

Chapter 6: Transcription and RNA Processing in Eukaryotes

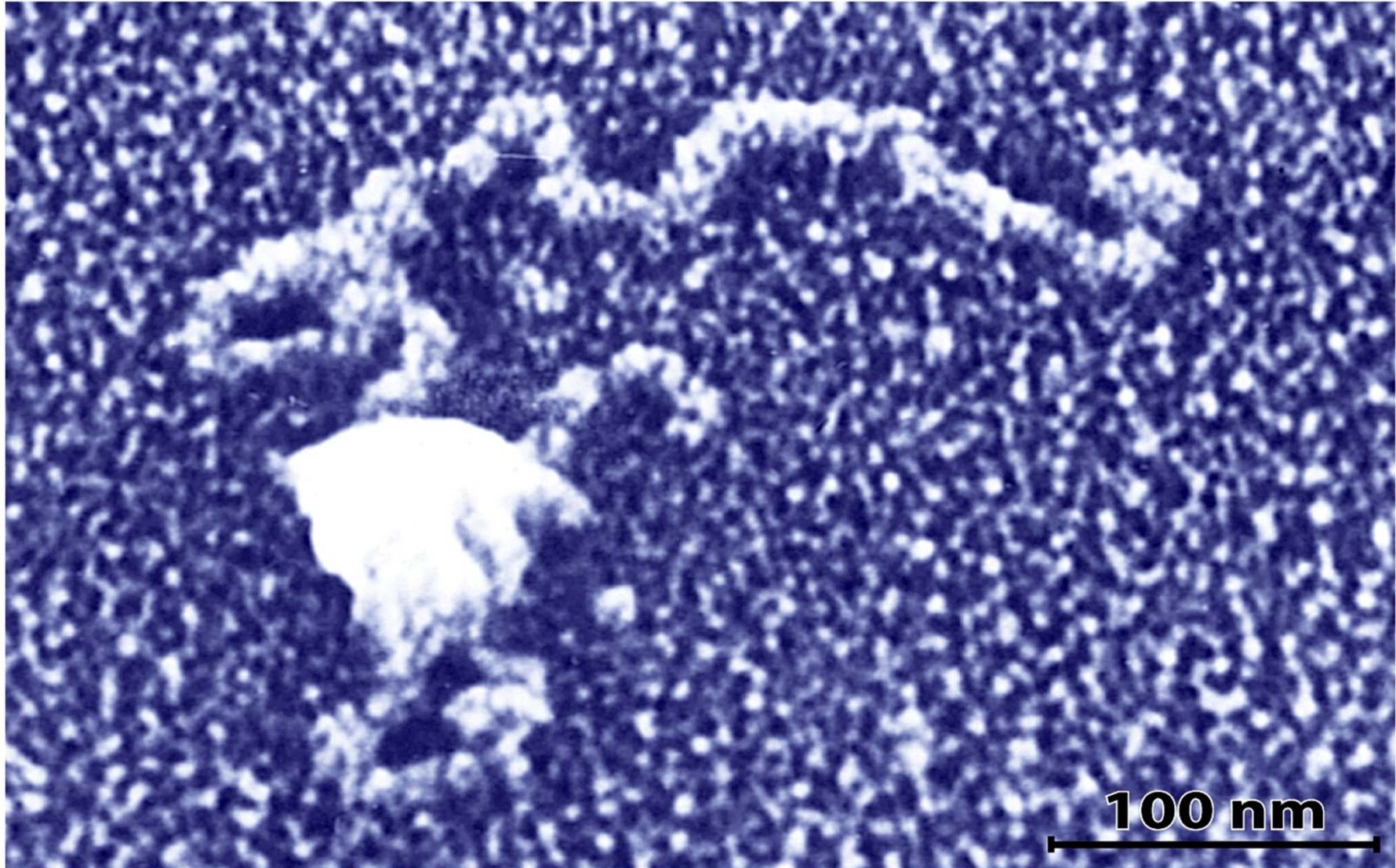
- Genetic organization in eukaryote
 - Transcription in eukaryote
 - RNA processing in eukaryote
 - Translation in eukaryotes

Transcription in Eukayotes

More complex!!.....πππ



Prokaryote VS. Eukaryote



Spliceosome processing a gene transcript

Genetic Organization in Prokaryote VS. Eukaryote

-Cell structure

- Eukaryote cells possess nucleus (nuclei)
 - separate compartment of cell
 - double-layer membrane or envelope
 - keep chromosomes carrying genetic information
- Eukaryote cells have membrane bound organelles
 - mitochondria: respiration
 - chloroplast: photosynthesis
 - both contain **circular DNA** molecules

Genetic Organization in Prokaryote VS. Eukaryote

-Cell structure

- Chromosome structure in eukaryotes
 - centromere, telomere, replication origins, chromosome arm
 - DNA is stored on the chromosome (chromatin = DNA + protein)
 - 2,000-fold shortening
- Chromosome folding and package
 - Level of folding: DNA double helix < nucleosome < 30 nm fiber < loop
< miniband < Chromatid

Genetic Organization in Prokaryote VS. Eukaryote

-Chromosomal structure

- Eukaryotic chromosome DNA sequence contains
 - repetitive sequences (ex. Alu element)
 - pseudogenes (defective duplicate copies of genuine genes)
 - functional genes (produce complete mRNAs)
 - intergenic regions (non-coding DNA)
- Eukaryotic genes consist of
 - introns (segment of a gene that is non-coding)
 - exons (segment of a gene that codes for protein)

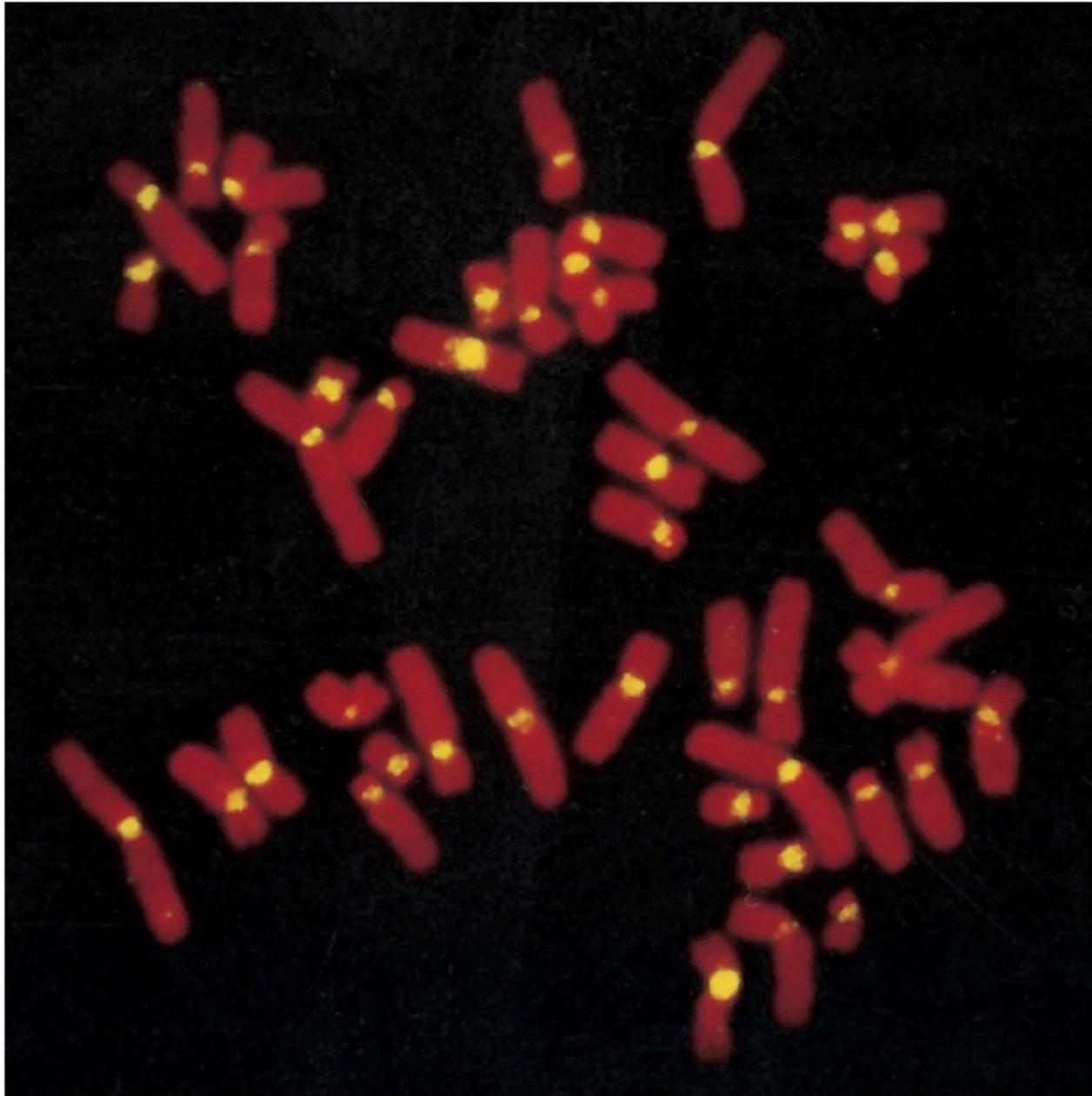


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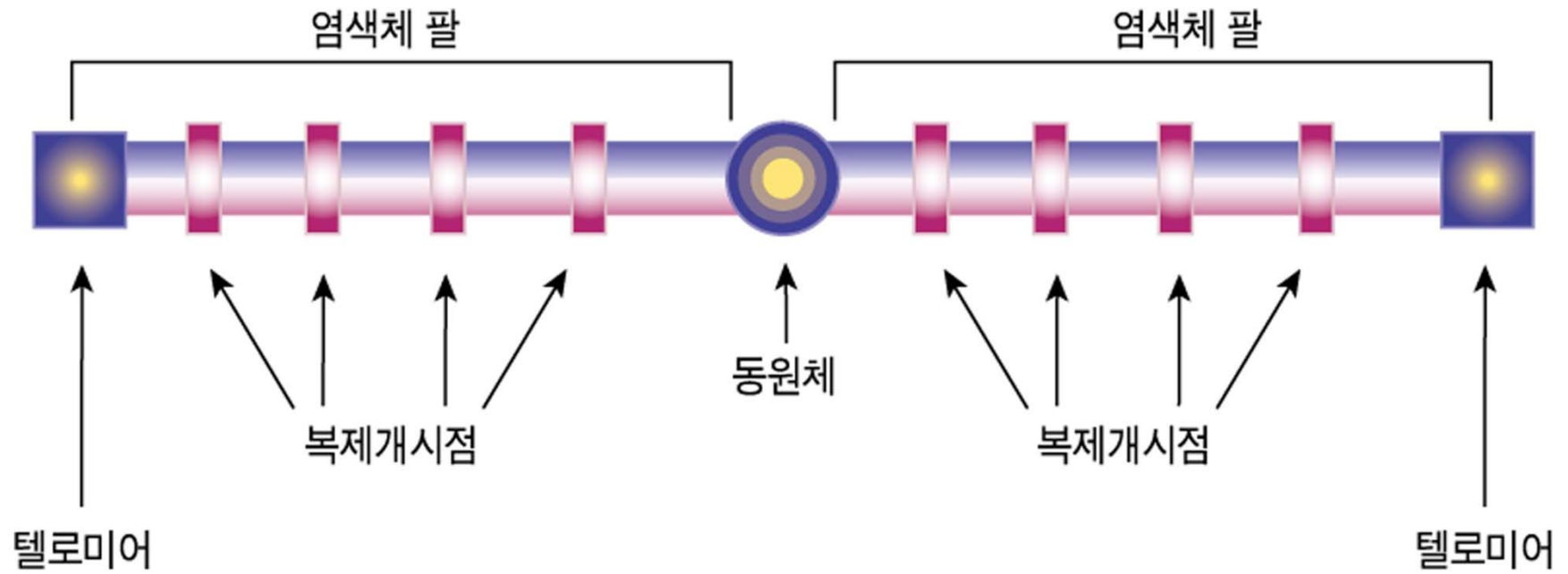


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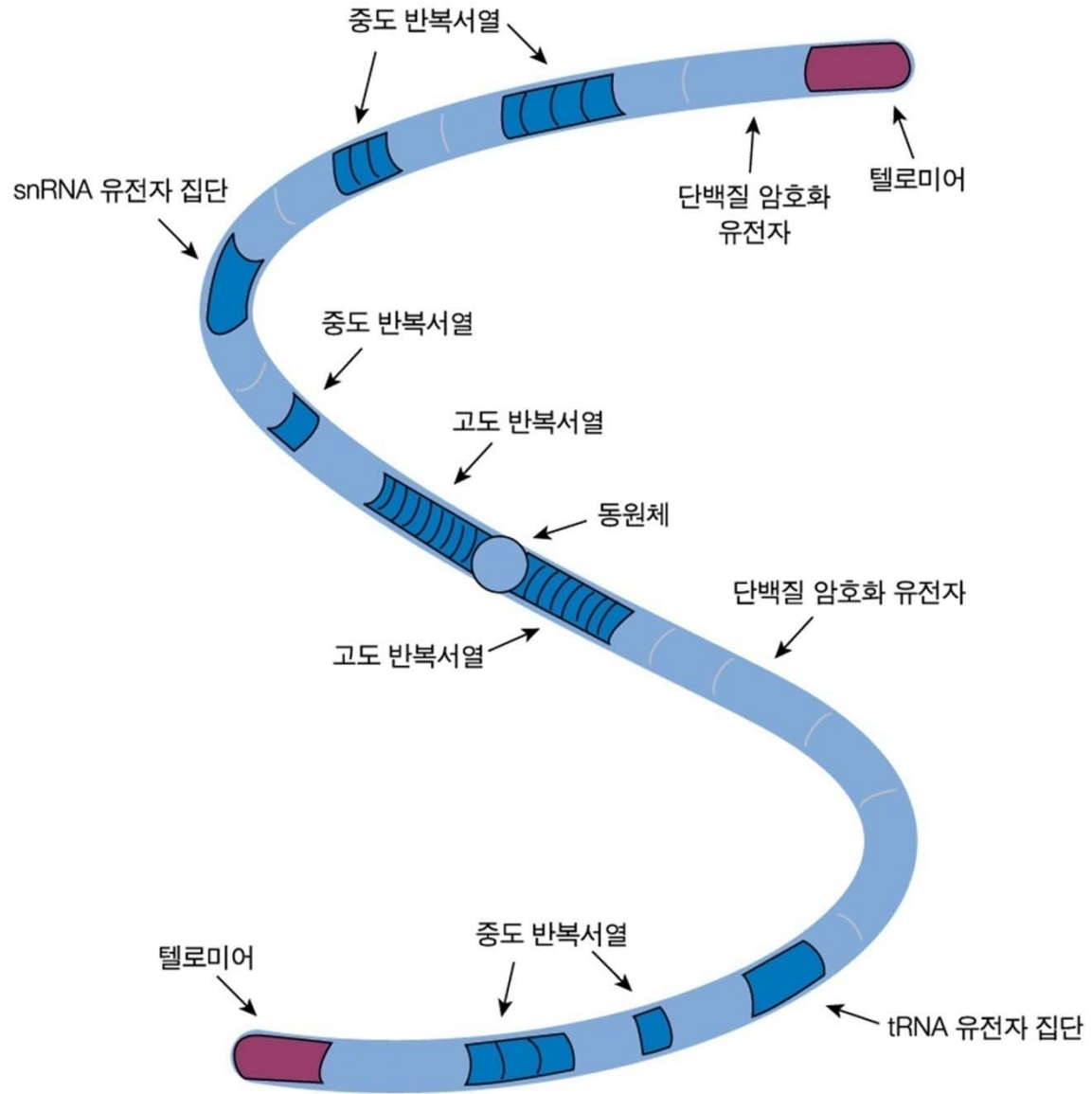


그림 11-10



↑
암호화 DNA

↑
비암호화 DNA



Transcription in Eukaryote

- RNA polymerases in eukaryote
 - RNA polymerase **I** : transcribes genes for large rRNA
 - RNA polymerase **II** : transcribes genes which code for protein
 - RNA polymerase **III** : transcribes genes for tRNA, 5S rRNA, miRNA
- The activity of RNA polymerase II is regulated by transcription factors which bind to and recognize specific sequences (promoter & enhancer) on the DNA

TABLE 11.1

Characteristics of the Three RNA Polymerases of Eukaryotes		
Enzyme	Location	Products
RNA polymerase I	Nucleolus	Ribosomal RNAs, excluding 5S rRNA
RNA polymerase II	Nucleus	Nuclear Pre-mRNAs
RNA polymerase III	Nucleus	tRNAs, 5S rRNA, and other small nuclear RNAs

Transcription in Eukaryote

-Gene regulation

- Eukaryotic promoter has three subcomponents
 - 1) Initiator box: transcription starts
 - 2) TATA box: RNA polymerase complex first binds
 - 3) upstream elements: specific control by transcription factors
- Transcription factors are specialized proteins that regulate gene expression by controlling transcription
- Transcription factors need **four domains** for:
 - 1) binding to a specific sequence on the DNA
 - 2) binding to the RNA polymerase II complex
 - 3) getting into the nucleus where the genes are kept
 - 4) responding to a stimulus which signals for gene turn-on

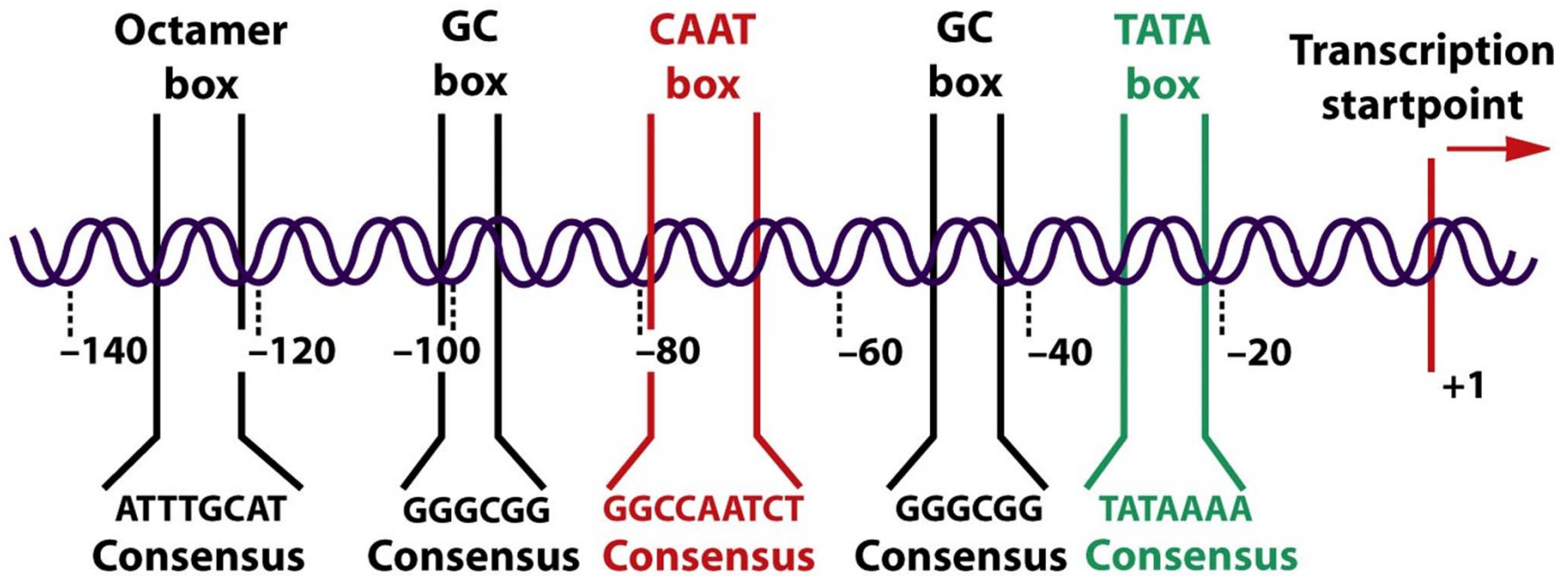
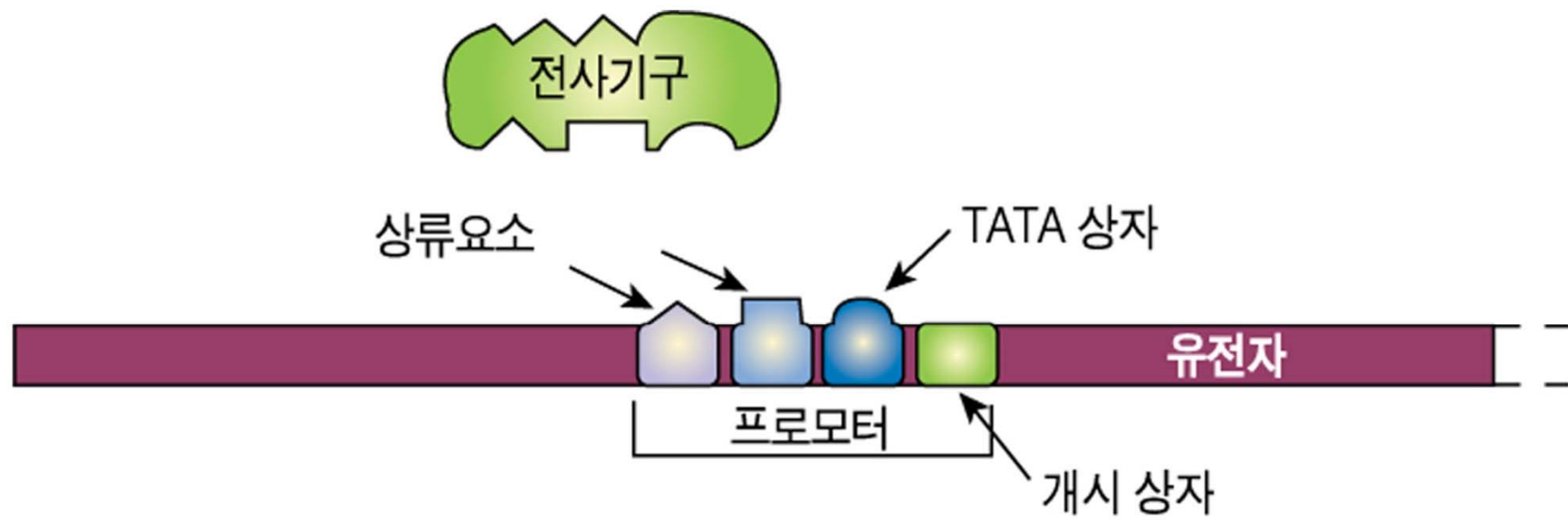


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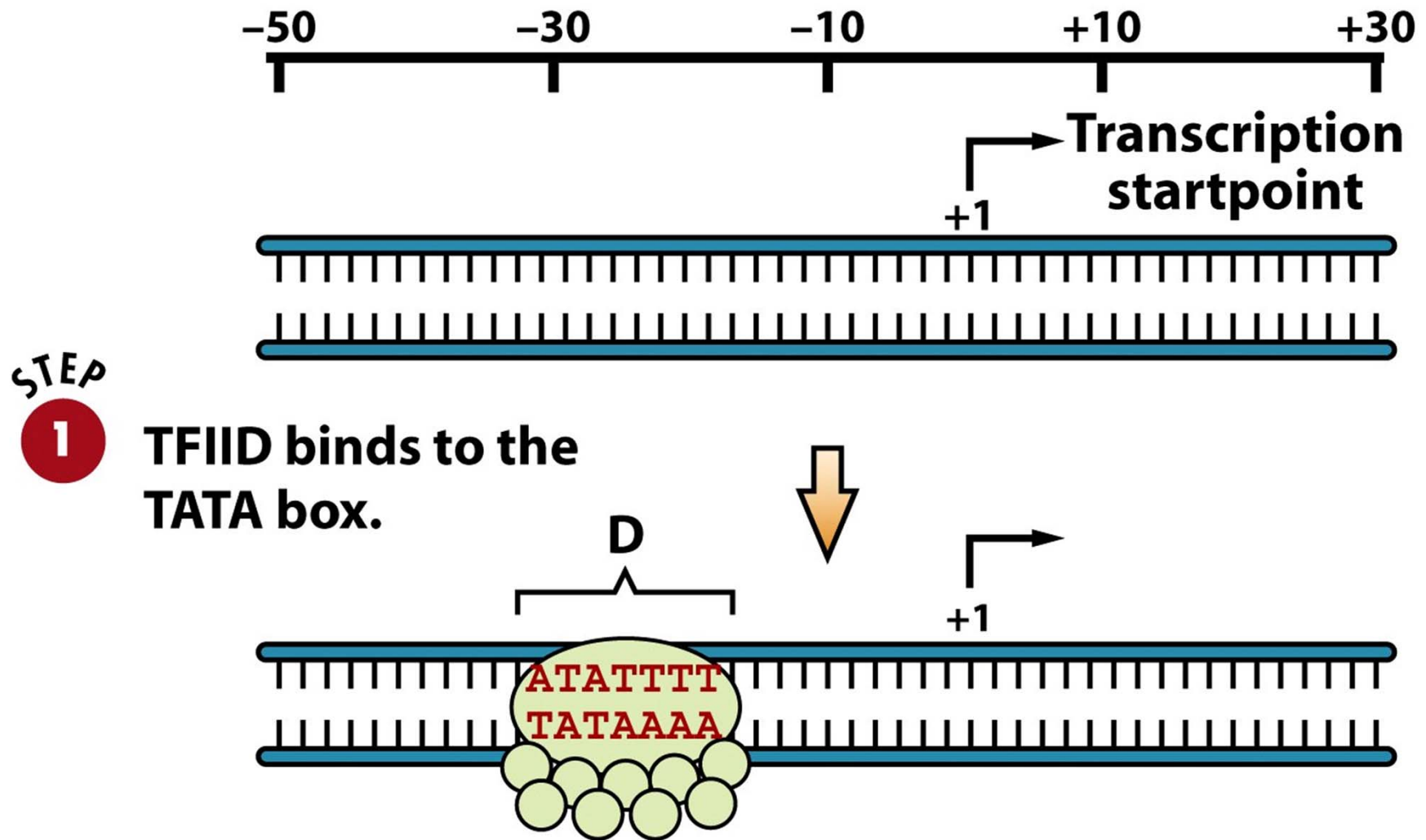


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STEP
2

TFIIA joins the initiation complex.

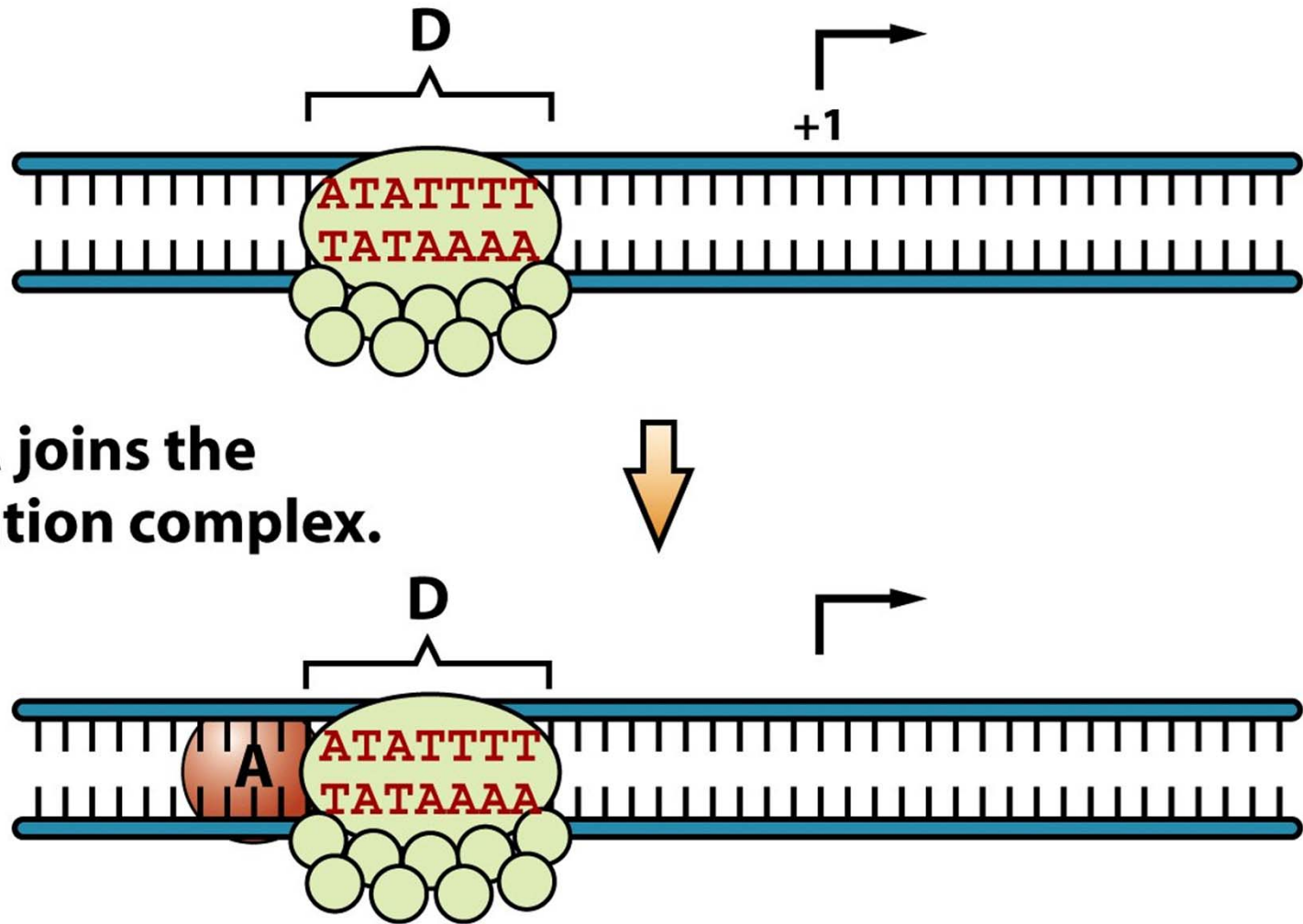


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STEP
3

TFIIB binds to the initiation complex.

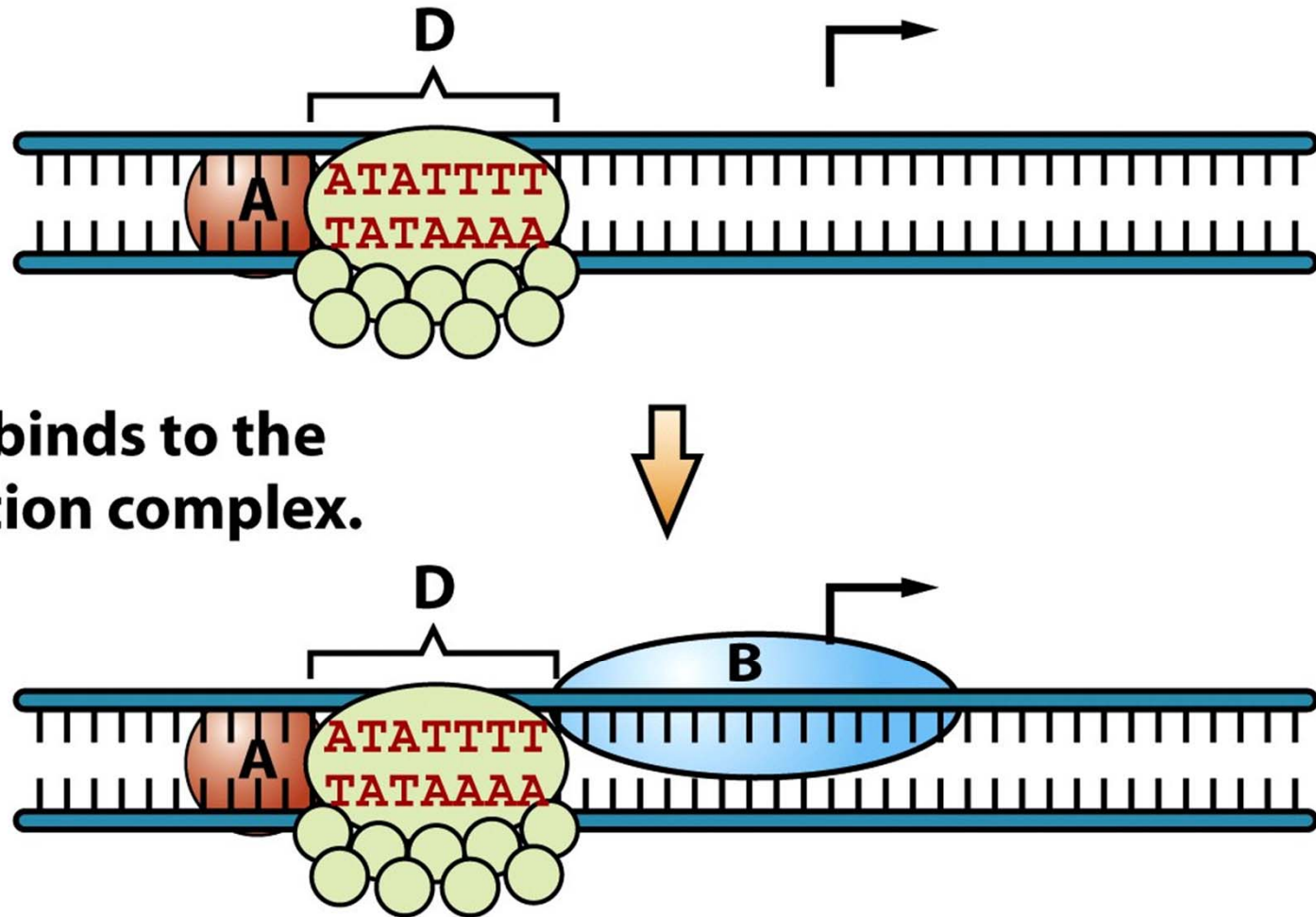
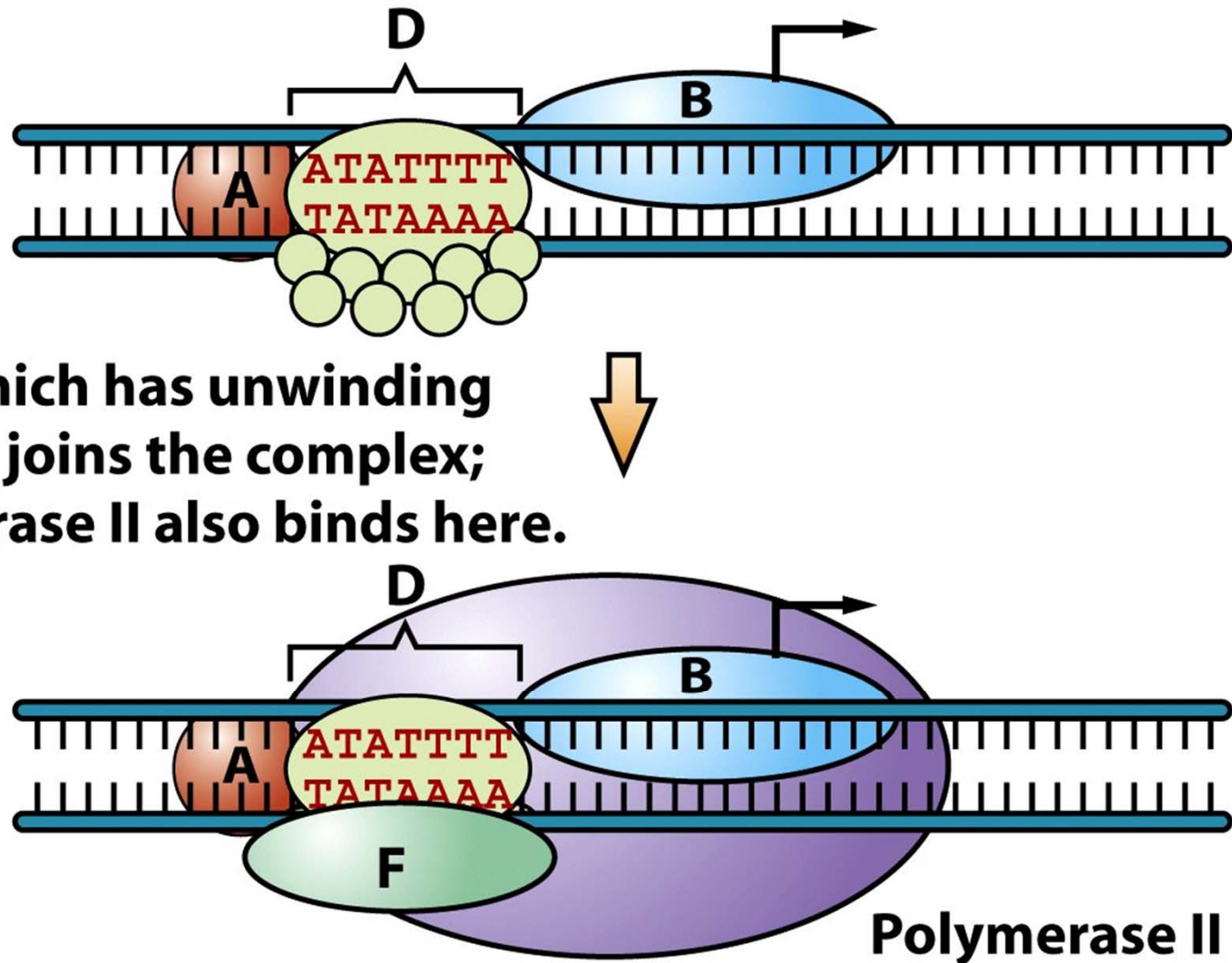
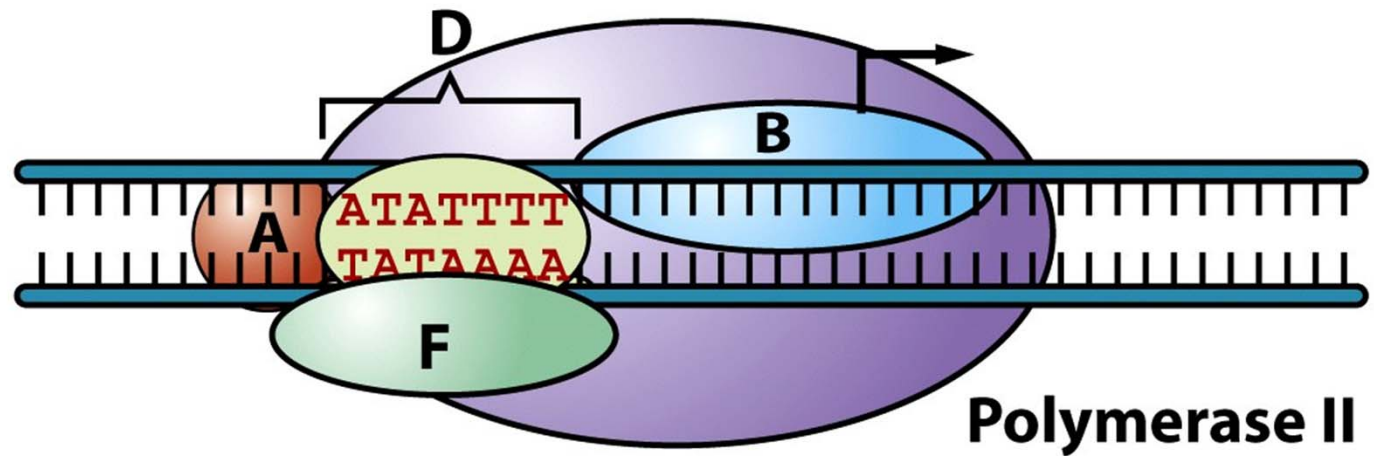


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STEP
4

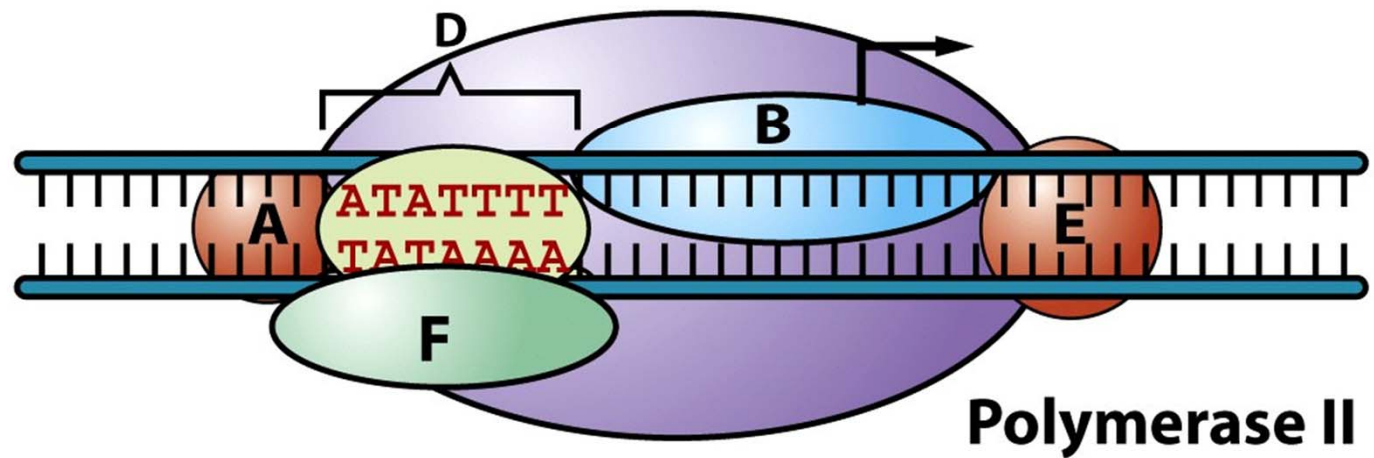
TFIIF, which has unwinding activity, joins the complex; polymerase II also binds here.





STEP
5

TFIIIE binds to the initiation complex.



Transcription in Eukaryote

-Gene regulation

- Enhancers are sequences involved in gene regulation during development or in different cell types
- Enhancers enhance the **rate of transcription** as a result of binding certain specific transcription factor

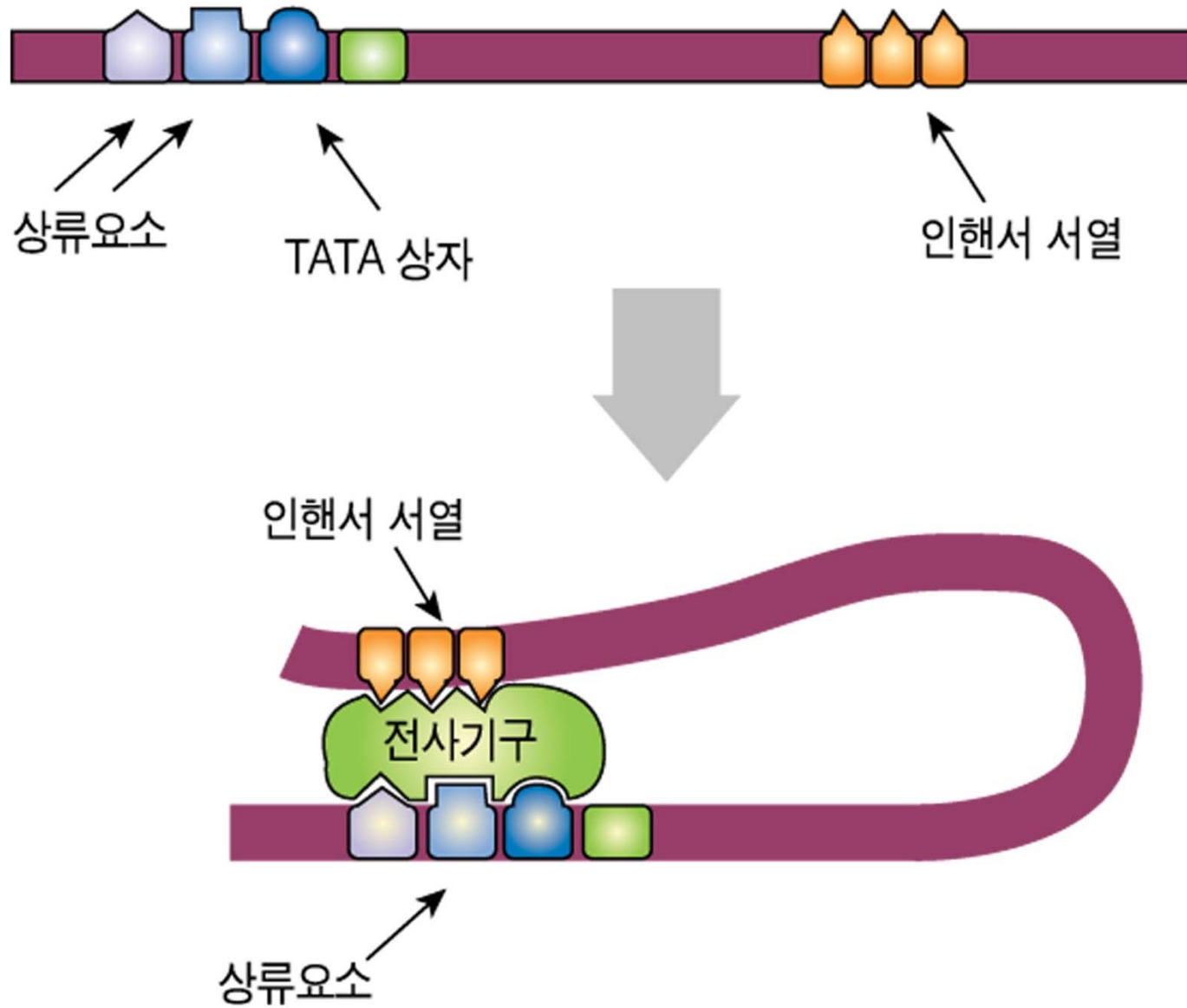


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Transcription in Eukaryote

-RNA Processing

- RNA processing occurs after transcription for primary transcript
- RNA processing of primary transcripts (= post-transcriptional modification)
 - 1) Capping: RNA chain elongation and the addition of 5' methyl guanosine caps (Guanosine monophosphate (GMP) residue is added to 5' end)
 - 2) Tailing: Termination by chain cleavage and the addition of 3' poly(A) tails (100 ~200 adenine residues are added to 3' end by poly(A) polymerase)
 - 3) Splicing: Introns are spliced out and exons are rejoined
- RNA editing occasionally occurs by replacing one base with another (ex. insertion or removal of uridin nucleotides in trypanosome transcript)

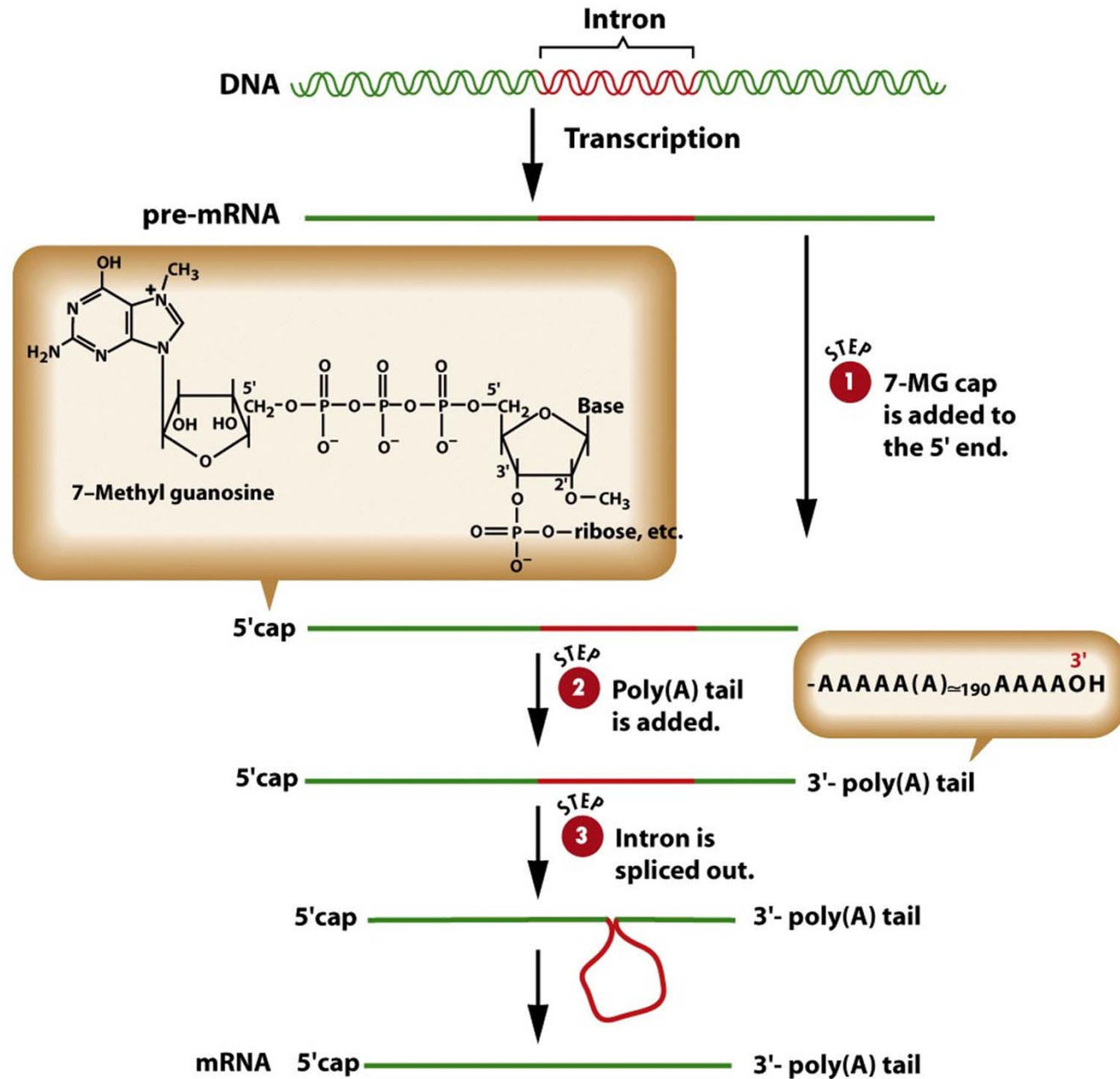
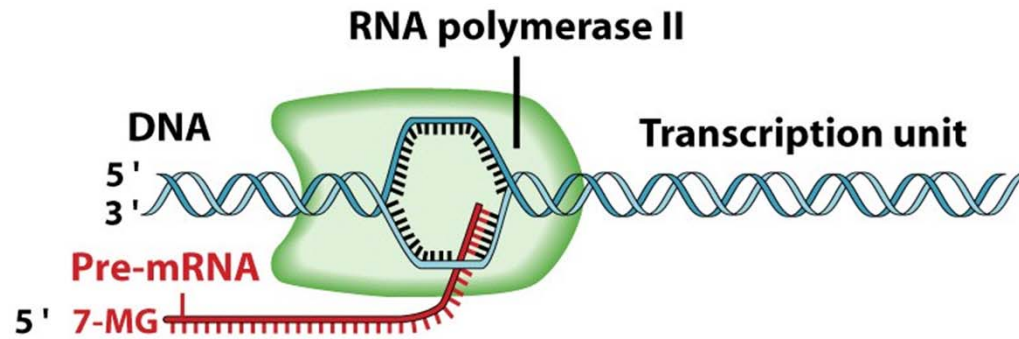
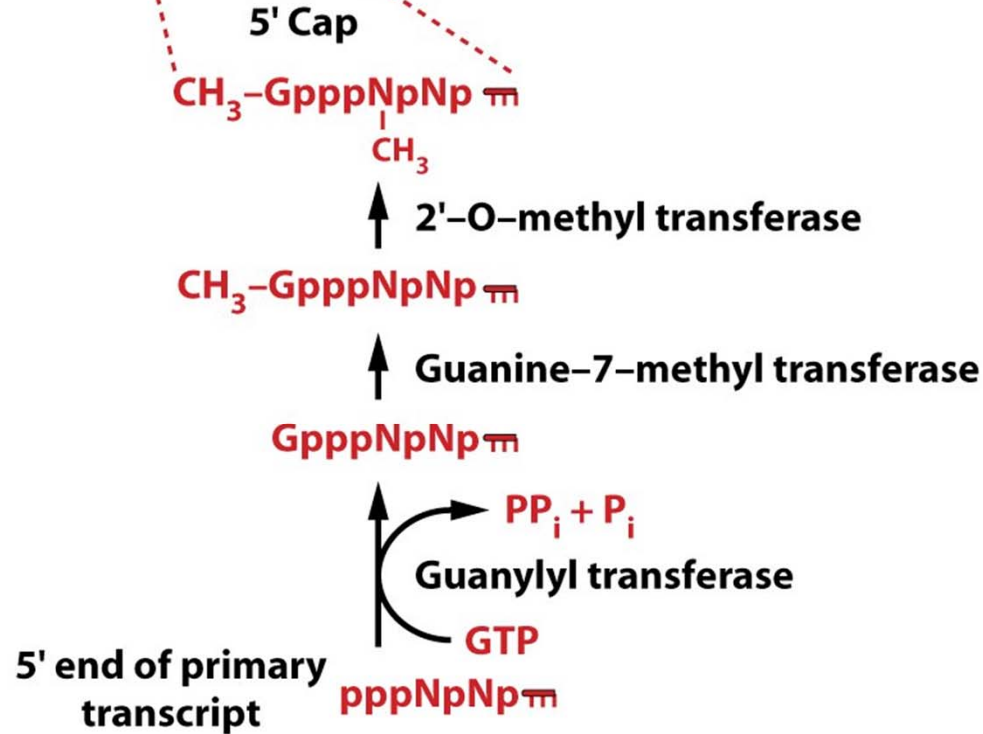


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(a) Early stage in the transcription of a gene by RNA polymerase II.



(b) Pathway of biosynthesis of the 7-MG cap.

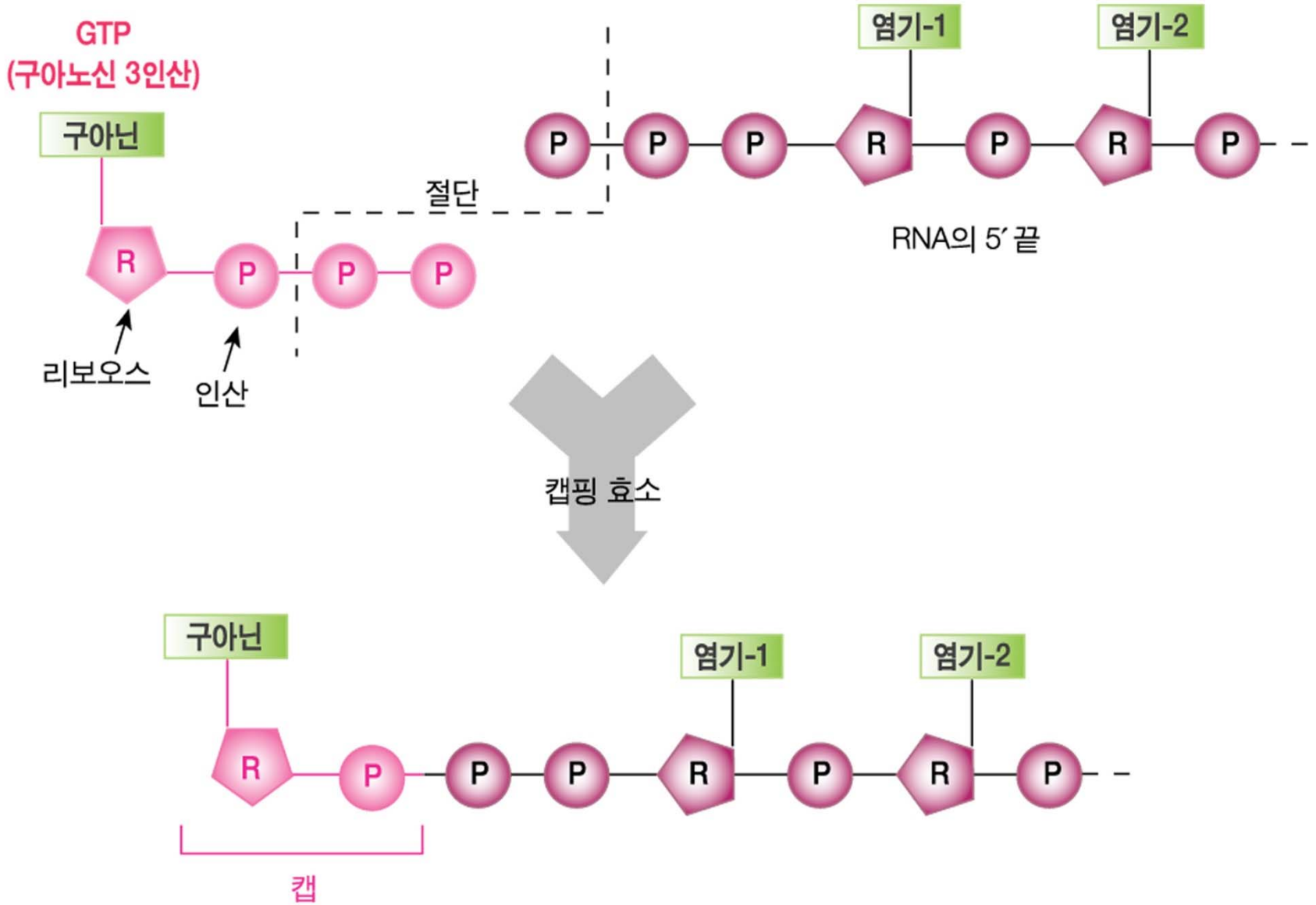


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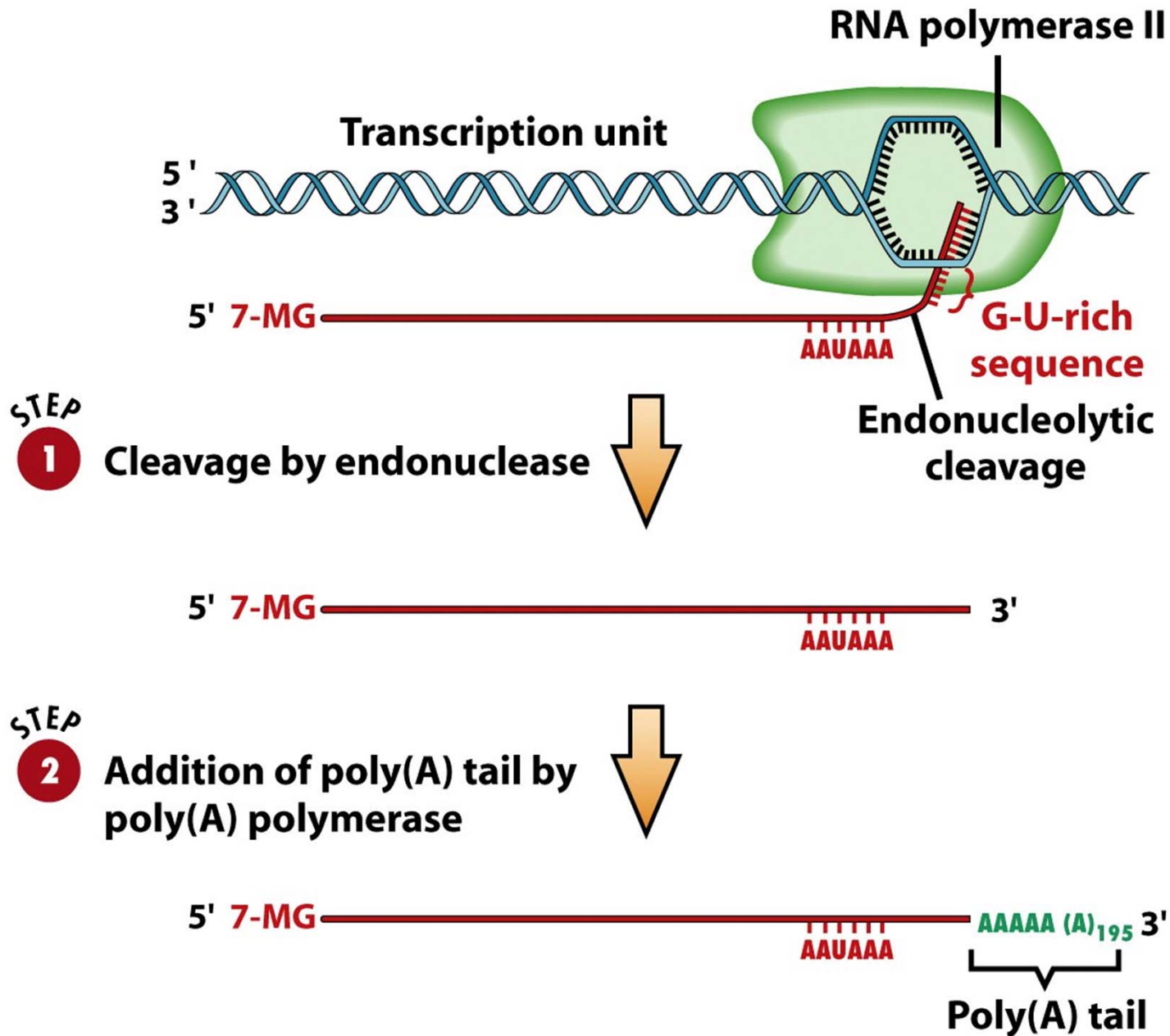
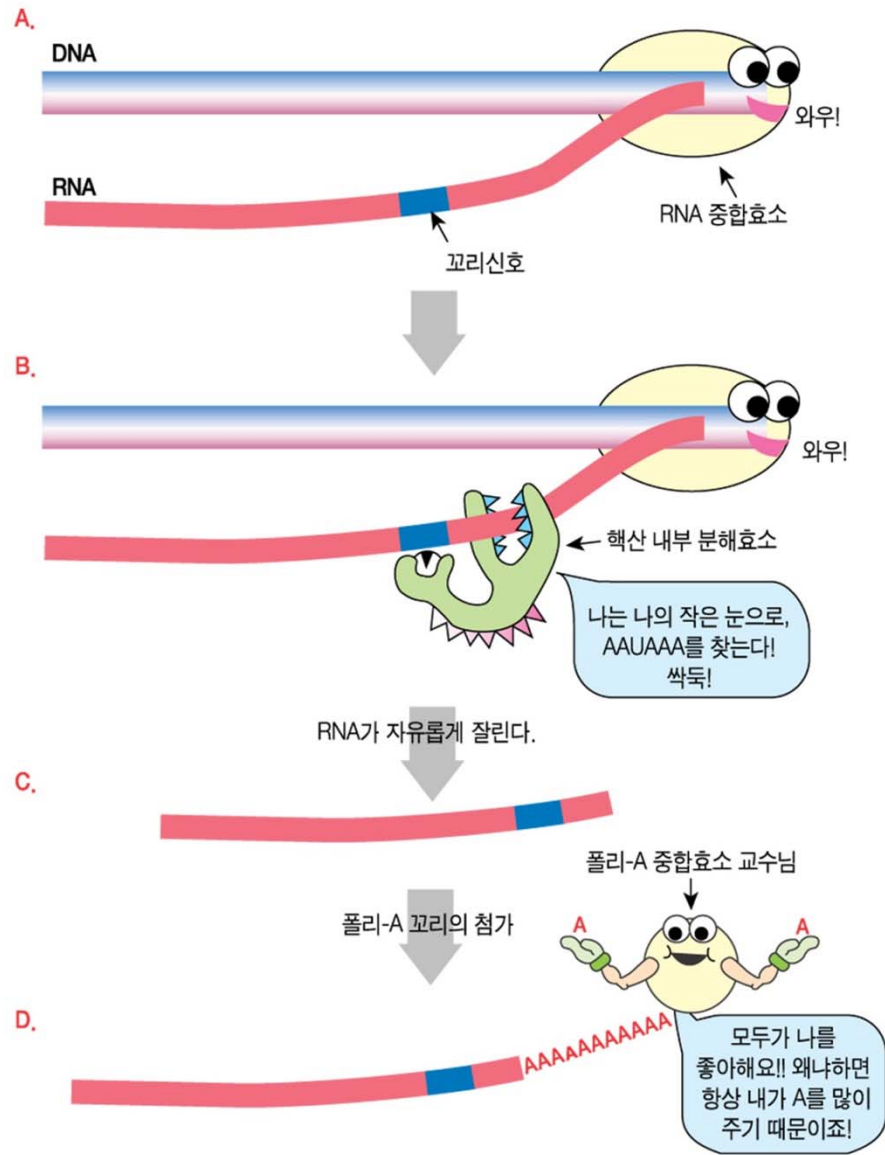


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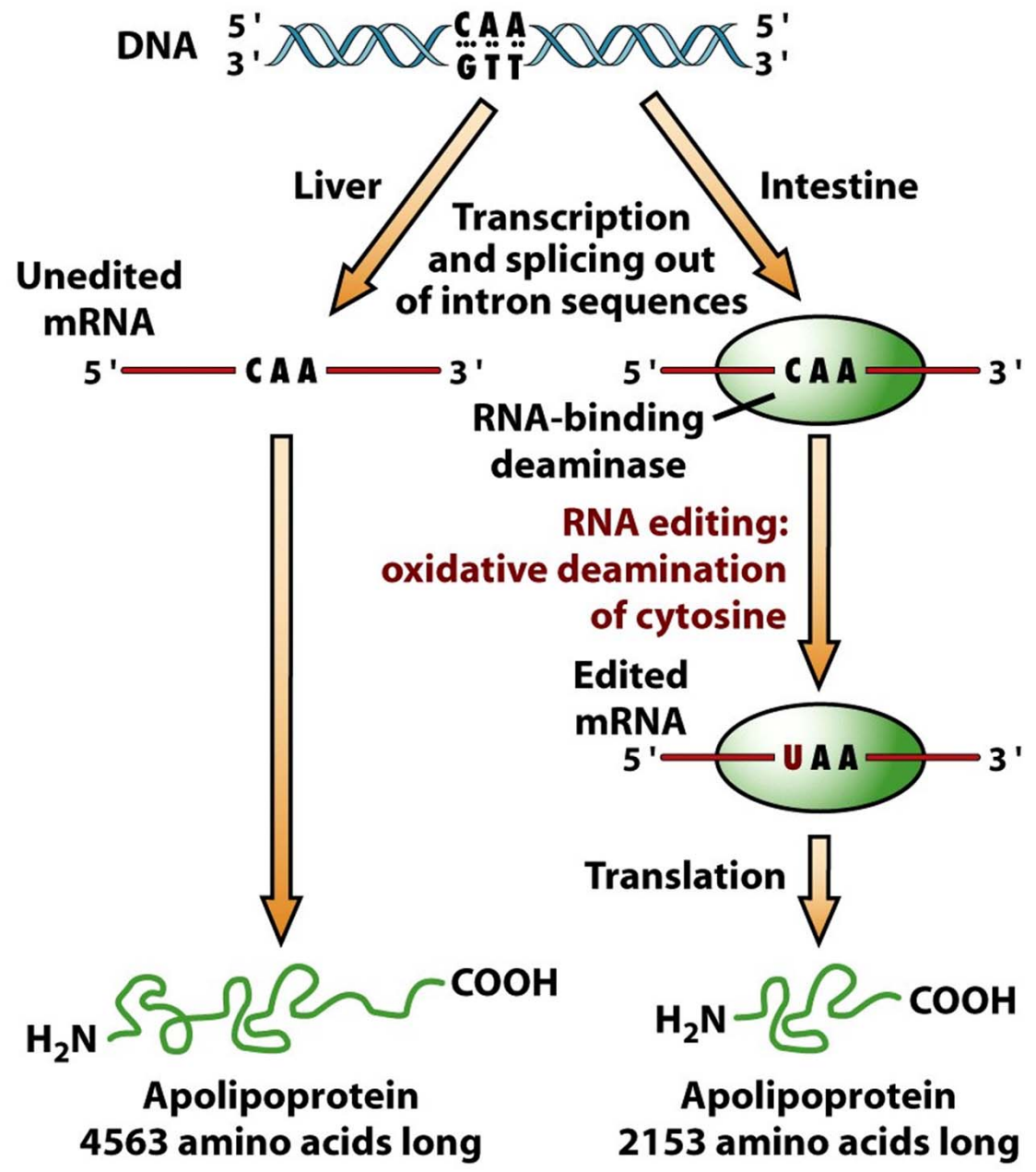


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Transcription in Eukaryote

-RNA Processing

- In RNA splicing, introns are removed by spliceosome
 - spliceosome complex = five small nuclear ribonucleoprotein
[snRNP=small nuclear RNA (snRNA) + proteins]
- snRNA recognize splice and branch site and proteins cut and stick
- Alternative splicing is used by different cell type and choose to use different splice site within the same gene

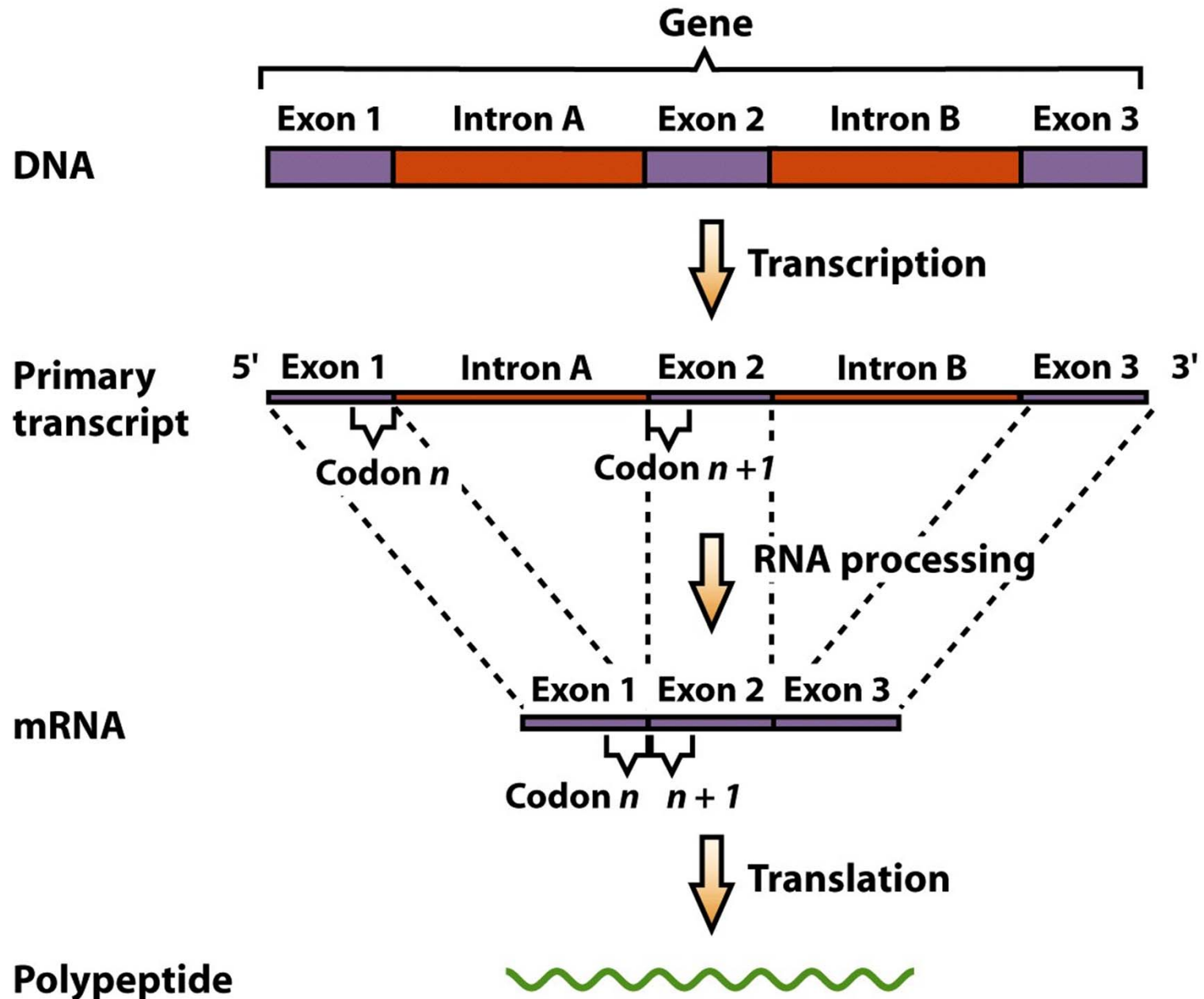
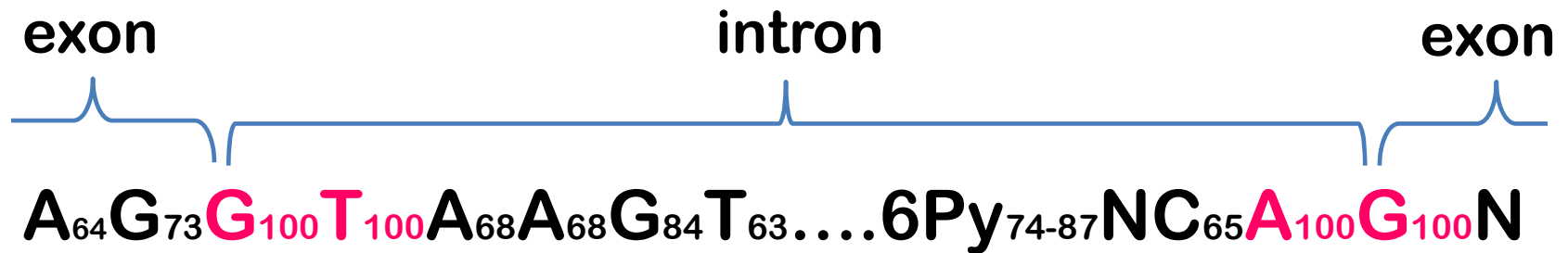
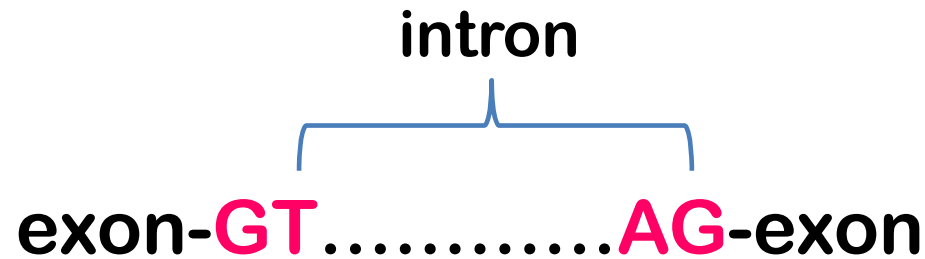


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Precise splicing signal: consensus sequences within introns and at the exon-intron junctions



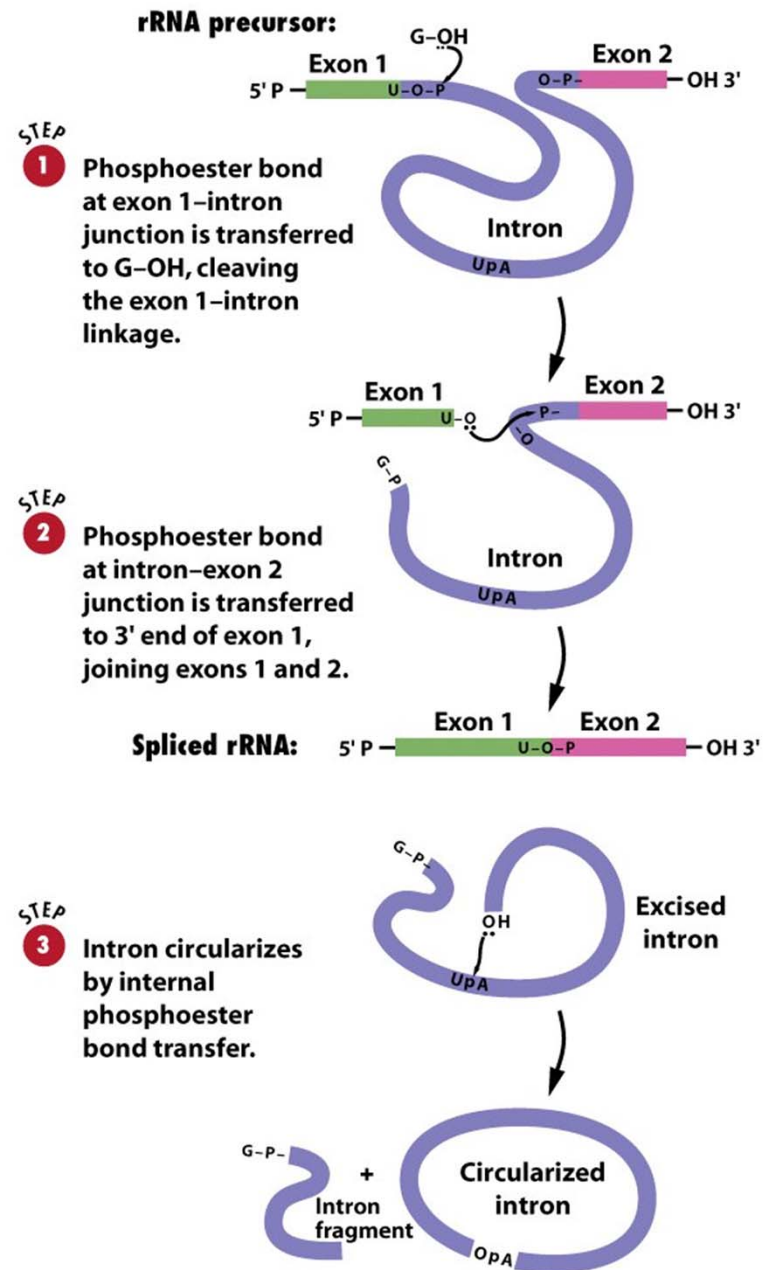


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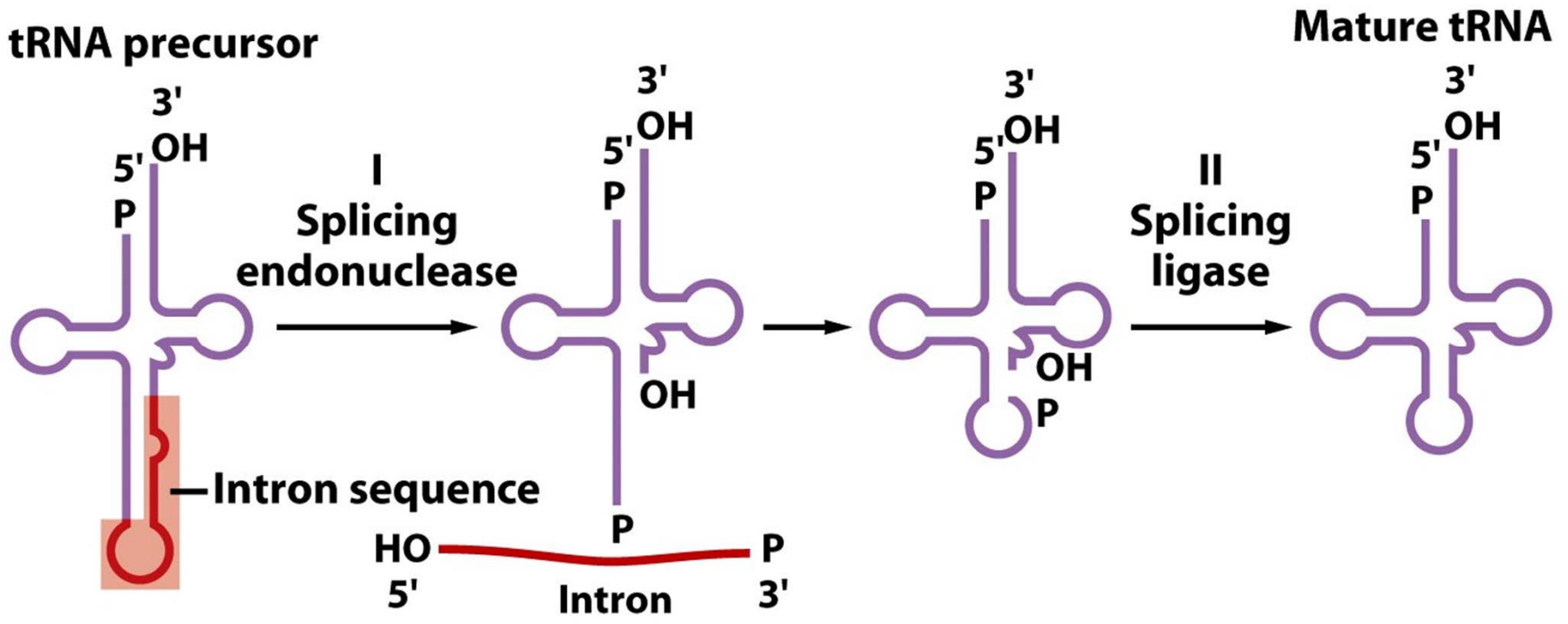


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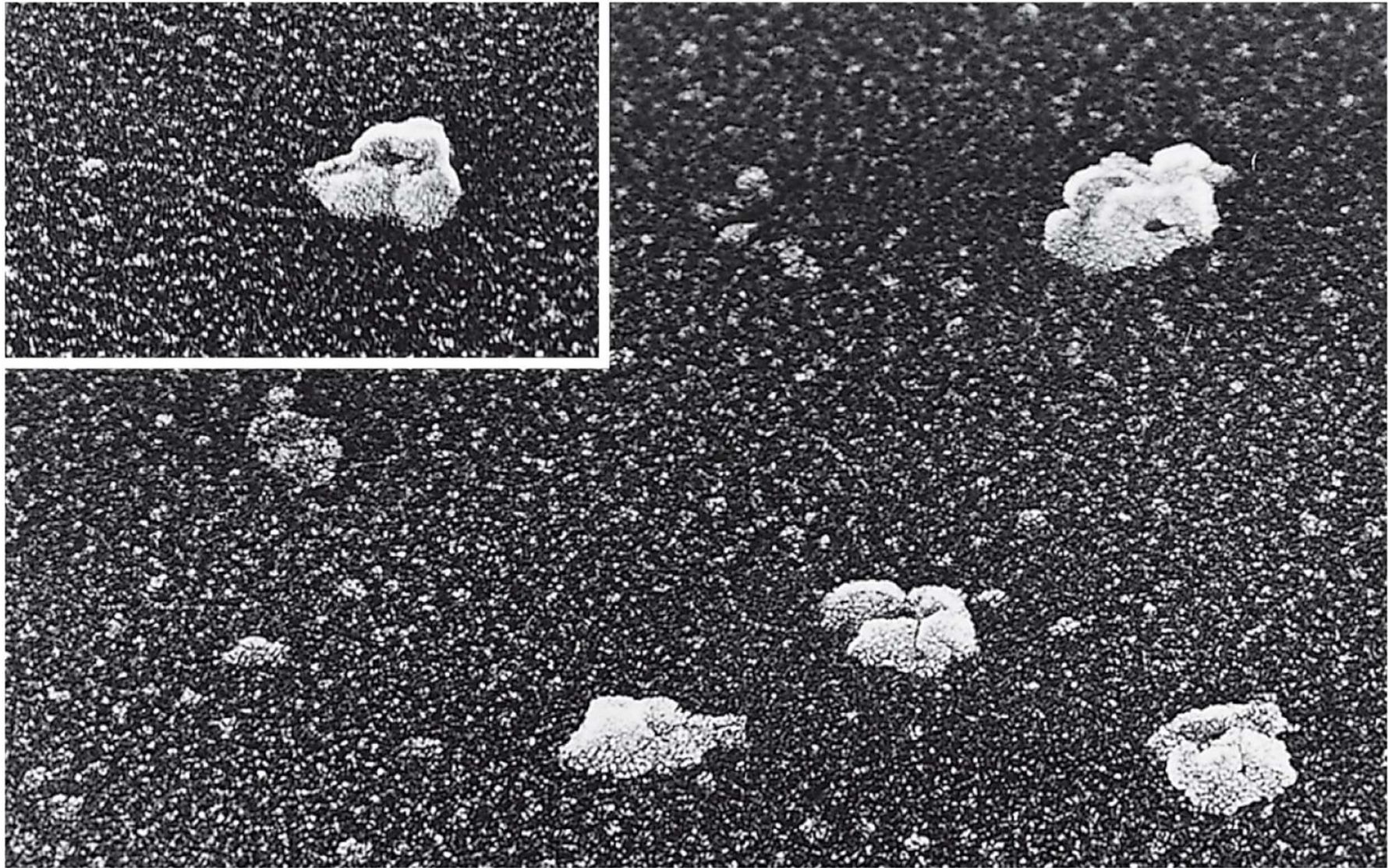
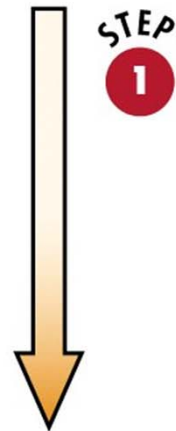
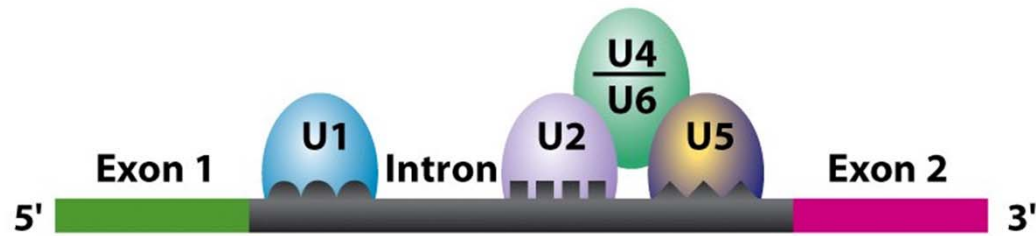


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Electron microscope photographs of purified spliceosomes



STEP 1 The complete spliceosome participates in the cleavage of the phosphoester linkage at the 5' intron splice site and the formation of a phosphodiester linkage between the 5' G of the intron and the conserved A near the 3' end of the intron. snRNA U4 is released.

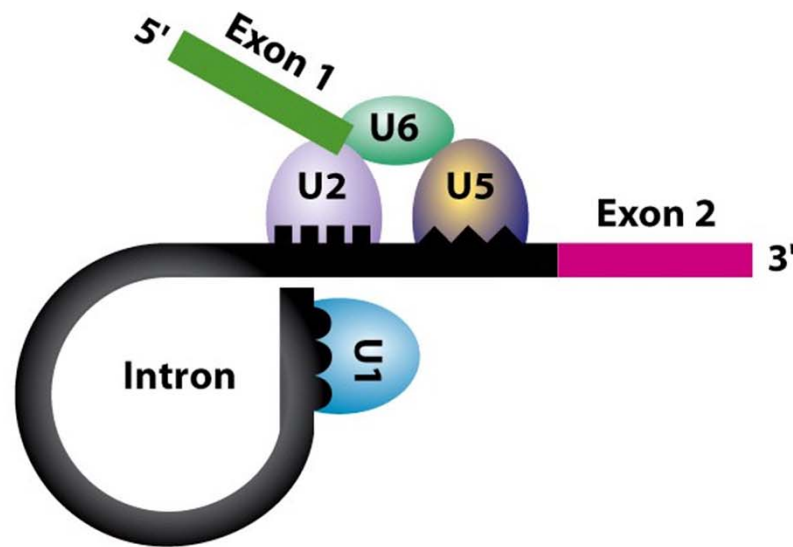


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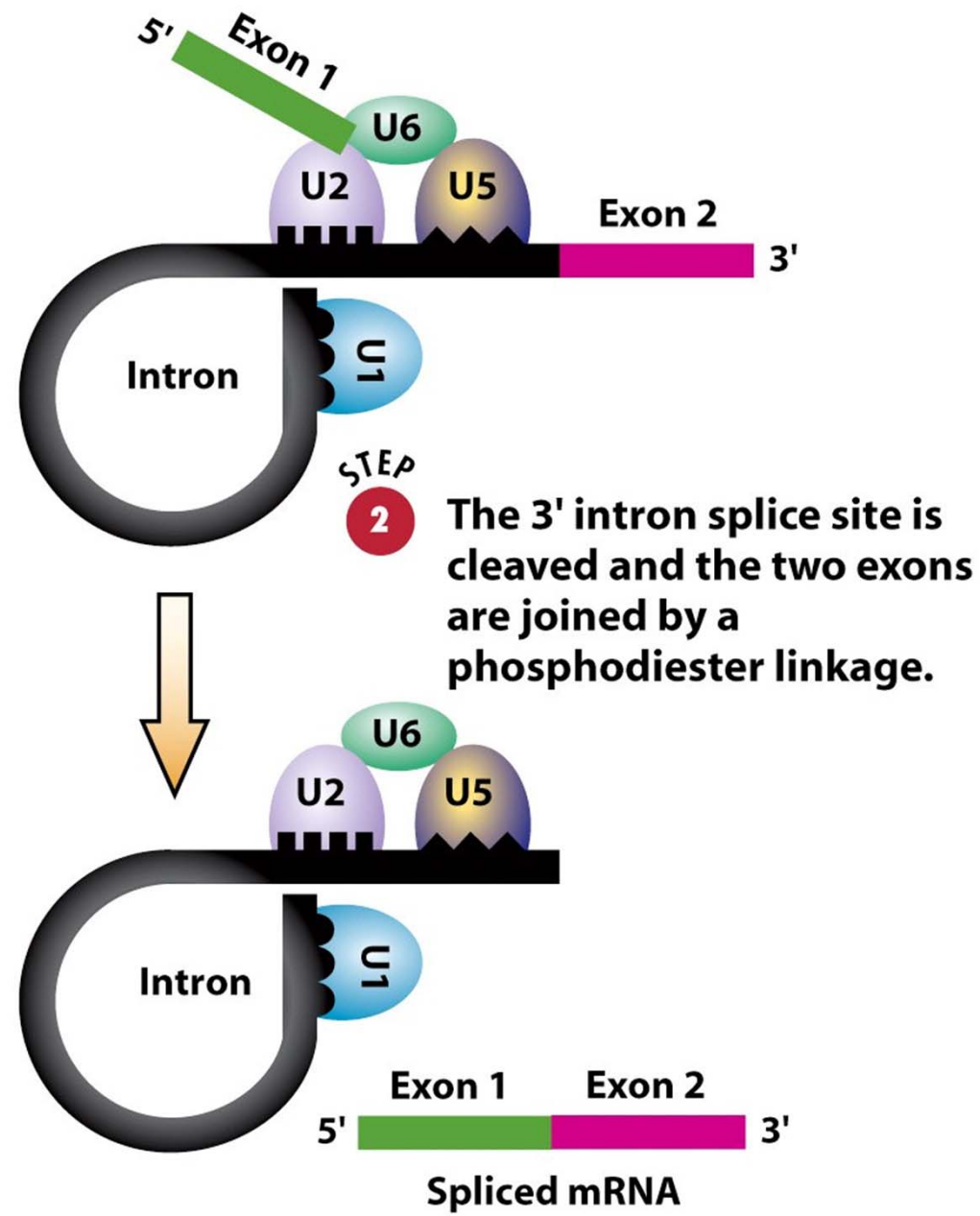


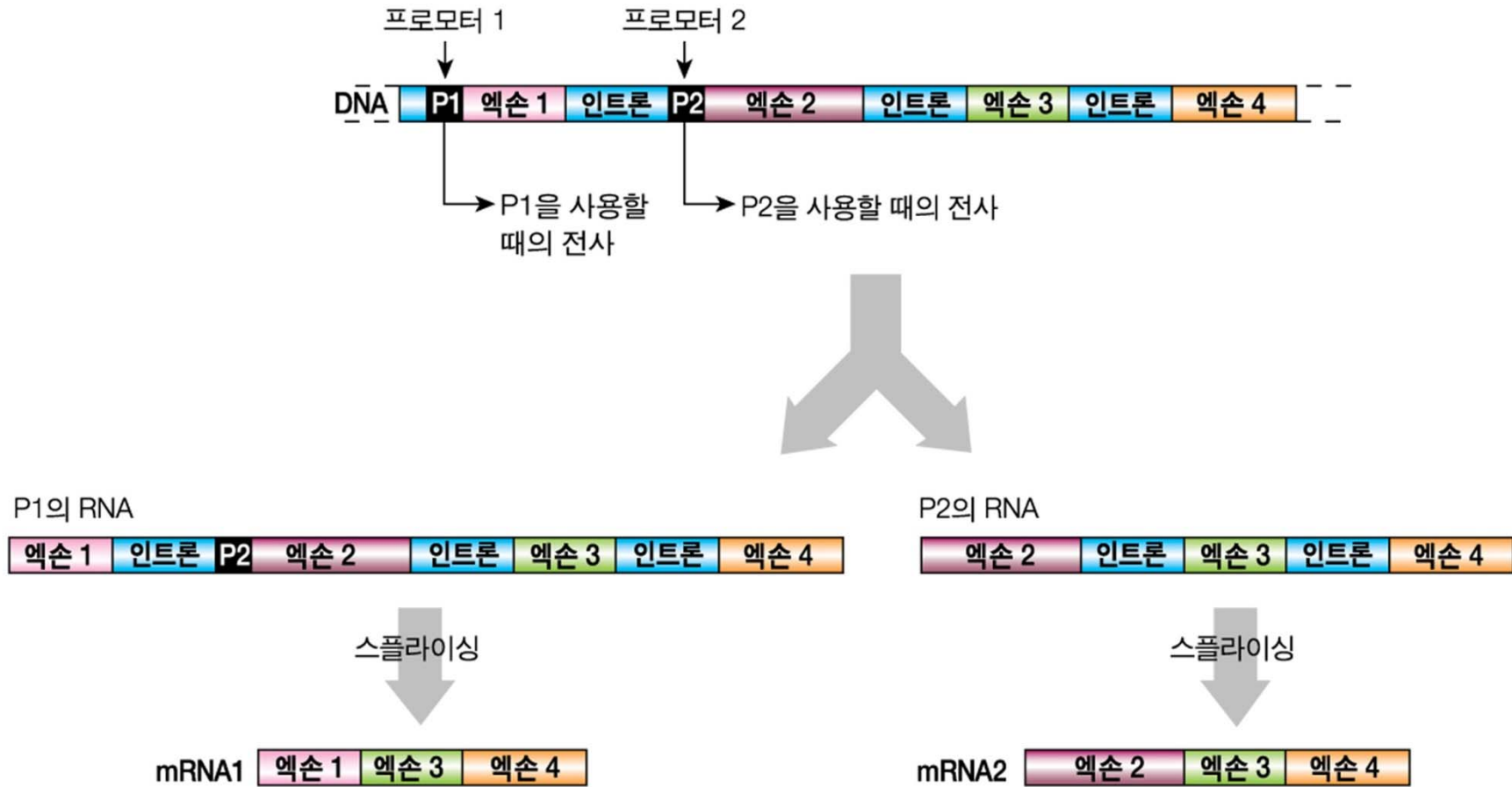
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Transcription in Eukaryote

-RNA Processing

- Four main types of alternative splicing
 - 1) Alternative promoter selection
 - 2) Alternative tail site selection
 - 3) Alternative splicing by exon cassette selection
 - 4) Trans-splicing

Alternative promoter selection



Alternative tail site selection

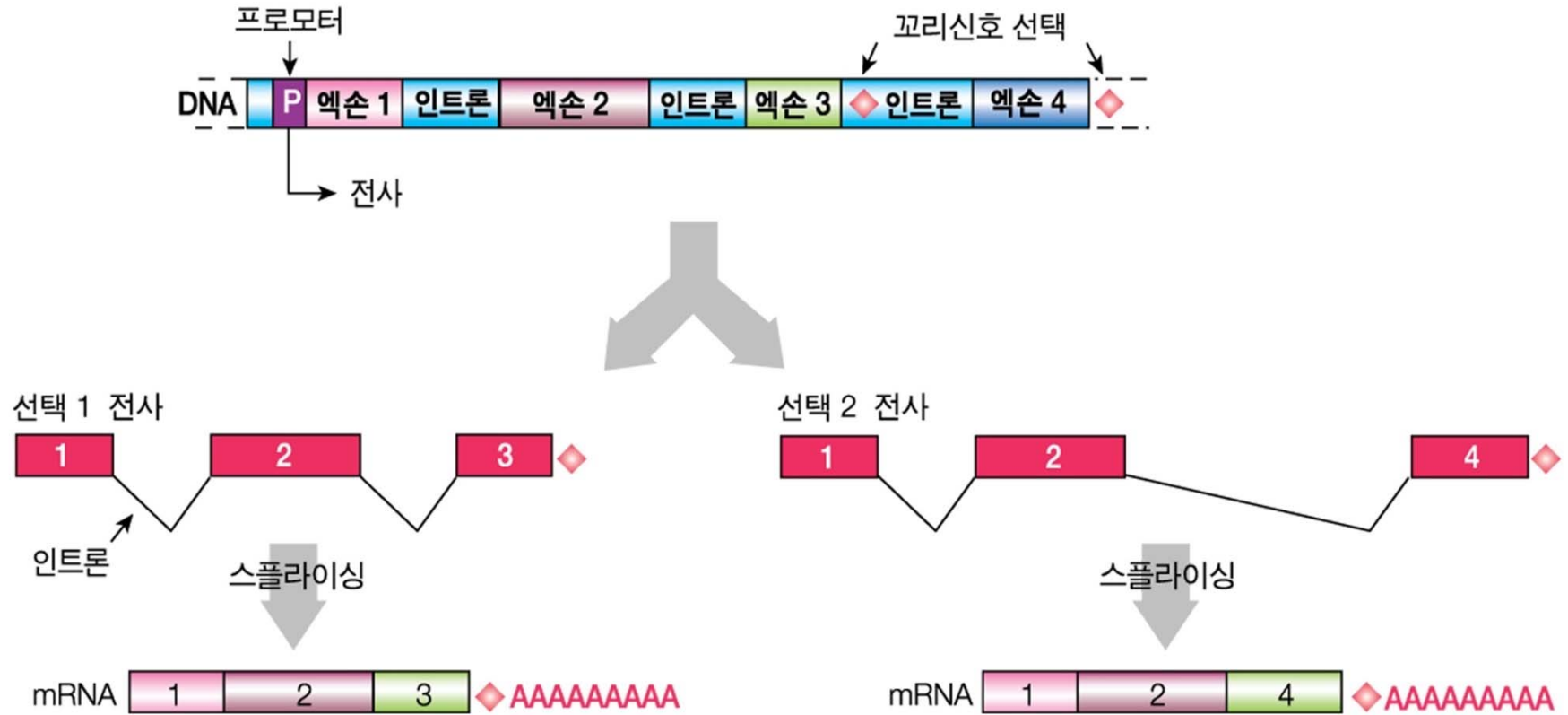


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Alternative splicing by exon cassette selection

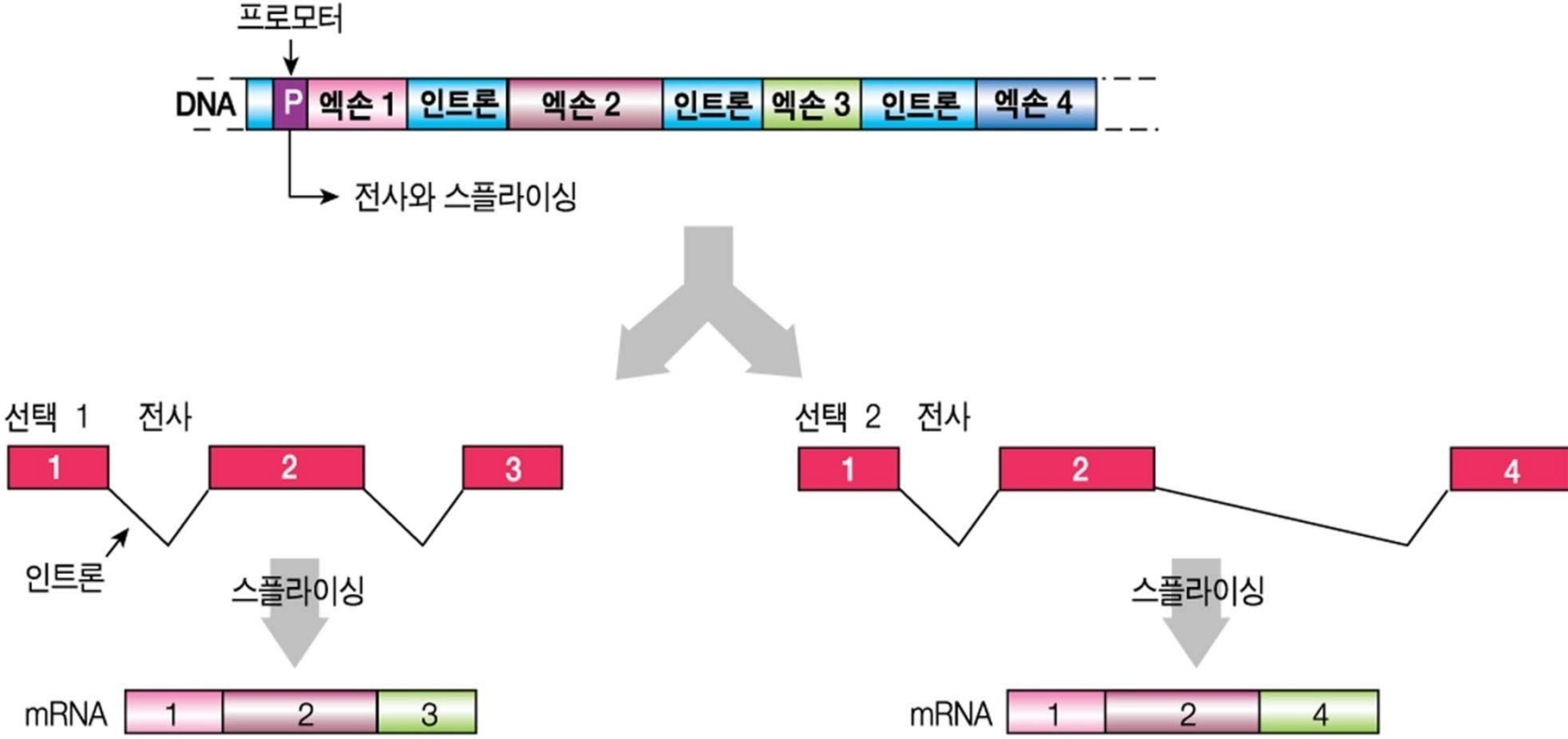
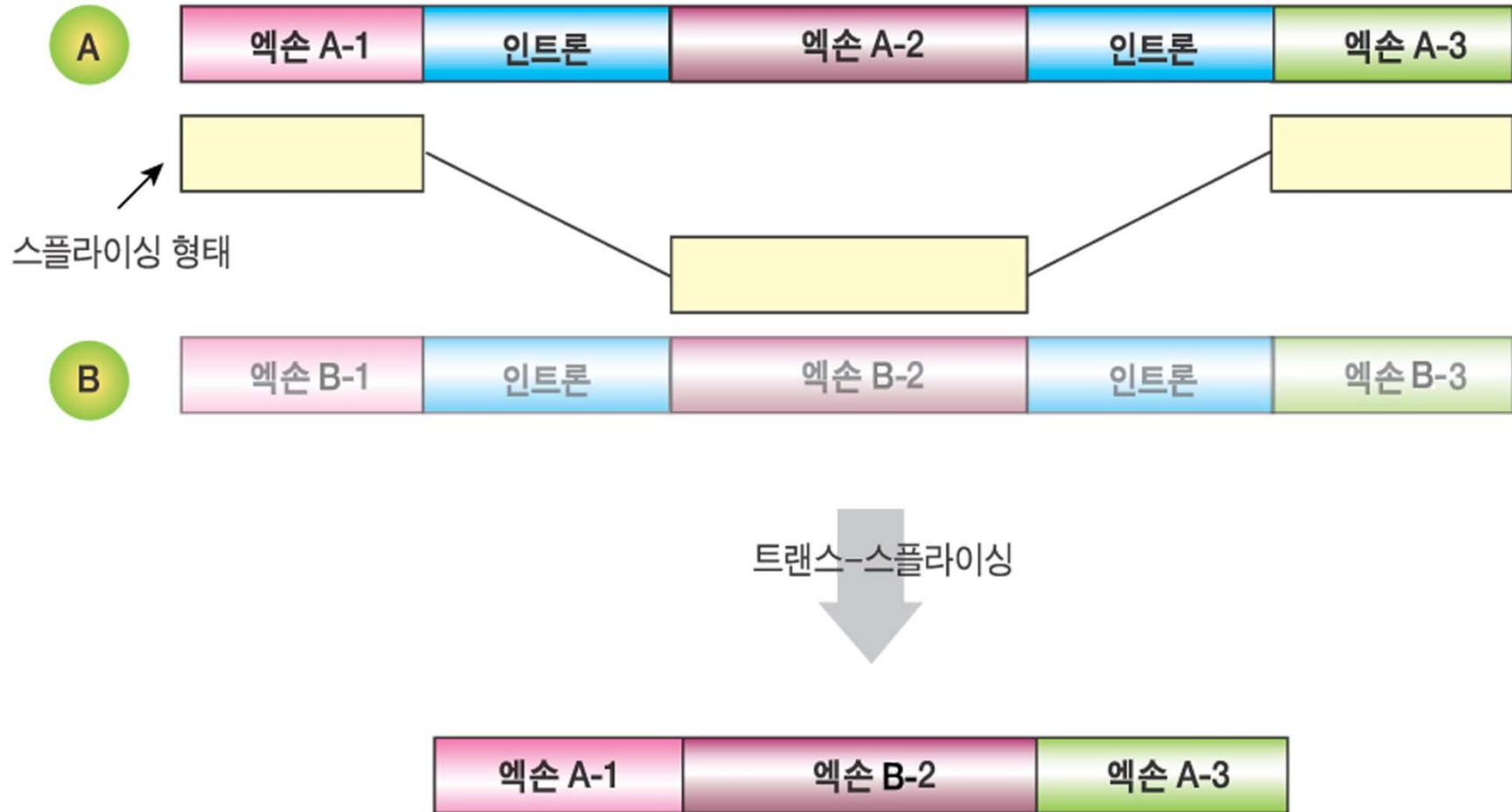


그림 11-24

Trans-splicing

A와 B는 관련된 유전자의 1차 전사체이다.



Translation in Eukaryote

- Translation in eukaryotes is same as in prokaryotes except for:
 - 1) mRNA has to be transported out of nucleus after RNA processing
 - 2) Ribosomes are bigger (80S) and consist of subunits, 40S and 60S
 - 3) No formyl-group is used to tag the first methionine by initiator tRNA
 - 4) 5' cap of mRNA is recognized by ribosome(40S) for binding
 - 5) Eukaryotes only have a single coding sequence on each mRNA

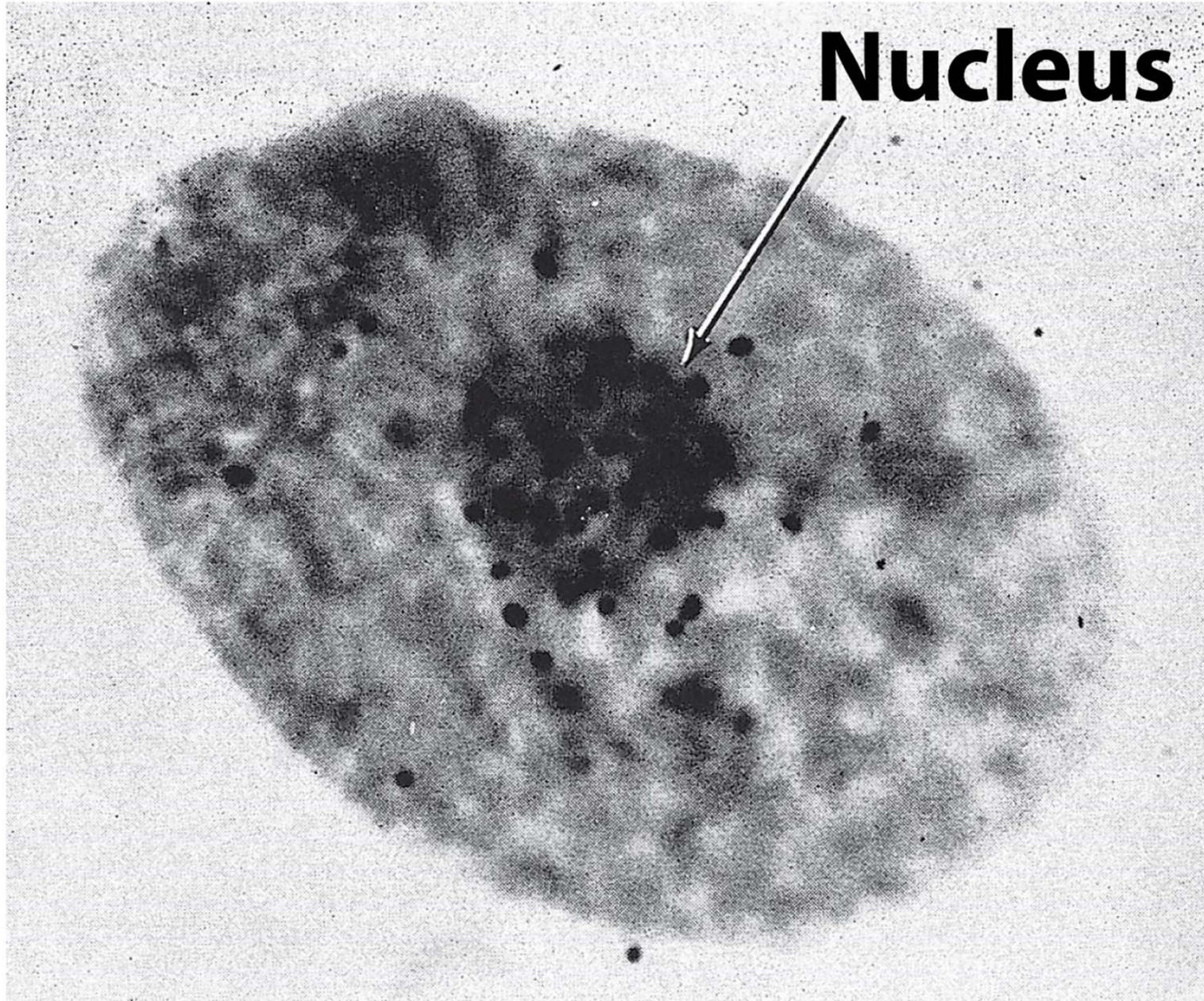


Figure 11-6a Principles of Genetics, 4/e

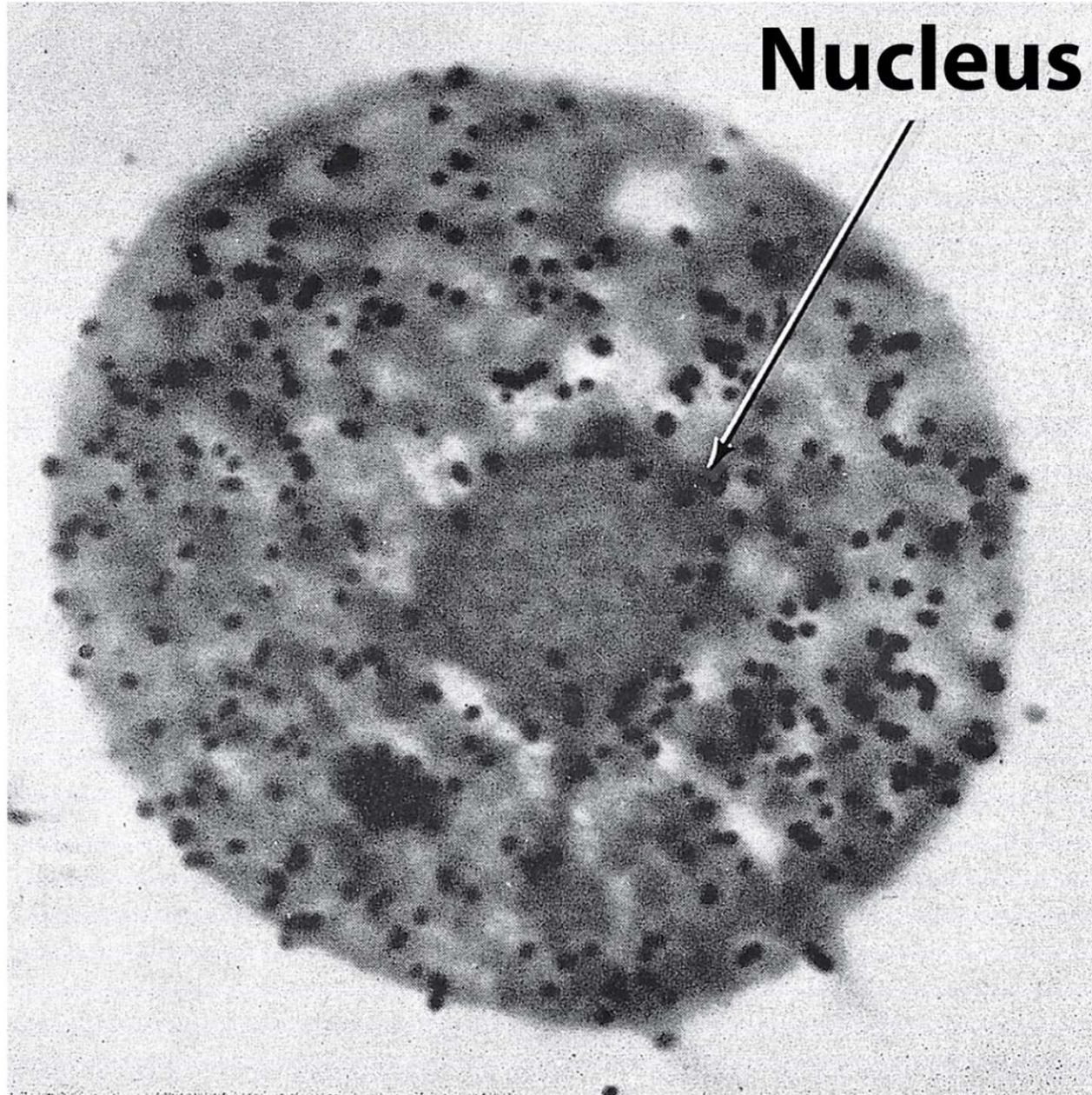


Figure 11-6b Principles of Genetics, 4/e

Take-Home Study

Q1. Biological significance of **INTRON**?

Q2. Biological significance of **Alternative SPLICING**?

Due?..... by next class ⇐⇐