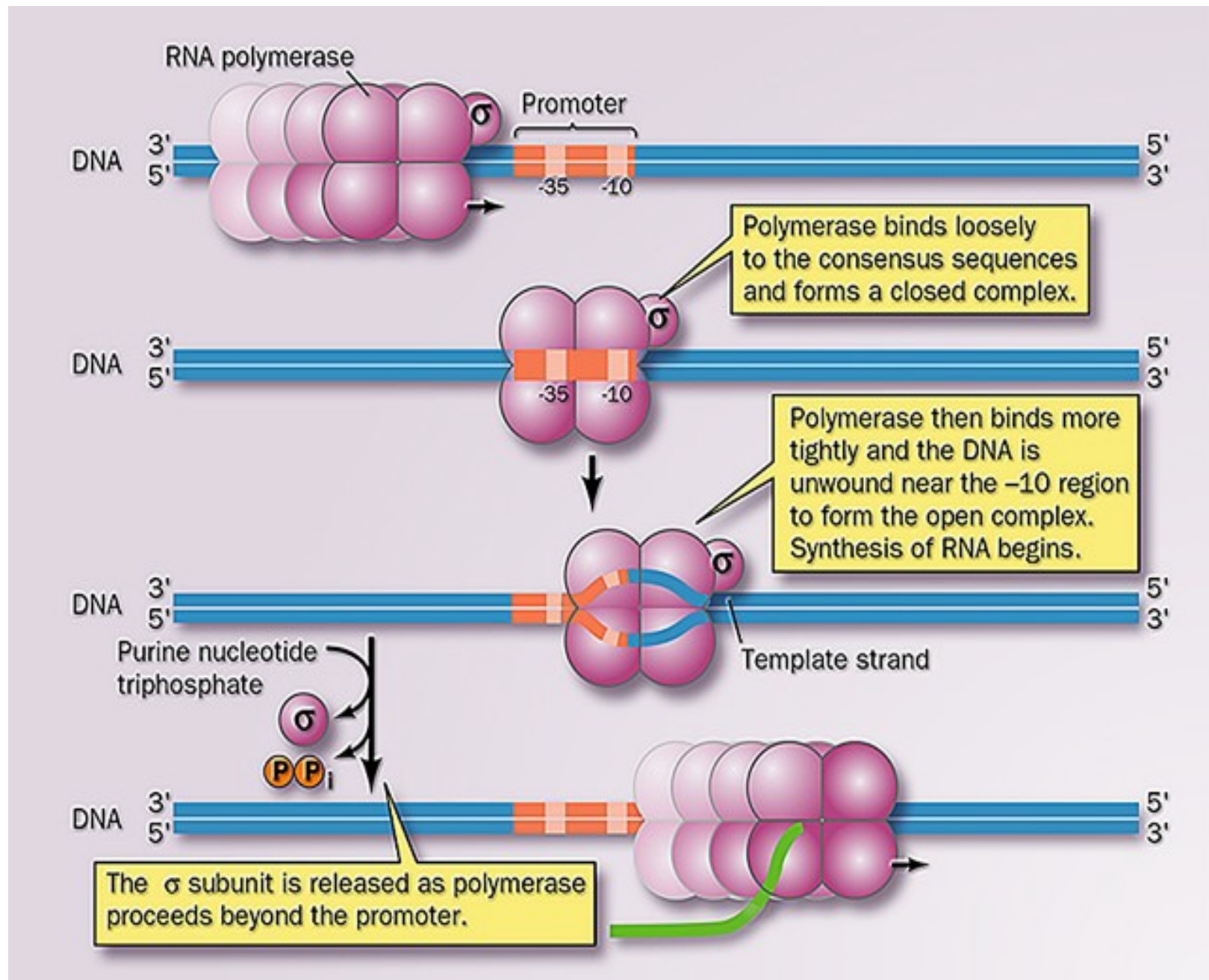
(5') CGCUAUAGCGUUU(3')

RNA transcript

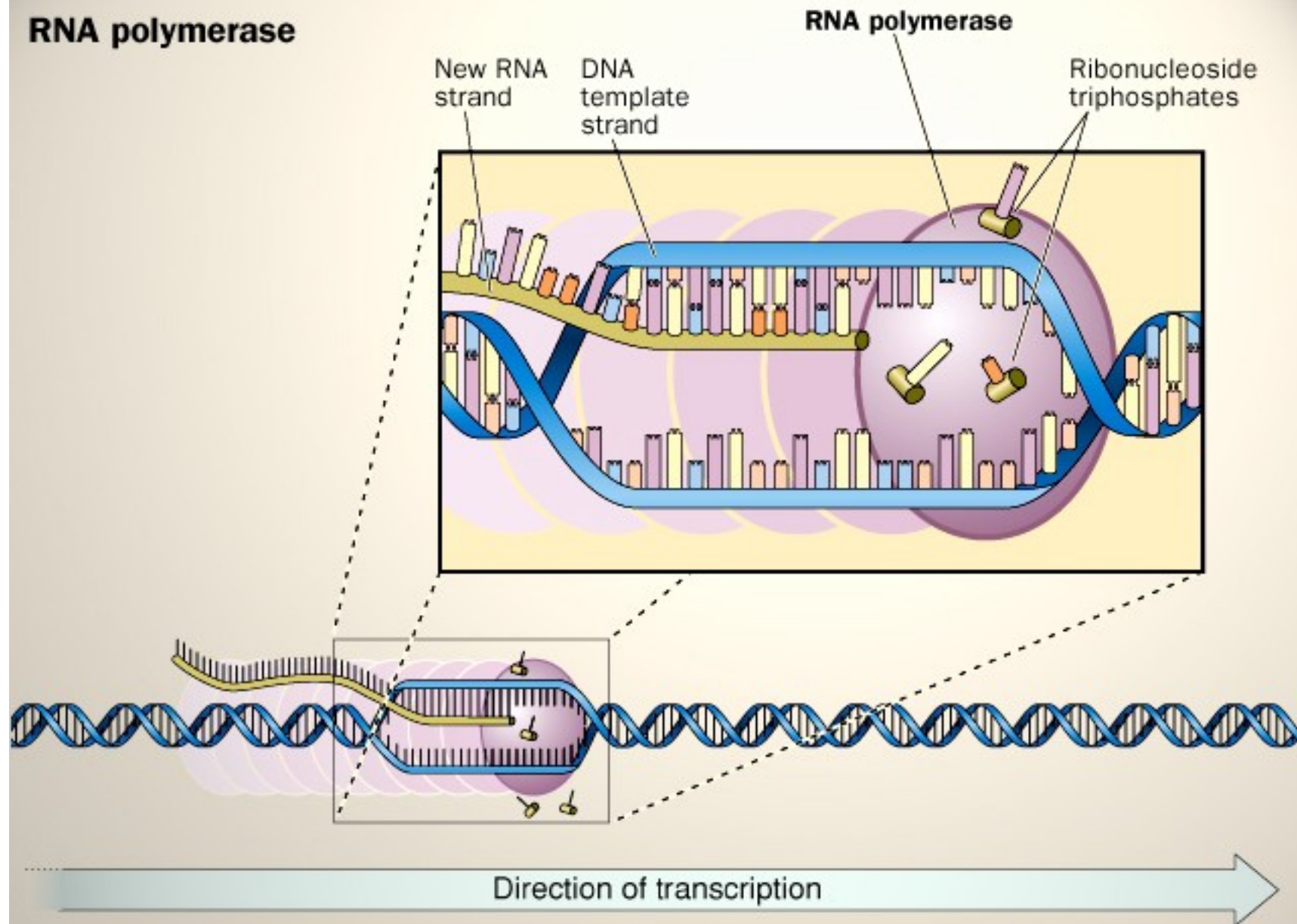




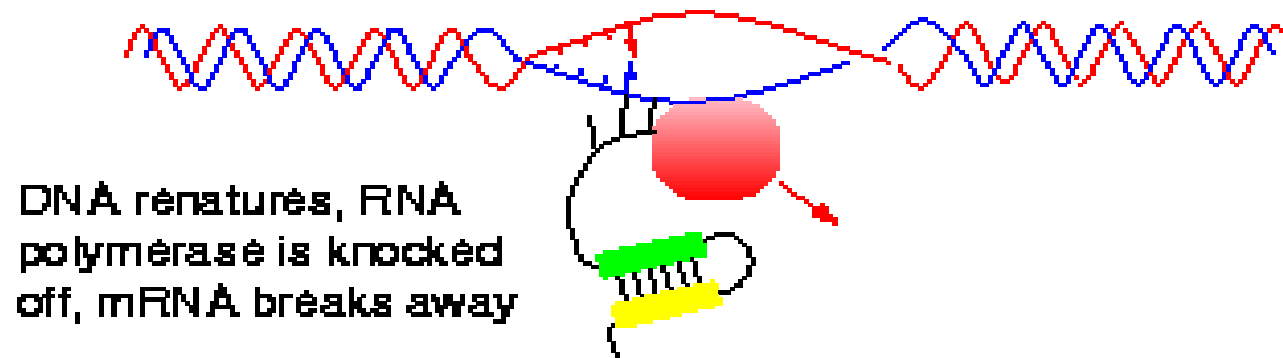
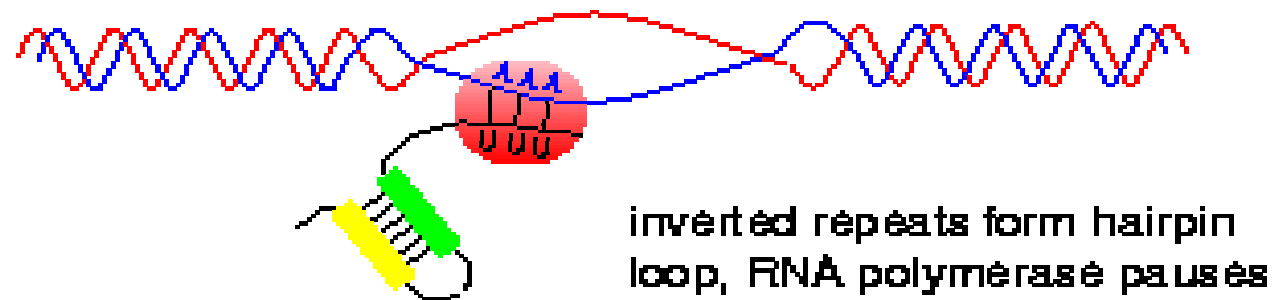
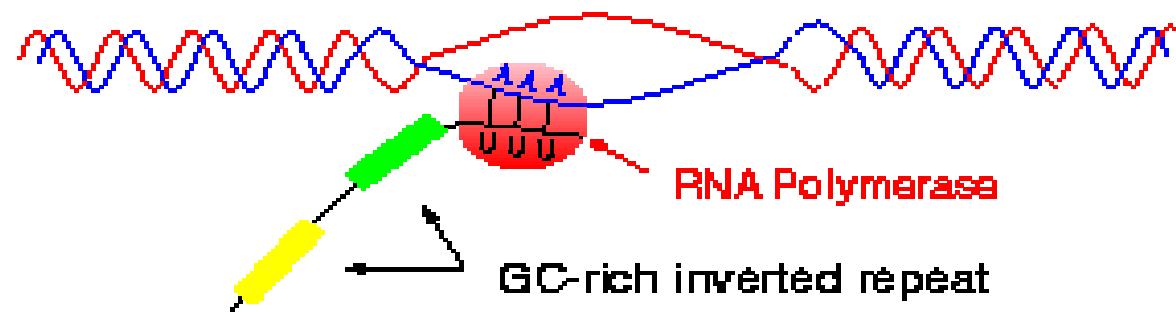
	UP element	-35 Region	Spacer	-10 Region	Spacer	RNA start
Consensus sequence	NNAAA ^{AA} _{TT} ^A _T TTTNNAAAANN	TTGACA	N ₁₇	TATAAT	N ₆	+1
<i>rrnB</i> P1	AGAAAATTATTTTAAATTCCT	GTGTCA	N ₁₆	TATAAT	N ₈	A
<i>trp</i>		TTGACA	N ₁₇	TTAACT	N ₇	A
<i>lac</i>		TTTACA	N ₁₇	TATGTT	N ₆	A
<i>recA</i>		TTGATA	N ₁₆	TATAAT	N ₇	A
<i>araBAD</i>		CTGACG	N ₁₈	TACTGT	N ₆	A

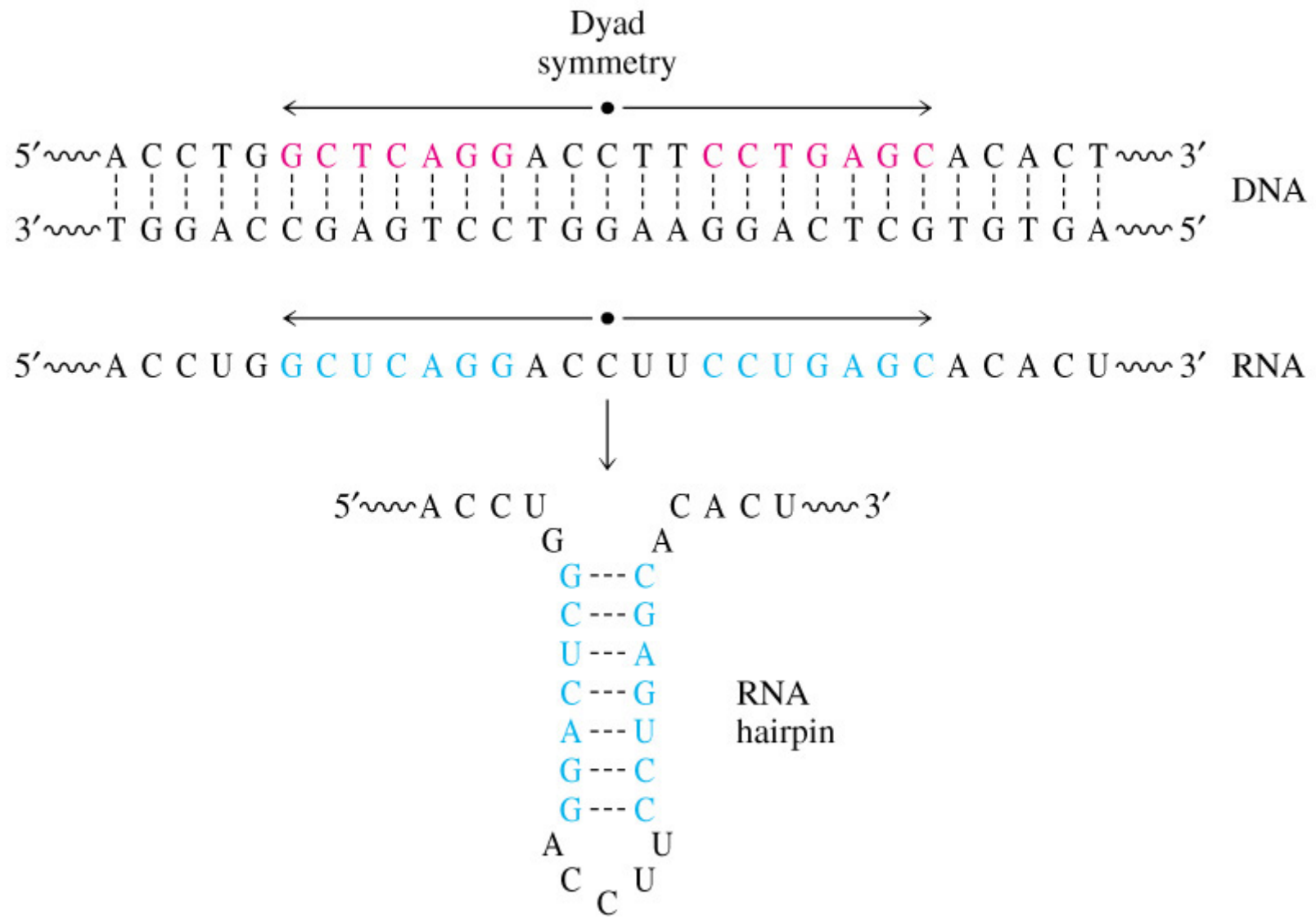


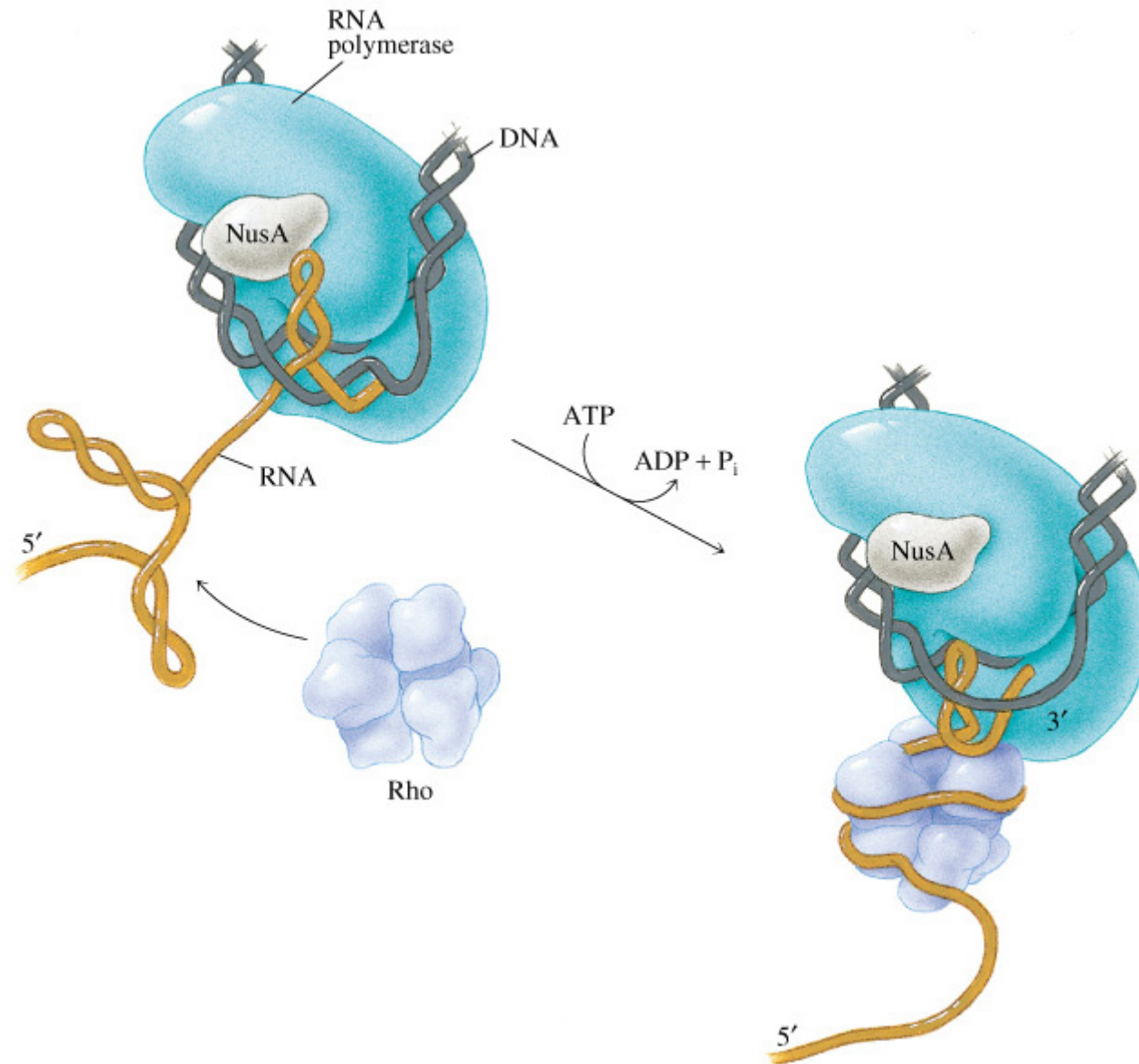
RNA polymerase



Chain Termination







FIN

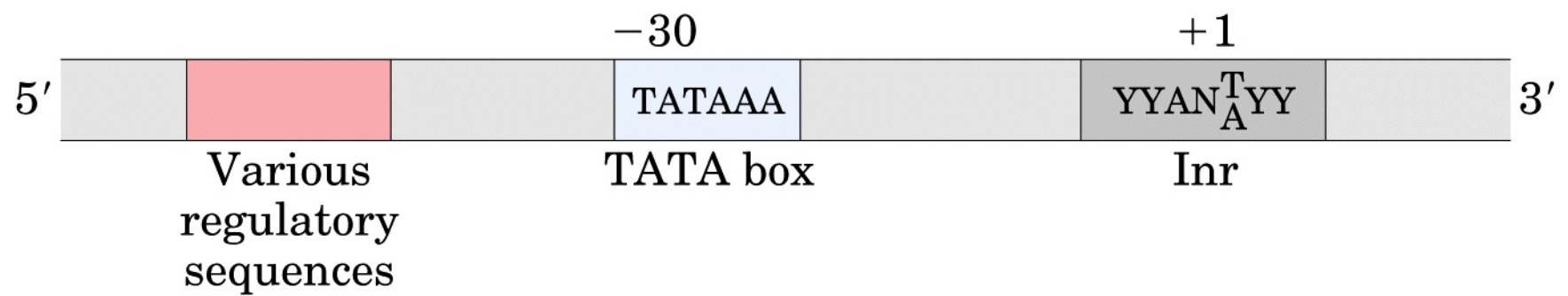
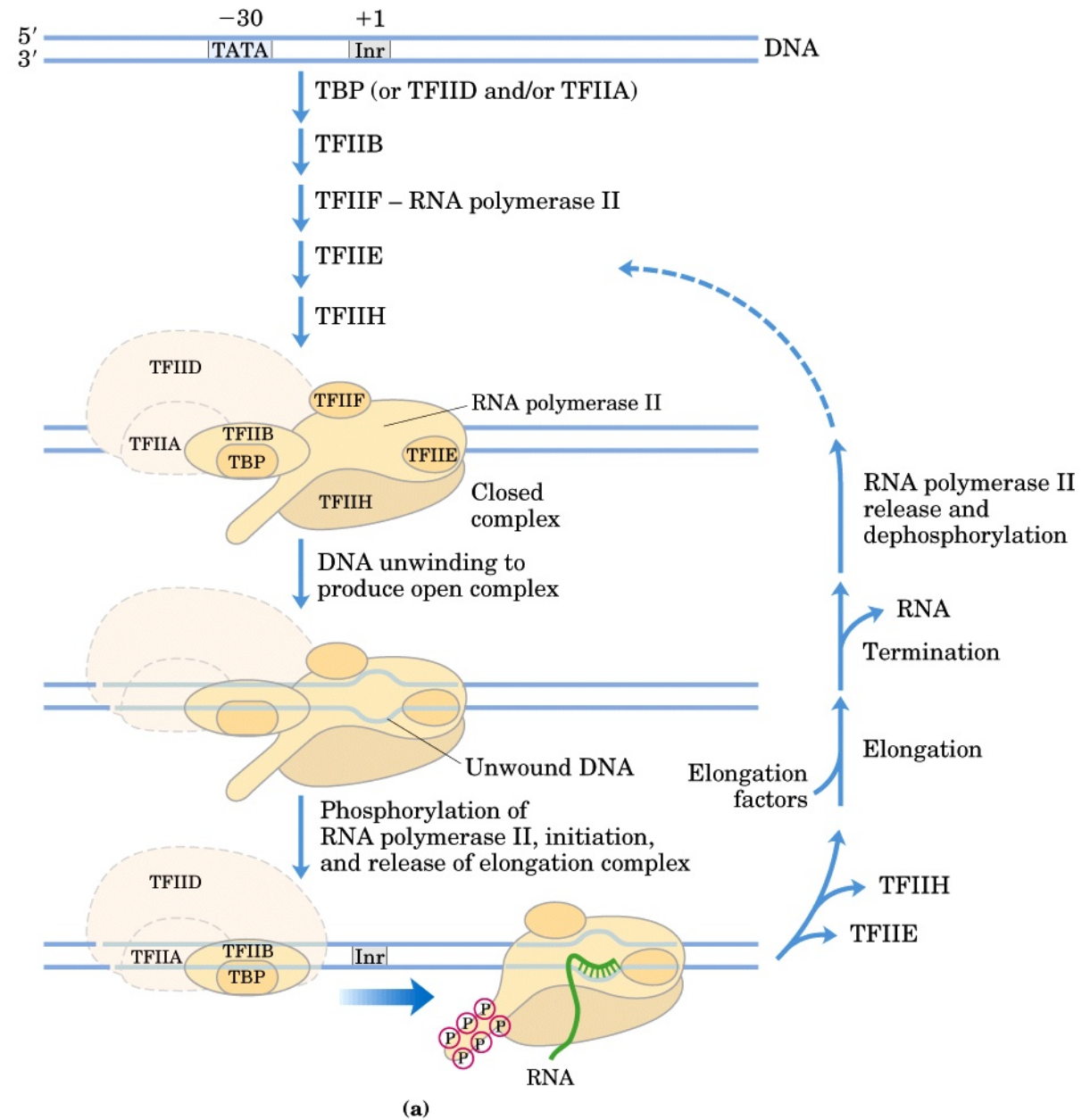


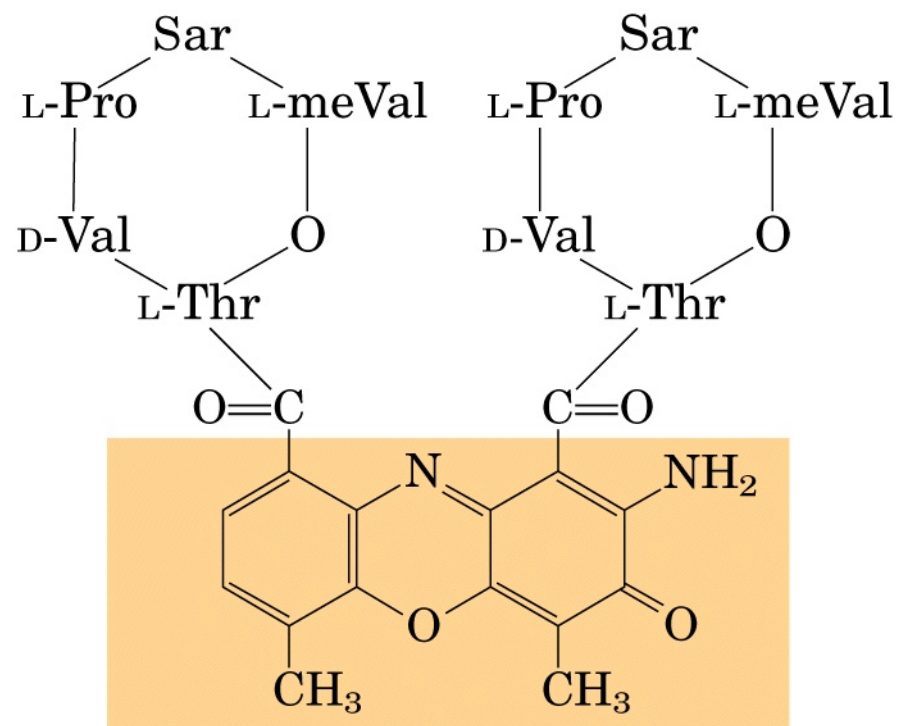
table 26–1

Proteins Required for Transcription at the RNA Polymerase II Promoters of Eukaryotes			
Transcription factor	Number of subunits	Subunit M_r	Functions
Initiation			
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
Elongation*			
ELL [†]	1	80,000	
P-TEFb	2	43,000, 124,000	
SII (TFIIS)	1	38,000	
Elongin (SIID)	3	15,000, 18,000, 110,000	

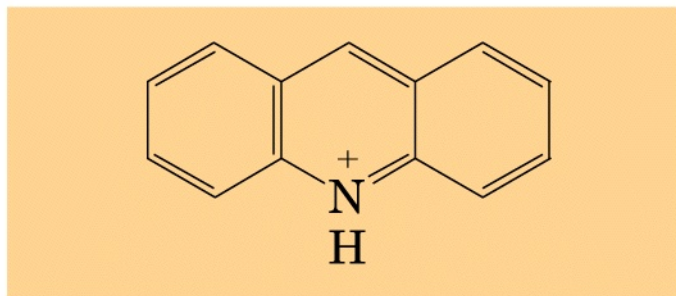
*All elongation factors suppress the pausing or arrest of transcription by the RNA polymerase II – TFIIF complex.

[†]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.

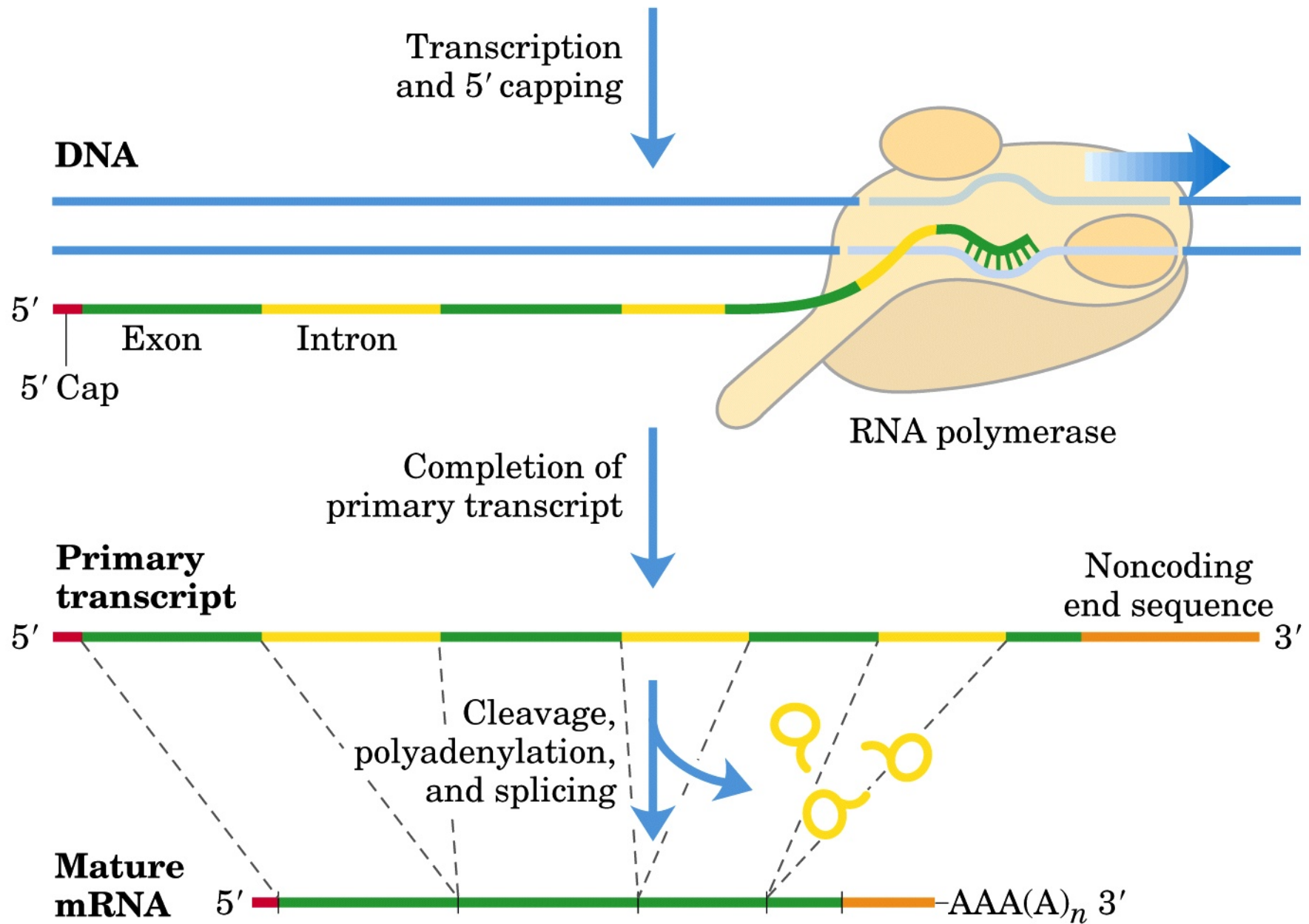


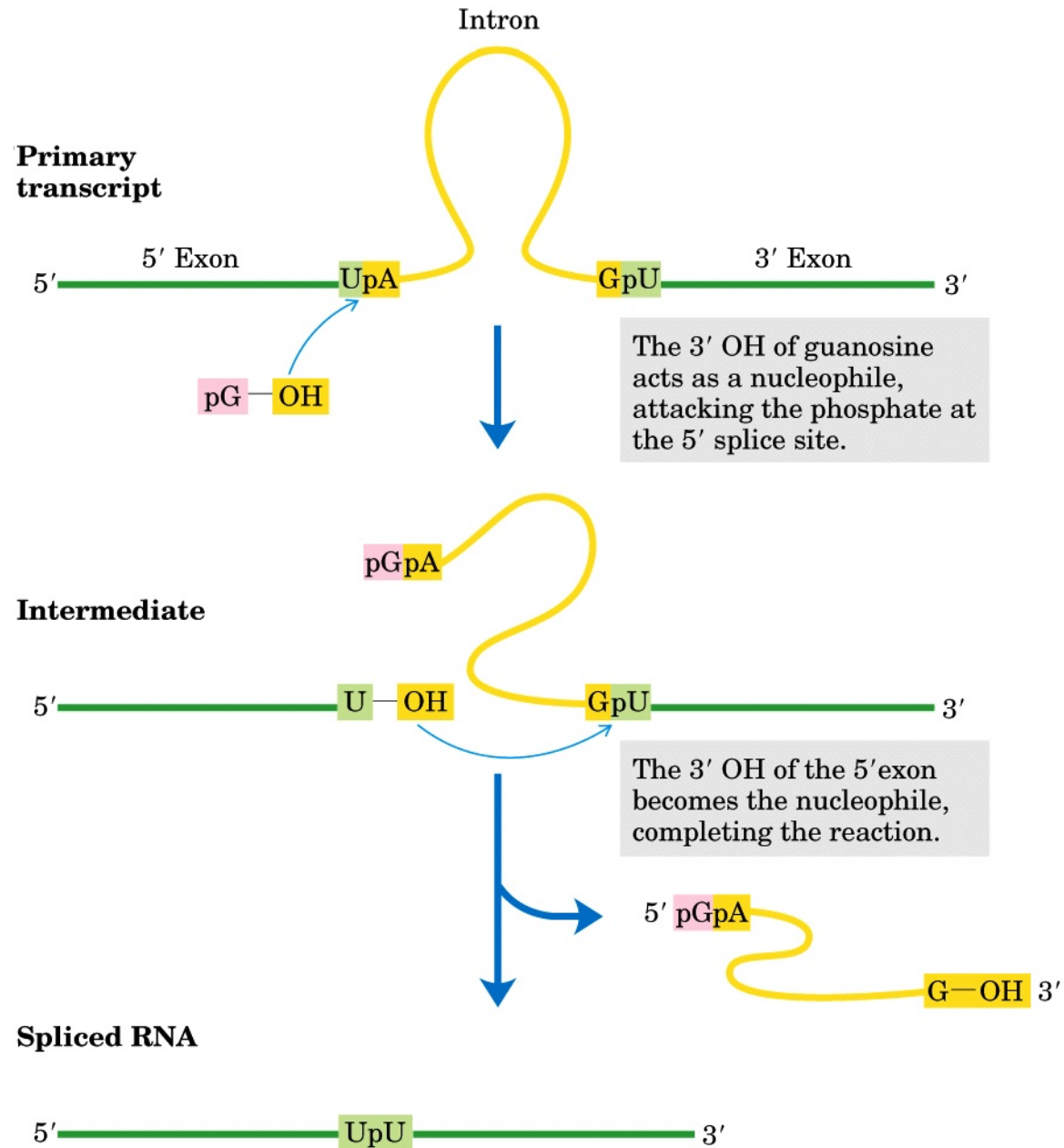


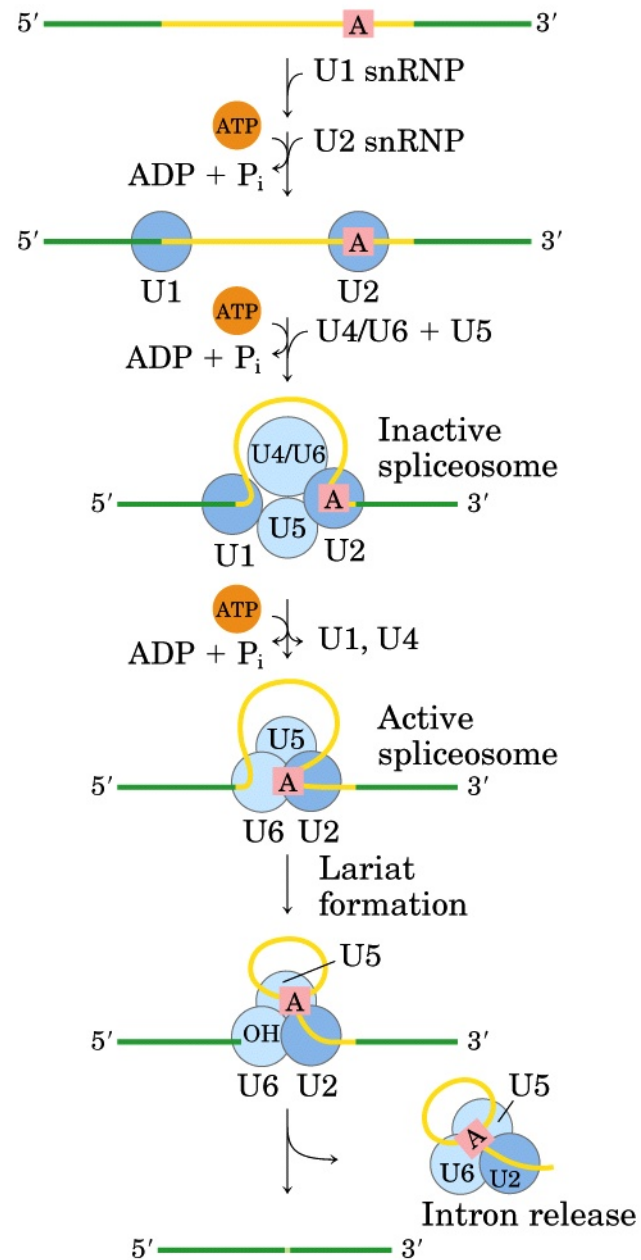
Actinomycin D



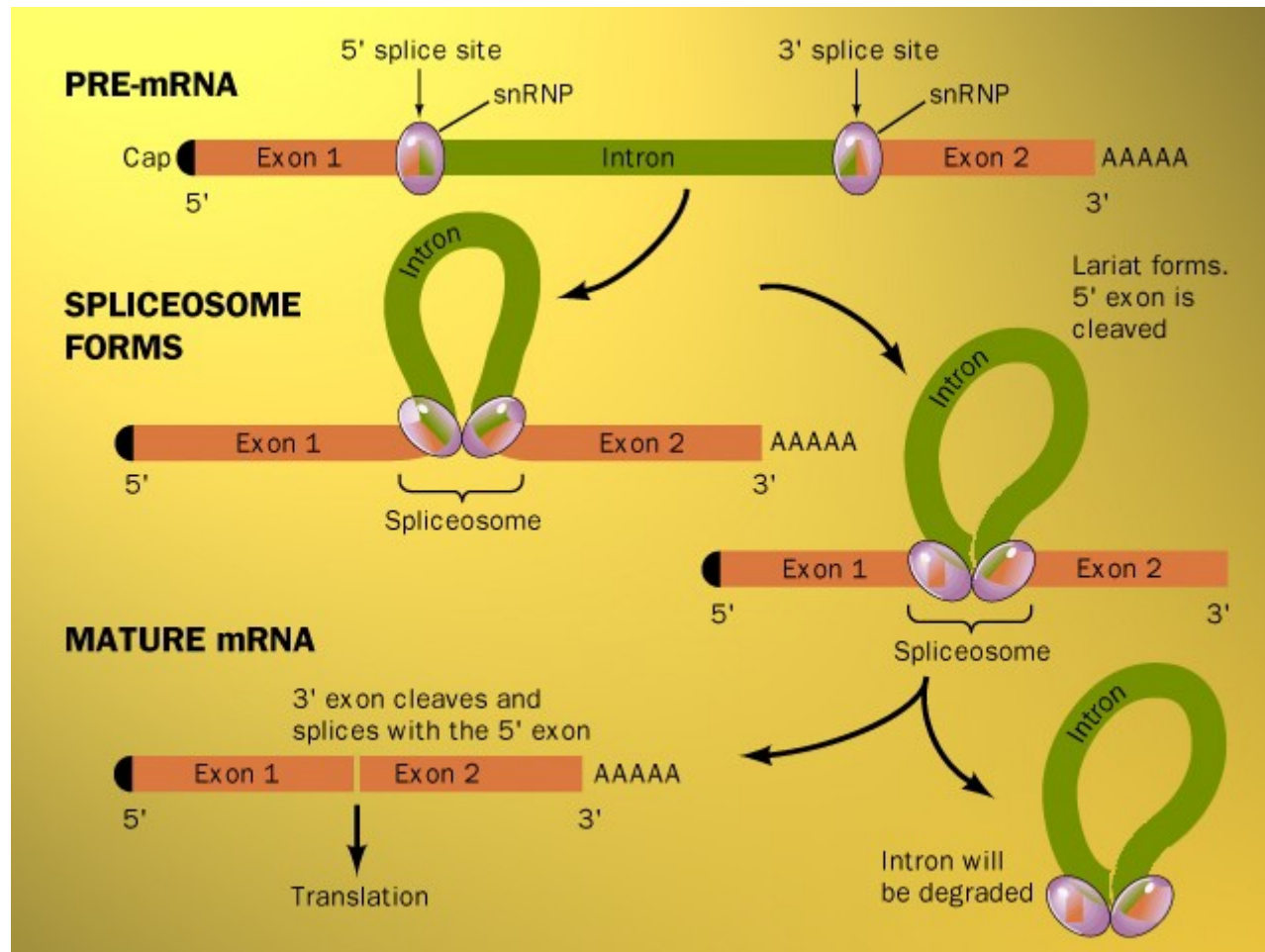
Acridine

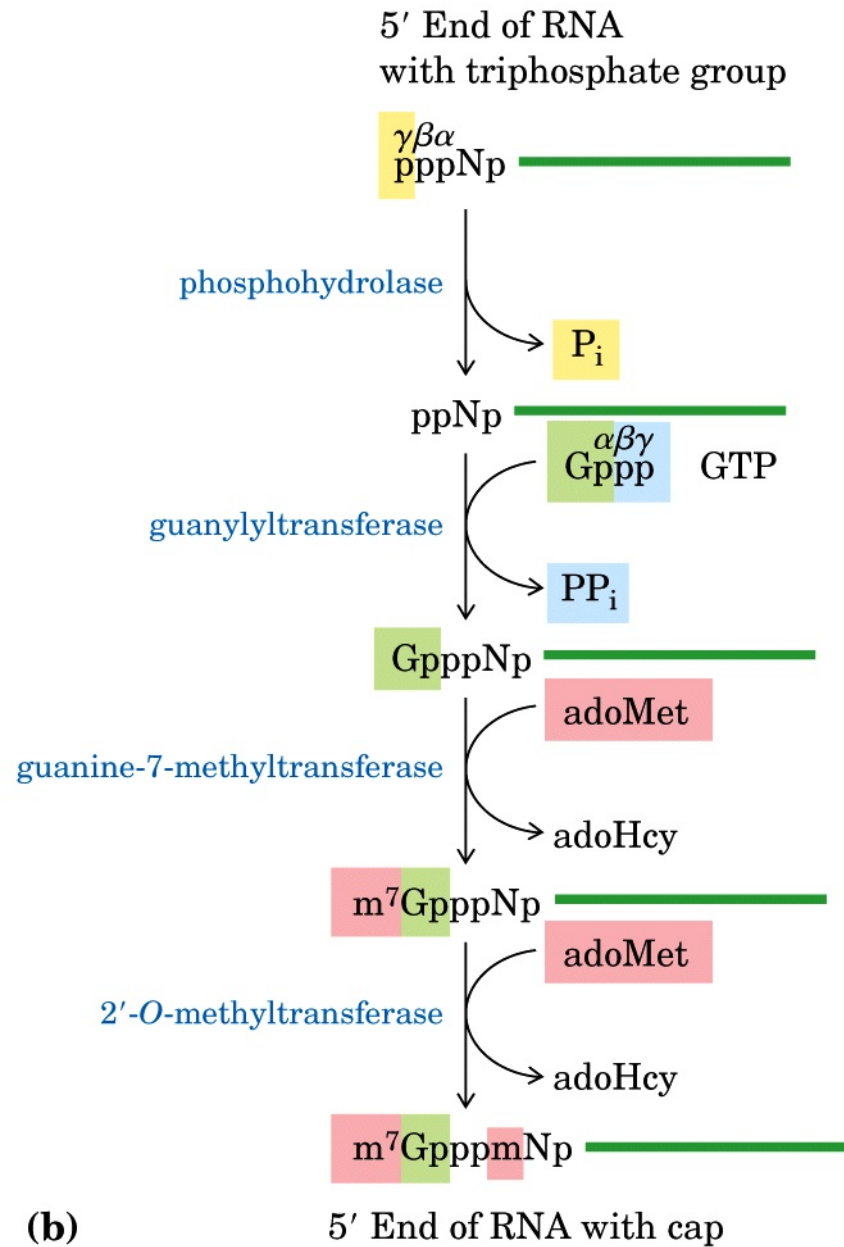


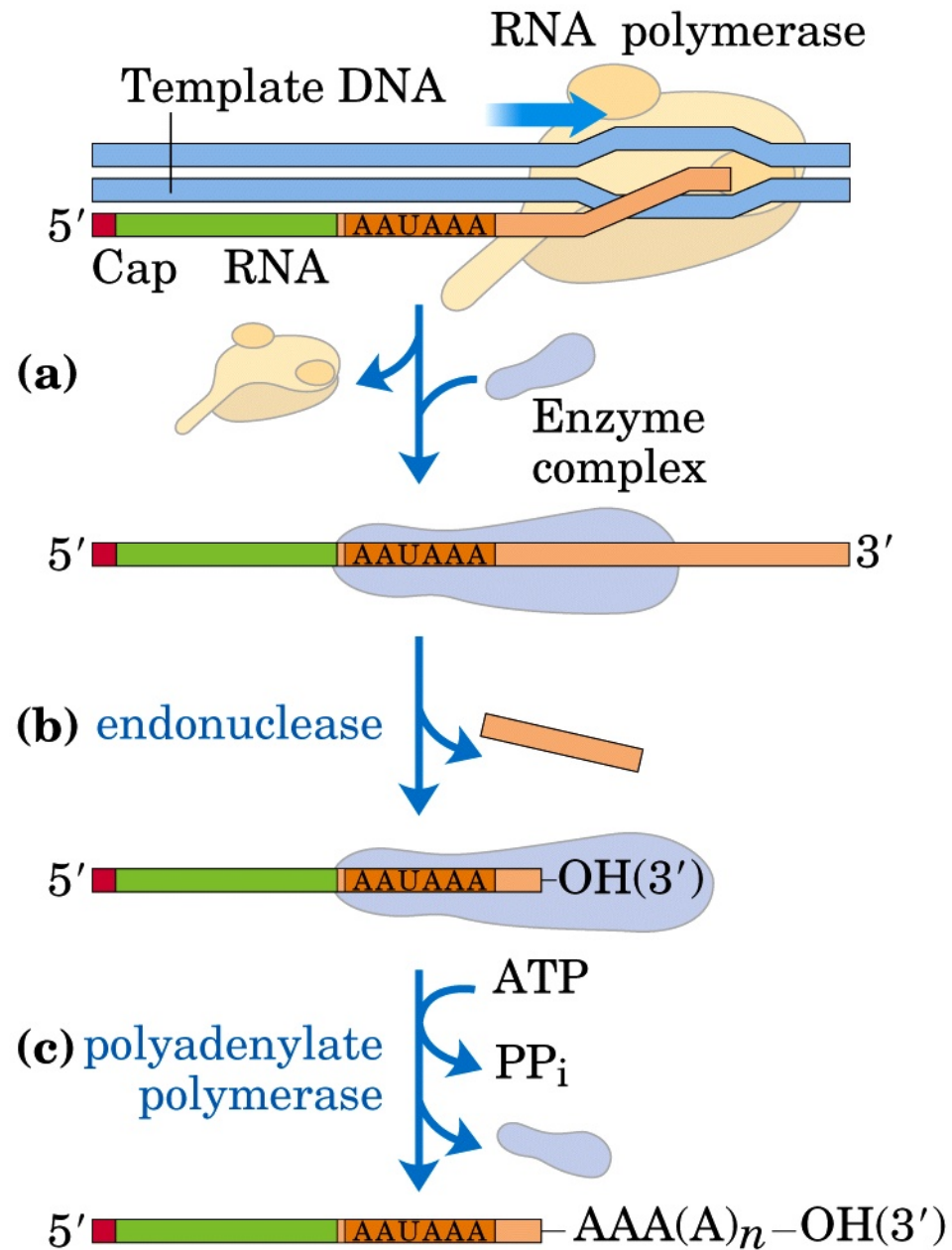


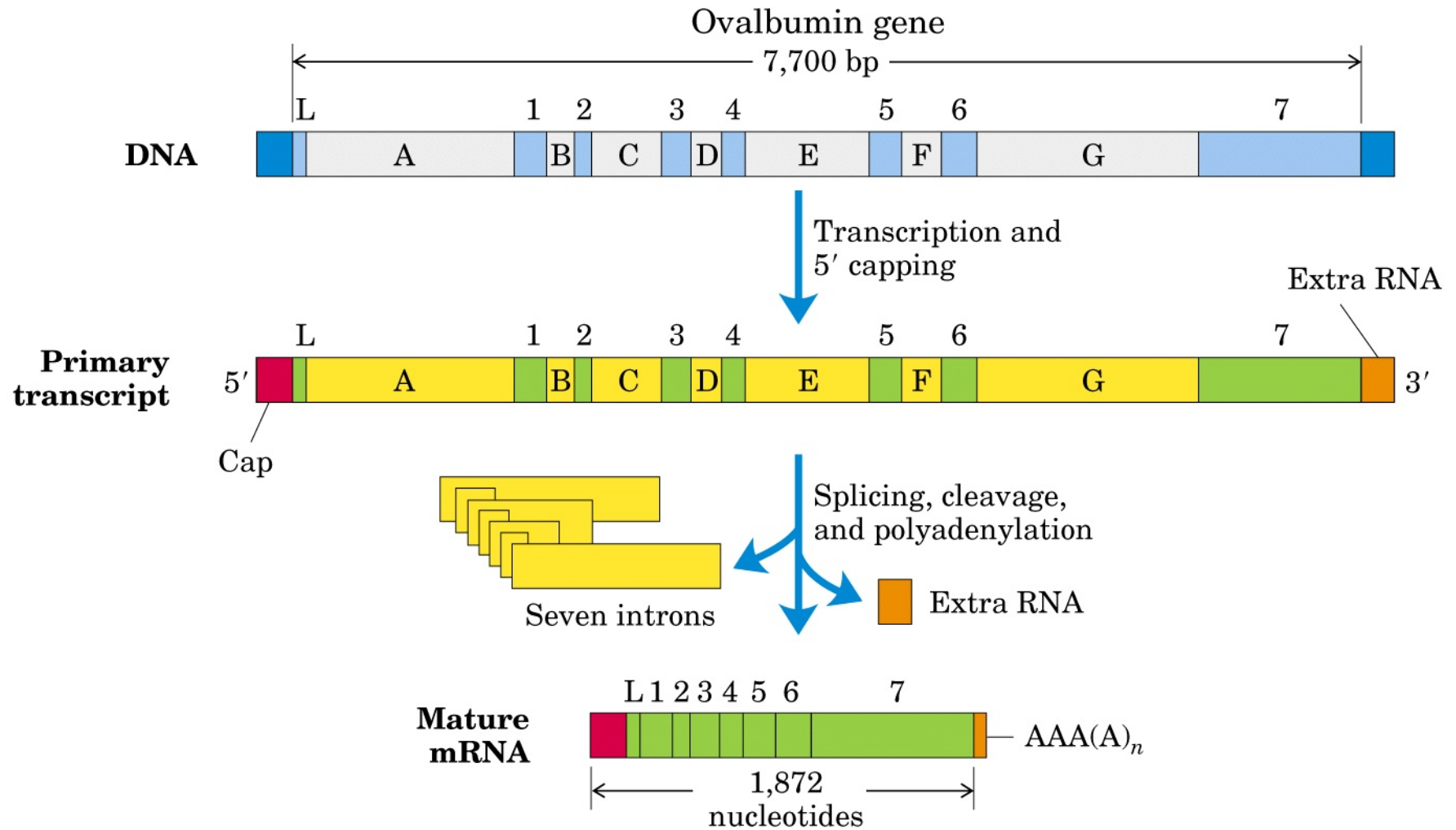


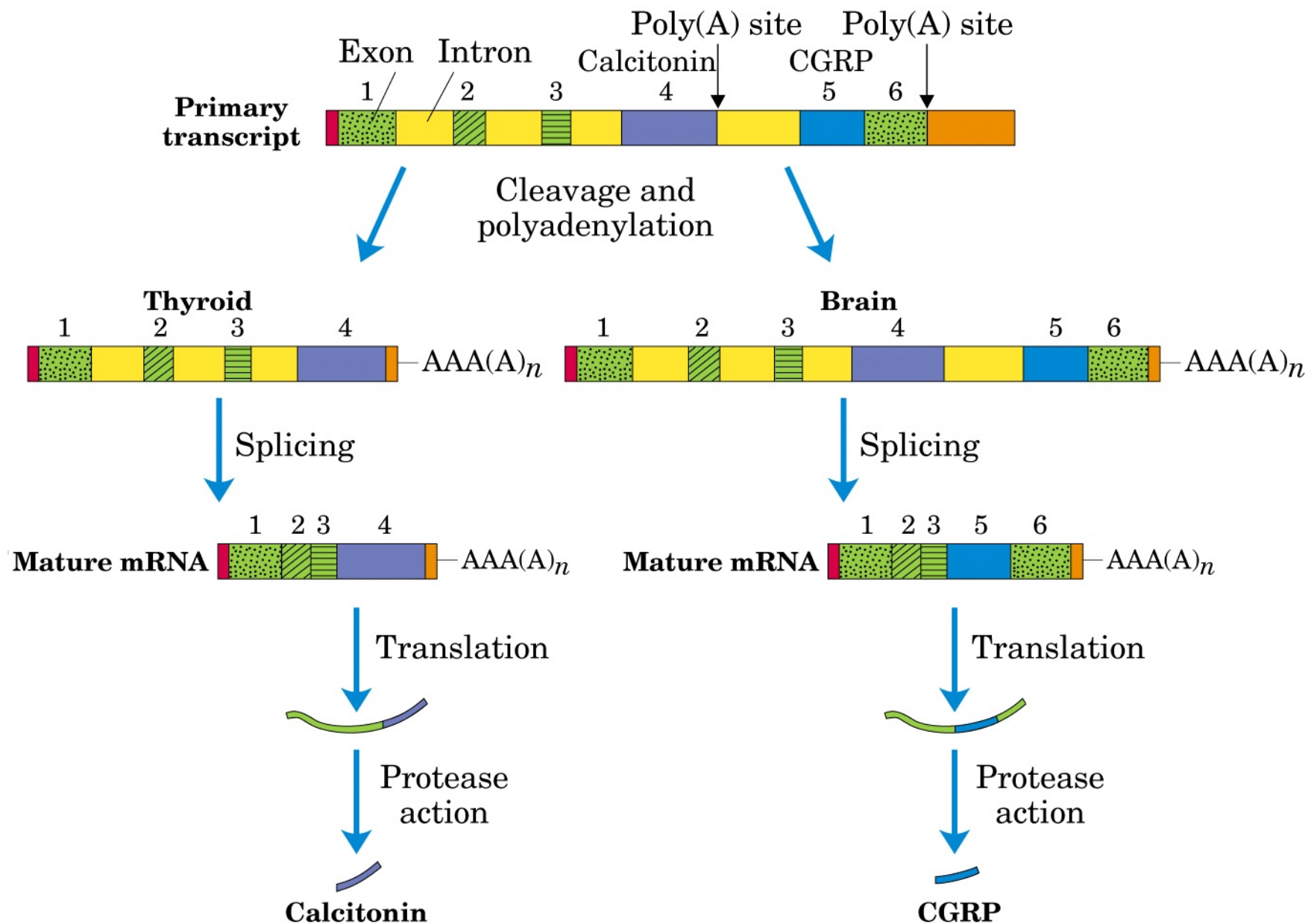
pre-RNA_m → RNA_m

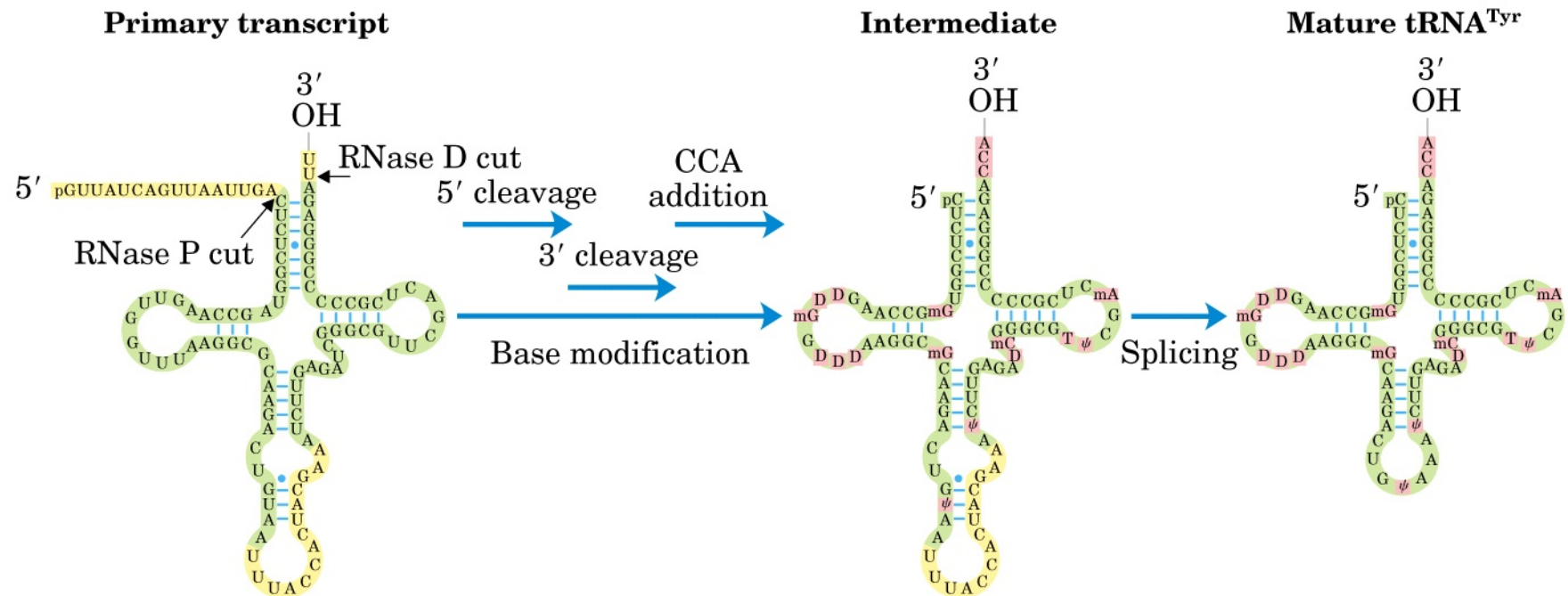











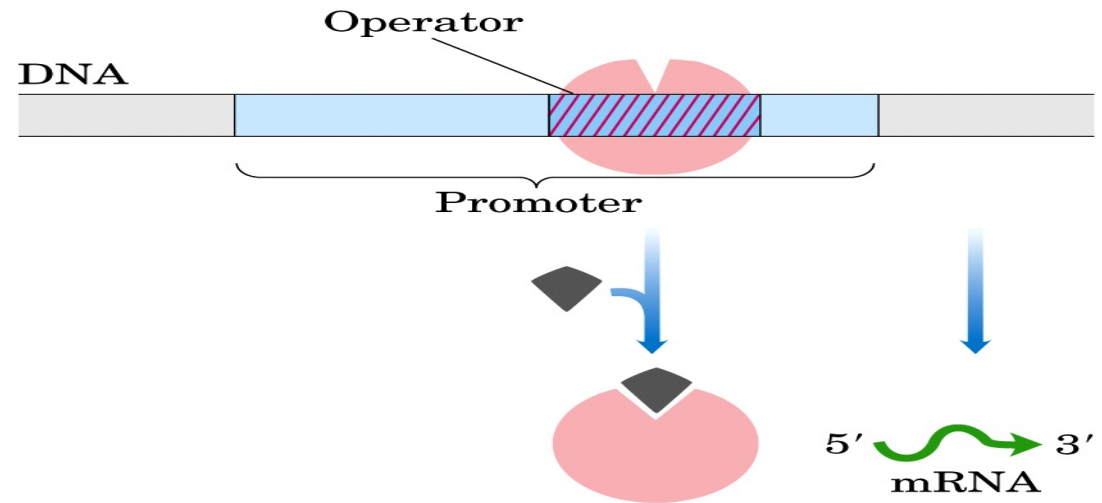


REGULACION GENICA


Negative regulation
(bound repressor inhibits transcription)

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

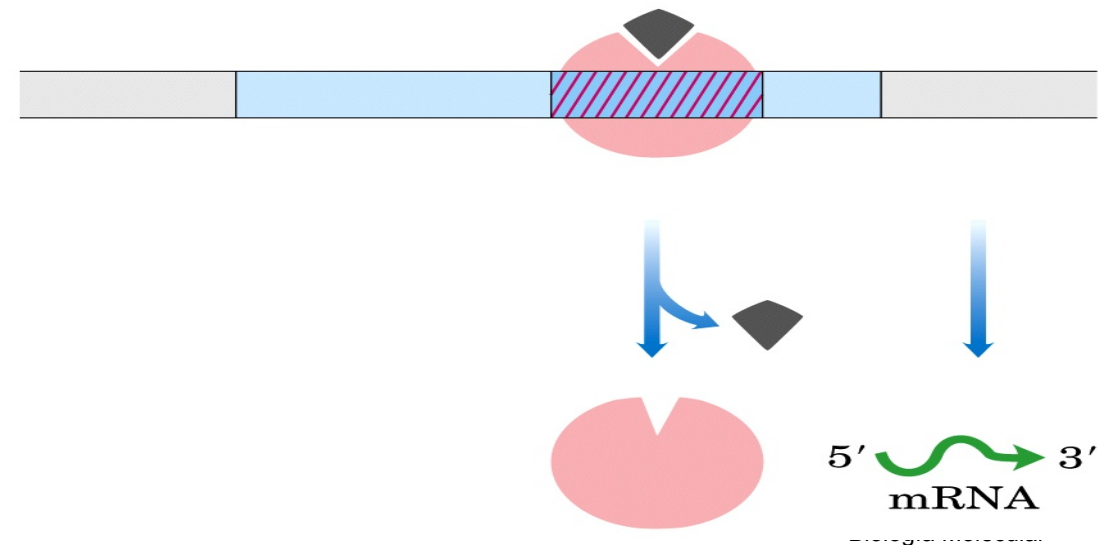
(a)



Negative regulation
(bound repressor inhibits transcription)

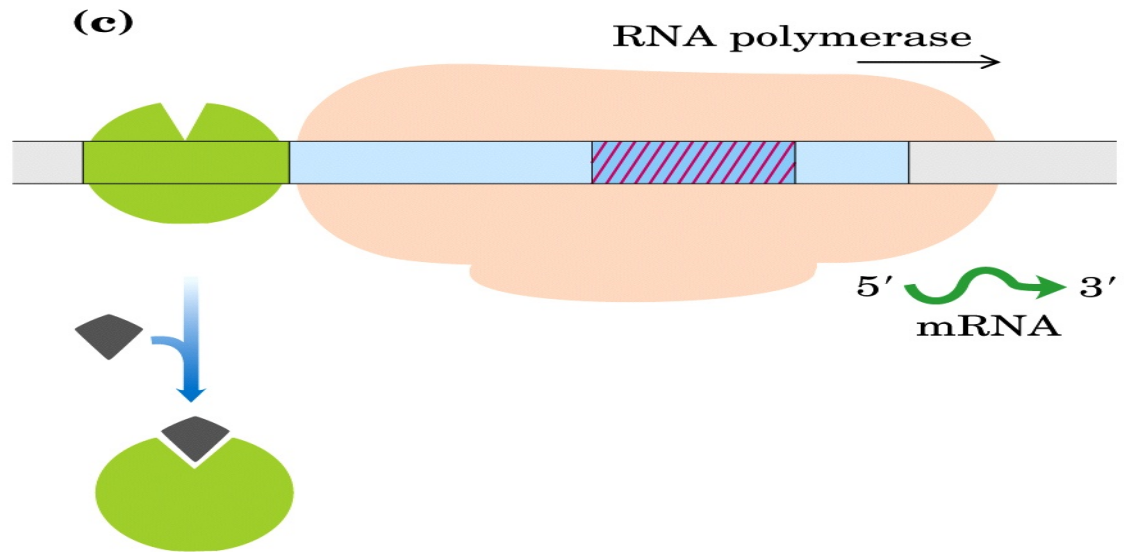
Molecular signal
() causes *binding*
of regulatory protein
to DNA

(b)



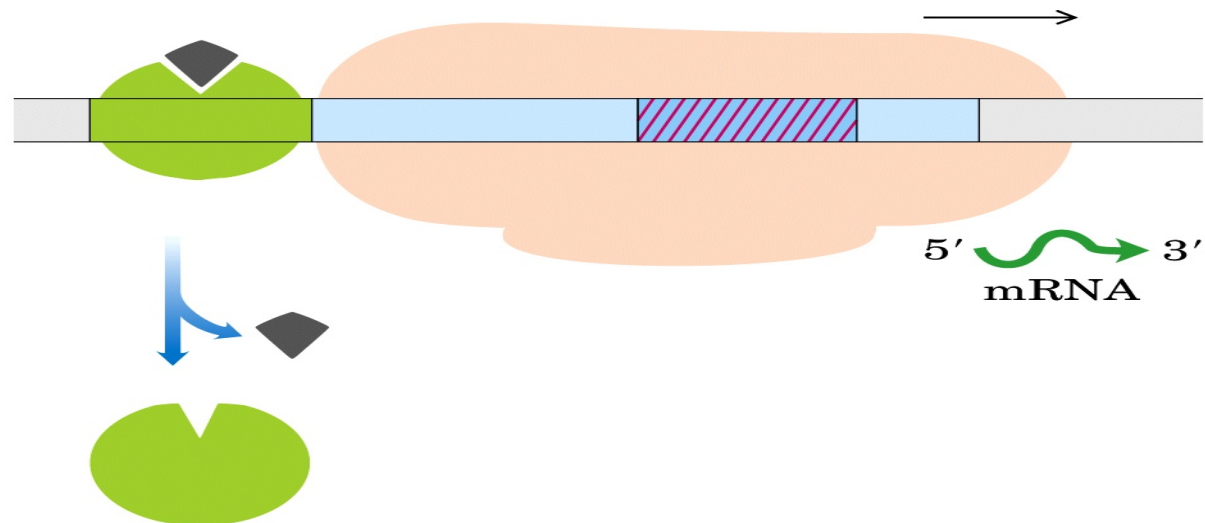
Positive regulation
(bound activator facilitates transcription)

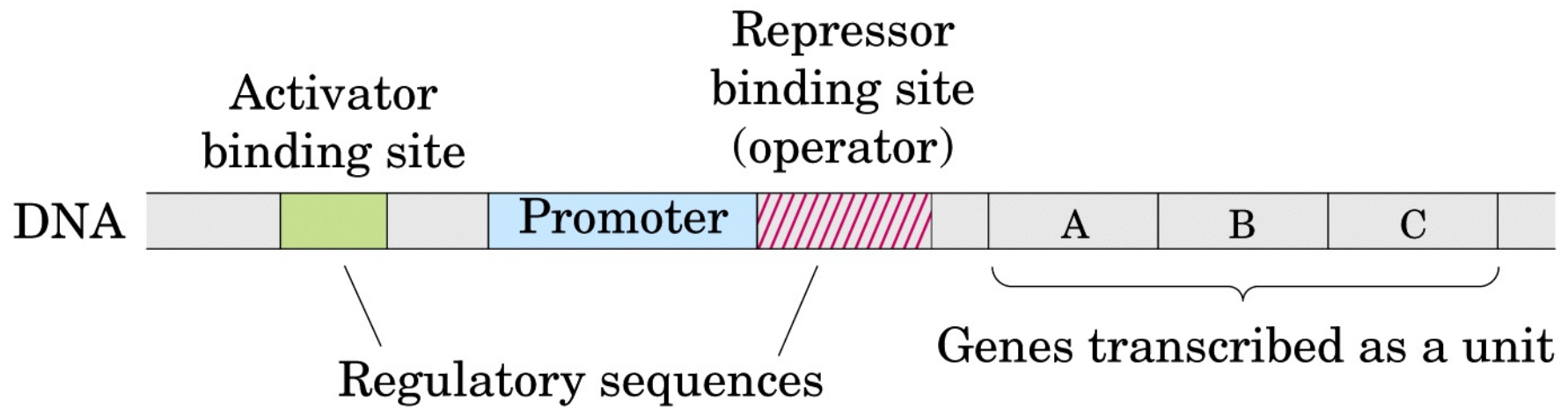
Molecular signal
(◆) causes *dissociation*
of regulatory protein
from DNA

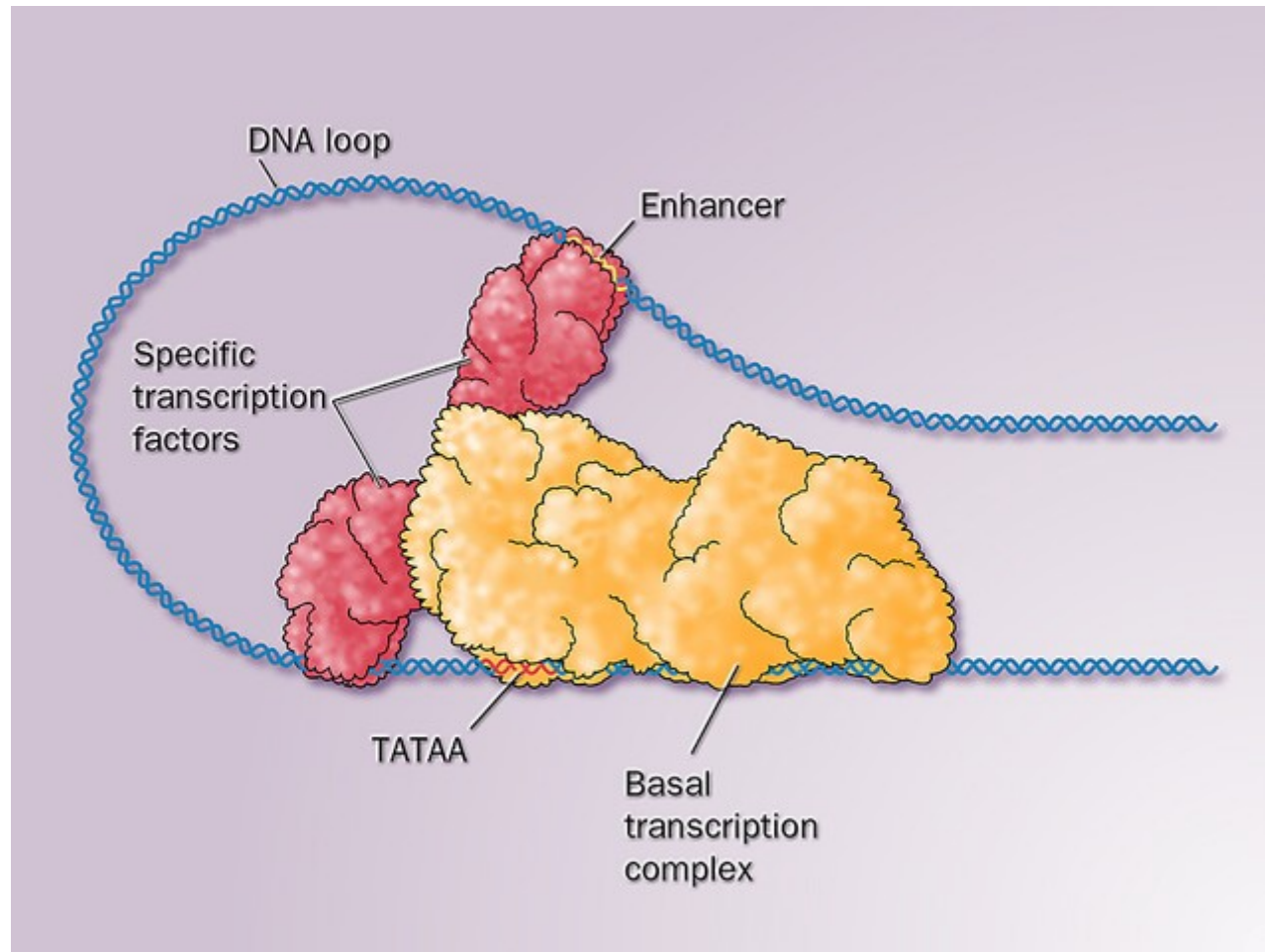


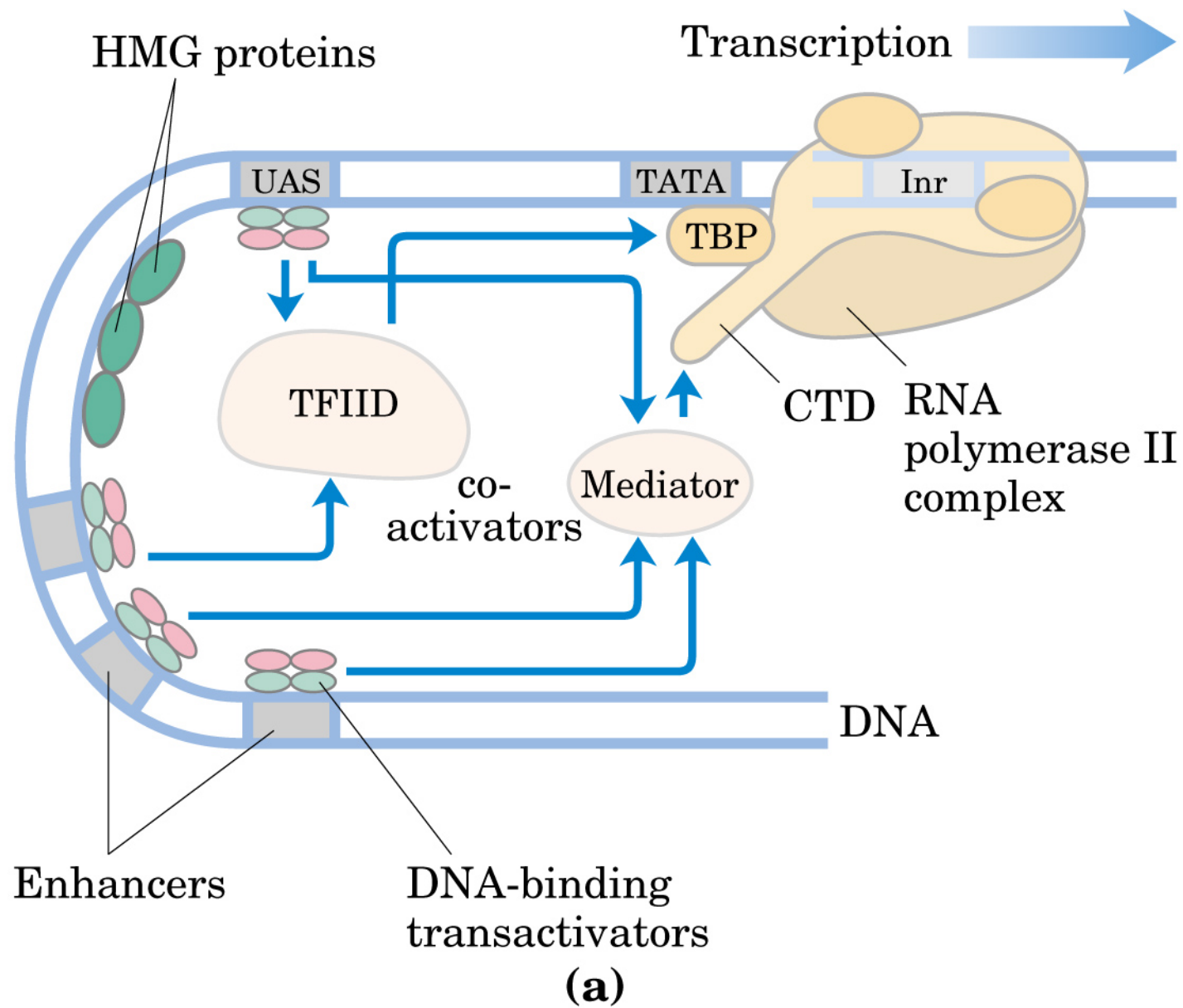
Positive regulation
(bound activator facilitates transcription)

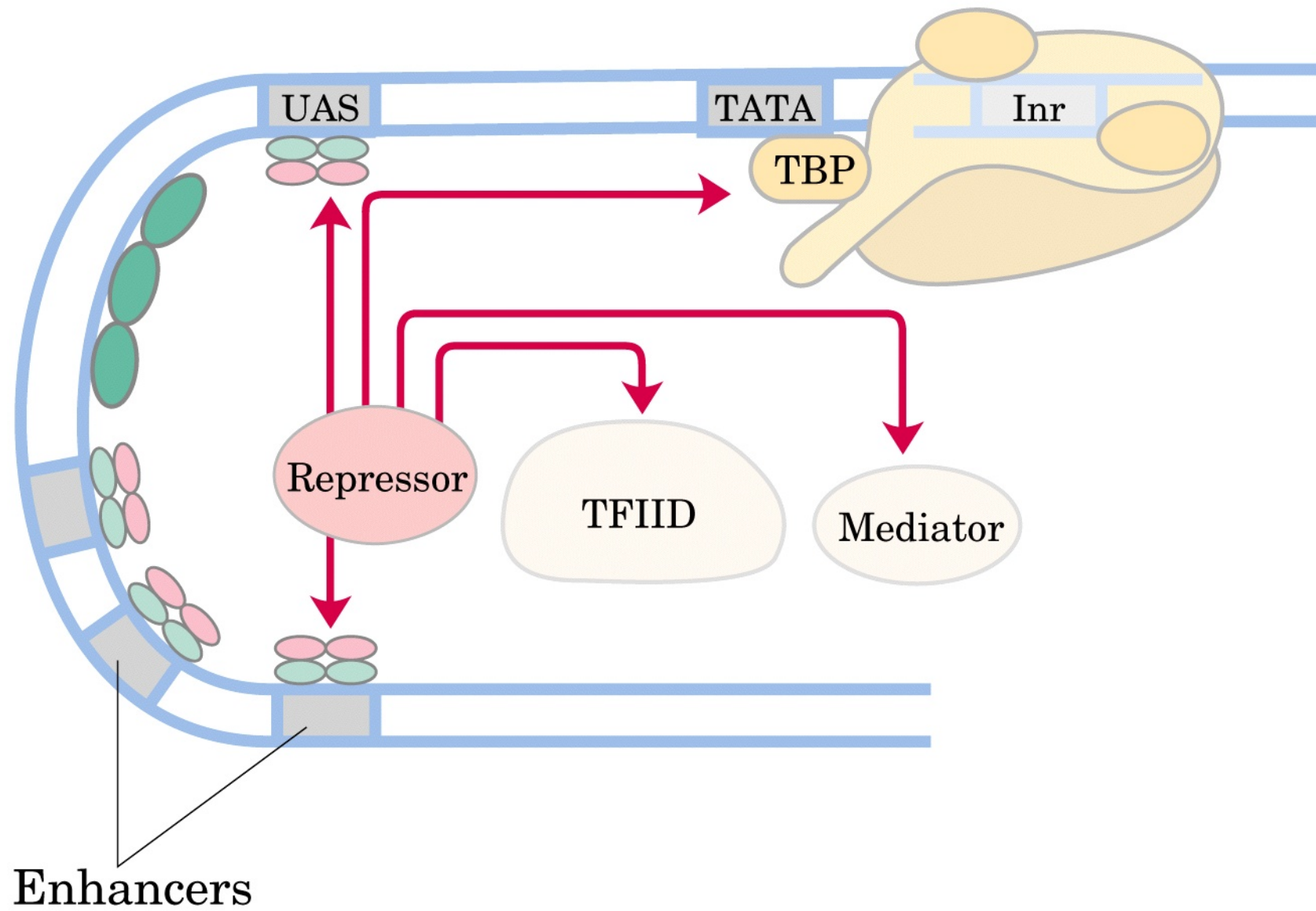
Molecular signal
(◆) causes *binding*
of regulatory protein
to DNA











(b)

FIN