

RNA Biosynthesis

**The DNA-dependent RNA polymerases
have the following properties:**

- 1. template dependent, requiring double-stranded DNA**
- 2. do not require a primer; synthesis begins with a nucleoside triphosphate**
- 3. require the four nucleoside triphosphates (ATP, GTP, CTP, and UTP)**
- 4. copy (read) the template DNA strand in the 3' to 5' direction**
- 5. synthesize the RNA in the 5' to 3' direction**

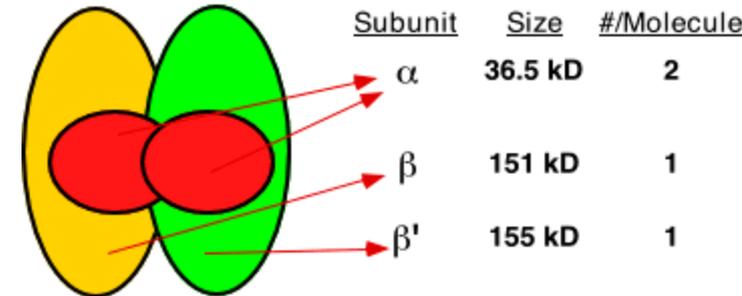
Prokaryotic RNA Biosynthesis

In prokaryotes, the same RNA polymerase catalyzes the synthesis of all three types of RNA: mRNA, rRNA and tRNA.

RNAP is a relatively large molecule.

The core enzyme is capable of initiating transcription **NON-SPECIFICALLY**

Prokaryotic RNA Polymerase:
Core Enzyme



The core enzyme has 5 subunits (~400 kDa):

- α (x2): the two α subunits assemble the enzyme and also recognizes regulatory factors.
- β: has the polymerase activity (catalyzes the synthesis of RNA).
- β': binds to DNA (nonspecifically).
- ω: function not known clearly.

However it has been observed to offer a protective/chaperone function to the β' subunit

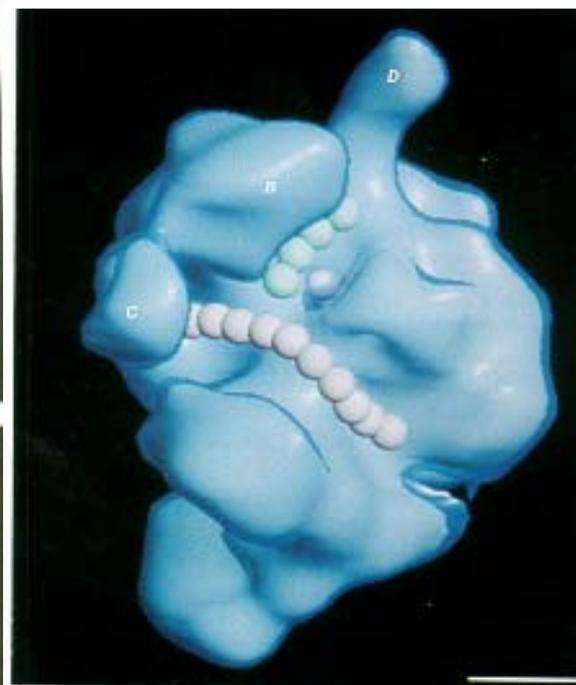
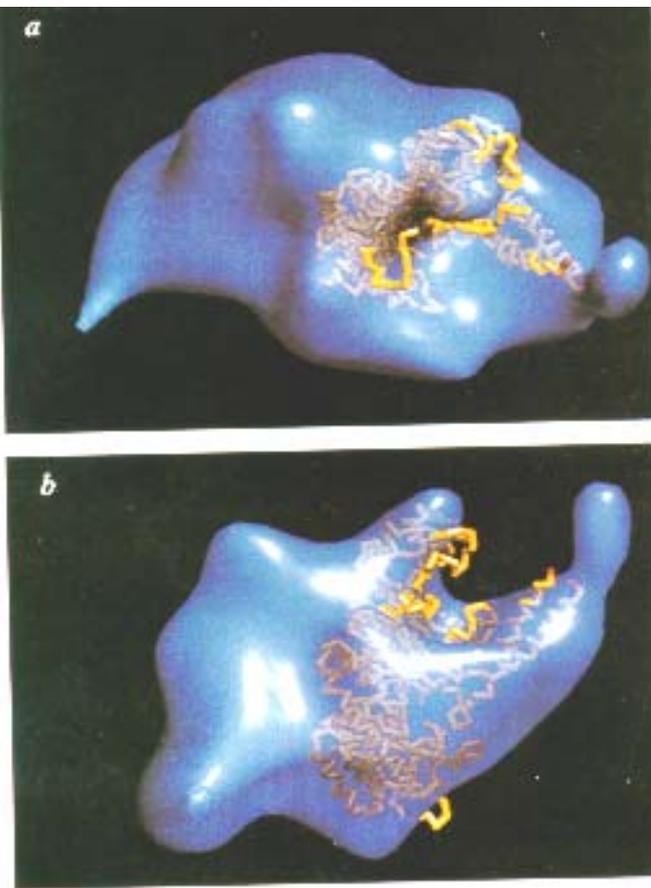


Figure 4. The Molecule on the Left in Figure 3, Viewed from the Left of Figure 3, Approximately down the Positive a Axis. The features labeled in Figure 3 are labeled here if visible (B-D). Chains of colored beads, the significance of which is described in the text, have been superimposed on the structure. The beads are 8 Å in diameter and are placed every 6.8 Å along the chain. The scale bar represents 25 Å.

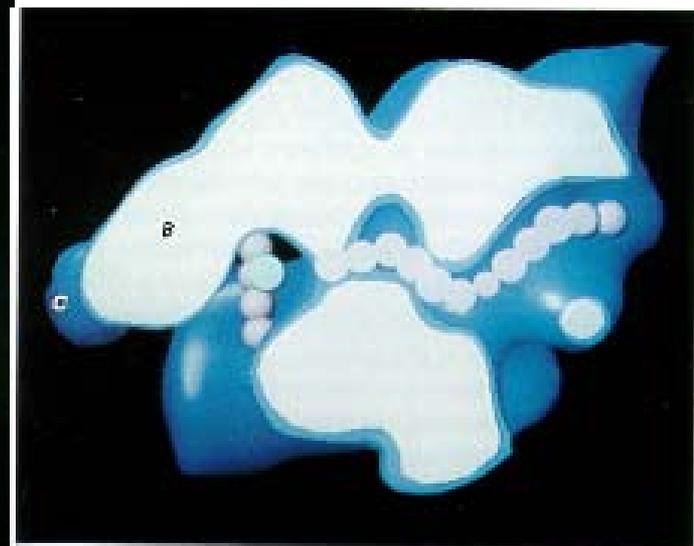


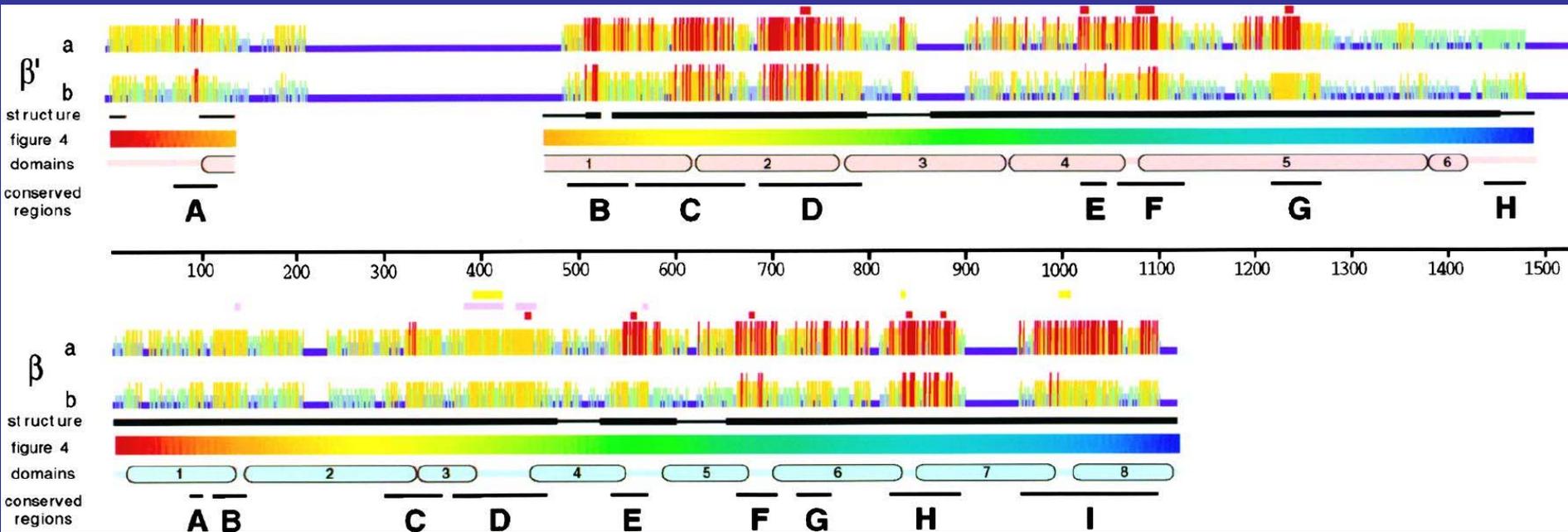
Figure 6. The Molecule of Figure 4, Viewed down the Axis of the Chain of Green Beads (from the Upper Right of Figure 4) and Sliced at the Level of the Tunnel, Which Passes Completely through the Molecule (Pink Beads).

**The structure RNAP exhibits a groove:
length of 55 Å
diameter of 25 Å.**

This groove fits well the 20 Å double strand of DNA.

The 55 Å length can accept 16 nucleotides.

RNA polymerase Sequence alignment from 50 bacteria

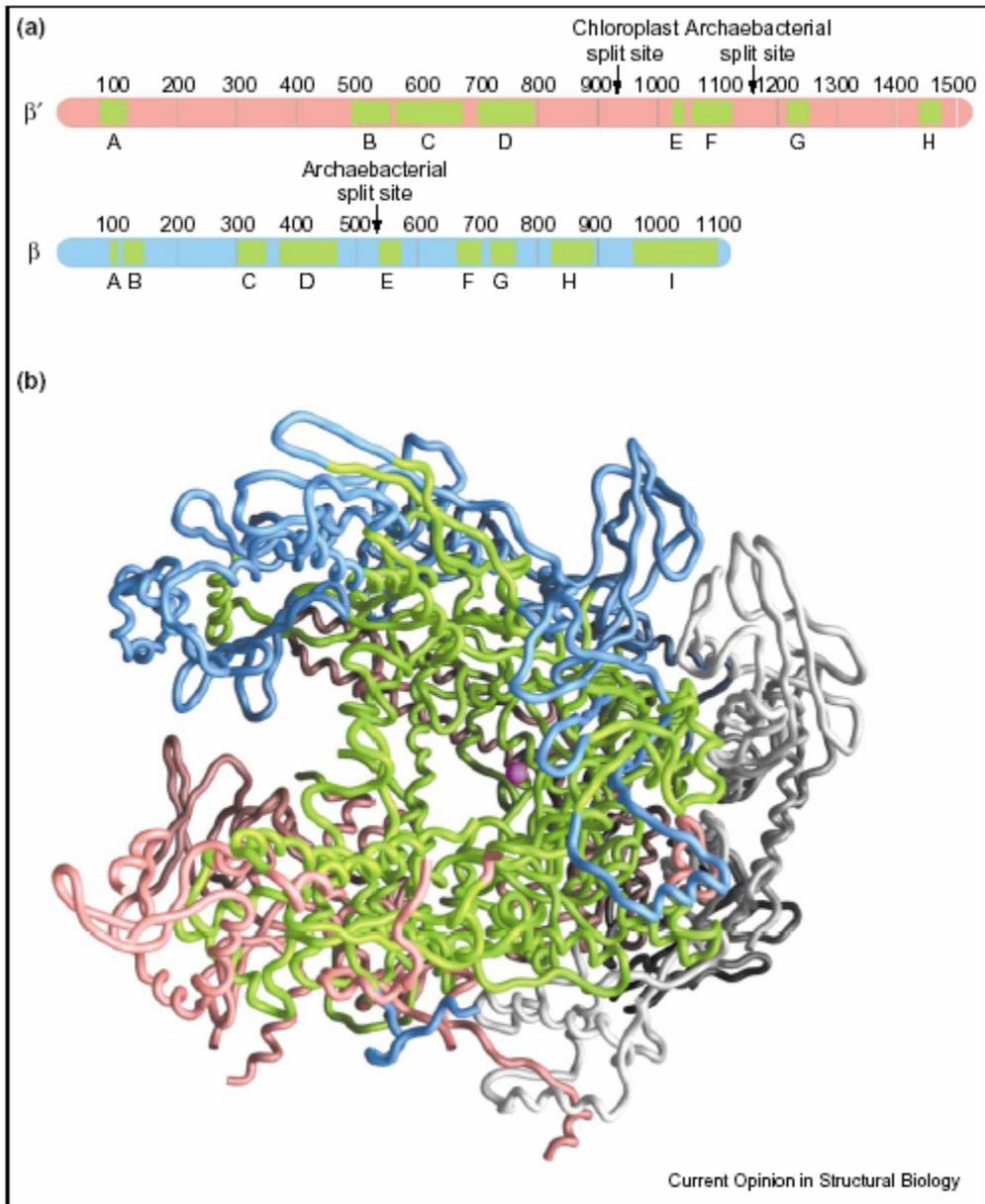


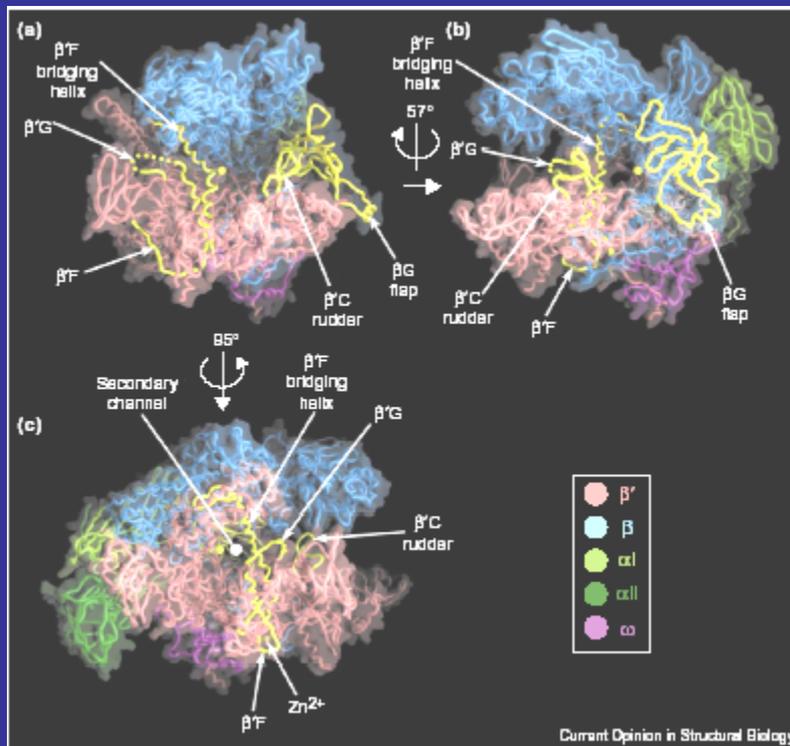
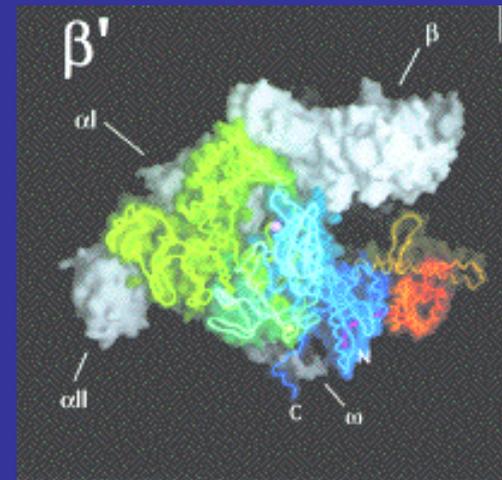
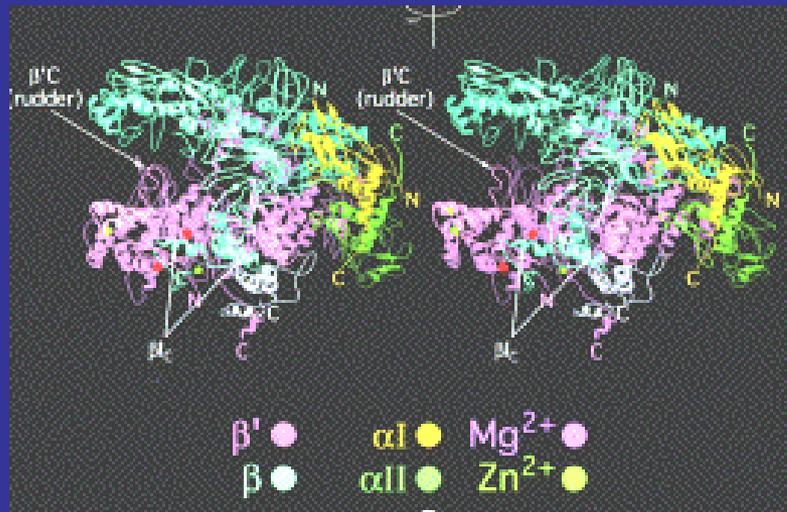
Red = 100% conserved followed by Yellow then Green then Blue

Zhang et al. Cell 98, 811–824, September, 1999

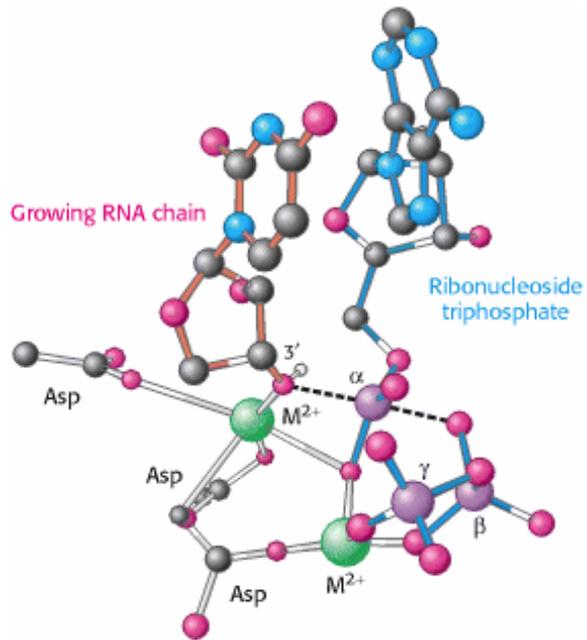
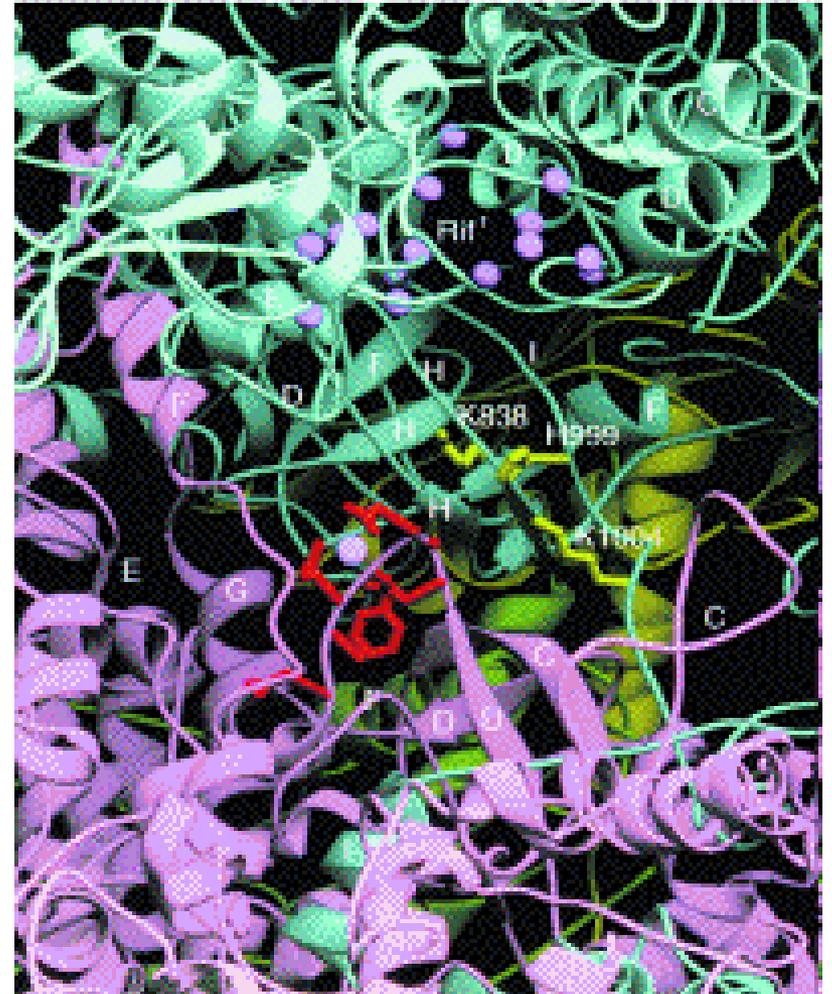
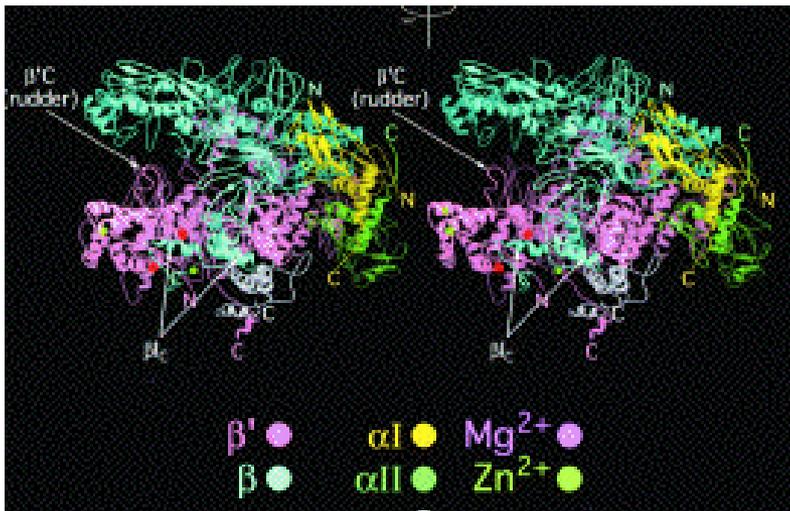
Evolutionarily conserved segments of the RNAP large subunits form the structural core. (a) The bars schematically represent the primary sequences of the *Taq* β' (top, pink) and β (bottom, blue) subunits, with amino acid numbering directly above the bars [4**]. The split sites of the large subunits, which occur as two separate peptides in chloroplast and archaeobacterial RNAPs, are also indicated. Evolutionarily conserved regions among prokaryotes, chloroplasts, archaeobacteria and eukaryotes [4**], originally defined for β' by Jakerst *et al.* [31] and for β by Sweetser *et al.* [32], are denoted as light green boxes and are labeled (A–H for β' , A–I for β) directly below.

(b) Backbone worm diagram of *Taq* core RNAP (same view as Figure 1b). The two α monomers and ω are colored white. The large subunits are colored pink (β') and blue (β), except for the evolutionarily conserved segments shown in (a), which are colored light green. The active site Mg^{2+} ion is shown as a magenta sphere.



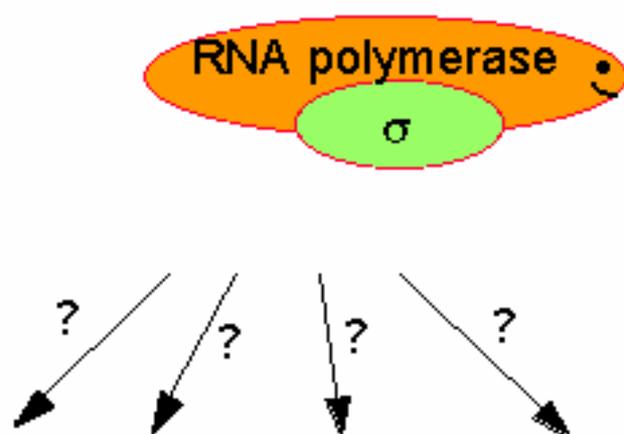


The *Tag* core RNAP structure. The α -carbon backbone is shown as worms, along with the transparent molecular surface. Various structural features discussed in the text are labeled and highlighted in yellow. The individual subunits are color-coded as indicated in the key. The Mg^{2+} ion chelated at the active center is indicated by a yellow sphere. The Zn^{2+} ion bound in β' is indicated by a light green sphere. (a) View looking into the active site channel, perpendicular to the axis of the main channel. This view is rotated (b) 57° clockwise about the vertical axis and (c) 95° counter-clockwise about the vertical axis (this view locks directly down the axis of the secondary channel).



TRANSCRIPTION

How does RNA polymerase know where to start transcription?



DNA

TRANSCRIPTION

RNA polymerase recognizes a sequence of nucleotides called the **PROMOTER**

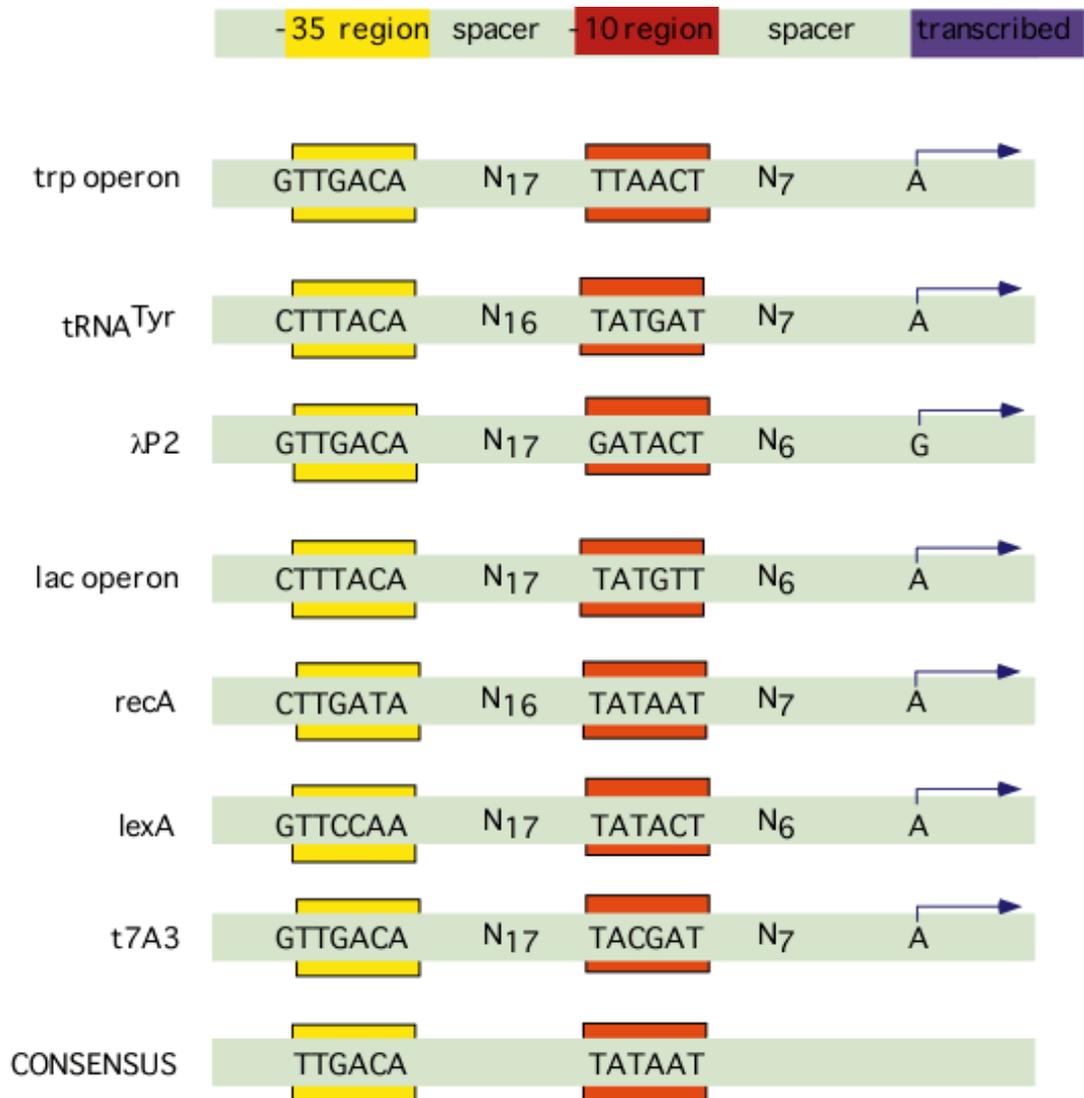


In prokaryotes, a promoter consists of two sequences “-35 box” and “-10 box”. Transcription starts approximately 7 nucleotides downstream from the “-10” box. Promoters of different genes may have slightly different sequences:

-35		-10
TTGACA	-(17 bp)	TATAAT
TTAACA	-(17 bp)	TATTAT
TTGCCA	-(17 bp)	TATTAT
TTGACT	-(17 bp)	TATCAT
TTGACA	-(17 bp)	TTTGAT
TTGATA	-(17 bp)	TAAAAT

The “average” promoter sequence is called the **consensus promoter sequence**. The closer the promoter sequence to the consensus, the better the promoter.

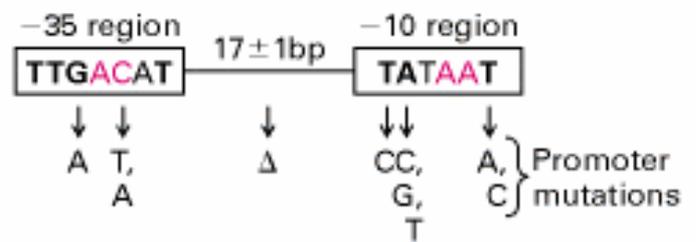
Some Promoter Sequences



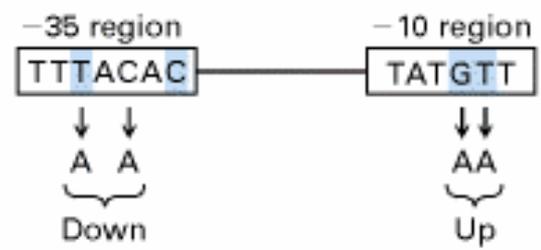
(a) Strong *E. coli* promoters

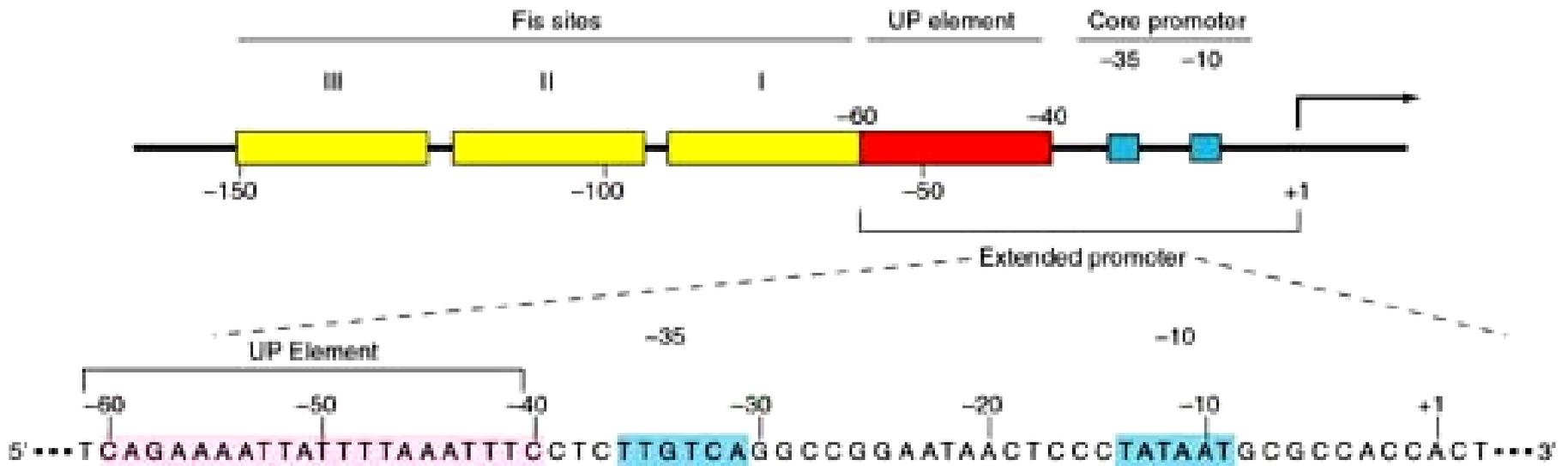
tyr tRNA	TCTCAACGTAACAC	TTTACAG	GCGGCG • • CGTCATTTGA	TATGAT	GC • GCCCCG	CCTTCCCGA
rrn D1	GATCAAAAAAATAC	TTGTG	CAAAAAA • • TTGGGATCCC	TATAAT	GCGCCTCCG	TTGAGACG
rrn X1	ATGCATTTTCCGC	TTGTCTT	CCTGA • • GCCGACTCCC	TATAAT	GCGCCTCCA	TCGACACG
rrn (DXE) ₂	CCTGAAATTCAGGG	TTGACTC	TGAAA • • GAGGAAAGCG	TAATATAC	GCCACCT	TCGCGACA
rrn E1	CTGCAATTTTCTA	TTGCGGC	CTGCG • • GAGAACTCCC	TATAAT	GCGCCTCCA	TCGACACG
rrn A1	TTTTAAATTTCTC	TTGTCA	GGCCGG • • AATAACTCCC	TATAAT	GCGCCACCA	CTGACACG
rrn A2	GCAAAAATAAATGC	TTGACTC	TGTAG • • CGGGAAGGCG	TATTAT	GC • ACACCC	CGCGCCGC
λ P _R	TAACACCGTGCGTG	TTGACTA	TTTTTA • • CCTCTGGCGGT	GTATAAT	GG • • TTGCAT	GTACTAA
λ P _L	TATCTCTGGCGGTG	TTGACAT	AAATA • • CCACTGGCGGT	GTACT	GA • • GCACAT	CAGCAGG
T7 A3	GTGAAACAAAACGG	TTGACA	ACATGA • • AGTAAACACGG	TACGAT	GT • ACCCAT	TGAAACGA
T7 A1	TATCAAAAAGAGTA	TTGACTT	AAAGT • • CTAACCTATAG	GATACTTA	CAGCCAT	TCGAGAGG
T7 A2	ACGAAAAACAGGTA	TTGACA	ACATGAAGTAA	ACATGCAGTAAGATAC	AAATCG	CTAGGTAA
fd VIII	GATACAAATCTCCG	TTGTACT	TTGTT • • TCGCGCTTGG	TATAAT	CG • CTGGGG	GTCAAAGA
		-35		-10		+1 

(b) Consensus sequences of σ^{70} promoters



(c) Lac promoter sequence





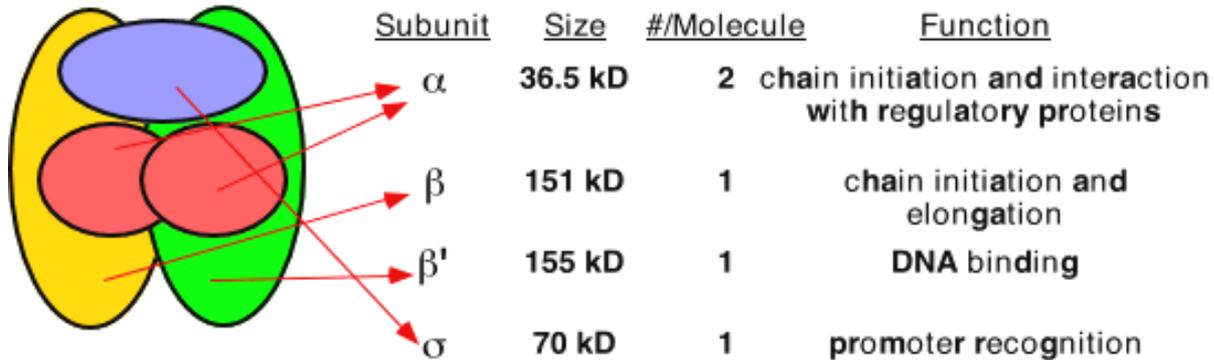
The core region in this promoter contains the -10 and -35 sequences.

In addition, many promoters contain an UP element that make them an even stronger promoters, by binding RNA polymerase more tightly).

Sigma factor (σ) is a specificity factor.

Core + σ = RNA polymerase Holoenzyme

**Prokaryotic RNA Polymerase:
Holoenzyme Enzyme**



Sigma confers upon the RNA polymerase holoenzyme the ability to initiate RNA synthesis at specific locations in DNA called **promoters.**

The holoenzyme binds tightly to promoters in DNA.

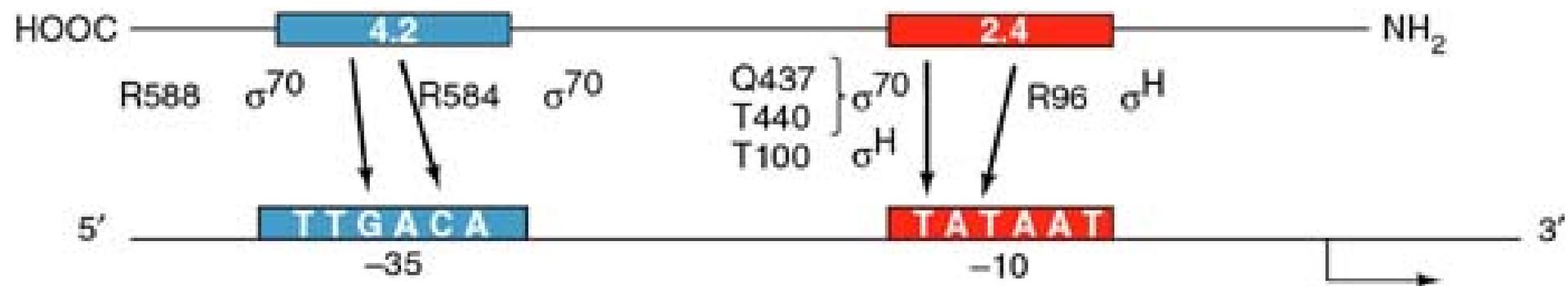
To bind promoter-specific regions, the core enzyme requires another subunit, sigma (σ).

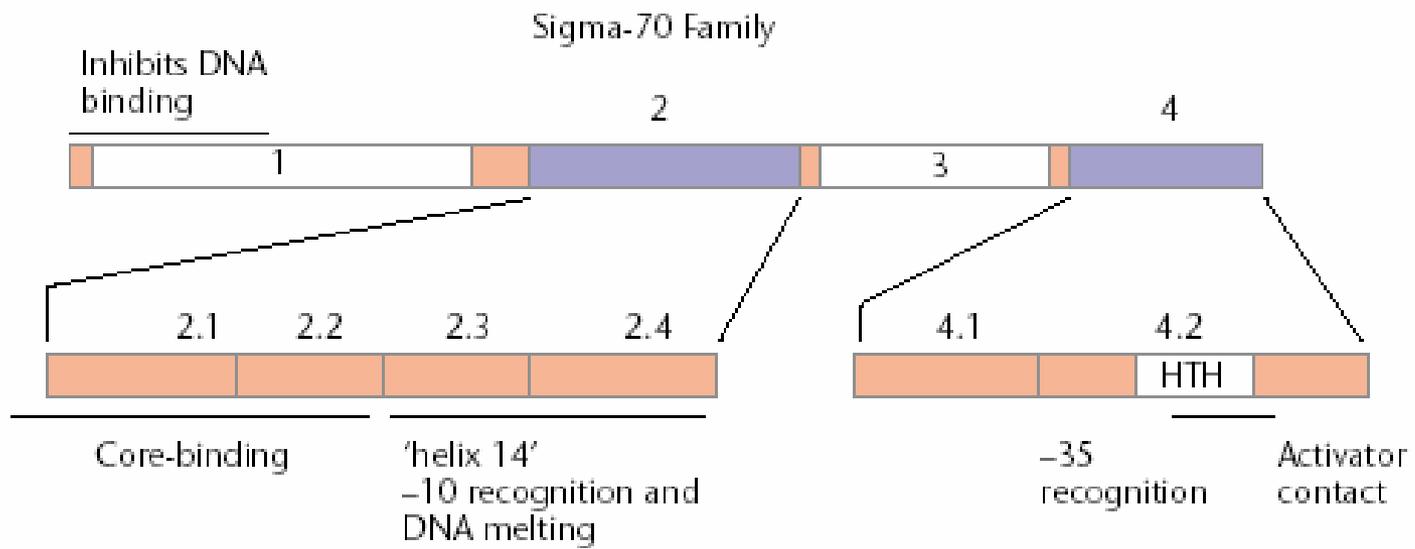
The sigma factor

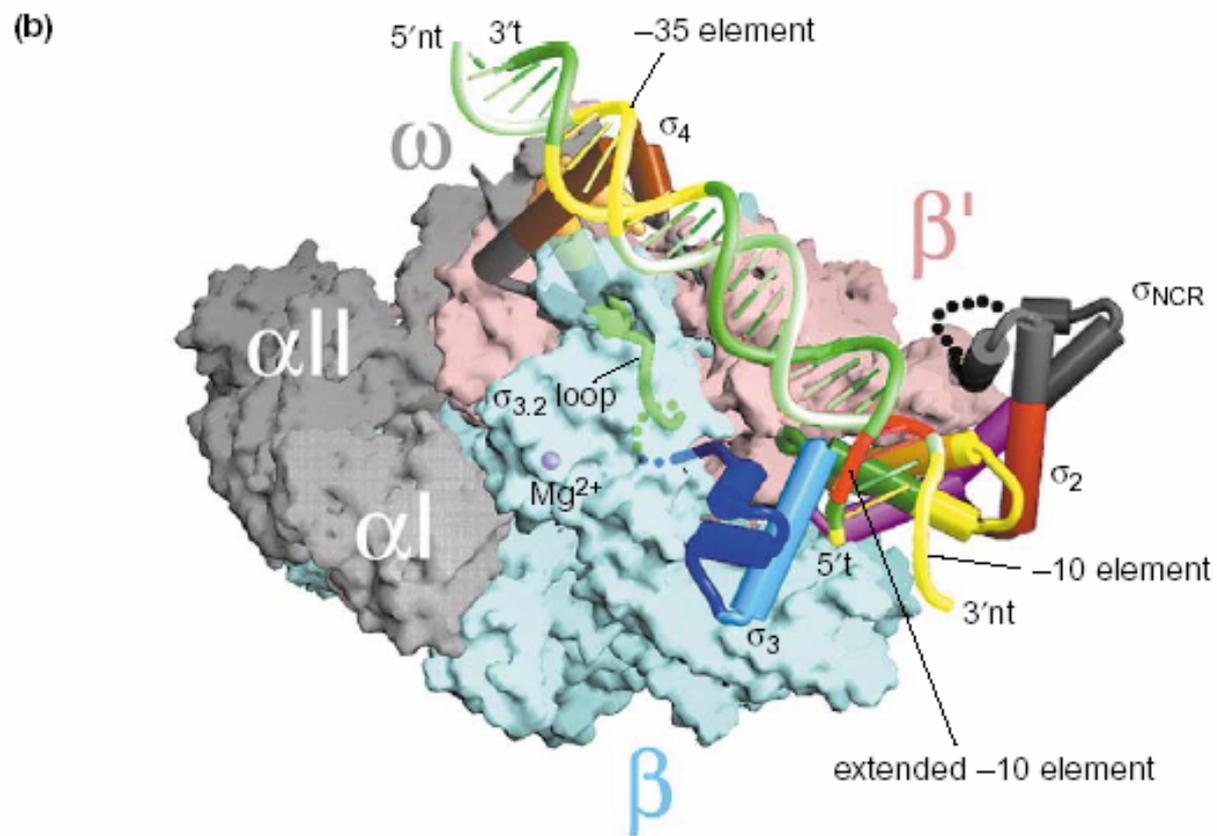
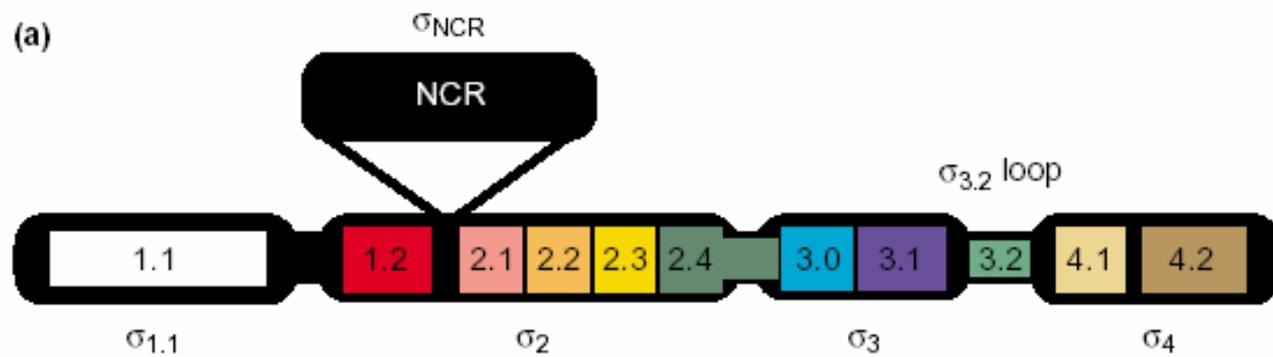
- greatly reduces the affinity of RNAP for nonspecific DNA
- increases the specificity for promoter regions

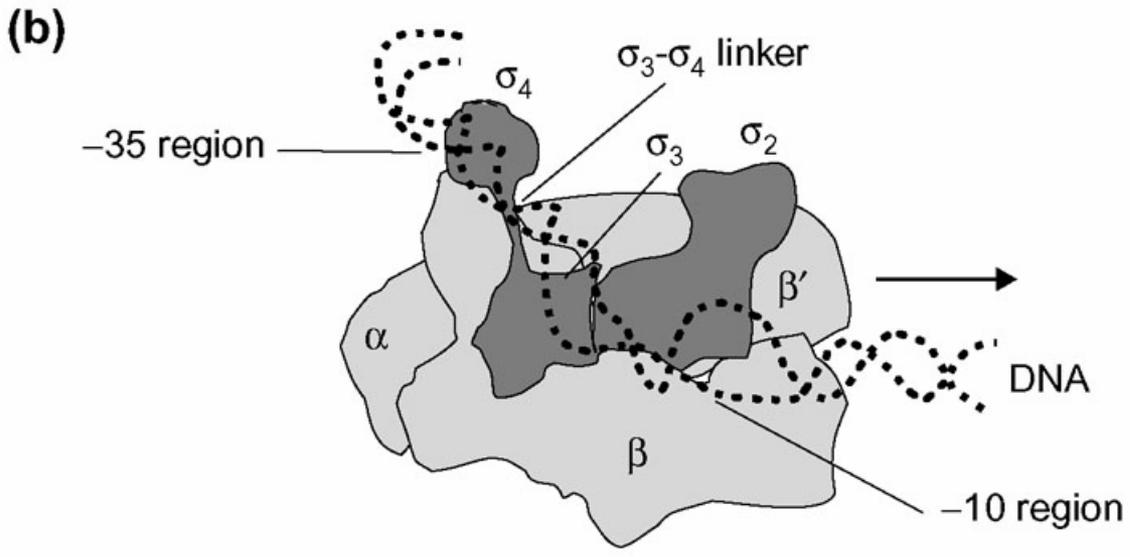
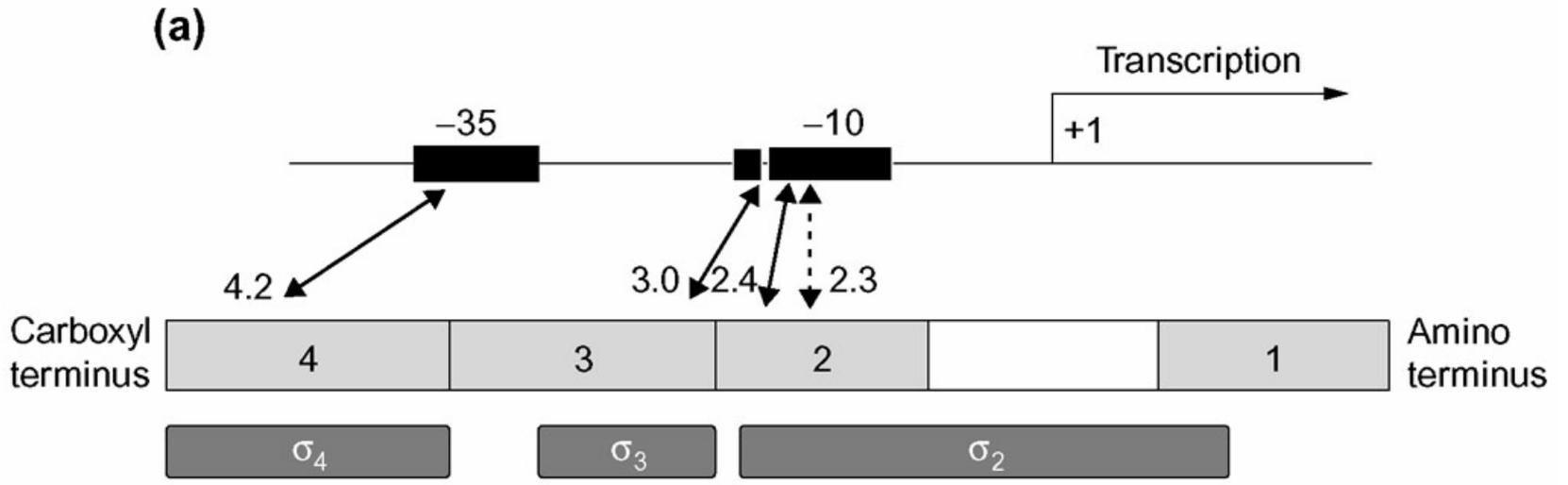
All prokaryotes contain multiple sigma factors.

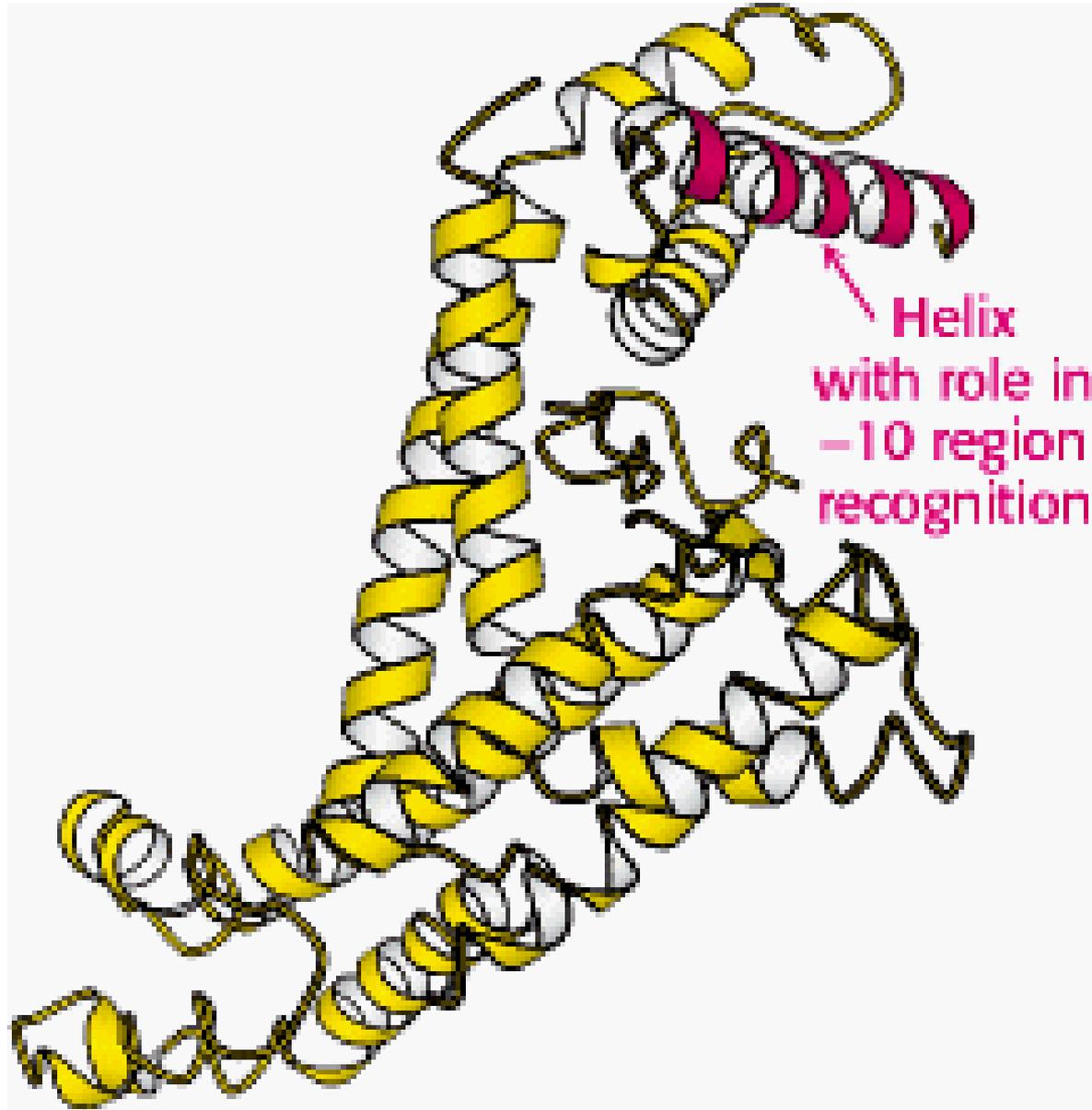
The complete holoenzyme, which is required for promoter-specific initiation has 6 subunits: $\alpha 2 \beta \beta' \sigma \omega$ (~480 kDa).







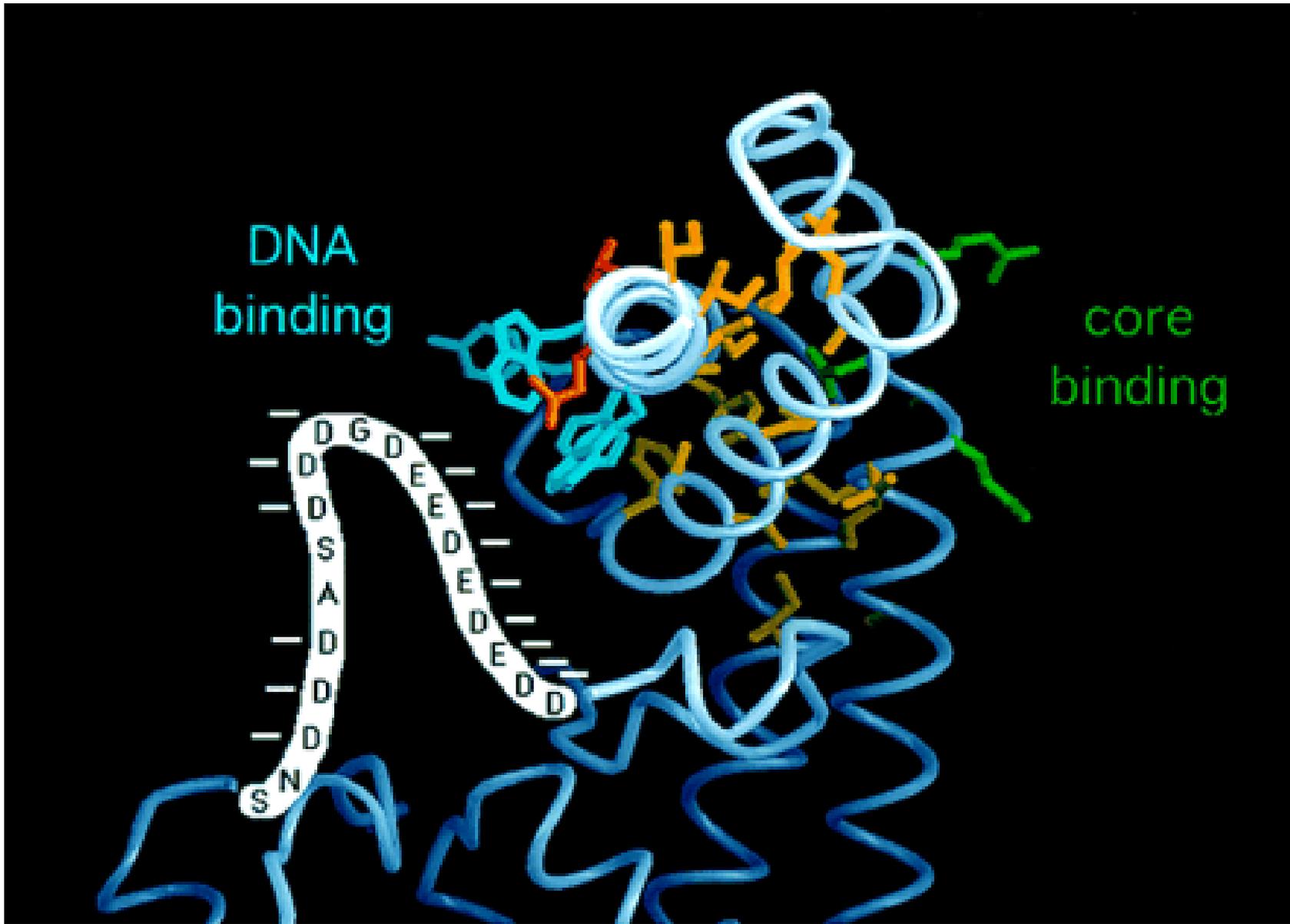




DNA
binding

core
binding

S N
D G D
D D E
D S A D E
D A D E
D D E
D D E
D D E



5'-----⁻³⁵TTGACA-----⁻¹⁰TATAAT-----3'

Standard promoter

5'-----TNNCNCNC TTGAA-----CCCATNT-----3'

Heat-shock promoter

5'-----CTGGGNA-----TTGCA-----3'

Nitrogen-starvation promoter

Sigma Factor	Promoters Recognized	Promoter Consensus	
		-35 Region	-10 Region
σ^{70}	Most genes	TTGACAT	TATAAT
σ^{32}	Genes induced by heat shock	TCTCNCCCTTGA A	CCCCATNT A
σ^{28}	Genes for motility and chemotaxis	CTAAA	CCGATAT
σ^{38}	Genes for stationary phase and stress response	?	?
		-24 Region	-12 Region
σ^{54}	Genes for nitrogen metabolism and other functions	CTGGNA	TTGCA

SOURCES: C. A. Gross, M. Lonetto, and R. Losick, 1992, in S. L. McKnight and K. R. Yamamoto, eds., *Transcriptional Regulation*, Cold Spring Harbor Laboratory Press; D. N. Arnosti and M. J. Chamberlin, 1989, *Proc. Nat'l. Acad. Sci. USA* **86**:830; R. Hengge-Aronsis, 1996, *Mol. Microbiol.* **21**:887.

A	Group 1	-----GTPDPVPRVYLKSGTVPILLTRREEVPLSKRIEKAQVQIE		97
		CTR RpoD	97	
CTR SigA	93	-----GTPDPVPRVYLKSGTVPILLTRREEVPLSKRIEKAQVQIE	136	
BSU SigA	97	-----PPGVKINPVRVYLKSGTVPILLTRREEVPLSKRIEKAQVQIE	131	
SAU PlaC	90	-----PPGVKINPVRVYLKSGTVPILLTRREEVPLSKRIEKAQVQIE	128	
ECO RpoD	86	-----SVSEIGRTTPVPRVYMRSGTVPILLTRREEVPLSKRIEKGINQVQ	131	
STY RpoD	88	-----SVSEIGRTTPVPRVYMRSGTVPILLTRREEVPLSKRIEKGINQVQ	133	
PAE RpoD	88	-----AVESDIGNTPVPRVYMRSGTVPILLTRREEVPLSKRIEKGIREVM	133	
MXA RpoD	187	-----EDDEPGGKSNPVRVYLKSGTVPILLTRREEVPLSKRIEKGSEKVL	232	
ANA SigA	77	-----YTESPVLKSGTVPILLTRREEVPLSKRIEKGSEKVL	115	
SCE HrdB	129	DDAPAQQVAAGATAPVPRVYLKSGTVPILLTRREEVPLSKRIEKG	174	
SCE HrdA	84	-----PPPTRTSEGGPSPVPRVYLKSGTVPILLTRREEVPLSKRIEKG	128	
SAE RpoD	15	-----GPSADLFRVYLKSGTVPILLTRREEVPLSKRIEKG	49	
SCE HrdD	32	-----DRPLVGLYDFAETVPLSKRIEKGSEKVL	64	
SCE HrdC	35	-----EPLVGLYDFAETVPLSKRIEKGSEKVL	68	
ECO SigS	65	-----RVLDATQVYVLEKSGTVPILLTRREEVPLSKRIEKG	99	
ECO RpoH	1	MTDRMQSLALAPVGNRDSYVTRAAANAWMLSDDEERALKKELHYHGD	46	
CFR HtpR	1	MTKEMQNLALAPVGNRDSYVTRAAANAWMLSDDEERALKKELHYHGD	46	
MXA SigB				
STY FliA	1		MNSLYTAE----- 9	
SCE WhiG	1	MPQHTSGSDRAAIPPAARDGGSVRPPAPSTLDLWRSYKTTG	43	
BSU SigD	1		MQSINYEDELWTRKKNK	
BSU SigG	1		MSRNKVEYCGVTSKSLVKNRMRKTRPIDEQD	
BSU SigF	1		MDVEVKKN-----GKNAQLKDEVKELKKSQ-NGD	
BLI SigF	1		MEVKKE-----NONTQLKDEVKELKKSQ-NGD	
BSU SigB	1		YTPSSHTKLRQDEVDRLISSDYTKQD	
BSU SigE	1		YIGGSEALPPLKDEVDRLISSDYTKQD	
BTH Sg35	1		YIGGSEALPPLKDEVDRLISSDYTKQD	
BSU SigK	1		YVKNNAFPQPLSSDEBKYLELMDKGD	
BTH Sg28	1		YVKNNAFPQPLSSDEBKYLELMDKGD	
BSU SigH	1		MNLQNNKGGKNGQ-----FCQLEDQVLEKHYHGD	
BLI SigH	1		MNLQNNKGGKNGQ-----FCQLEDQVLEKHYHGD	

d 562 g p6L1a3336 ba226e G

B	Group 1	-----Core Binding		313
		CTR RpoD	313	
CTR SigA	313	KSQERARKEWVESNLRLLVSIKAKYV	398	
BSU SigA	132	--EESKRRLAESNLRLLVSIKAKYV	215	
SAU PlaC	129	--EVAKSRRLAESNLRLLVSIKAKYV	212	
ECO RpoD	371	KARAKKEWVESNLRLLVSIKAKYV	456	
STY RpoD	373	KARAKKEWVESNLRLLVSIKAKYV	458	
PAE RpoD	375	KARAKKEWVESNLRLLVSIKAKYV	450	
MXA RpoD	466	RAERARSELVESNLRLLVSIKAKYV	561	
ANA SigA	150	IGRERARKEWVESNLRLLVSIKAKYV	235	
SCE HrdB	201	DGRERAKHLLVESNLRLLVSIKAKYV	286	
SCE HrdA	155	LGRERAKRRLVESNLRLLVSIKAKYV	240	
SAE RpoD	76	MGRARKRRLVESNLRLLVSIKAKYV	160	
SCE HrdD	92	ESERARKEWVESNLRLLVSIKAKYV	177	
SCE HrdC	98	DGQERARKEWVESNLRLLVSIKAKYV	183	
ECO SigS	100	--VASRRMIESNLRLLVSIKAKYV	183	
ECO RpoH	47	--LEBAKTLTSLHRLVSIKAKYV	129	
CFR HtpR	47	--LEBAKTLTSLHRLVSIKAKYV	129	
MXA SigB	1			
STY FliA	1		VMRHSLSRQRYVVRHRLDQVRLPVSAGVSDLLDQEGEGLLVAVDRYDALQGLTFTTYAVORIRGAV	
SCE WhiG	44	--EERSLTLLHYSPLVYKVAAGSVGLPNEQAVYSSVGLDAIEKKTVEHREKFTYATFRIRGAV	127	
BSU SigD	21	--PFGGDLRMRVYRLVYVHWGRIYVGLPRLSHKDDLSLELGLDIALEKFPDSDQIKFTIYASVFRIRGAV	104	
BSU SigG	37	--DSAREKLVNLRLLVSIKAKYV	119	
BSU SigF	31	--QARSLTLESNLRLLVSIKAKYV	113	
BLI SigF	29	--QARSLTLESNLRLLVSIKAKYV	111	
BSU SigB	28	--EQAARSLTLESNLRLLVSIKAKYV	111	
BSU SigE	29	--QARSLTLESNLRLLVSIKAKYV	107	
BTH Sg35	29	--QARSLTLESNLRLLVSIKAKYV	107	
BSU SigK	28	--EQRANMLTESNLRLLVSIKAKYV	106	
BTH Sg28	28	--AQANMLTESNLRLLVSIKAKYV	106	
BSU SigH	32	--SDALVYLTIKYRNVVARRARSLFL	115	
BLI SigH	37	--SDALVYLTIKYRNVVARRARSLFL	120	

A2 66EAN6RLV6S6A225 n 2G6 F1D66QEGN6GL62A63253 2G 2F115A15W124A6 Ra6a34a21626P6h6



C	Group 1	-----EHTNKVIRGAKRITAME		398
		CTR RpoD	398	
CTR SigA	398	-----EHTNKVIRGAKRITAME	477	
BSU SigA	215	-----EHTNKVIRGAKRITAME	294	
SAU PlaC	212	-----EHTNKVIRGAKRITAME	291	
ECO RpoD	456	-----EHTNKVIRGAKRITAME	535	
STY RpoD	458	-----EHTNKVIRGAKRITAME	537	
PAE RpoD	460	-----EHTNKVIRGAKRITAME	539	
MXA RpoD	551	-----EHTNKVIRGAKRITAME	630	
ANA SigA	235	-----EHTNKVIRGAKRITAME	313	
SCE HrdB	286	-----EHTNKVIRGAKRITAME	365	
SCE HrdA	240	-----EHTNKVIRGAKRITAME	319	
SAE RpoD	161	-----EHTNKVIRGAKRITAME	256	
SCE HrdD	177	-----EHTNKVIRGAKRITAME	262	
SCE HrdC	183	-----EHTNKVIRGAKRITAME	262	
ECO SigS	183	-----EHTNKVIRGAKRITAME	216	
ECO RpoH	130	-----EHTNKVIRGAKRITAME	216	
CFR HtpR	130	-----EHTNKVIRGAKRITAME	167	
MXA SigB	78	-----EHTNKVIRGAKRITAME	173	
STY FliA	93	-----EHTNKVIRGAKRITAME	212	
SCE WhiG	127	-----EHTNKVIRGAKRITAME	186	
BSU SigD	104	-----EHTNKVIRGAKRITAME	195	
BSU SigG	119	-----EHTNKVIRGAKRITAME	187	
BSU SigF	113	-----EHTNKVIRGAKRITAME	185	
BLI SigF	111	-----EHTNKVIRGAKRITAME	190	
BSU SigB	111	-----EHTNKVIRGAKRITAME	147	
BSU SigE	108	-----EHTNKVIRGAKRITAME	147	
BTH Sg35	108	-----EHTNKVIRGAKRITAME	146	
BSU SigK	107	-----EHTNKVIRGAKRITAME	146	
BTH Sg28	107	-----EHTNKVIRGAKRITAME	162	
BSU SigH	115	-----EHTNKVIRGAKRITAME	167	
BLI SigH	120	-----EHTNKVIRGAKRITAME		

3 6 26 2 2 6 q3 6G23P1 p336A3 6 6 3 6r36 62a 3P616 tp6g33 3 gD 6e3 P 3

-----ESSFDFEDFAVESPBAT	477
-----ESSFDFEDFAVESPBAT	477
-----SHGDFEDFAVESPBAT	294
-----SHGDFEDFAVESPBAT	291
-----SHGDFEDFAVESPBAT	535
-----SHGDFEDFAVESPBAT	537
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-----SRFDFEDFAVESPBAT	313
-----SEFTDFEDFAVESPBAT	365
-----VAIGDFEDFAVESPBAT	319
-----VAIGDFEDFAVESPBAT	256
-----VAIGDFEDFAVESPBAT	262
-----KALDFEDFAVESPBAT	262
-----SDSQPMAPVLYLDKSSNFADGIEDN	216
-----SDSQPMAPVLYLDKSSNFADGIEDN	216
-----EHTNKVIRGAKRITAME	167
-----SEELTDFEDFAVESPBAT	173
-----EHTNKVIRGAKRITAME	212
-----EHTNKVIRGAKRITAME	186
-----NDGGDFYVMDQSDERNDT	195
-----NDGGDFYVMDQSDERNDT	187
-----NDGGDFYVMDQSDERNDT	185
-----NDGGDFYVMDQSDERNDT	190
-----EHTNKVIRGAKRITAME	147
-----EHTNKVIRGAKRITAME	147
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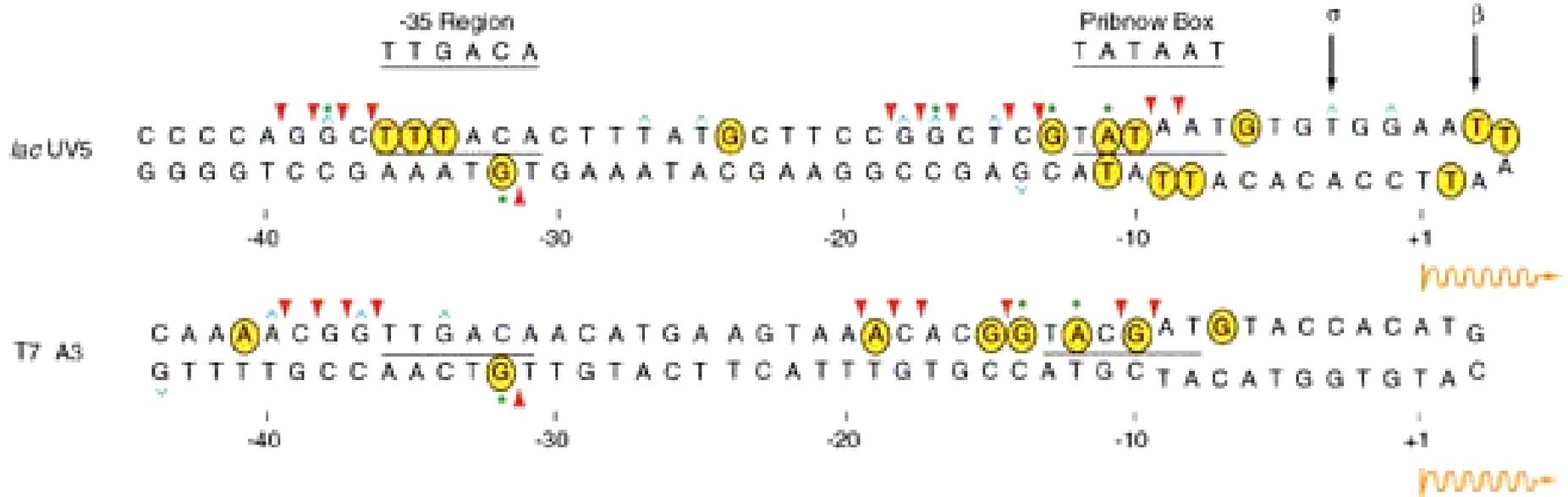
3.1 32

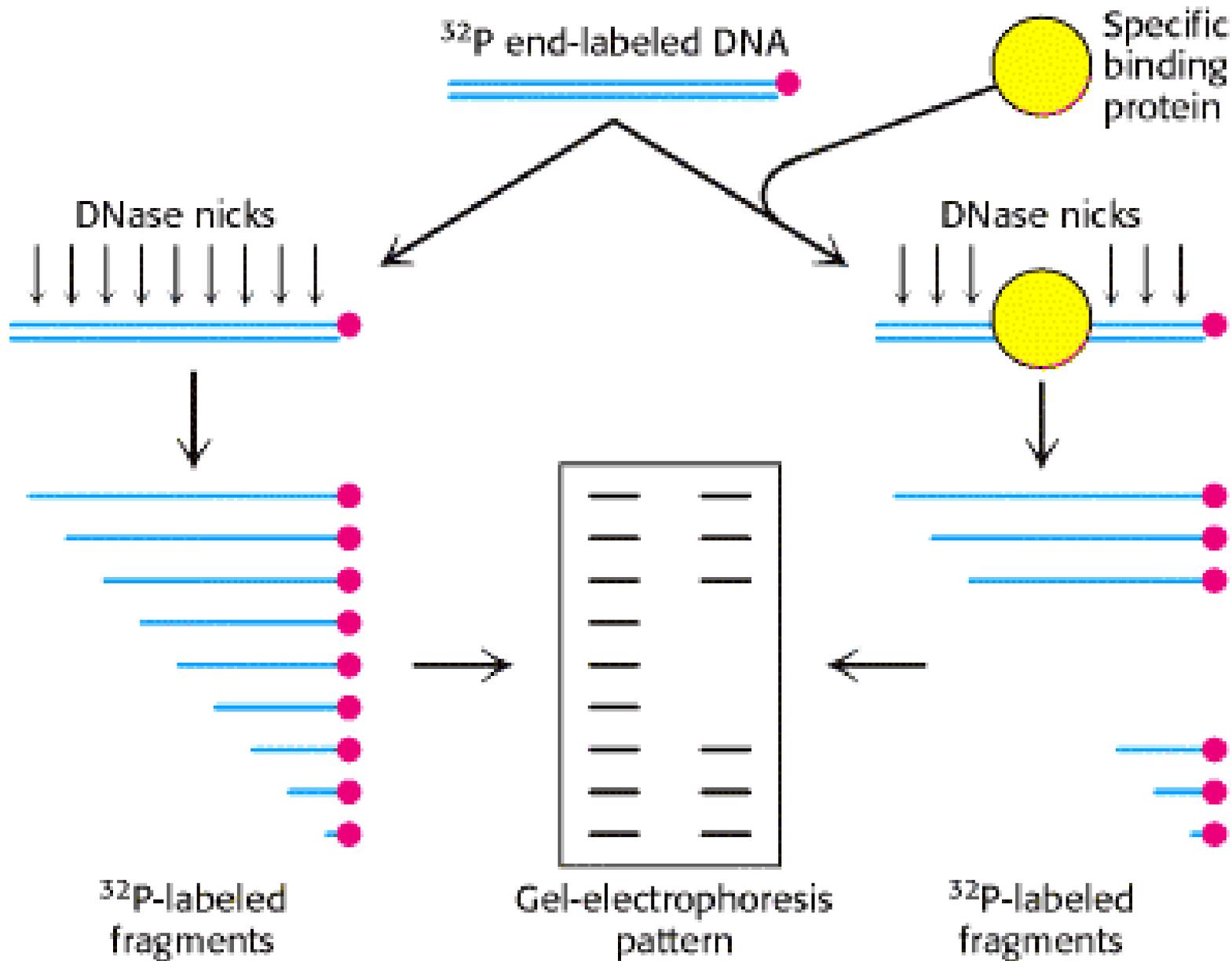
Group 1	Group 2	Group 3
CTR RpoD 478	GYSNFKKVKKMKTLDDRERFVLIHFRGILLGHPKTLDEVGSAFNVTRERIRQIEAKALRKMRFHPSKQIKAEFLDALLEEKIGSGKIKSYKN	572
CTR SigA 478	GYSNFKKVKKMKTLDDRERFVLIHFRGILLGHPKTLDEVGSAFNVTRERIRQIEAKALRKMRFHPSKQIKAEFLDALLEEKIGSGKIKSYKN	572
BSU SigA 295	AYEHLKEQLEPMVSTLDDRENVLSLRFGIAGGRTTLDEVGKVFVTRERIRQIEAKALRKLRFHPSKQIKAEFLDALLEEKIGSGKIKSYKN	371
SAU PlaC 292	AYEHLKEQLEPMVSTLDDRENVLSLRFGIAGGRTTLDEVGKVFVTRERIRQIEAKALRKLRFHPSKQIKAEFLDALLEEKIGSGKIKSYKN	368
ECO RpoD 536	TTESKAAATHPLAGLTAREAKVLMRFGIMNTDHTLDEVGKQFDVTRERIRQIEAKALRKLRFHPSKQIKAEFLDALLEEKIGSGKIKSYKN	613
STY RpoD 538	TTESKAAATHPLAGLTAREAKVLMRFGIMNTDHTLDEVGKQFDVTRERIRQIEAKALRKLRFHPSKQIKAEFLDALLEEKIGSGKIKSYKN	615
PAE RpoD 540	TSESKESTREPLAGLTAREAKVLMRFGIMNTDHTLDEVGKQFDVTRERIRQIEAKALRKLRFHPSKQIKAEFLDALLEEKIGSGKIKSYKN	617
MXA RpoD 631	INMNAEQTRKQATLTPREKVLVLRFGIAGGRTTLDEVGKQFDVTRERIRQIEAKALRKLRFHPSKQIKAEFLDALLEEKIGSGKIKSYKN	709
ANA SigA 314	SKNFKREDLEKMLVLSRPERDVLRLRYGLAGGRTTLDEVGKQFDVTRERIRQIEAKALRKLRFHPSKQIKAEFLDALLEEKIGSGKIKSYKN	390
SCE HrdB 366	SFTLQEQHLSMLTLSEREAQVSMRFGITGCPKTLVEIGKHYGVTRERIRQIESKTMKSLRFHPSKQIKAEFLDALLEEKIGSGKIKSYKN	441
SCE HrdA 320	AFLDQEQHLSMLTLGERERVWVLRFGIAGGRTTLVEIGKHYGVTRERIRQIESKTMKSLRFHPSKQIKAEFLDALLEEKIGSGKIKSYKN	395
SAE RpoD 241	AFFRCEHLEAMSTLGERERVWVLRFGIAGGRTTLVEIGKHYGVTRERIRQIESKTMKSLRFHPSKQIKAEFLDALLEEKIGSGKIKSYKN	317
SCE HrdD 257	LTLRSEELDPLGRLOPRTASIIKRYGIAGGRTTLVEGKHYGLTRERIRQIEAKALRKLRFHPSKQIKAEFLDALLEEKIGSGKIKSYKN	331
SCE HrdC 263	EFOAIAAELEAVGTLAPRESTILSLRYGLAGGRTTLQVQVHGLTRERIRQIEAKALRKLRFHPSKQIKAEFLDALLEEKIGSGKIKSYKN	338
ECO SigS 263	QDDNQQSIVKWFELNAKQEVNLRREFGLGYEAATLDEVGKHYGLTRERIRQIEAKALRKLRFHPSKQIKAEFLDALLEEKIGSGKIKSYKN	362
ECO RpoH 217	WEEQAANRLLTHAQGLDERSQDIIBARVLDGEDNKSTLQELADRYGVSVAERVROLEKAMKKLRAAEA	284
CFR HtpR 217	WEDQAANKLTHAQGLDERSQDIIBARVLDGEDNKSTLQELADRYGVSVAERVROLEKAMKKLRAAEA	281
MXA SigB 168	--GGINARVKAAMRLDPREFPIEQRVYAFSPMTLNLGGEHFGSRRERROLEIPAKDKLASEAALMAEVDPEAVAAQQ	246
STY FliA 174	LEGDNRQVMAEESLPEREQVLTLYN---QEEINKEIGAVVGVGESRVSQIHTKSVLQLRAKAGFGR	239
SCE WhiG 213	EDRELRLLARAVLPERERIVVTLIYN---YEGLTAEIGAVVGVTESRVSQIHTKSVLQLRAKAGFGR	280
BSU SigD 187	MKDELIAQLAEKHELSEKEQIVVSLFY---KEELTTEIGQVNLSTSRISQIHTKSVLQLRAKAGFGR	254
BSU SigG 196	SQWEEELALDQRRINDREKMLKRF---FOGKTQEVGEEFGISQAQVSRLEKPAIKQANKNT-HQ	260
BSU SigF 188	EKWFDIALAEKDLDEREKIVYLRY---YKKTQSEVADRGISQVQVSRLEKPAIKQANKNT-HQ	255
BLI SigF 186	EKWFDIALAEKDLDEREKIVYLRY---YKKTQSEVADRGISQVQVSRLEKPAIKQANKNT-HQ	253
BSU SigB 191	ERVNQQLMLOSALHVISDREKQIIDLTY---IQNKSQETGDFGISQMHVSRLEKPAIKQANKNT-HQ	262
BSU SigE 148	-----KLLKALHQLNDREKQIMPLRFGIAGGRTTLDEVGKQFDVTRERIRQIEAKALRKLRFHPSKQIKAEFLDALLEEKIGSGKIKSYKN	212
BTH Sg35 148	-----HLLMKAHQLNDREKQIMPLRFGIAGGRTTLDEVGKQFDVTRERIRQIEAKALRKLRFHPSKQIKAEFLDALLEEKIGSGKIKSYKN	212
BSU SigK 147	-----EKWQYVTLDDREKQIVVLRFGIAGGRTTLDEVGKQFDVTRERIRQIEAKALRKLRFHPSKQIKAEFLDALLEEKIGSGKIKSYKN	221
BTH Sg28 147	-----EKWQYVTLDDREKQIVVLRFGIAGGRTTLDEVGKQFDVTRERIRQIEAKALRKLRFHPSKQIKAEFLDALLEEKIGSGKIKSYKN	218
BSU SigH 163	-----ELLSDLERVLAALYL---DGRSYQEISDEANRHVKSIDNALQVKKLEKYDELREISL	218
BLI SigH 168	-----ELLSDLERVLAALYL---DGRSYQEISDEANRHVKSIDNALQVKKLEKYDELREISL	223

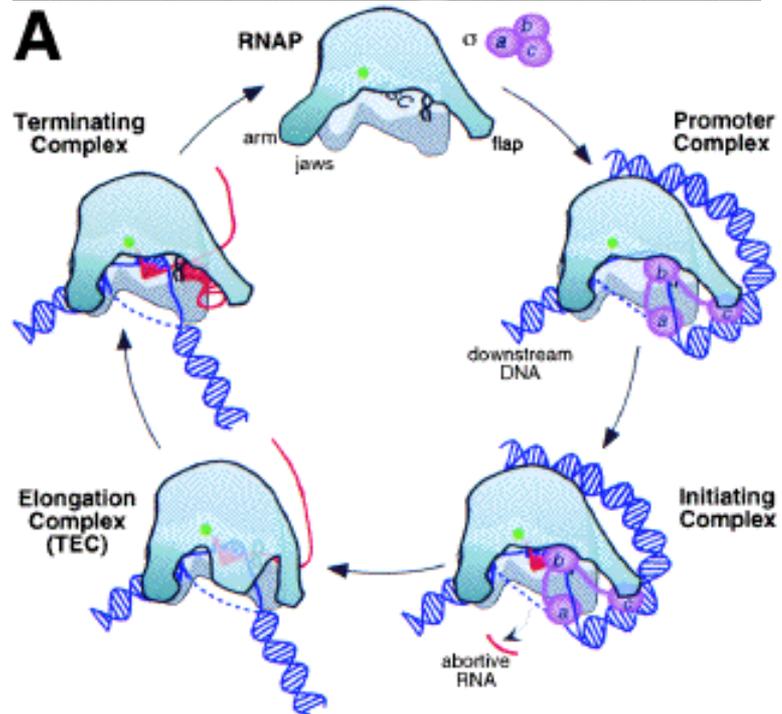
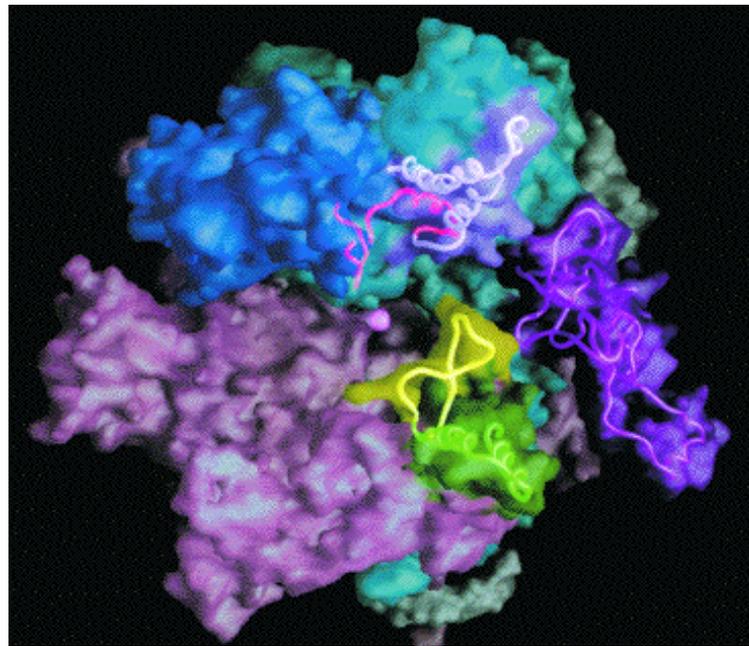
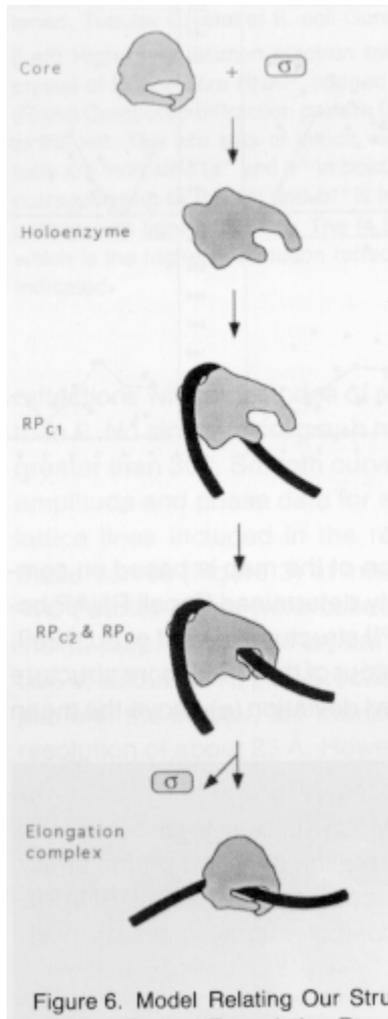
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4.1 4.2

H T H

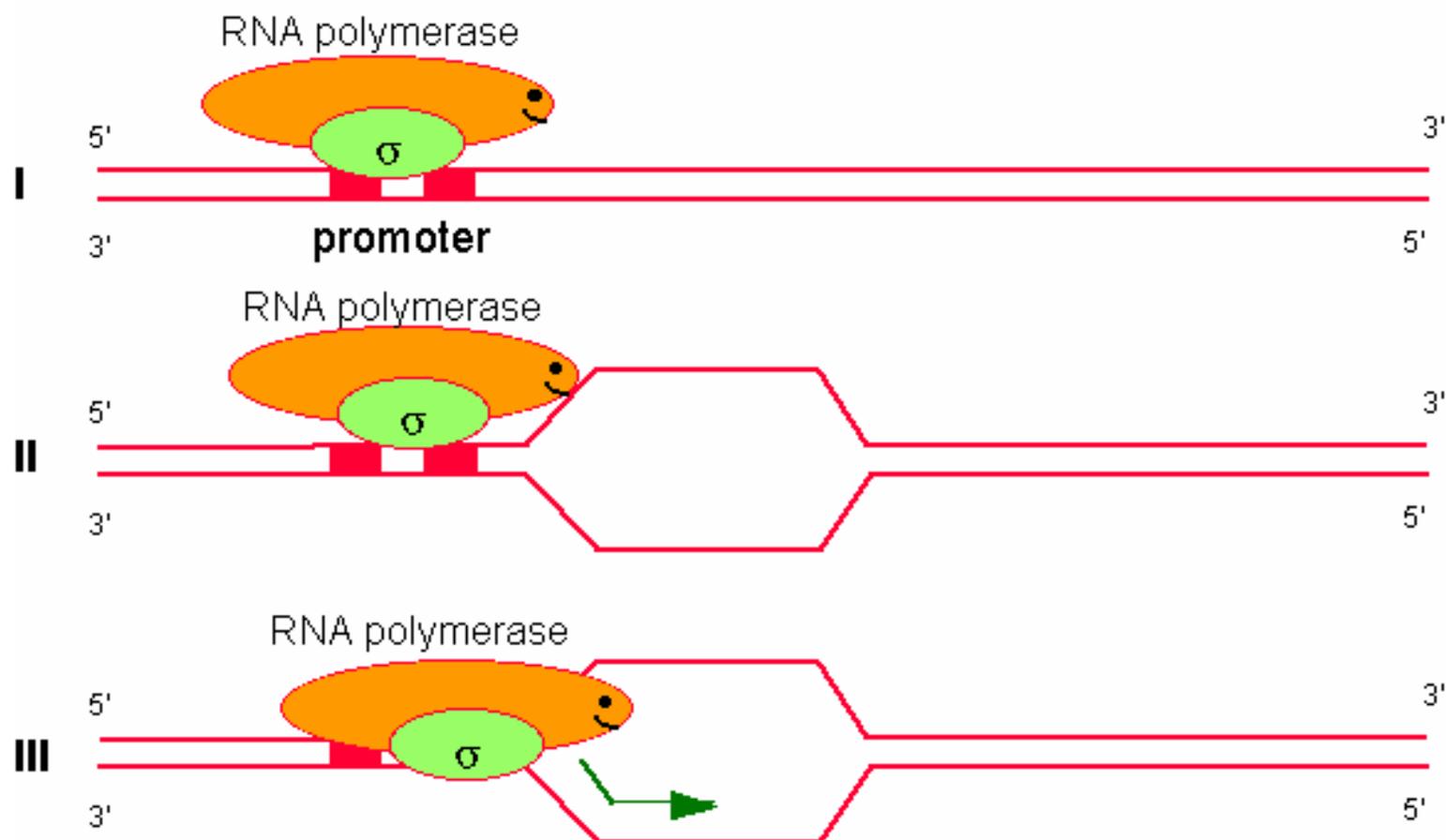


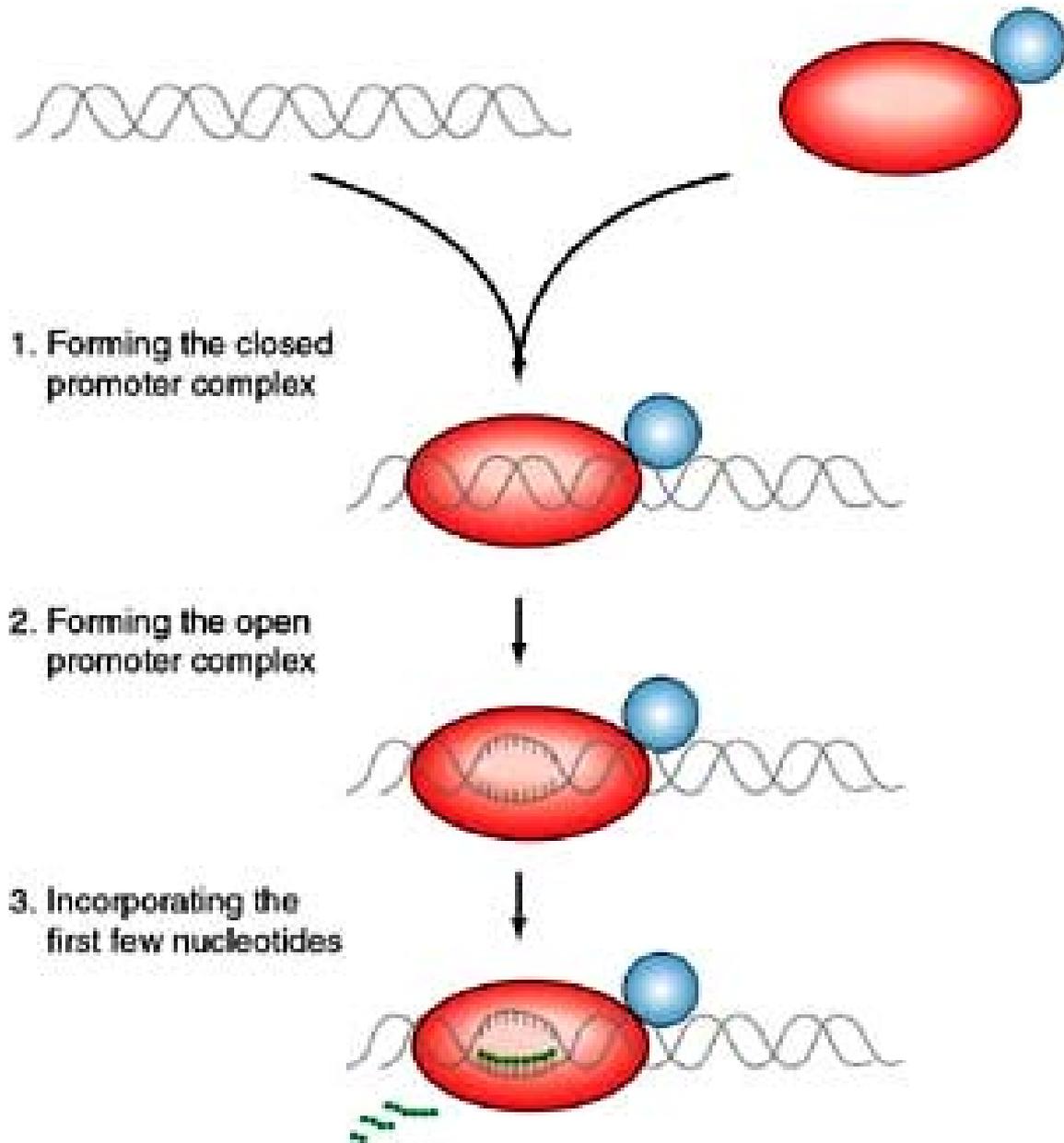




TRANSCRIPTION

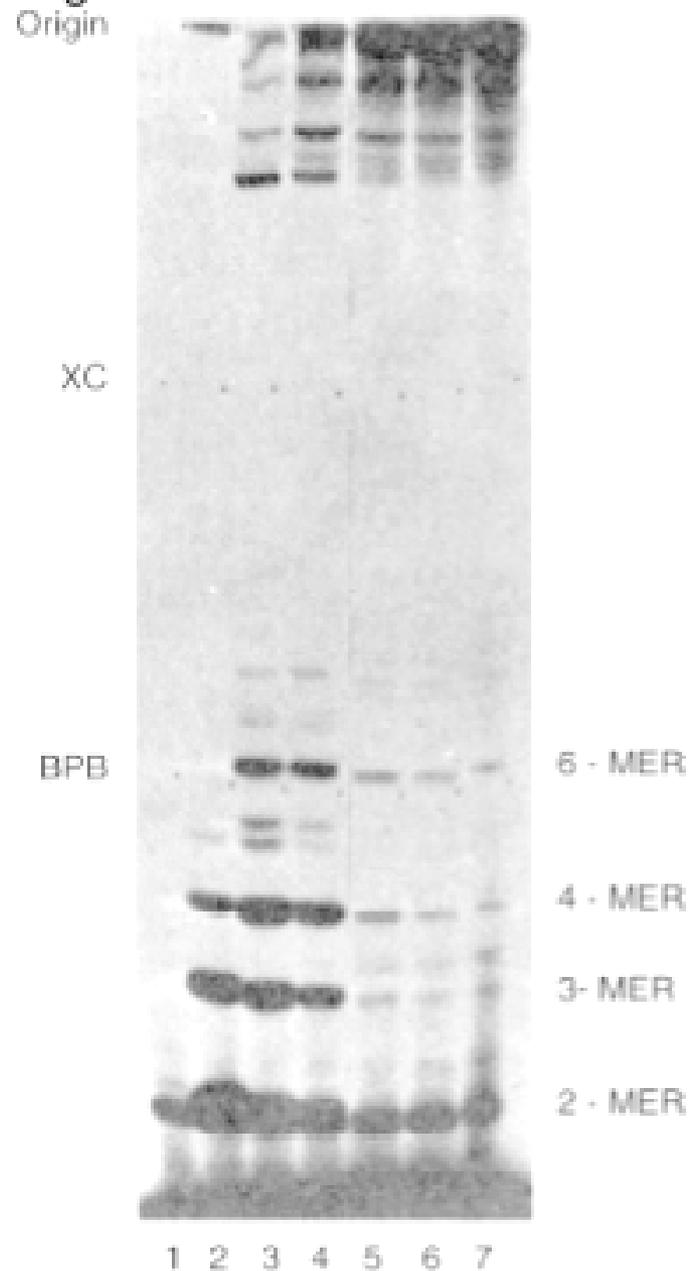
During initiation of transcription, RNA polymerase binds to the promoter, separates DNA strands in front of it and starts transcribing RNA from the template DNA strand.

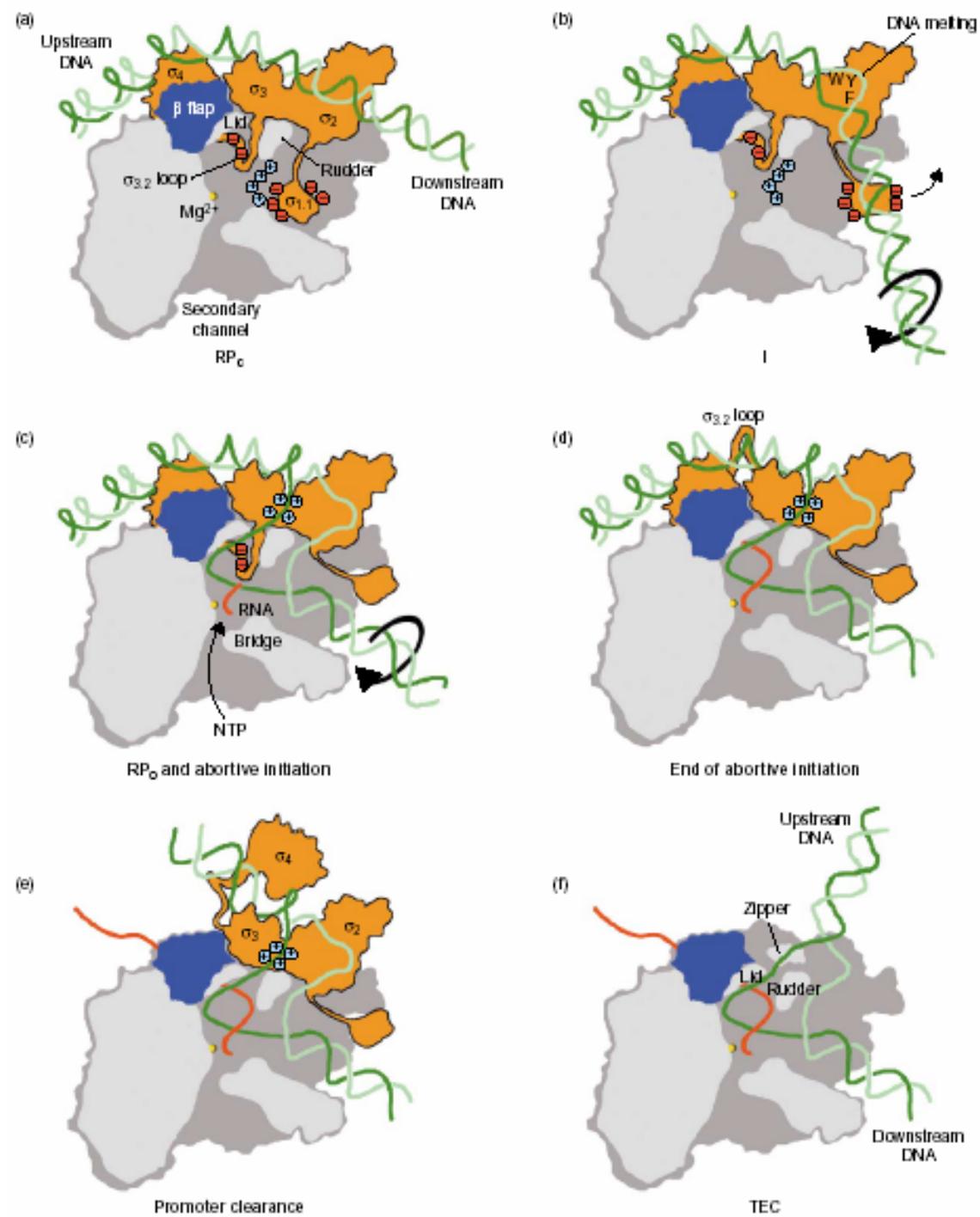




Synthesis of short transcripts by RNAP bound to a promoter

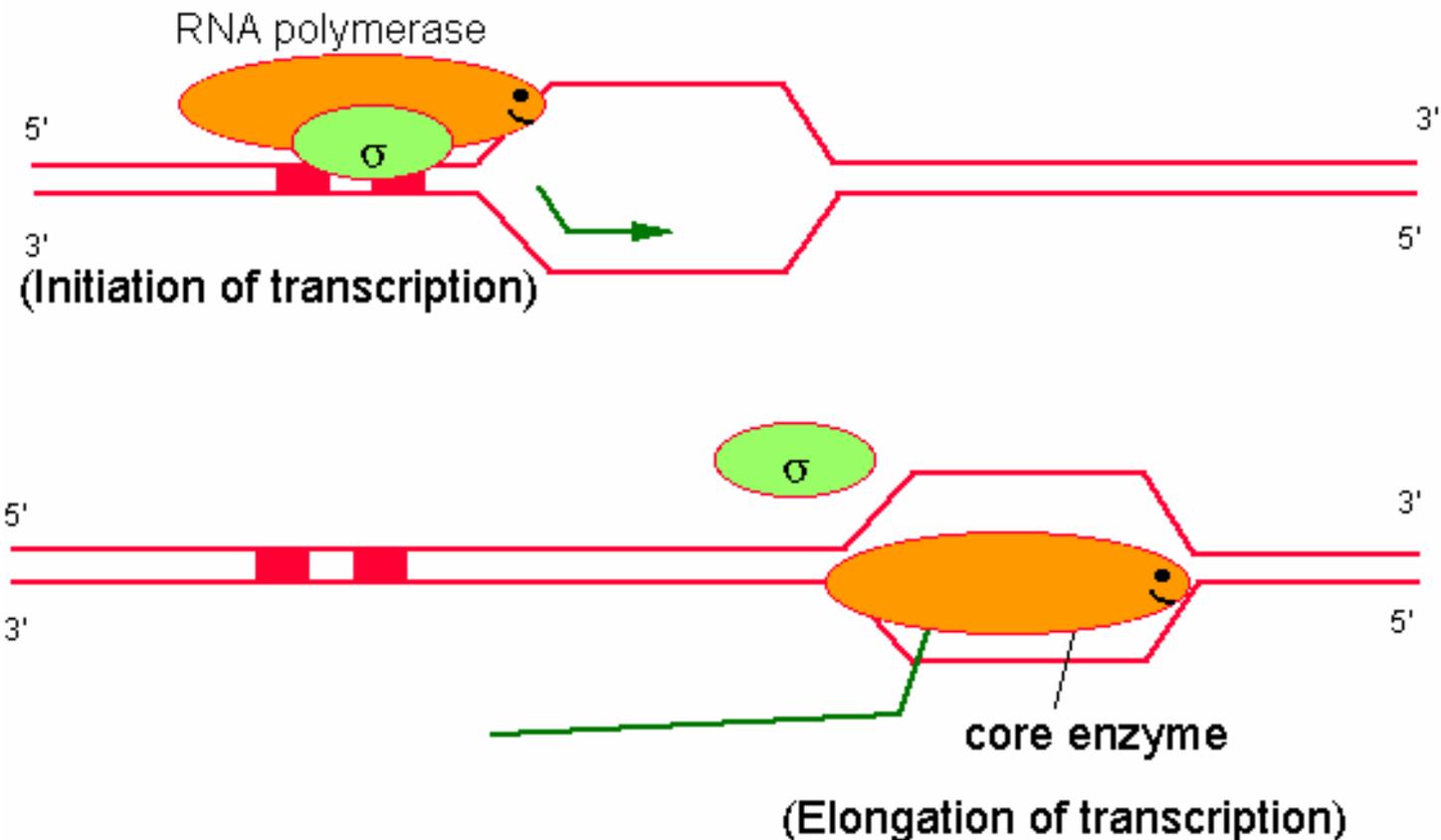
Figure 6.12

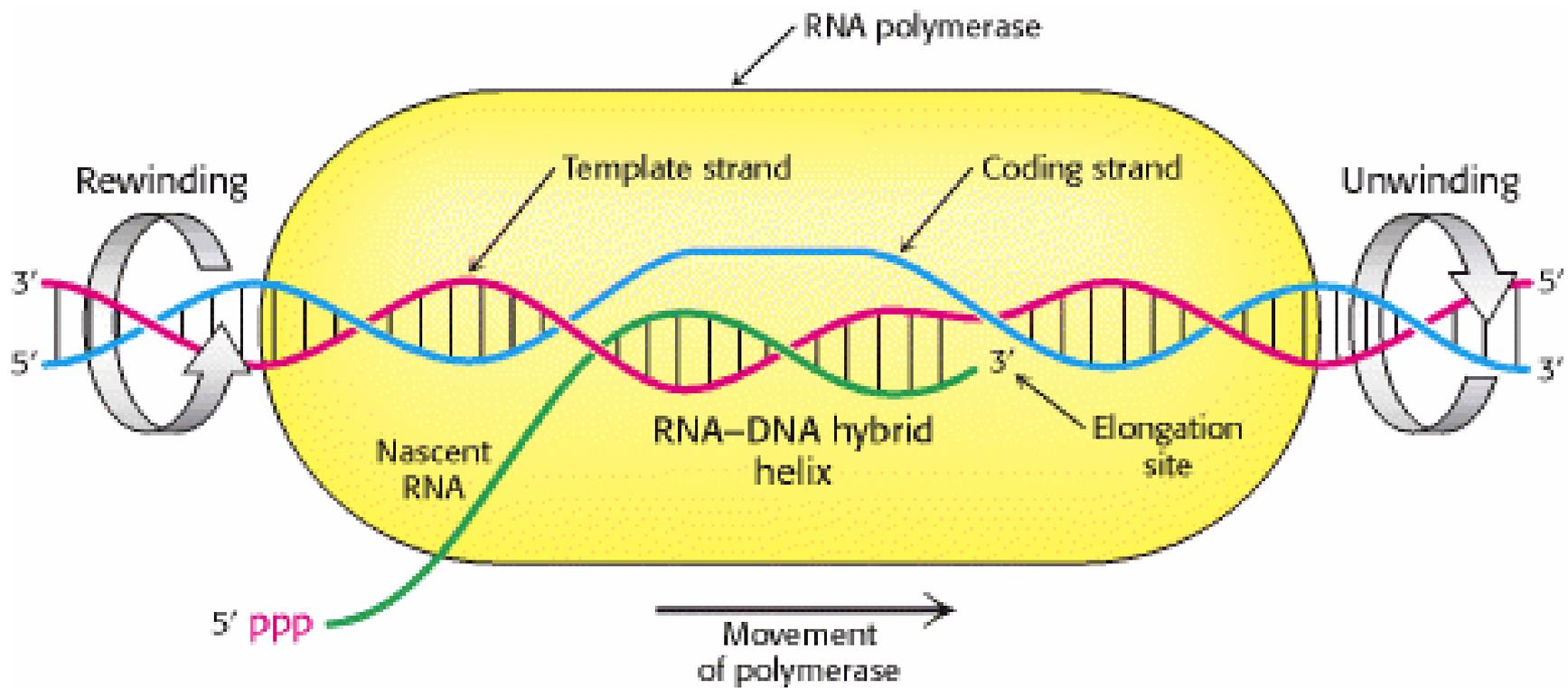


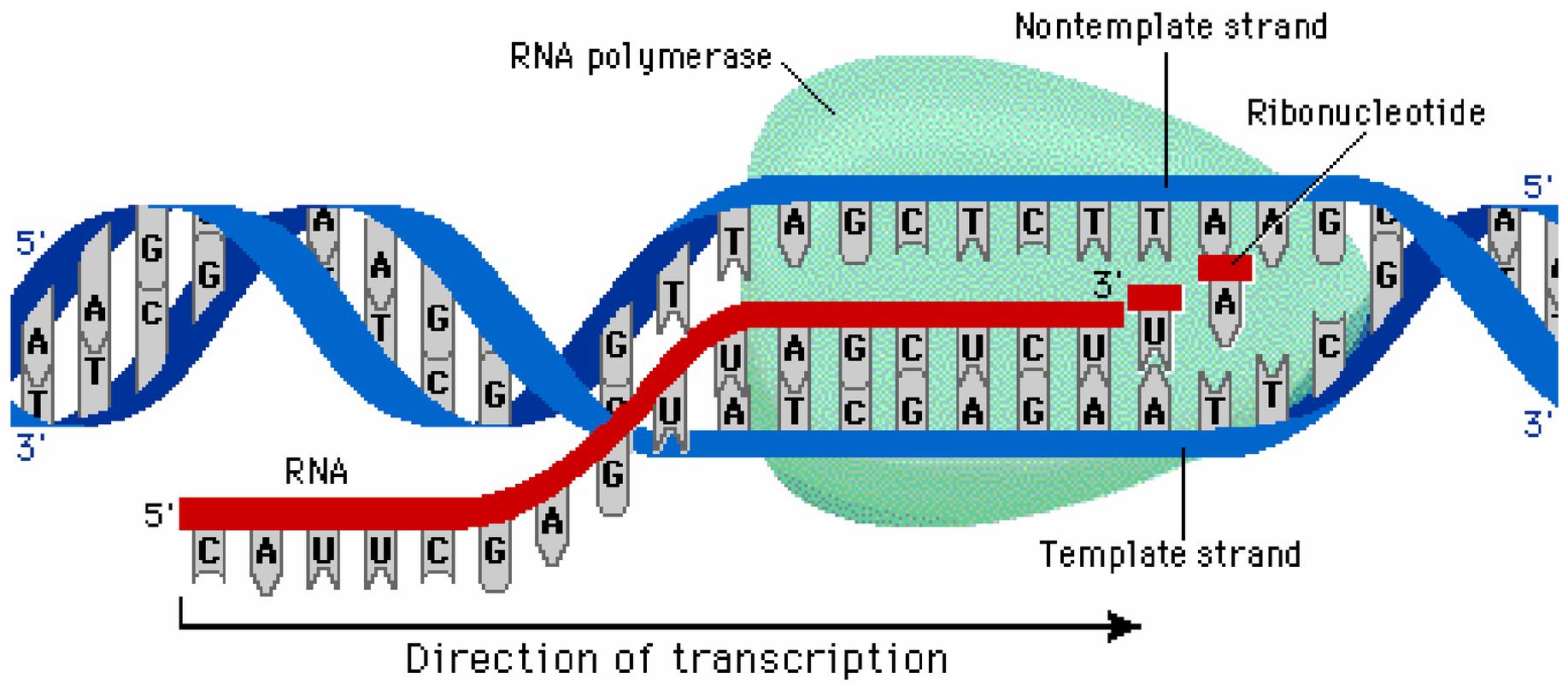


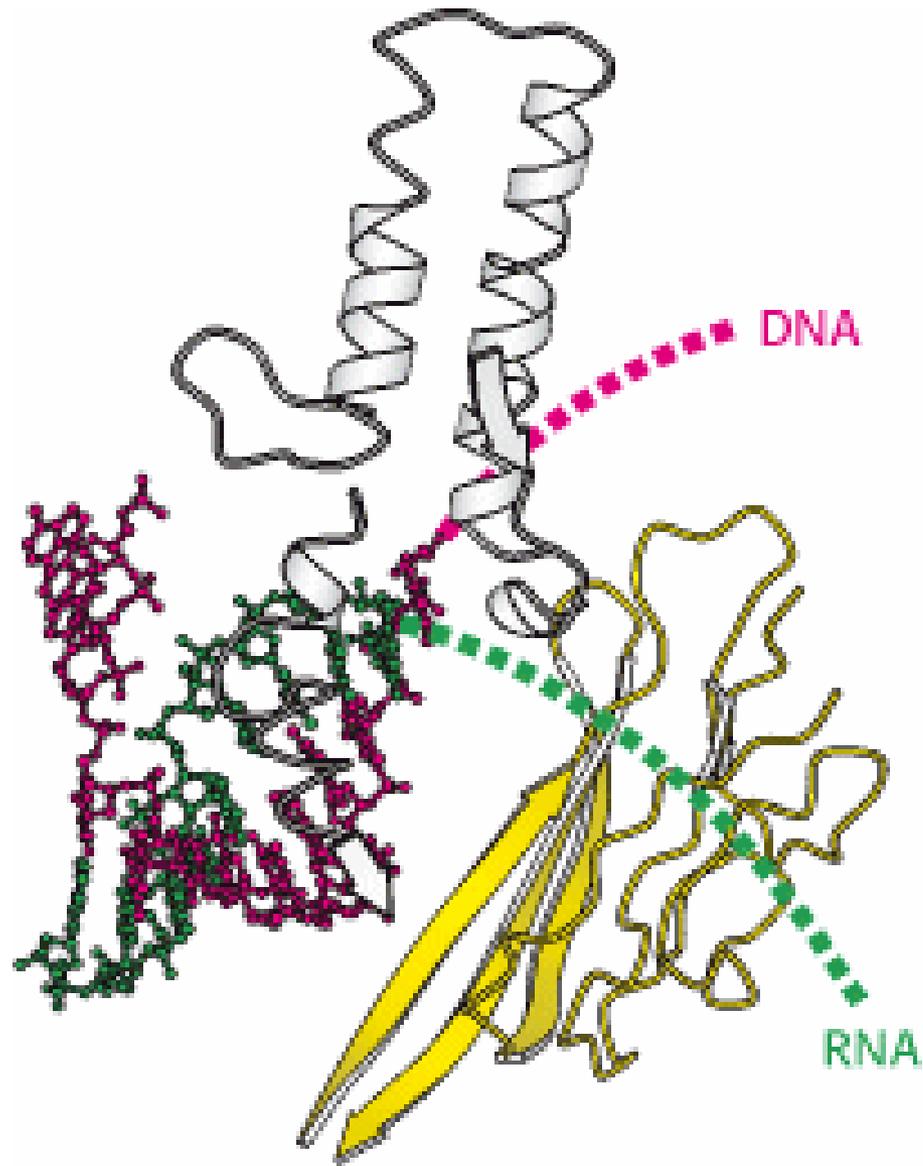
TRANSCRIPTION

Soon after RNA polymerase started transcription, the σ subunit dissociates. The σ subunit is required only for the initiation of transcription. The core enzyme continues to synthesize RNA

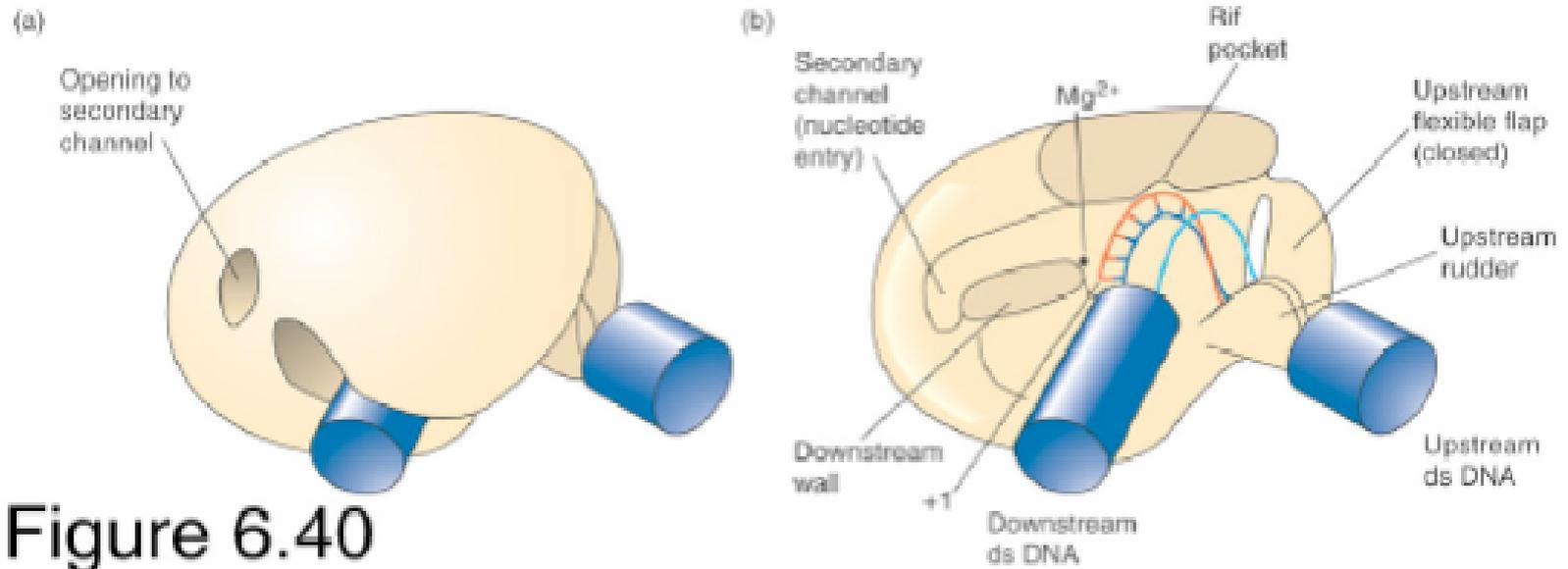








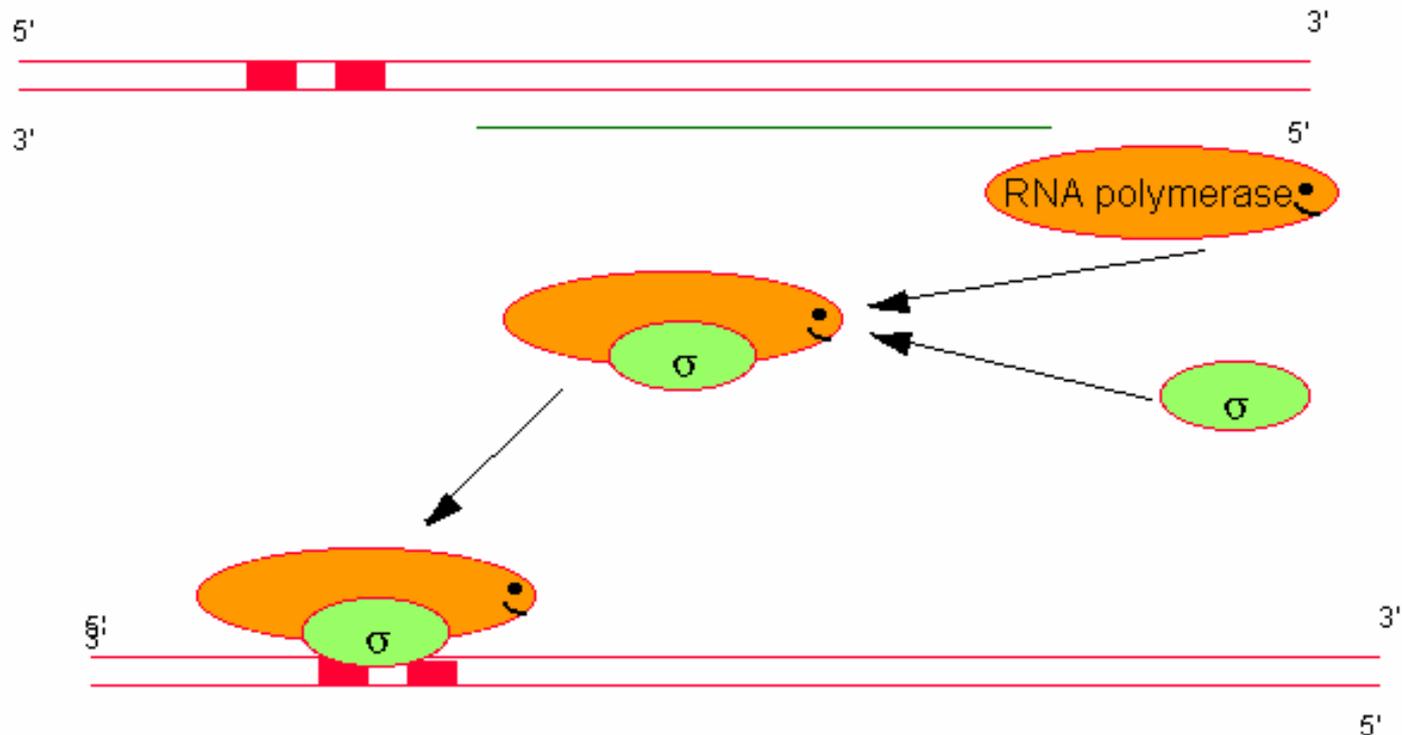
The Elongation Complex

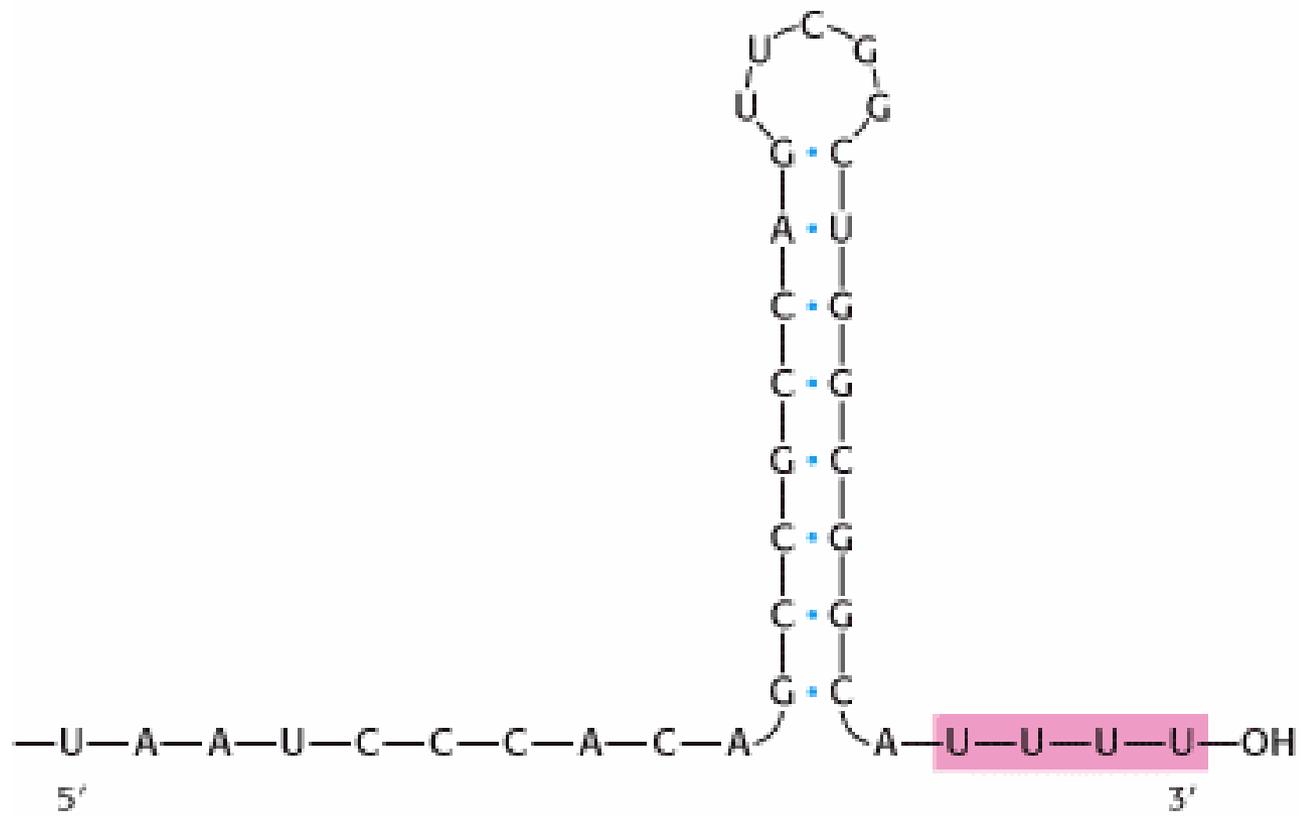


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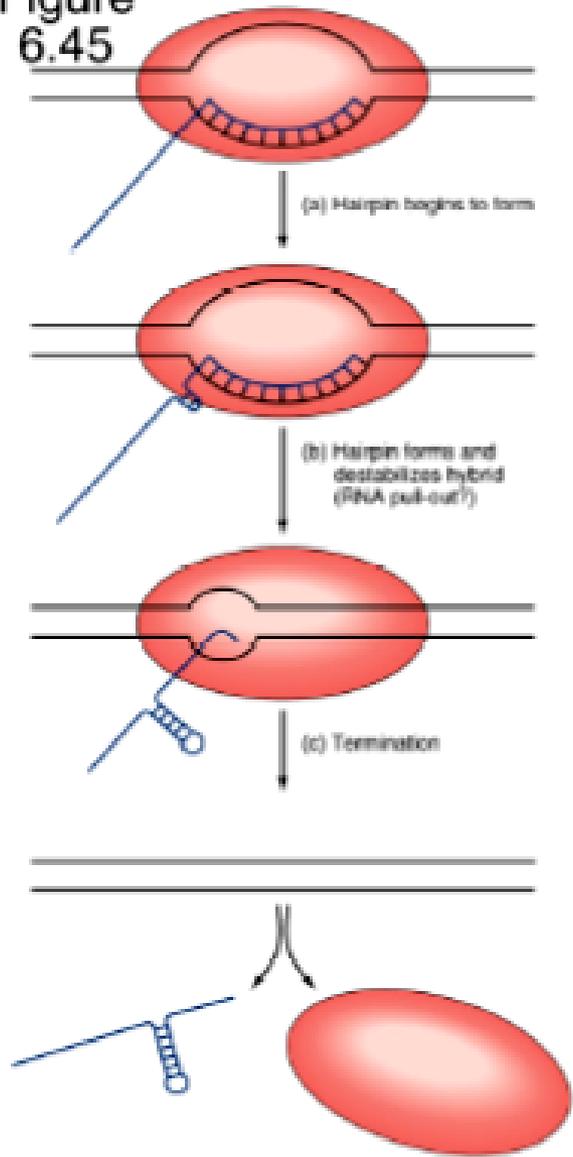
Transcription is terminated when the RNA polymerase encounters a special signal in DNA called transcription terminator. The RNA polymerase dissociates from DNA and the RNA transcript is released.

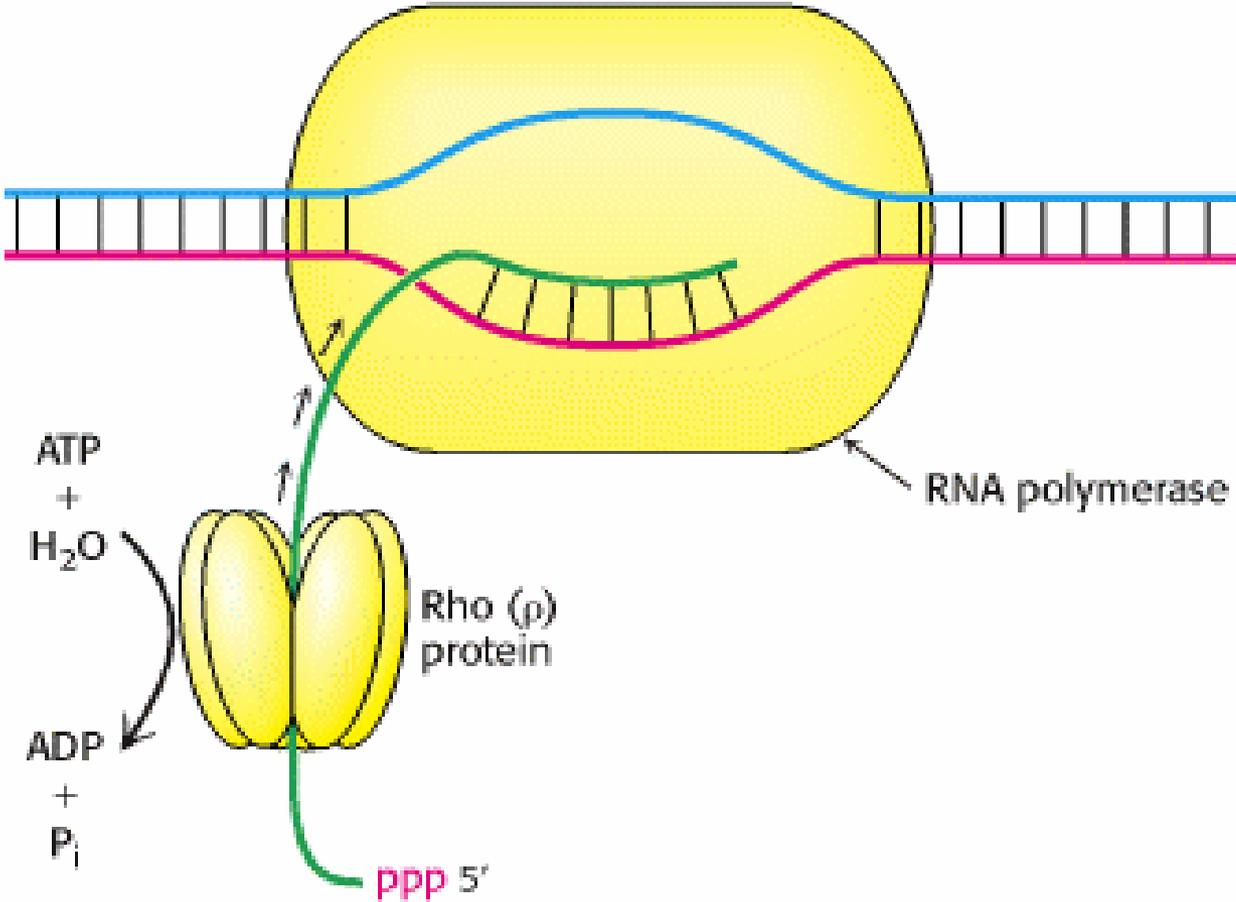
Now RNA polymerase core enzyme can re-unite with the σ subunit, and initiate transcription of another gene.





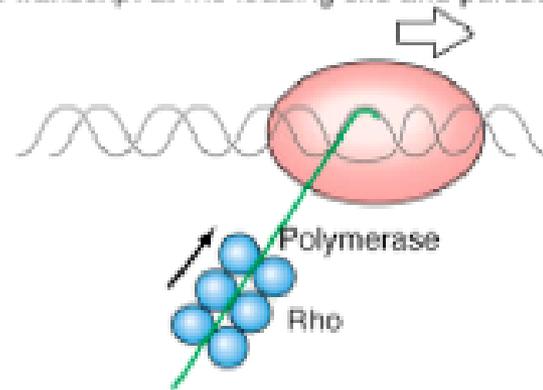
Rho-independent termination
Figure 6.45



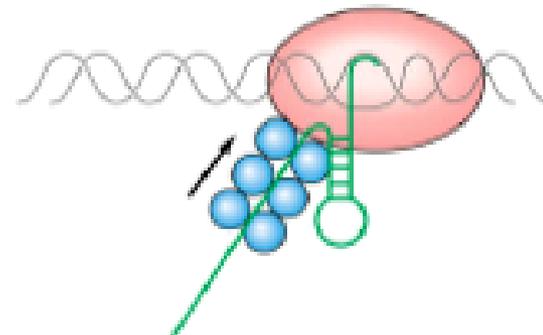


Rho-dependent termination

(a) Rho binds to transcript at rho loading site and pursues polymerase.



(b) Hairpin forms; polymerase pauses; rho catches up.



(c) Rho helicase releases transcript and causes termination.

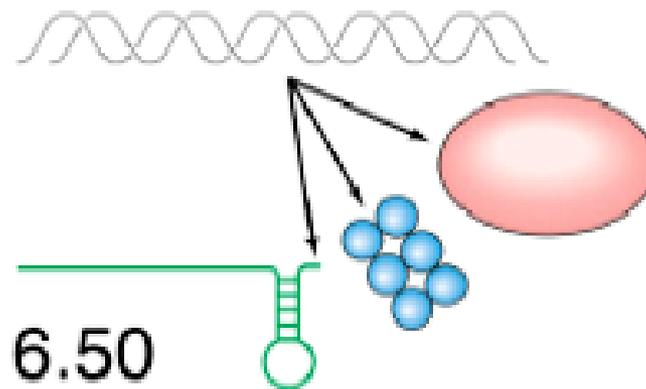
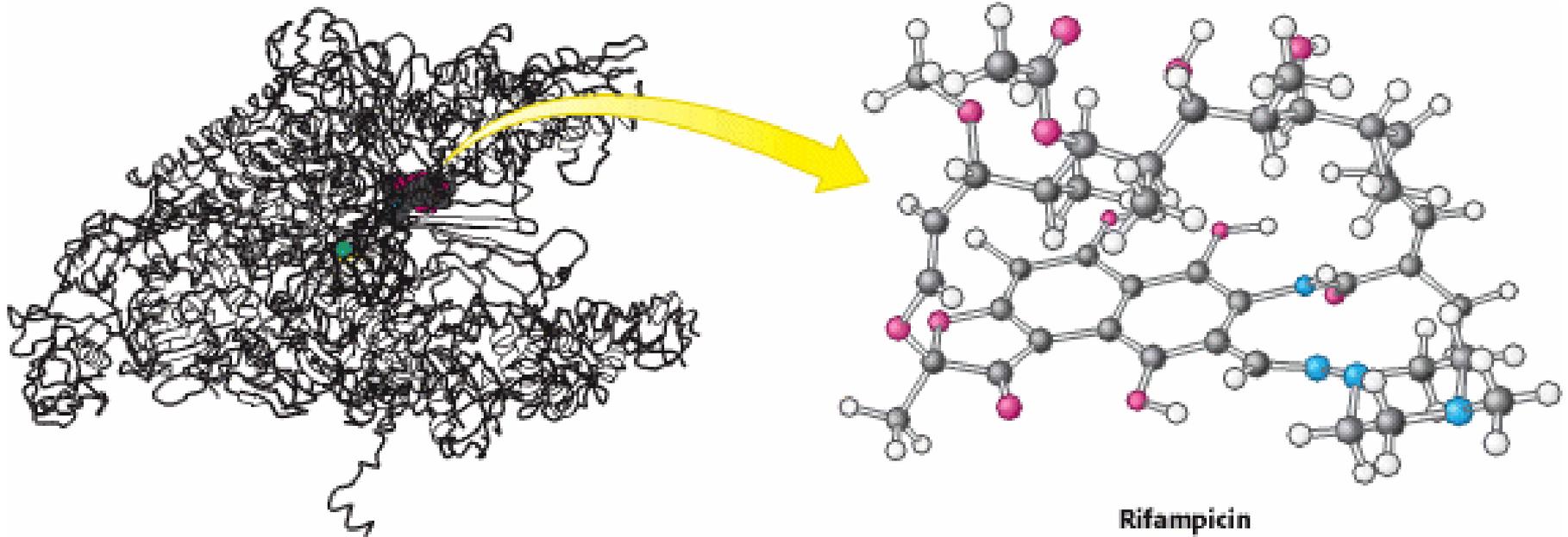


Figure 6.50



Rifampicin binds to a pocket in the channel that is normally occupied by the newly formed RNA-DNA hybrid. Thus the antibiotic blocks elongation after only two or three nucleotides have been added.

http://www.lsic.ucla.edu/l3/tutorials/gene_expression.html