

LEHNINGER
PRINCIPLES OF BIOCHEMISTRY
Fifth Edition

CHAPTER 26

RNA Metabolism

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Transcription

The synthesis of RNA molecules using DNA strands as the templates so that the genetic information can be transferred from DNA to RNA.

(Similarity between
replication and transcription)

- Both processes use DNA as the template.
- Phosphodiester bonds are formed in both cases.
- Both synthesis directions are from 5' to 3'.

→ Base Pair In DNA its Thyamine, in RNA it's Uracil

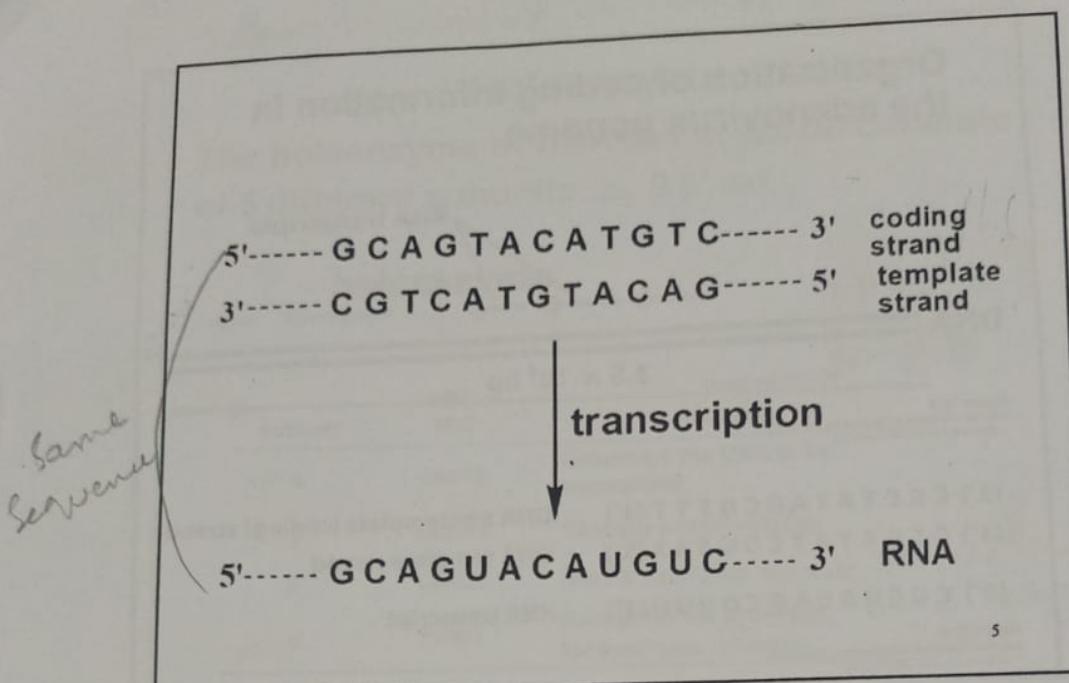
- In DNA there is deoxyribose sugar in RNA it's Ribose sugar

Differences between replication and transcription

DNA	replication	RNA	transcription
template	used Both strands as template		single strand
substrate	dNTP (in DNA)	NTP (Nucleoside triphosphate in RNA)	
primer	yes	no	
Enzyme	DNA polymerase	RNA polymerase	
product	dsDNA	ssRNA	
base pair	A-T, G-C	A-U, G-C	

Template

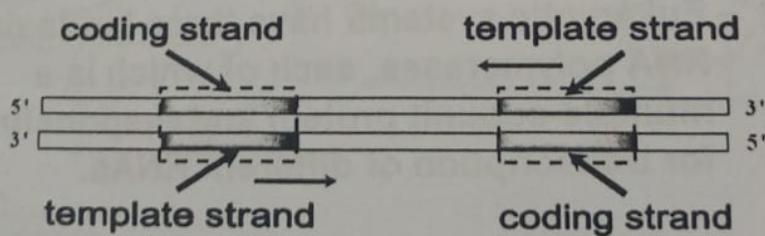
- The strand which we use for synthesis of DNA is called template strand.
- The whole genome of DNA needs to be replicated, but only small portion of genome is transcribed in response to the development requirement, physiological need and environmental changes.
 - DNA regions that can be transcribed into RNA are called structural genes or Transcription unit.
 - (The template strand is the strand from which the RNA is actually transcribed. It is also termed as antisense strand.)
 - (The coding strand is the strand whose base sequence specifies the amino acid sequence of the encoded protein. Therefore, it is also called as sense strand.)



(it's wrong me etc
strand or etc as template
hoga to it
is asymmetric
mode of
transcription)

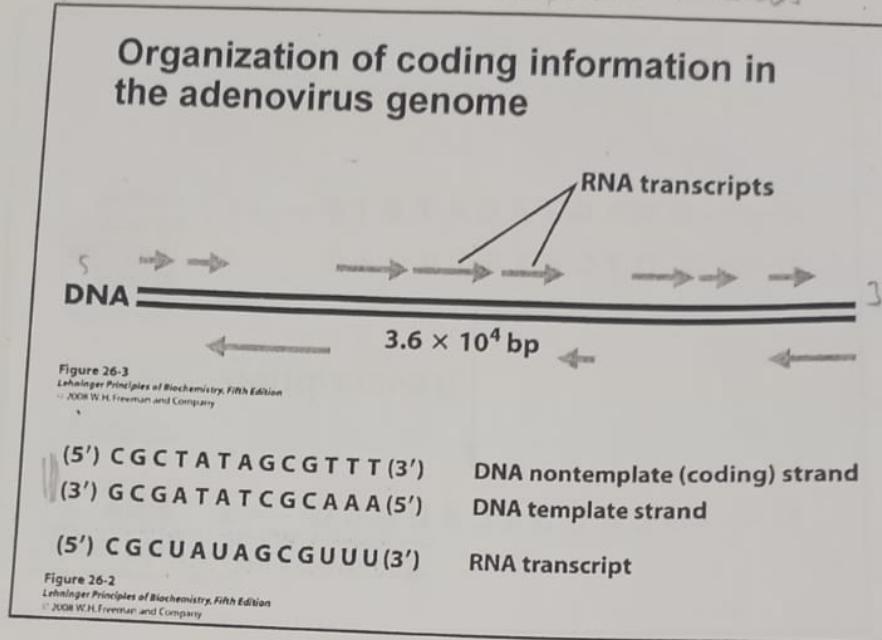
Asymmetric transcription

- Only the template strand is used for the transcription, but the coding strand is not.
- Both strands can be used as the templates.
- The transcription direction on different strands is opposite.
- This feature is referred to as the asymmetric transcription.



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- # do strands have opposite polarity in diff areas
- # no transcrib bra rule no template strands



§ 1.2 RNA Polymerase : Responsible to synthesize phosphodiester bond

- The enzyme responsible for the RNA synthesis is DNA-dependent RNA polymerase.

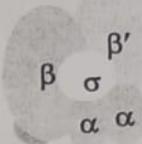
- The prokaryotic RNA polymerase is a multiple-subunit protein of ~480kD.
- Eukaryotic systems have three kinds of RNA polymerases, each of which is a multiple-subunit protein and responsible for transcription of different RNAs.

RNA MRNA
bra teens
bra wa hai

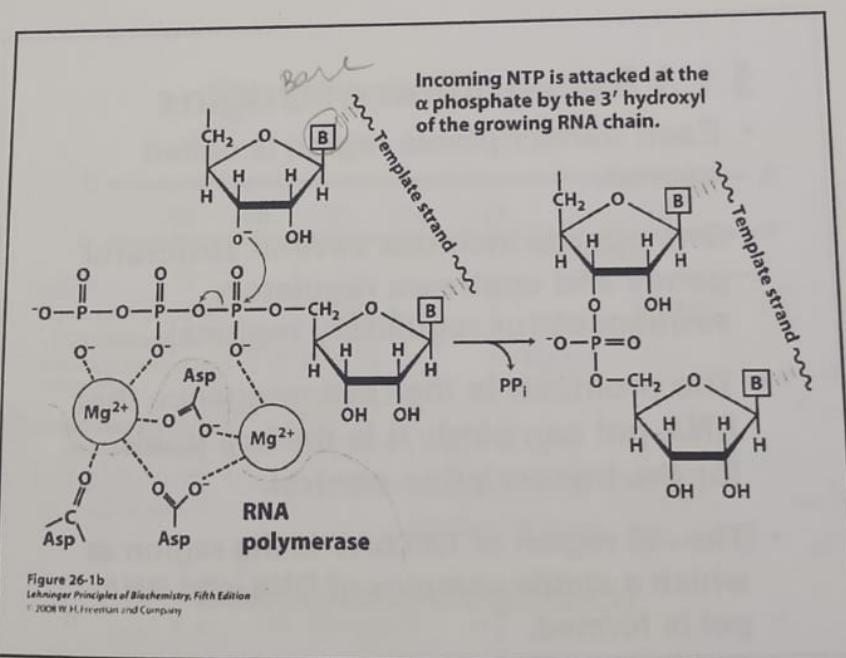
Holoenzyme

The holoenzyme of RNA-pol in *E.coli* consists of 5 different subunits: $\alpha_2 \beta \beta' \omega \sigma$.

holoenzyme



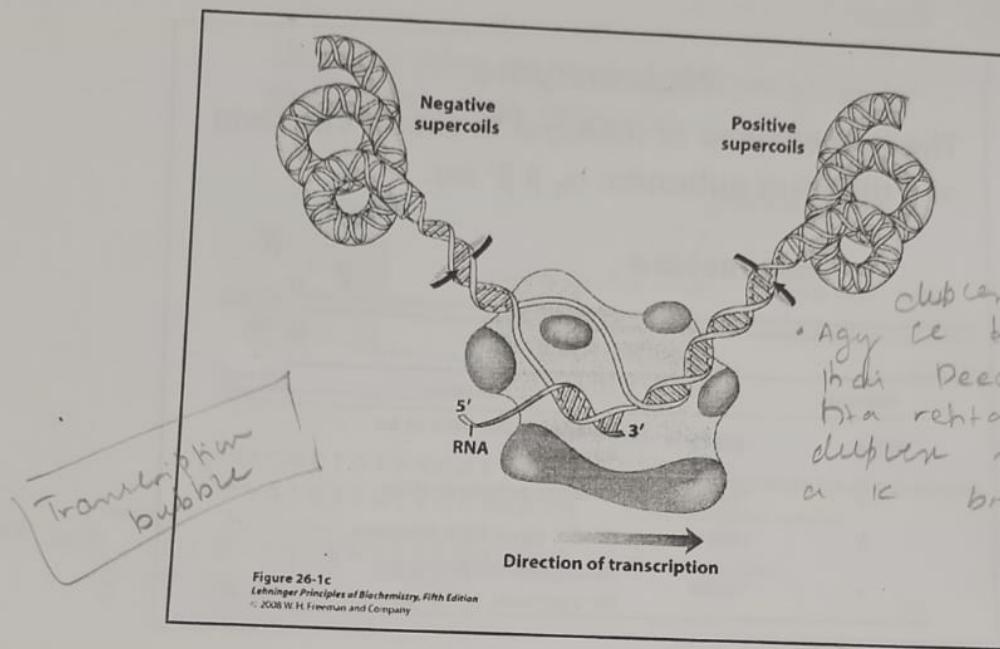
subunit	MW	function
$\checkmark \alpha$	36512	Determine the DNA to be transcribed
β	150618	Catalyze polymerization
β'	155613	Bind & open DNA template, <i>Initiate Process area jahan ke transcription start hogi</i>
$\checkmark \sigma$	70263	Recognize the <u>promoter</u> for synthesis initiation



An Active Site of RNA Polymerase having mag ion which join with Aspartate. Its work is to hold up phosphate to bond to break it to monophosphate for diya sake off groups to pass Pyrophosphate to remove it to.

It have enzyme monophosphatase that help it out to remove it to release 19 kJ/mol energy

"Open area 17 base pair lca hita-hu"

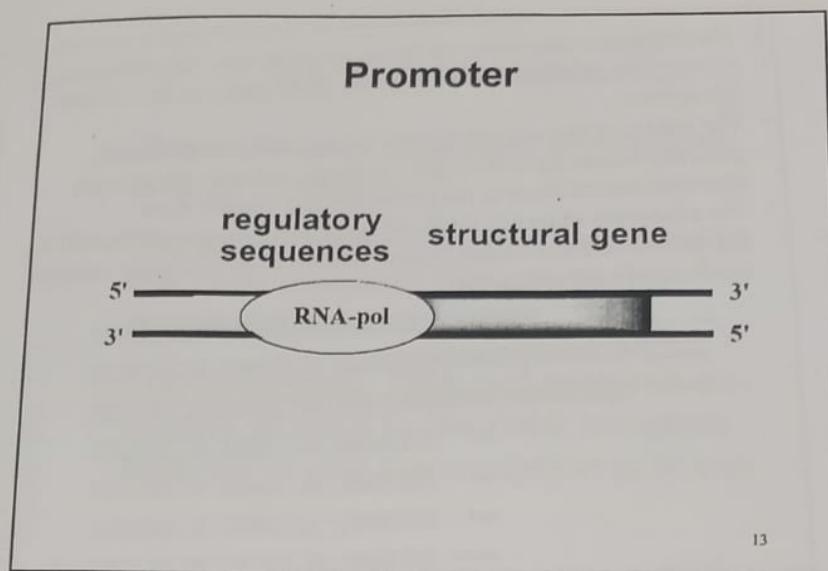


• Agt ce bimulta rehta
hdi Deecce ce bad
hxa rehta hoi. dNA
duplex me nucleo
a ic bad we ha

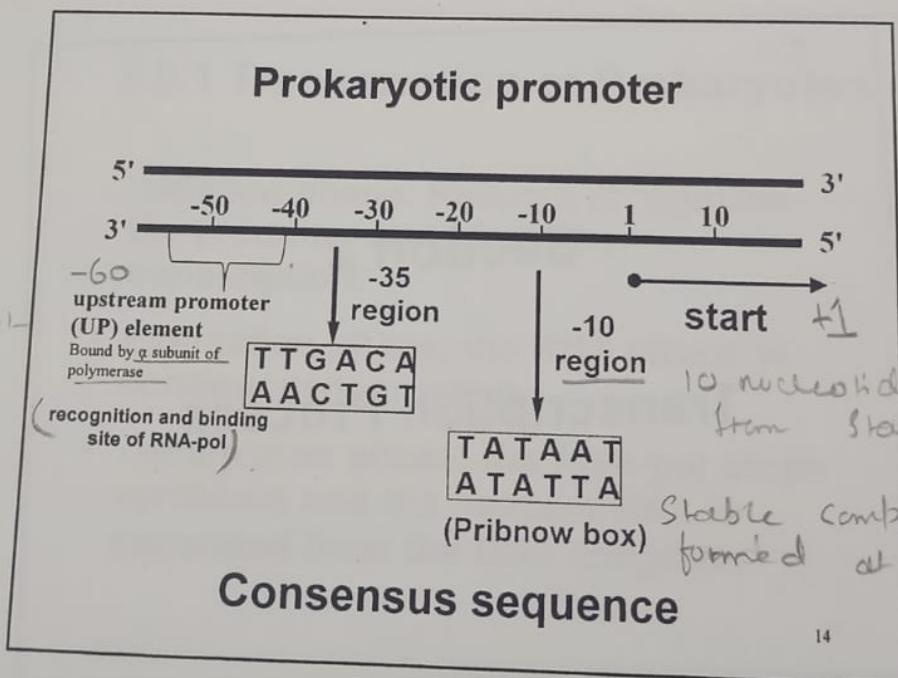
§ 1.3 Recognition of Origins

- Each translatable region is called **operon**.
- One **operon** includes several structural genes and upstream regulatory sequences (or regulatory regions).
- The promoter is the DNA sequence that RNA-pol can bind. It is the key point for the transcription control.
to add first nucleotide.
Initiates the process of transcription.
- The -10 region of TATAAT is the region at which a stable complex of DNA and RNA-pol is formed.
In Promoter region 12

• Structural gene may
single or mul
+ re
by



13



14

-10 -35 one consensus seq
 which are similar in diff sites having
 similar structure & function.
 or minor variation

- The sequences vary from one promoter to the next, but comparisons of many promoters reveal similarities, particularly in the -10 and -35 regions.
- The sequence element UP, not present in all E. coli promoters, generally occurring in the region between -40 and -60, strongly stimulate transcription at the promoters that contain them.
- The consensus sequence for E. coli promoters recognized by σ 70 is shown second from the top. Spacer regions contain slightly variable numbers of nucleotides (N).

Consensus sequence	UP element	-35 Region	Spacer	-10 Region	Spacer	RNA start
NNAAA _n A _m A _p T _q T _r T _s T _t T _u T _v NAAANNNNN						+1
<i>rrnB P1</i>	TTGACA	N ₁₇	TATAAT	N ₆		
AGAAAAATTATTTAAATTTCCTN	GTTGCA	N ₁₆	TATAAT	N ₆	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	

Figure 26-5
Lodish et al., Molecular Cell Biology, 5th Edition

Nucleotide

(Ovarian
charge her
hair) accord
to cellular
area of fun

Fifth nucleotide
breaks the Purine
base ring. It's
one of the four
Choices. Zyclo
Yahan Glutamine
is Lysine here
but it's opposite
sequence here
here RNA A.

Section 2

Transcription Process

General concepts

- Three phases: initiation, elongation, and termination.
- The prokaryotic RNA-pol can bind to the DNA template directly in the transcription process. *Promoter region*
- The eukaryotic RNA-pol requires co-factors to bind to the DNA template together in the transcription process.

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§ 2.1 Transcription of Prokaryotes

- Initiation phase: RNA-pol recognizes the promoter and starts the transcription.
- Elongation phase: the RNA strand is continuously growing.
- Termination phase: the RNA-pol stops synthesis and the nascent RNA is separated from the DNA template.

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a. Initiation

- No primer is needed for RNA synthesis.
- RNA-pol recognizes the TTGACA region, ⁻³⁵ and slides to the TATAAT region, then opens the DNA duplex. ^{To add first nucleotide}
- The unwound region is about 17 ± 1 bp.

4 form stable
Lambourne at
-10 hex is
TATAAT box

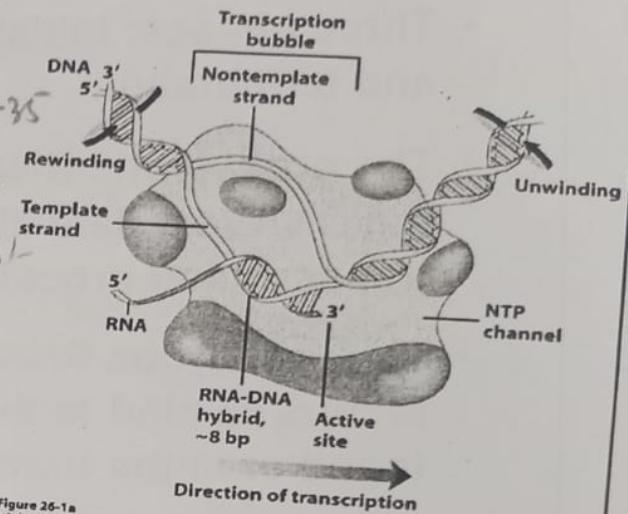


Figure 25-1a
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- The first nucleotide on RNA transcript is always purine triphosphate. GTP is more often than ATP.
- The pppGpN-OH structure remains on the RNA transcript until the RNA synthesis is completed.
- The three molecules form a transcription initiation complex.

RNA pol ($\alpha_2\beta\beta'\sigma$) - DNA - pppGpN- OH 3'

m'ihahen Campione

- ① RNA Polymerase which is in the holoenzyme form with all sigma's bind with DNA duplex to form stable complex
 ② In +1 region RNA polymerase open DNA duplex by add one nucleotide
 ③ Initiation complex begins then it provides signal that initiation complete move towards elongation.

- Transcription is initiated within the complex
- The σ (sigma) subunit falls off once the first 3',5' phosphodiester bond is formed.
- Leading to a conformational change that converts the complex to the elongation form followed by movement of the transcription complex away from the promoter (promoter clearance)



Figure 26-6b
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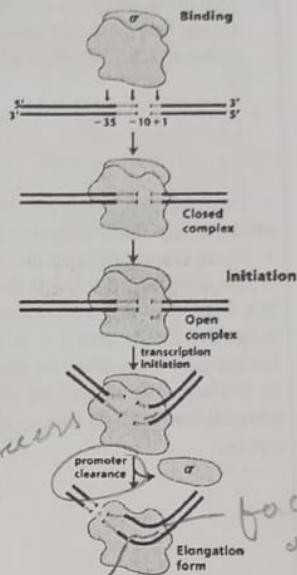


Figure 26-6a
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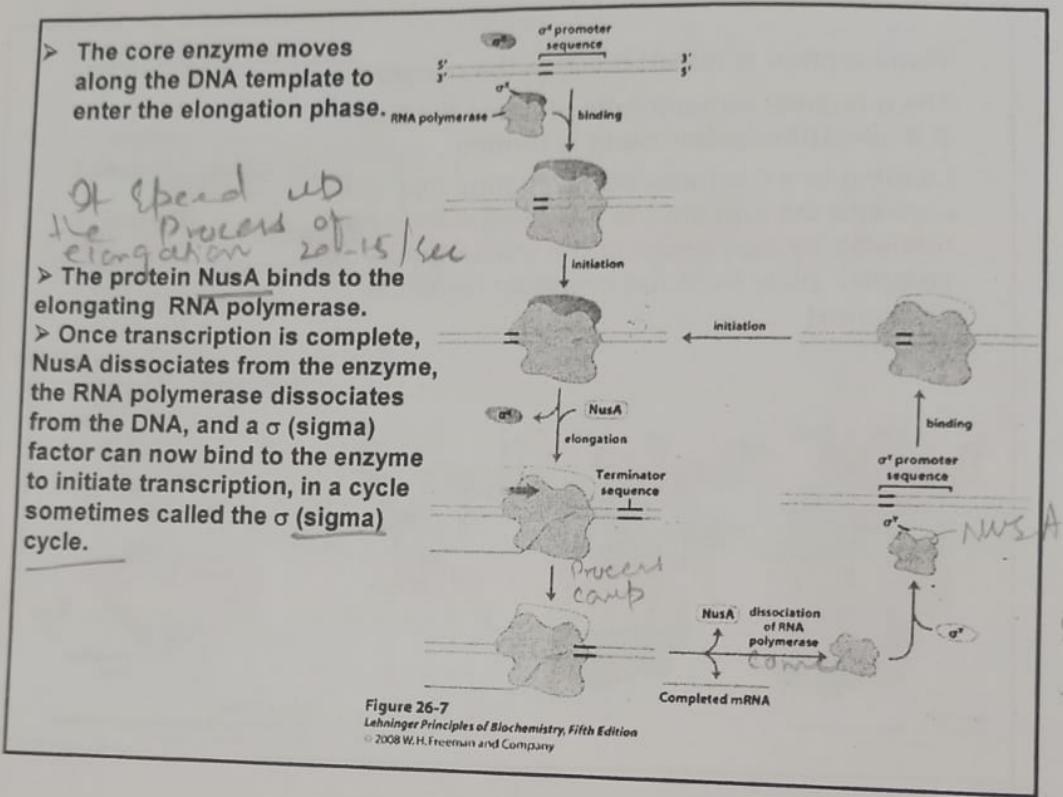
- ④ Now σ -subunit separate
 ⑤ First Phospho-diesther bond is formed

is becoming DNA

Promoter Clearance and Elongation

- Occurs after 4- 10 nt are added
- First rnt becomes unpaired from antisense (template) strand. \therefore DNA strands re-anneal
- Polymerase loses sigma, sigma recycled
 - Result "Closed hand" surrounds DNA
- NusA binds to core polymerase
- As each nt added to 3', another is melted from 5', allowing DNA to re-anneal.
- RNA pol/NusA complex stays on until termination. Rate=20-50nt/second.

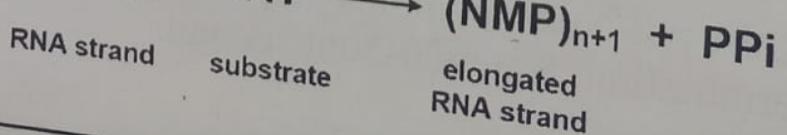
• Sigma can be recycled



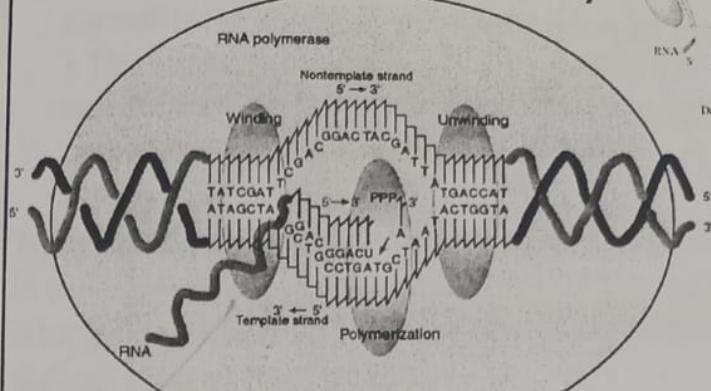
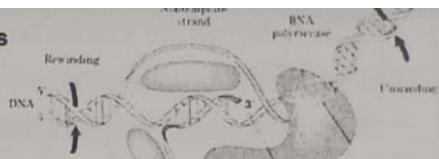
b. Elongation

- The release of the σ subunit causes the conformational change of the core enzyme. The core enzyme slides on the DNA template toward the 3' end.
 - Free NTPs are added sequentially to the 3' -OH of the nascent RNA strand.

$$(NMP)_n + NTP \longrightarrow (NMP)_n NTP$$



The 3' segment of the nascent RNA hybridizes with the DNA template, and its 5' end extends out the transcription bubble as the synthesis is processing.



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Intrinsic Protein

DNA transcrips me
know me as:
sequence may good
how to process
do terminate
knows how -

No-dependent
need special
process to end
up the process
release transcript
come to its original position.

Termination

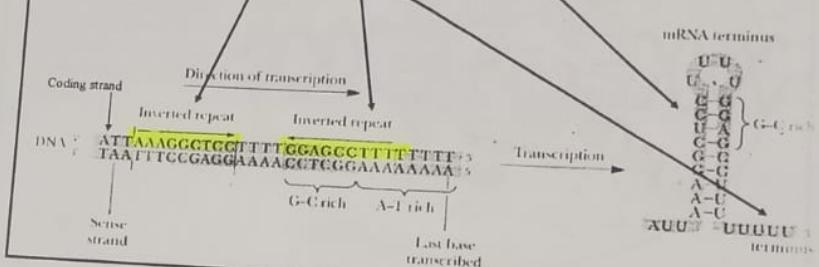
- Occurs at specific sites on template strand, called Terminators
- Two types of termination
 - Intrinsic terminators # Some sequences used for transcription.
 - Rho (ρ) dependent terminators
- Sequences required for termination are in transcript
- Variation in efficiencies.

- Inverted repeats have similar sequence with complementary base pairs or 5' - 3'
- direction -
- Hair Pin like structure is formed because of complementary base pair. helps to terminate the process.

Intrinsic Terminators

In Intrinsic Terminator there are

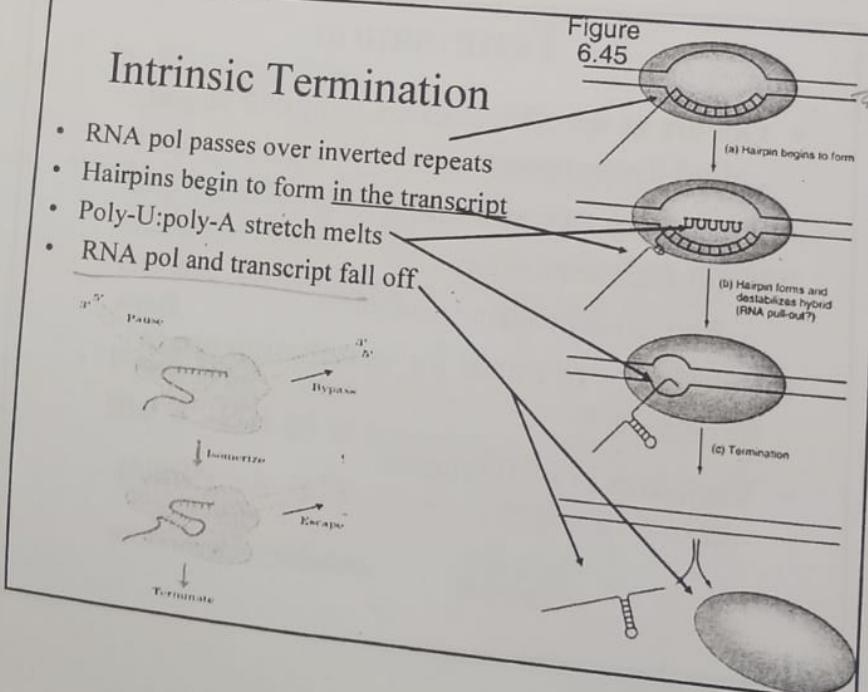
- DNA template contains inverted repeats (**G-C rich**)
 - ∴ Can form hairpins
- **6 to 8 A** sequence on the DNA template that codes for **U**
- Consequences of poly-U:poly-A stretch?



A cu u
have long
base pair,

Intrinsic Termination

- RNA pol passes over inverted repeats
- Hairpins begin to form in the transcript
- Poly-U:poly-A stretch melts
- RNA pol and transcript fall off



of DNA-DNA hyb
hair elc new
RNA-RNA hyb
bra - A
ici bare par
ko wosler
IC din ko
delog nne m
madad del
hau

ρ -independent termination

Have two distinguishing features.

- The first is a region that produces an RNA transcript with **self complementary sequences**, permitting the formation of a hairpin structure
- The second feature is a highly conserved string of three A residues in the template strand that are transcribed into U residues near the 3' end of the hairpin.

This structural transformation disrupts several A=U base pairs in the RNA-DNA hybrid segment and may disrupt important interactions between RNA and the RNA polymerase, facilitating dissociation of the transcript.

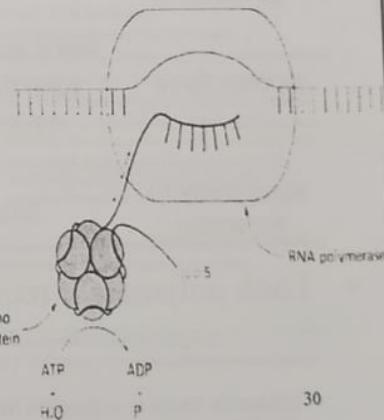
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The termination function of ρ factor

The ρ factor, is a hexameric protein, having ATP-dependent helicase activity.

The protein associates with the RNA at specific binding sites and migrates in the 5' \rightarrow 3' direction until it reaches the transcription complex that is paused at a termination site.

Here it contributes to release of the RNA transcript. The protein has an ATP-dependent RNA-DNA helicase activity that promotes translocation of the protein along the RNA, and ATP is hydrolyzed by protein during the termination process.



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Transcription of Eukaryotes

we
need some enzymes.

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RNA-polymerase of eukaryotes

RNA-pol	I	II	III
products	rRNA	mRNA <i>Bachot soon promoterico</i>	tRNA <i>bachot</i>
promoters	Vary greatly specie to specie	<u>Recognize</u> thousands of promoter	Well defined
Sensitivity to Amanitin	No	high	moderate

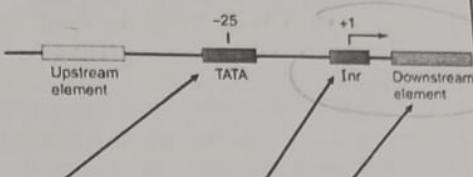
- Each polymerase recognizes a distinct promoter

Amanitin Toxin is a specific inhibitor of RNA-pol II and III.



Eukaryotic Polymerase II Promoters

- Much more complicated
- Two parts
 - Core promoter
 - Upstream element
- Core promoter
 - TATA box at ~30 bases
 - Initiator—on the transcription start site
 - Downstream element—further downstream
- Many natural promoters lack recognizable versions of one or more of these sequences



start point +1

Some genes transcribed by RNA pol II lack the TATA box. Ex: Housekeeping genes (expressed constitutively).

no TATA mechanism of

Downstream of
initiator
gene
recognition
property to
rel.

help in recognition
area

control the
housekeeping
genes

Regulatory gene: we can control
the mechanism of genes, i.e. changing
the biology.

Transcription Factors for eukaryotic transcription

RNA-pol does not bind the promoter directly.

RNA-pol II associates with six transcription factors, TFII A - TFII H.

TABLE 26-2 Proteins Required for Initiation of Transcription at the RNA Polymerase II (Pol II) Promoters of Eukaryotes

Transcription protein	Number of subunits	Subunit(s) M _r	Function(s)
Initiation			
Pol 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 TFIIIB and TBP to the promoter
TFIIB	1	35,000	Binds to TBP; recruits Pol II-TFIIF complex
TFIIE	2	34,000, 57,000	Recruits TFIIF; has ATPase and helicase activities
TFIIF	2	30,000, 74,000	Binds tightly to Pol II; binds to TFIIIB and prevents binding of Pol II to nonspecific DNA sequences
TFIIF	12	35,000–89,000	Unwinds DNA at promoter (helicase activity); phosphorylates Pol II (within the CTD); recruits nucleotide-excision repair proteins
Elongation*			
ELL [†]	1	80,000	Phosphorylates Pol II (within the CTD)
pTEF _b	2	43,000, 124,000	
SII (TFIIS)	1	38,000	
Elongin (SIII)	3	15,000, 18,000, 110,000	

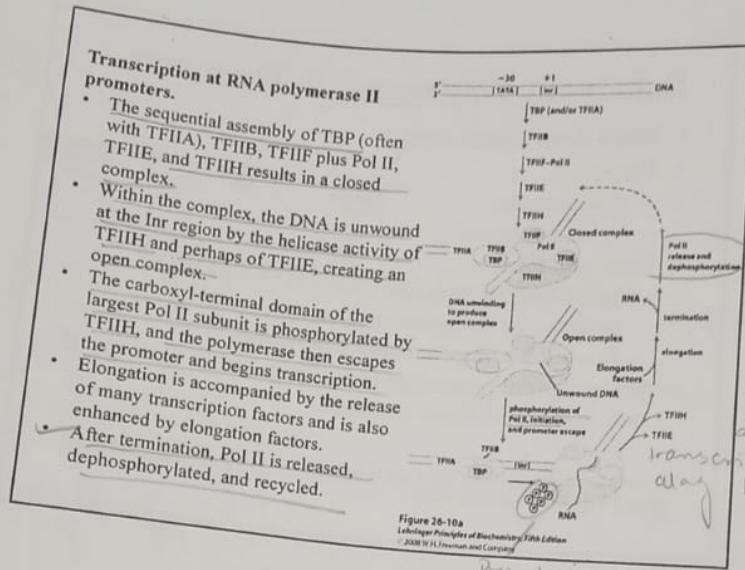
*The function of all elongation factors is to suppress the pausing or arrest of transcription by the Pol II-TFIIF complex.

[†]Name derived from eleven-nineteen lysine-rich leukemia. The gene for ELL is the site of chromosomal recombination events frequently associated with acute myeloid leukemia.

Table 26-2
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Transcription at RNA polymerase II promoters.

- The sequential assembly of TBP (often with TFIIA), TFIB, TFIF plus Pol II, TFIE, and TFIIH results in a closed complex.
- Within the complex, the DNA is unwound at the Inr region by the helicase activity of TFIIH and perhaps of TFIE, creating an open complex.
- The carboxyl-terminal domain of the largest Pol II subunit is phosphorylated by TFIIH, and the polymerase then escapes the promoter and begins transcription.
- Elongation is accompanied by the release of many transcription factors and is also enhanced by elongation factors.
- After termination, Pol II is released, dephosphorylated, and recycled.



b. Elongation

- The elongation is similar to that of prokaryotes. *diff factors of elongation are req*
- The transcription and translation do not take place simultaneously since they are separated by nuclear membrane.

c. Termination

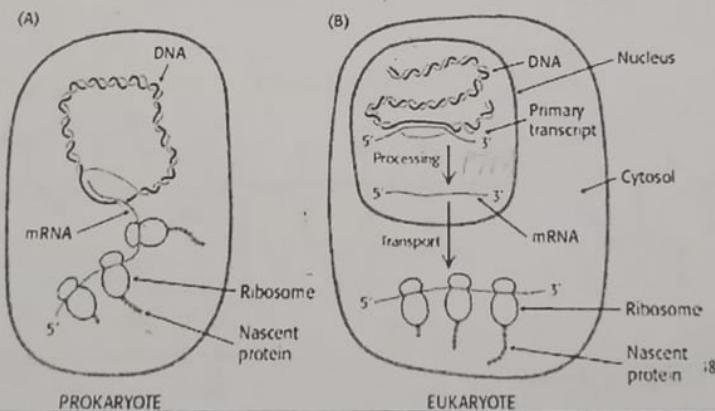
- The termination sequence is AATAAA followed by GT repeats.
- The termination is closely related to the post-transcriptional modification.

After Transcription complete
cy start PTM

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Post-Transcriptional Modification

- The nascent RNA, also known as primary transcript, needs to be modified to become functional tRNAs, rRNAs, and mRNAs.
- The modification is critical to eukaryotic systems.



(modification)
Processing reg

Polysomes: Single RNA
K thread Pr multiple
Ribosome agt hor.
(It will found in both
Prokaryote & Eukaryote.)

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capping: soft modeul early + transcript, then
 basal detach, bya jata hoi, then tailing
 me again ek addhara sequence attach hoi hoi,
 at 3' end. job initial transcript banta hoi to
 us hoi length both zyada hogi because of additional
 sequence go to Protein Synthesis & hoi ni chalye e

Sequence hoi
 hoi remove
 hoi hoi s in ho
 inner kala jata
 after removing
 stem we made
 functional transcript

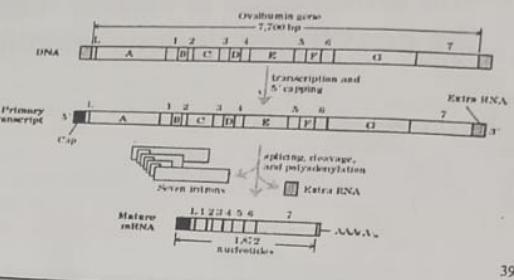
In fig green
 portion are req
 for Protein synthesis
 by yellow are
 removed so we
 remove it by
 pieces of
 splicing. a made it functional.

§ 3.1 Modification of Nascent RNA

- Primary transcripts of mRNA are larger than matured mRNA by many folds.

- Modification includes

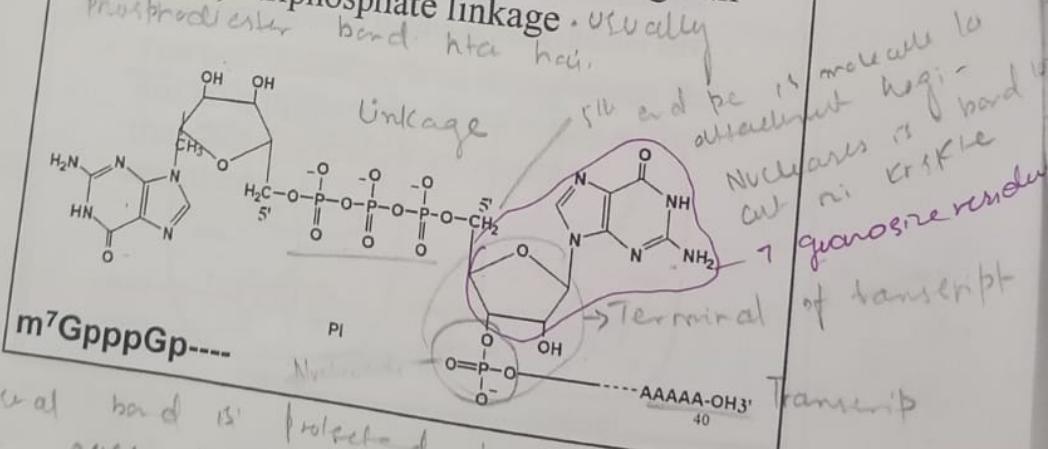
- Capping at the 5'- end
- Tailing at the 3'- end
- mRNA splicing



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Capping

Addition of 7-methylguanosine linked to the 5 terminal residue of the mRNA through an unusual 5,5-triphosphate linkage. Usually



This unusual bond is
 When it goes to
 This is the bond
 protected by Nucleus in cytoplasm
 which is form during capping

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On details:

- Capping
- > Guanosine 7-methyl-Guanosine residue which is going to attach the transcript by 5'-5' triphosphate linkage jis ki waaj se ye whole transcript se jyr jaega ga.
 - > First nucleotide jure ga we triphosphated ruyga to form the value ga dusra aye ga us k 2-phosphate release hoga.
 - > sb se phle phosphotydrilase enzyme act on it, than release its first phosphate.
 - > In second stage guanosine residue is going to attach to it, than 2 phosphate of guanosine residue release or mono-phosphate attach hogae ga aik.
 - > 2 phosphate phle le hai or ek phosphate k saath nucleotide aye ga or attach hogae with 5'-5' triphosphate bond.
 - > After that methylation occur, On methylation methyl group is attach to guanosine residue at the 7th position & this is carried out by methyl-transferase enzyme. Adenosine guan methionine is a molecule which provide methyl group & it is converted into homologous cysteine one.
 - > Methyl group after methylation sometimes is going to be methylated by other nucleotide as well.

termination
ylate hogae
ai / is one
to Synthesize
ing complete
rakhe
complete
phle
hogae
polymer
saath ye
completion
releases.

caption
base
me' ag
at 5'
vs 1c
Sequence
Sequence
bhu remov
hna hui
inhar kabo
after remov
hem we
functional b

jahan HC guanoosine residue hai
HC methylation hogi - phela jo kega
hoga methylated us 1co ap capting bering
Walter
group
berg

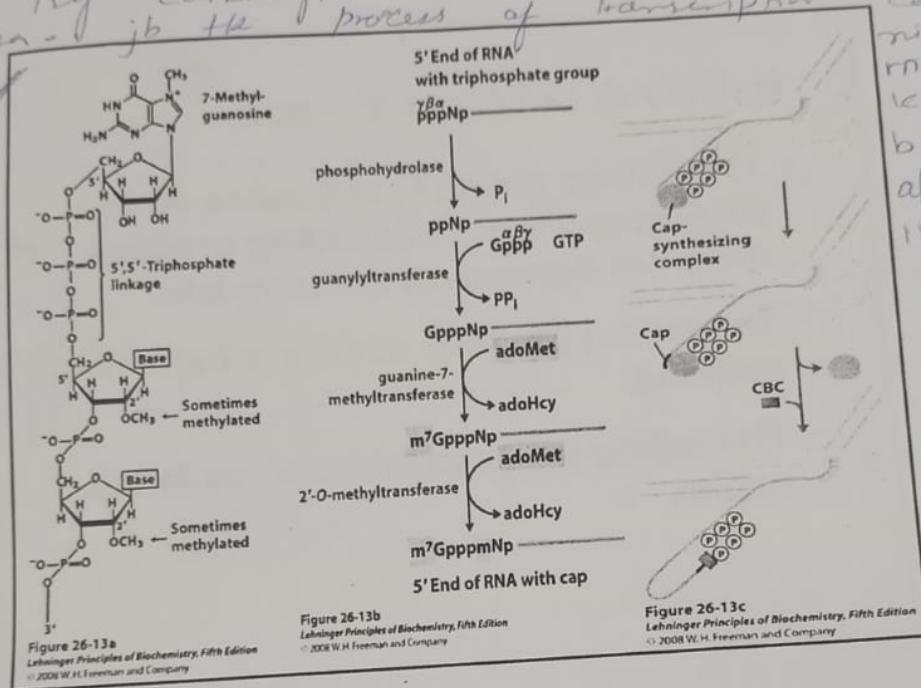
- All the process is going on while attached
to Eukaryotic RNA Polymerases by CEE,
PPA) Brown Structure is Eukaryotic RNA

Polymerase who does doing Process of
transcription jere hi process off transcription
initiate hua , jere hi 5' terminal bahan
mikta , vollar is ke saath cap lagta dyta

In Ag g,
portion are
for Protein
by Yellow
yellow &
orange &
process of
splicing

jae ga , cap is in bound form
After completion of Process , RNA Polymerase
se complex aay hogi or aay ja
ka further afna kaam Karay

→ In transcription of eukaryotes, before termination capping begins. carbonyl terminal phosphorylate has one phosphate group. It is the same enzyme that adds the cap. After formation of cap, cap-synthesizing complex releases digo, or CBC attach. Finally, carbonyl terminal is added by the process complete. In addition, it is the process of transcription complete.



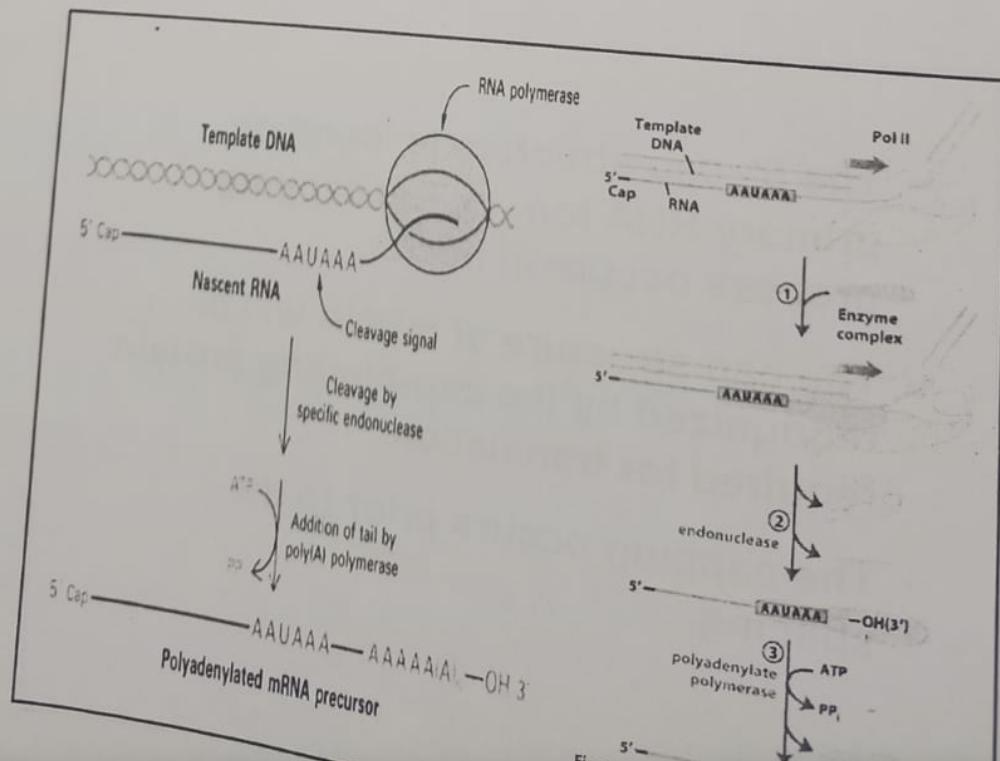
- The 5'- cap structure is found on primary RNA too. \Rightarrow The capping process occurs in nuclei.
- The cap structure of mRNA will be recognized by the cap-binding protein required for translation.
- The capping occurs prior to the splicing.

- In tailing 3' end K base multiple residues of adenine attach (A) hence a K base adenine residues add after completion of process of transcription.

b. Poly-A tailing at 3' - end

- There is no poly(dT) sequence on the DNA template. \Rightarrow The tailing process dose not depend on the template.
- The tailing process occurs prior to the splicing.
- The tailing process takes place in the nuclei.

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- On ^{RNA} Splicing, non coding part introns ko remove karne ke or trim ke, ^{is} ^{from} ^{that may we call it Poly-A strand multiplet}

Poly adenylic Polymers are attracted towards ^{were present} ^{adenine & guanine} ^{int.} ^{base bond hai.} Phosphodiester ^{A m} ^{esters being cut by}

Poly adenylic Polymers are cut bhi karega ⁱⁿ ^{adenine & guanine} ^{esters being} ^{so end} ^{get eq-} ^{or adenine ko attach bhi karega}

Transesterification:

GLC ester bond toote g ek toote g as a result of transesterification intron remove ho! & exon rejoin hoga

Spliceosomal Splicing:

Internal Molecule ^{adenine} bond ko disperse karega end ko loose chunega ka or exon ko rejoin karega jis se Lariat format hoga, then free end again break karega, & Lariat release hoga, wo again rejoin hoga

Why Lariat is form? Because of Internal Mol.

- Different Protein Collectively we call it Splicesomes jo ^{is} Mechanism ko facilitate karega, in ka kaam hai identify karo intron ko ta k wo vry remove/cut karen.

- U₁, U₂, U₃ are RNA along with Protein

- In tailing 3' end K pair multiple residues of adenine attach (A) hinge a K-Tac and

Poly-A tailing at 3'-end:

- Firstly one sequence came that will provide cleavage signal then it will break or adenine(A) residues attach hinge, the red sequence (coming from DNA) on blue nucleotide so bad one day be jerry jake hair. That's why we call it tailing process, held in nucleus, After completion of transcription ye cytoplasm me aata hai, starting be pheta hta hai.

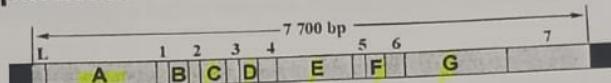
- If we fragment

Diagrammatically:

During transcription, A sequence came and provide signal to cleave, cleavage signal here is aata hai, An enzyme complex will bind to it, i.e. one 2 enzyme hinge, this will bind to this cleavage signal, [AAUAAA] this will provide signal to terminate, protein will bind to this sequence, then cut it, and sample all hinge, transcript separated. After separation of transcript, multiple adenine residues will go to attack it, ATP Ki form one nucleotide aata hai, Pyrophosphate release hta hai monophosphate jar jata hai. Ho mataba ATP ayega Adenine de kha chala ja jar, around 80-200 Adenine residues attach hta hai.

- In RNA splicing, non coding part introns ko remove karengya or exons ko rejoin karengya Because we need exons.
- If we remove these non-coding part to be sequence fragmentize hope ga so we don't need fragment sequence for protein synthesis - we need cont. sequence.

The structural genes are composed of EXONS (coding) and INTRONS (non-coding) regions that are alternatively separated.



A~G no-coding region 1~7 coding region

ARPP mRNA
1224 @base

45

45

In RNA Splicing m which useless part is being cutted by terminal will rejoin, so in the end we will get cont. seq.

Exon and intron

Exons are the coding sequences that appear on split genes and primary transcripts, and will be expressed to matured mRNA.

Introns are the non-coding sequences that are transcribed into primary mRNAs, and will be cleaved out in the later splicing process.

- The matured mRNAs are much shorter than the DNA templates.

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RNA splicing is the process by which introns, regions of RNA that do not code for protein, are removed from the pre-mRNA and the remaining exons connected to re-form a single continuous molecule.

ph
kr
repeat

Types:

- **Spliceosomal Splicing:** Their removal occurs within and is catalyzed by a large protein complex called a **spliceosome**.
- **Self-splicing:** no protein enzymes are involved.
 - Group I | en mode of cutting
 - Group II
- **tRNA splicing:**

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Terminal =
Point where
intron or exon
join

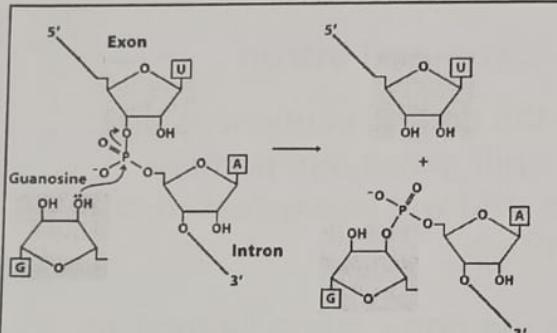


Figure 26-14 Molecular Principles of Biochemistry, 7th Edition
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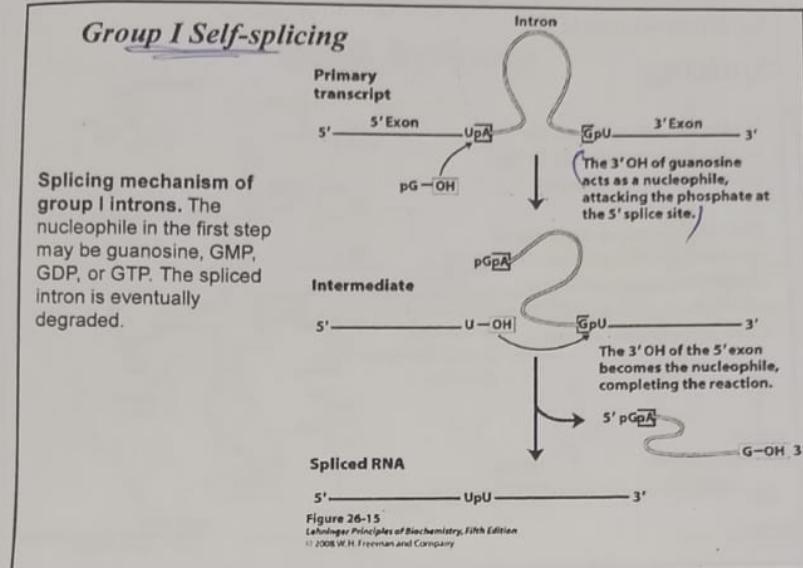
FIGURE 26-14 Transesterification reaction. Shown here is the first step in the two-step splicing of group I introns. In this example, the 3' OH of a guanosine molecule acts as nucleophile, attacking the phosphodiester linkage between U and A residues at an exon-intron junction of an mRNA molecule (see Fig. 26-15).

48

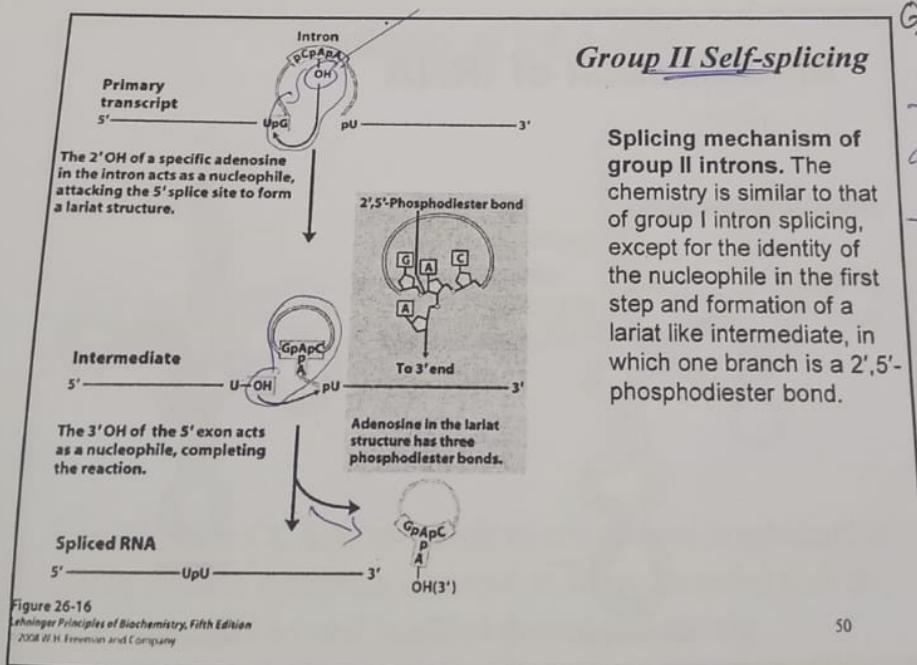
Mechanism of Remaining Intron: ek attacker molecule aye ga
jo bhar le aye ga ya Intron ke andr hoga phosphodiester
bond ke tareg ga, free karega exon ko, then rejoin it.
After exon repeat this reaction at another terminal. where
it will free Intron by exon ko abne sahi rejoin karyga.

is m
OH
Ade
les
is
lit

attack kore molecule intron ke andar hai
 toh inciy be Trichloro Mono Phosphate because Guanosine ka OH residue reaction karwa raha. Thats why it is important to phosphate OH residue bard ko break ker ke exon ko free khol jain hoga. exon k saath. Then exon ne repeat kiya process n mhan ko free clara.



Break bond ay rejoin exon.



Q) Why we call it self Splicing
 → Because we don't need an additional Protein.

ester attack kore wala molecule intron ke andar hai
 toh m adenine break the terminal ay rejoin exon
 2 bond me involve hai, so tohne k baad Guanosine
 the same jorta hai ,ard make unusual bond, which
 phosphodiester bond thats why it will form lariat
 structure. Station.

→ Spliceosomal Splicing additional Protein Kriwate han
 → U₁, U₂, U₃, U₄ in terminal ko identify Kr K m le attach
 hage, then in ko nazdeek lacingy, other Process ko
 facilitate lacingy, inactive Spliceosome Active me convne
 hoga, then ye off attack Kr K lariat bnae ga, exon Ko
 region Kr K intron Ko free clyor dega. lariat release.
 Internal Mol first Terminal second terminal

RNA nucle
 base
 fr. atke
 functional

function of Snurps:

To Identify
 the Intron
 by cut it

Spliceosomal Splicing

Within the spliceosome, the introns undergo splicing by the lariat-forming mechanism.

The spliceosome is made up of specialized RNA-protein (U₁, U₂, U₃) complexes, small nuclear ribonucleoproteins (snRNPs, often pronounced "snurps").

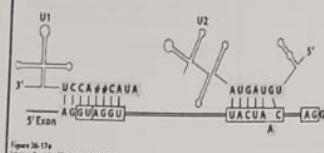


Figure 26-15a
Principles of Biochemistry, Fifth Edition
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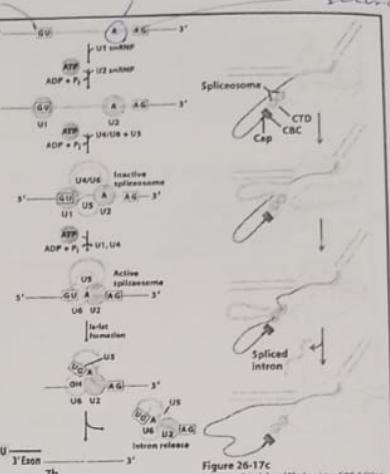
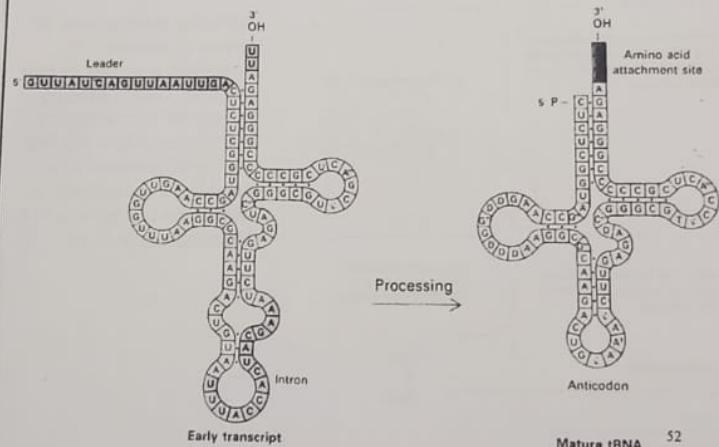


Figure 26-17c
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Modification of tRNA

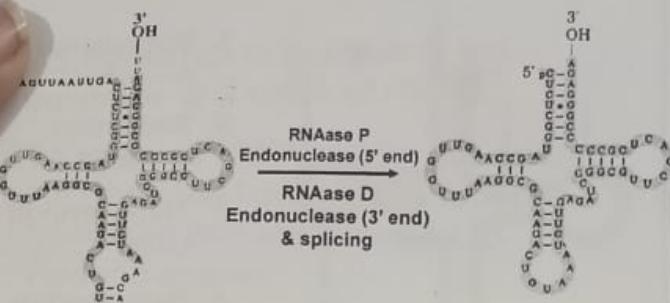


Mature tRNA 52

tRNA in early transcript non-functional hta hai by certain modification key functional bnae jata hai which include, removal of Leader, removal of 2-nucleotide seq, addition of AAC mol which is going to attach a a at later stage, splicing. 26

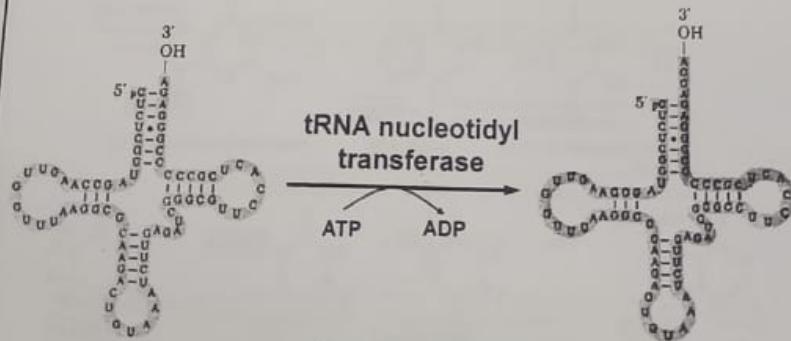
RNA nucleases no enzyme have to be cut
 like hair, so it will remove two nucleotides of
 tRNA. But it is not completely functional

tRNA Splicing



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Addition of CCA-OH tri-nucleotide

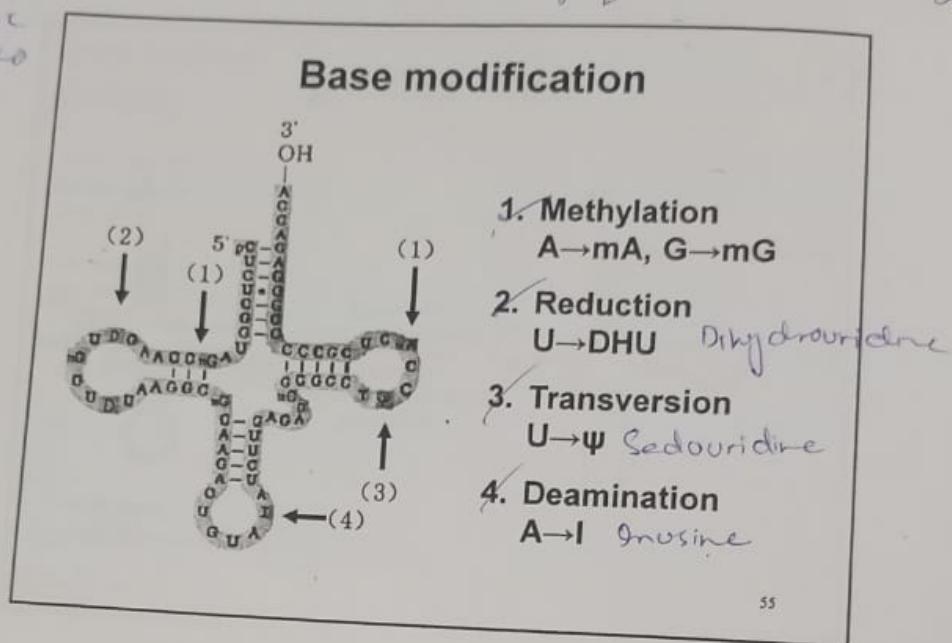


54

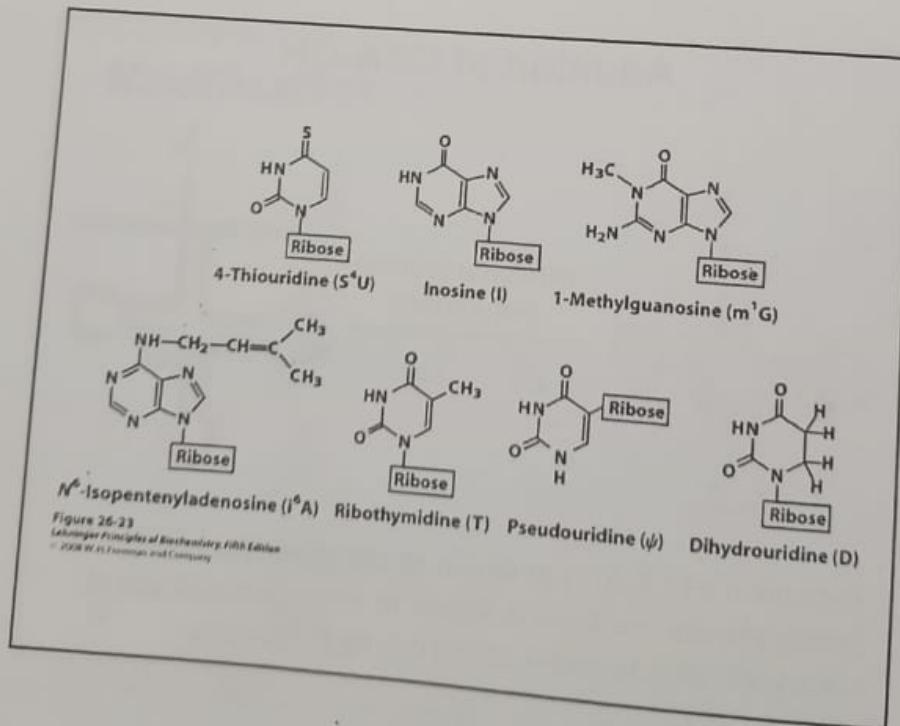
Trinucleotide CCA(3) to which an amino acid is attached is during protein synthesis is absent in some bacterial and all eukaryotic tRNAs and is added during processing

It is unusual require it require ATP

→ kuch reaction kr base pr heterogeneous base change hoga
 J- nucleotide me change ata hai, kuch recognition point
 hote hai m base modification ki wajah se jin ko saay
 ja ke genetic code ko through recognize kr le m. pr. a. b.
 jara jata hai - Because 19 a.a 32 tRNA ay tRNA is
 specific for a.a. us ko recognize keta hai or us
 ko specific a.a. code ko jarta hai.



55

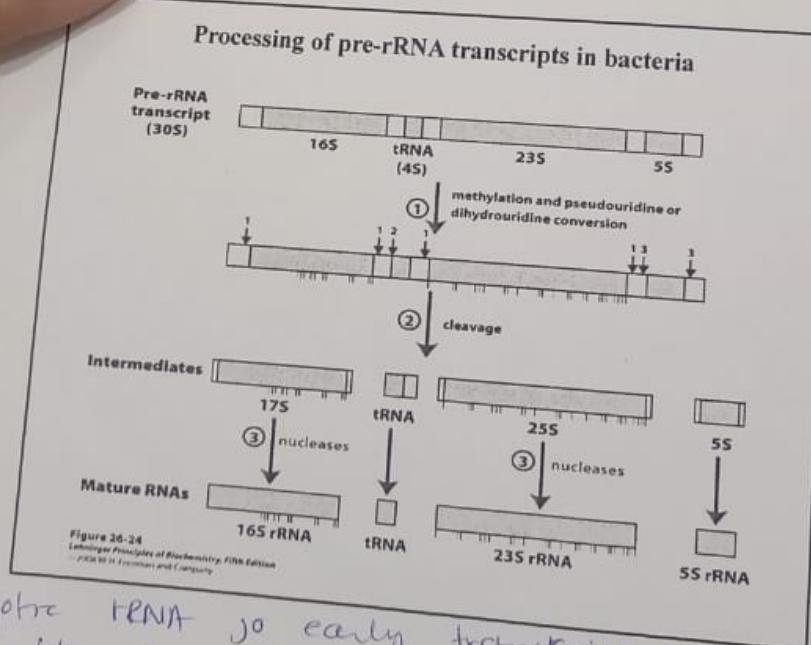


After certain modification rRNA to be functional molecule, it has including methylation, pseudouridylation, after cleavage it will divide early transcript in to five parts, After intron removal, functional transcript in to three hair So it will assemble to Protein ribosome

§ 3.3 Modification of rRNA

- 45S transcript in nucleus is the precursor of 3 kinds of rRNAs.
- The matured rRNA will be assembled with ribosomal proteins to form ribosomes that are exported to cytosolic space.

57



On Prokaryotic rRNA to early transcript has no 30S RNA in own me ita has After certain modification ye functional RNA bne ja ye finally protein le sally mill k ribosome bne hair 29