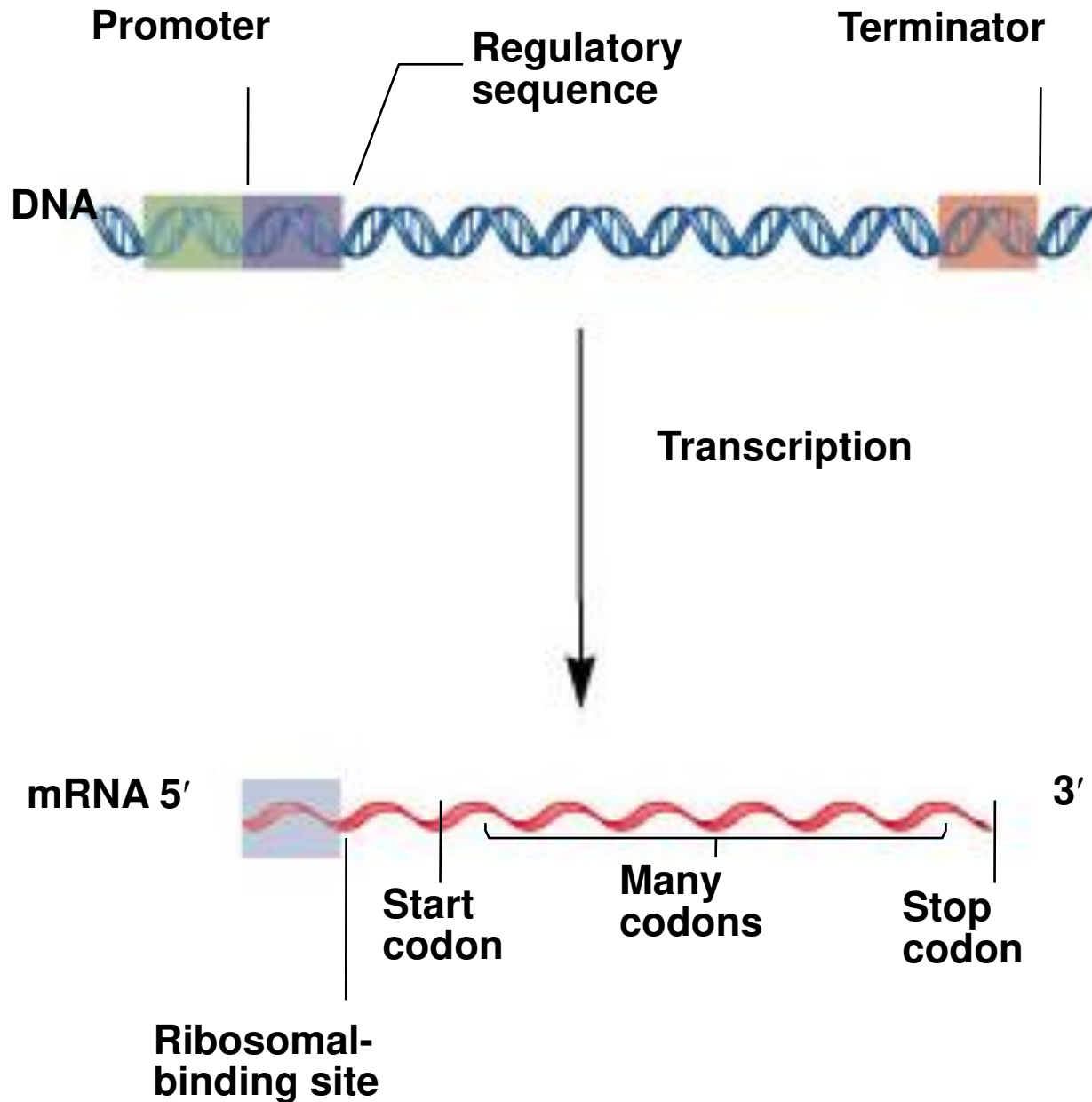


Transcription in Prokaryotes & Eukaryotes

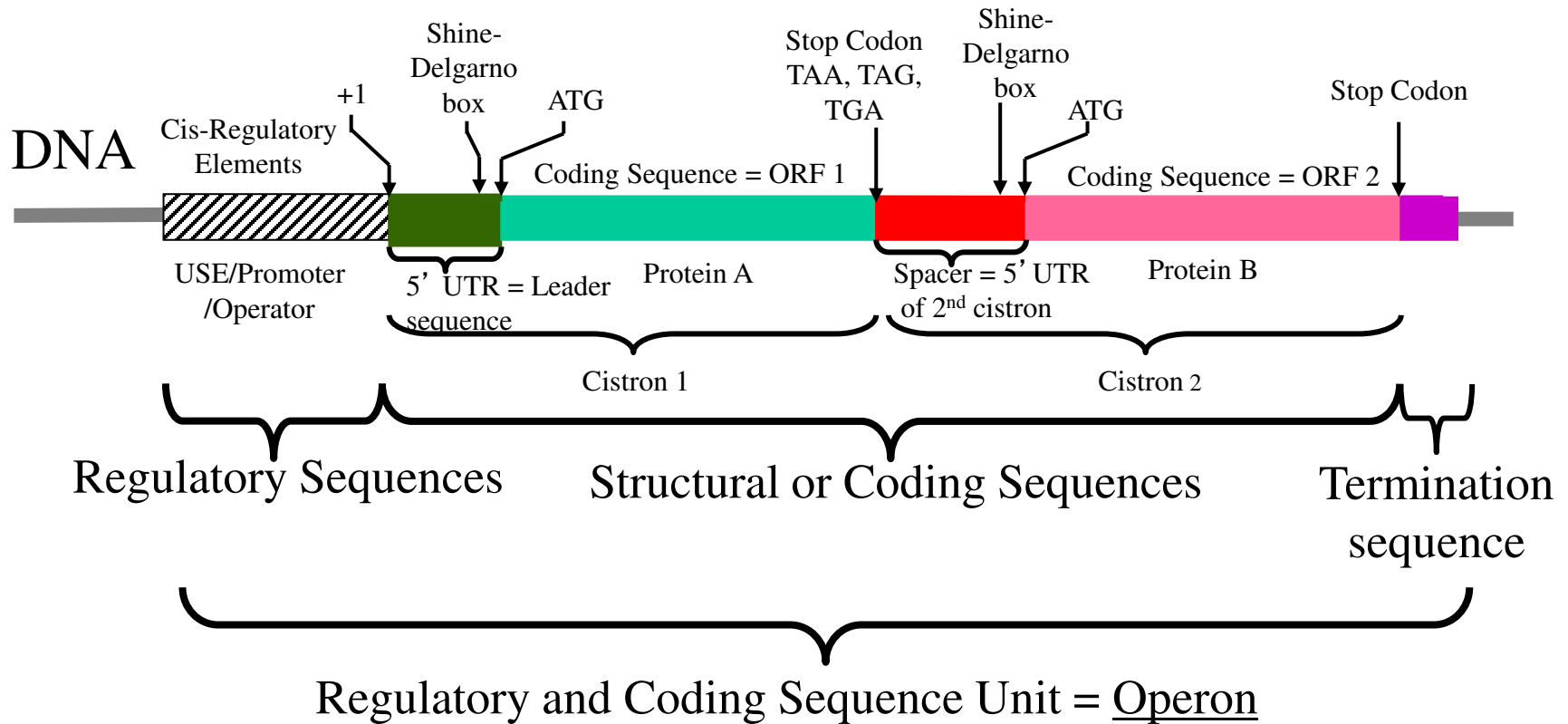
Gene Expression

- There are 4 major events that occur during the process of gene expression
 - Transcription
 - RNA processing
 - Translation
 - Protein processing

A Gene is a Transcription Unit

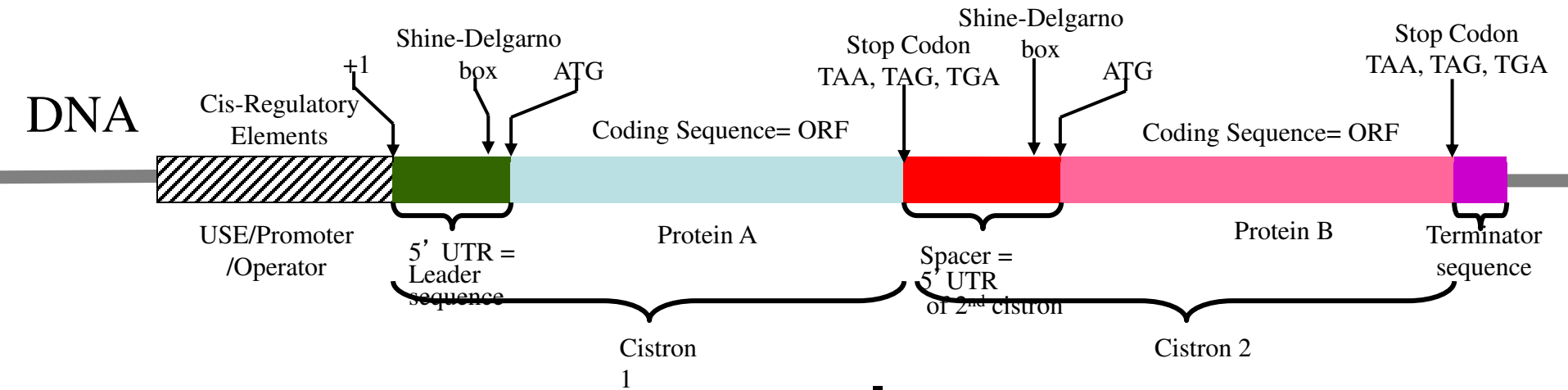


Prokaryotic Gene Structure

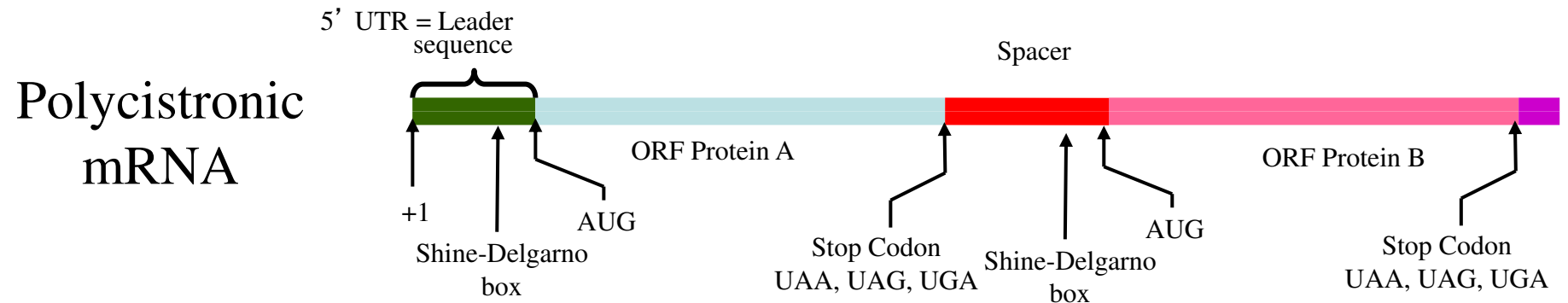


Polycistronic structure

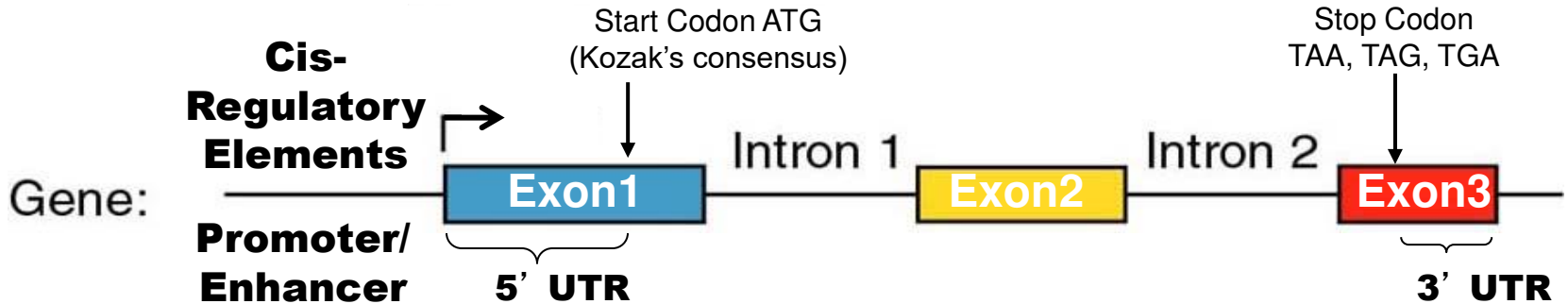
Prokaryotic Gene Structure



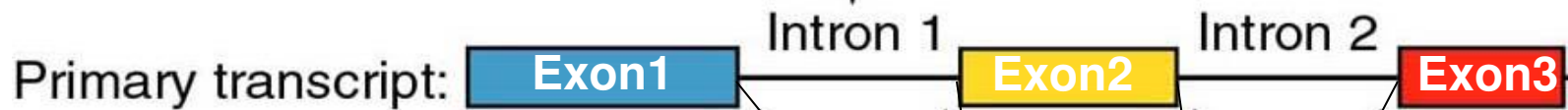
TRANSCRIPTION ↓



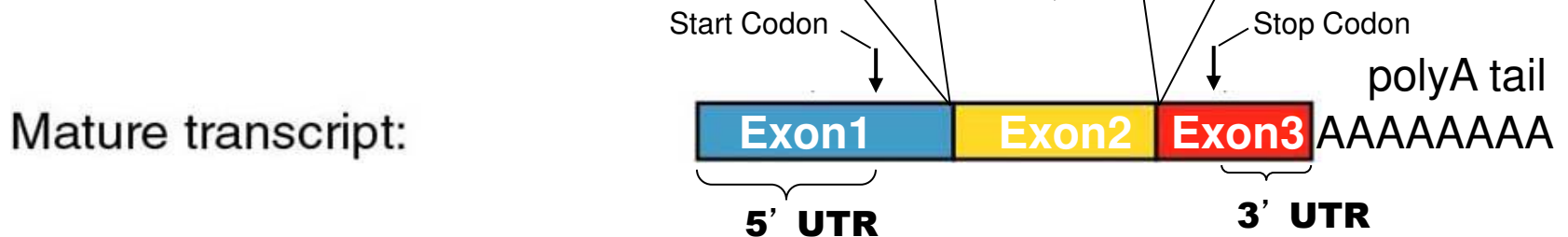
Eukaryotic Gene Structure



TRANSCRIPTION ↓

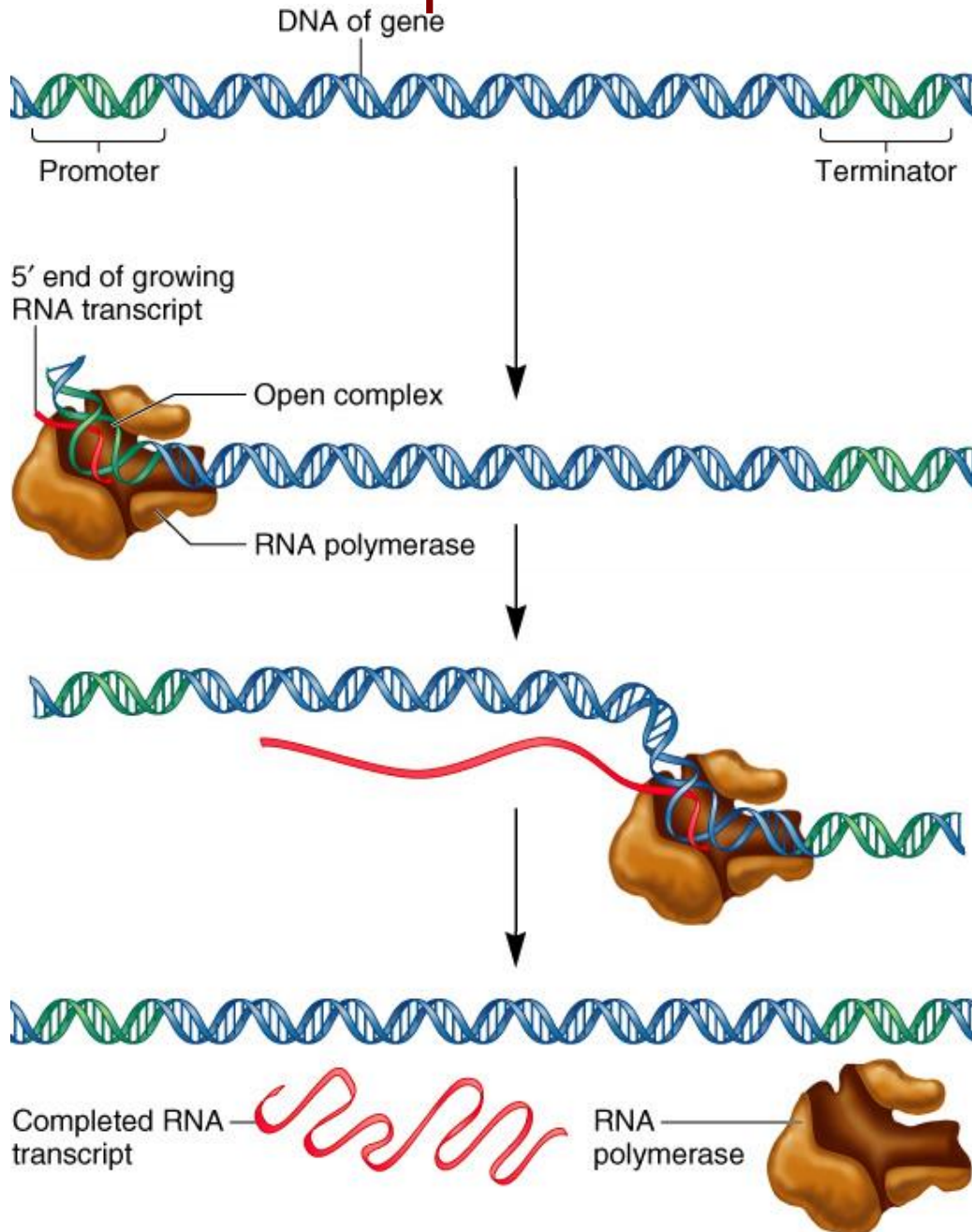


RNA Processing



Monocistronic structure

Transcription Proceeds Through 3 Steps



Initiation

- **Transcription factors & RNA polymerase recognize & bind the promoter**
- **DNA adjacent to the promoter is denatured forming the open promoter complex**

Elongation

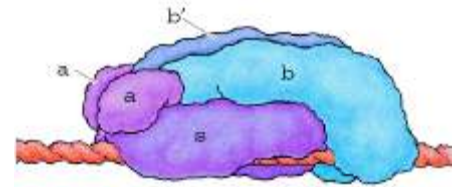
- **RNA polymerase moves along the DNA in synthesizing a RNA transcript. Synthesis is 5' → 3' – Only 1 strand of DNA is read as a template.**

Termination

- **A termination signal is reached causing RNA polymerase to dissociate from the DNA**

Initiation

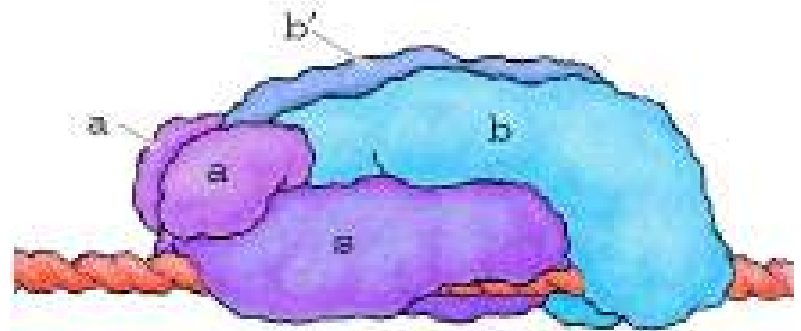
- RNA polymerase $\alpha \alpha \beta \beta' \sigma$
- Transcription factors
- Promoter DNA
 - RNAP binding sites
 - Operator - repressor binding
 - Other TF binding sites



Start site of transcription is +1

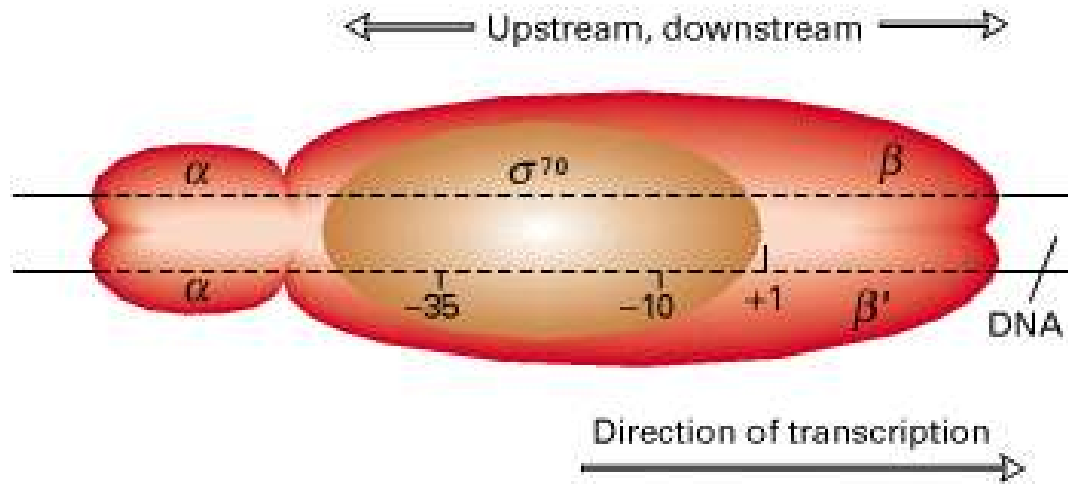
Initiation

- RNA polymerase
 - 4 core subunits
 - **Sigma factor** (σ)-
determines promoter
specificity
 - Core + σ = **holoenzyme**
 - Binds promoter sequence
 - Catalyzes “open complex” and
transcription of DNA to RNA

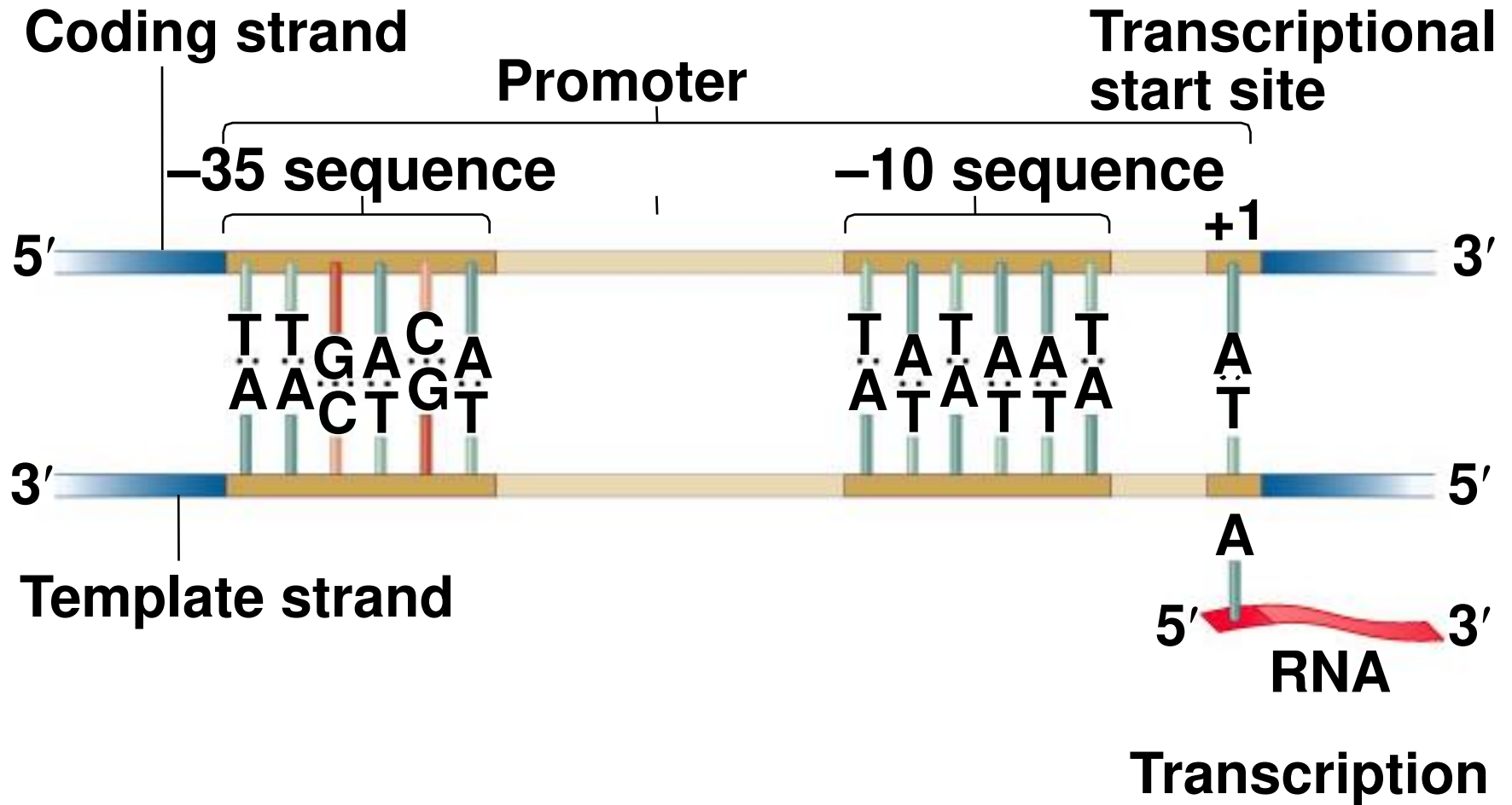


RNAP binds specific promoter sequences

- Sigma factors recognize consensus -10 and -35 sequences



A Prokaryotic Promoter



Reaching A Consensus

-35 region -10 region +1 Transcribed

lac operon TTTACA N₁₇ TATGTT N₆ A

lacI GCGCAAN₁₇ CATGAT N₇ A

trp operon TTGACA N₁₇ TTAACT N₇ A

rrnX TTGTCT N₁₆ TAATAT N₇ A

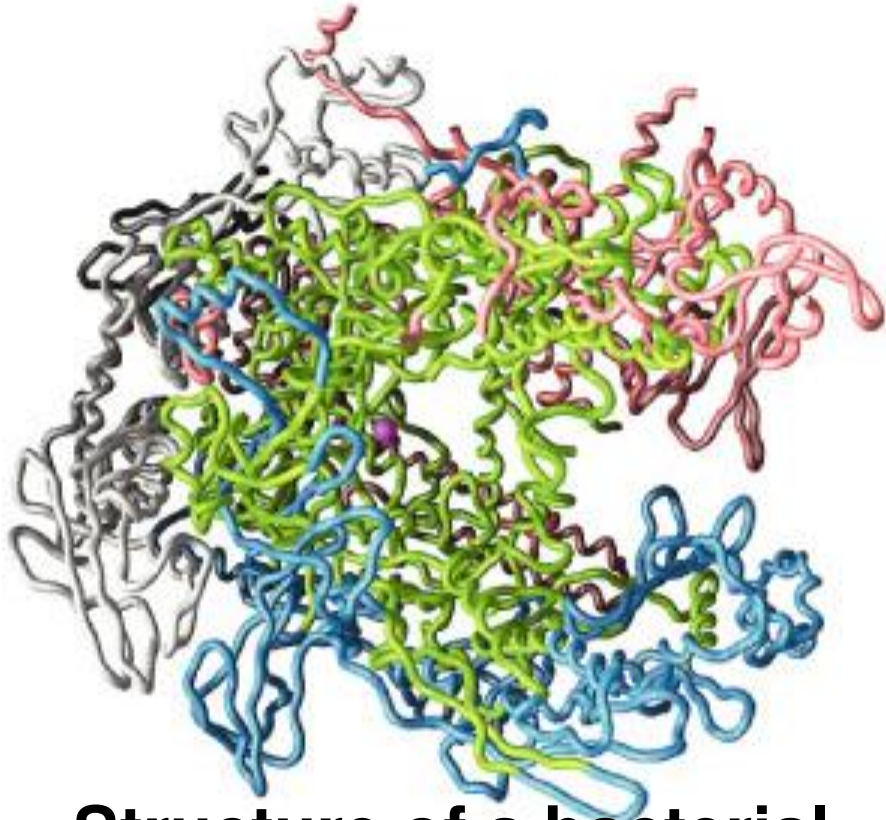
recA TTGATA N₁₆ TATAAT N₇ A

lexA TTCCAA N₁₇ TATACT N₆ A

tRNA^{tyr} TTTACA N₁₆ TATGAT N₇ A

Consensus TTGACA TATAAT

RNA Polymerases



Structure of a bacterial RNA polymerase



Structure of a eukaryotic RNA polymerase II

RNA Polymerases

- Differences between eukaryotes & prokaryotes
- Prokaryotes
 - 1 enzyme with 4 subunits
 - 2 α' s, 1 β , & 1 β'
 - actual polymerase function
 - Sigma factors (σ)
 - recognize & bind promoter DNA sequence
- Eukaryotes
 - 3 separate holoenzymes – each has ~12 subunits
 - RNA Pol I – 28S, 18S, 5.8S rRNA
 - RNA Pol II – mRNA, snRNA
 - RNA Pol III – tRNA, 5S rRNA
 - 3 sets of basal transcription factors
 - recognize promoter DNA sequences

The Process of Transcription

- **Initiation**

- Where/when most regulation of gene expression occurs
- Different between prok:s & euk:s

- **Elongation**

- Essentially same between prok:s & euk:s
- Some regulation, more in prok:s than euk:s

- **Termination**

- Different between prok:s & euk:s
- Some regulation

Prok:s-prokaryote

Euk:s-eukaryotes

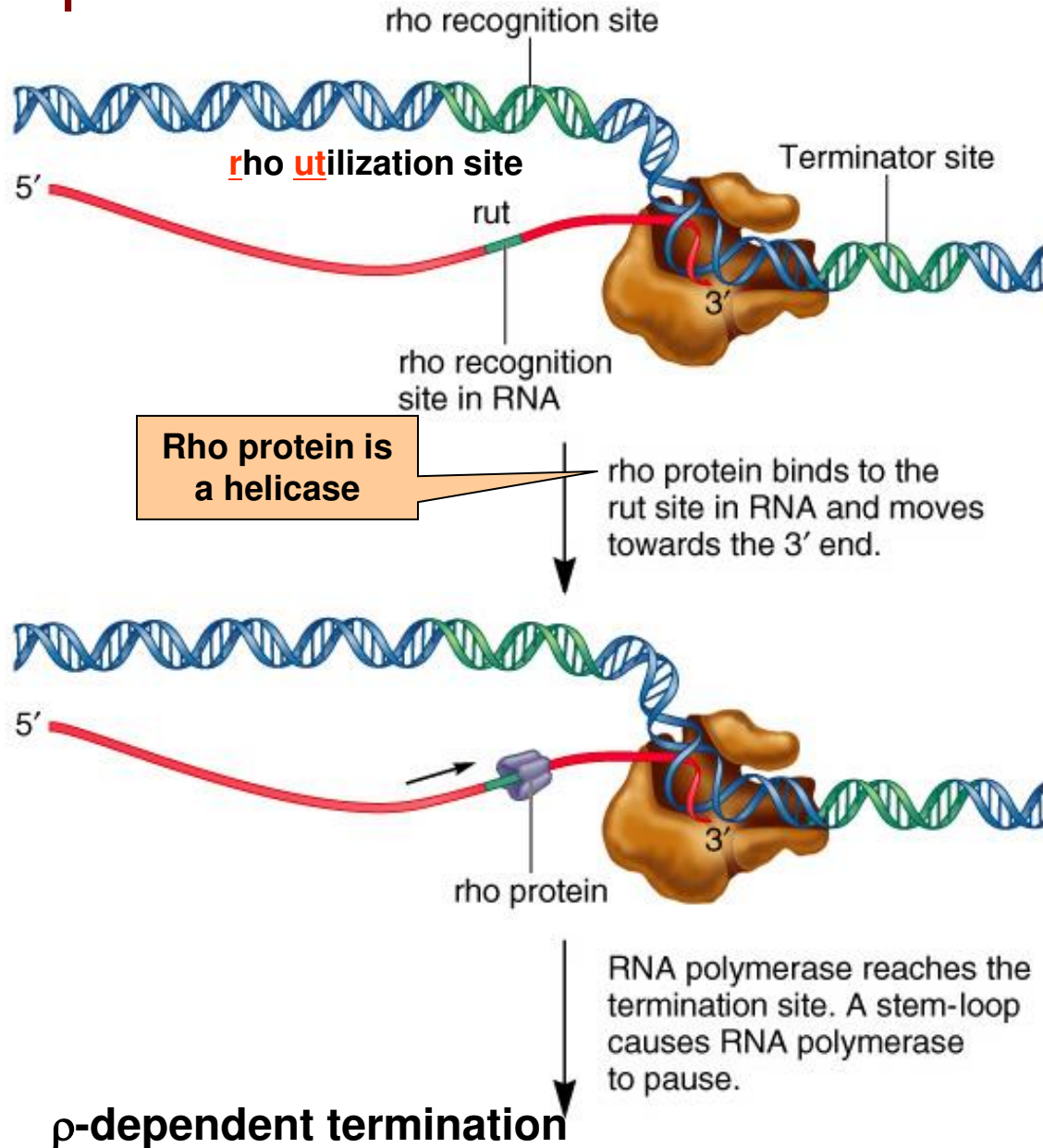
Elongation

- Once the RNA polymerase has synthesized a short stretch of RNA (~ 10 nt), transcription shifts into the elongation phase.
- **This transition** requires further conformational change in polymerase that leads it to grip the template more firmly.
- **Functions:** synthesis RNA, unwinds the DNA in front, re-anneals it behind, dissociates the growing RNA chain

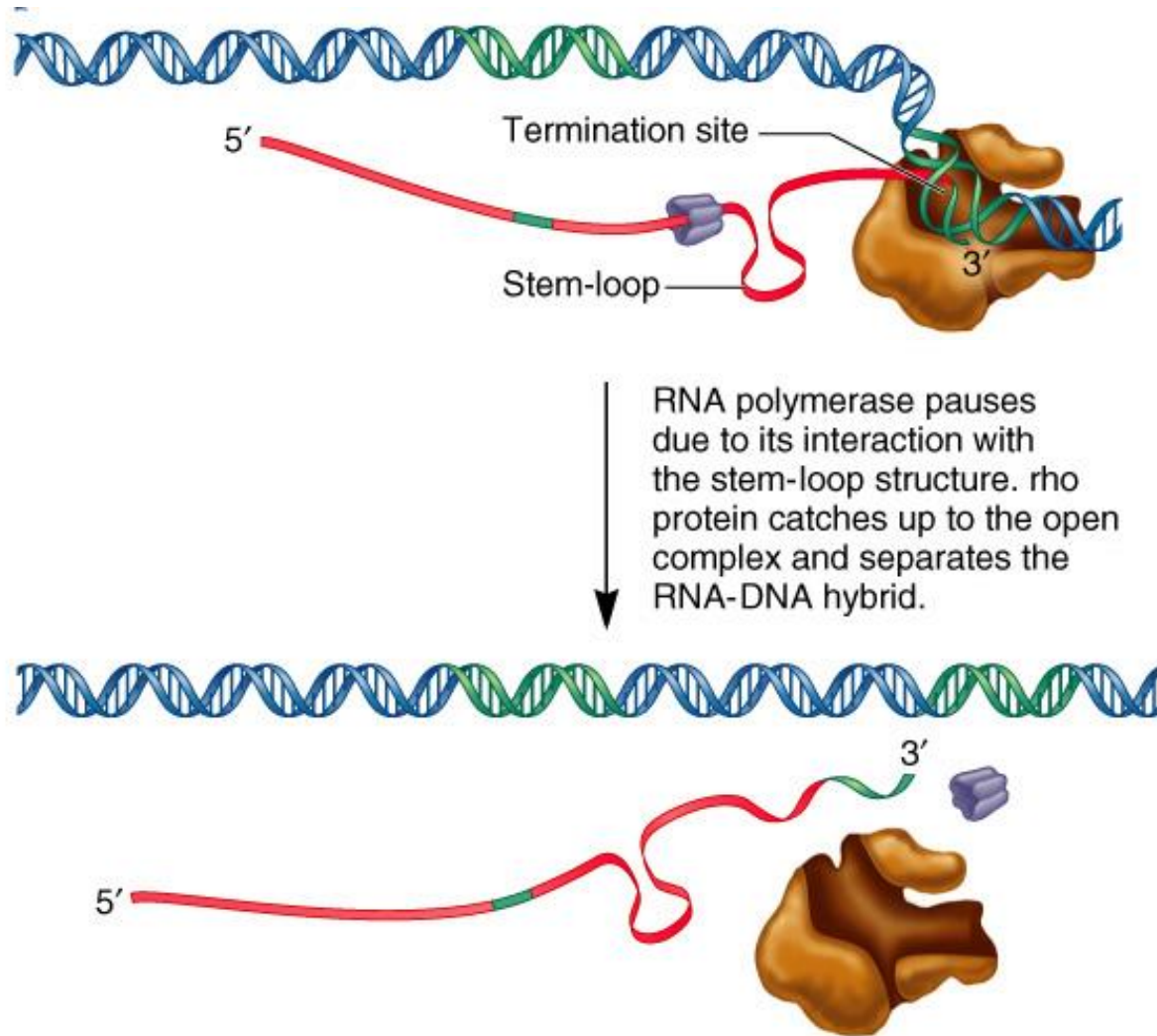
Termination

- After the polymerase transcribes the length of the **gene (or genes)**, it will stop and release the RNA transcript.
- In some cells, termination occurs at the specific and well-defined DNA sequences called **terminators**. Some cells lack such termination sequences.

Rho Dependent Termination in Prokaryotes



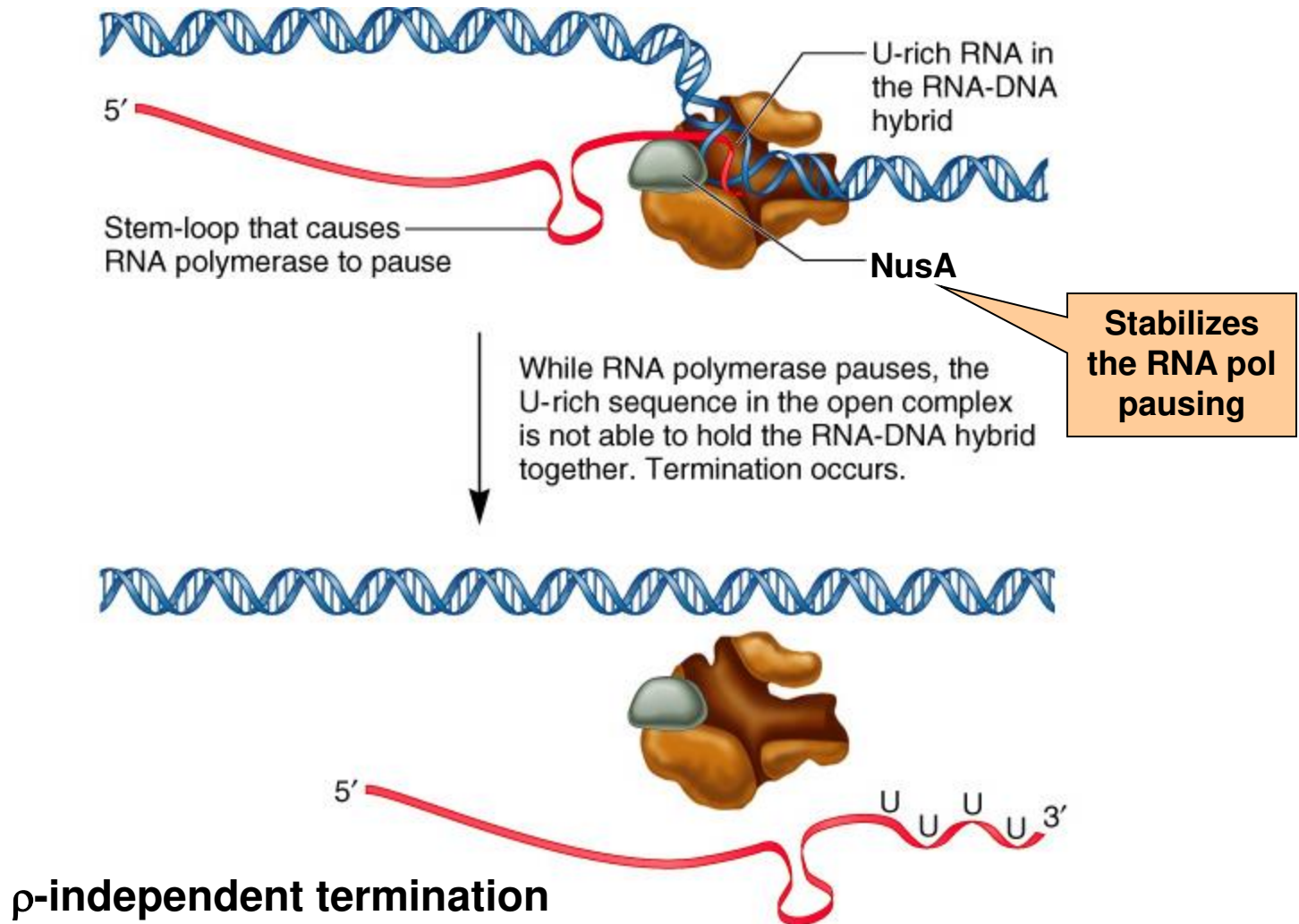
Rho Dependent Termination in Prokaryotes



ρ -dependent termination

Rho Independent Termination in Prokaryotes

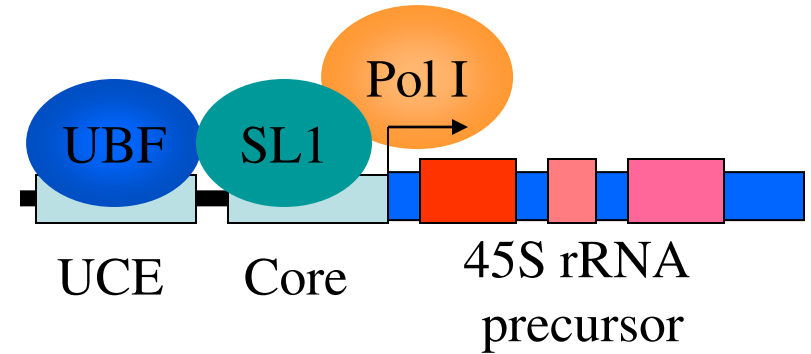
- ρ -independent termination requires two sequences in the RNA
 - A stem-loop structure upstream of 7-9 U residues



Eukaryotic Promoters

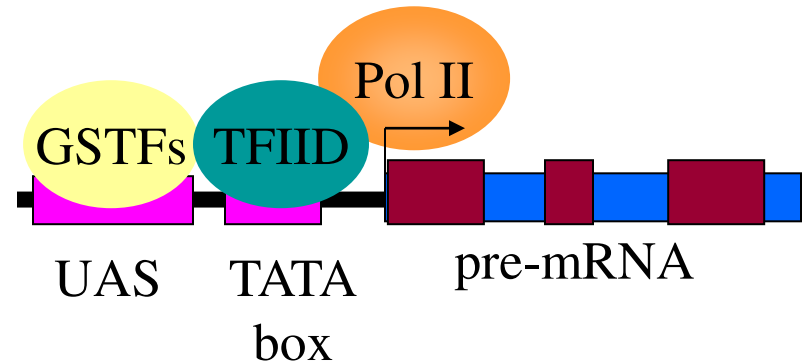
- RNA Pol I

- rRNA precursor



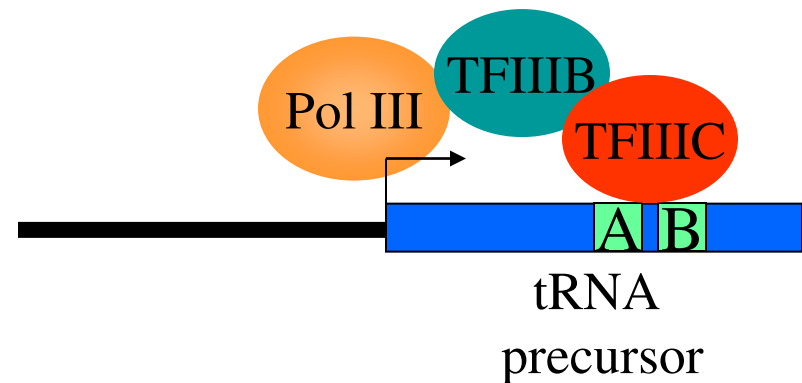
- RNA Pol II

- mRNAs,
U6 snRNA



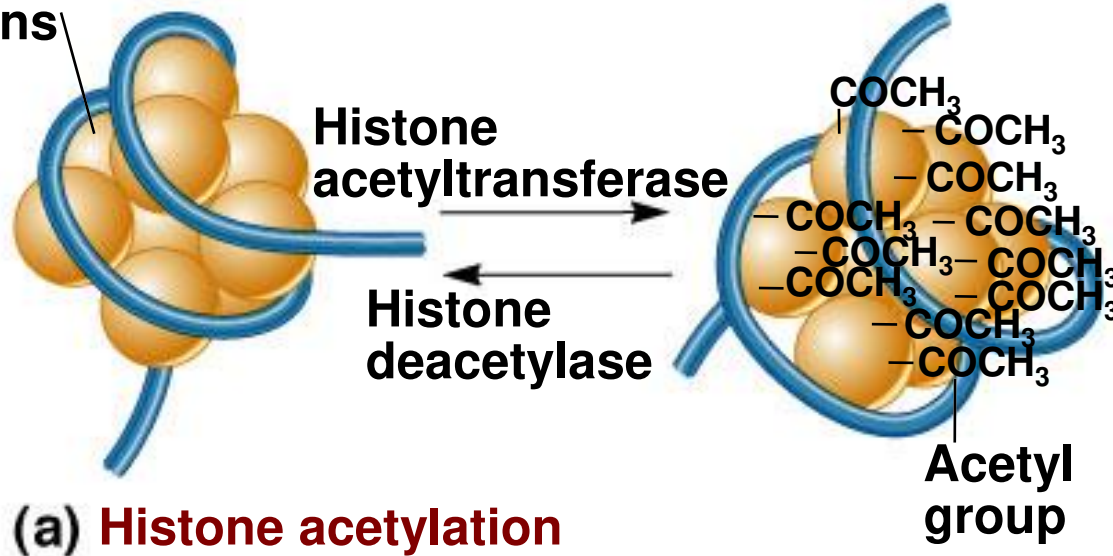
- RNA Pol III

- tRNA, 5S
rRNA, U1-U5
snRNAs



Chromatin Structure Affects Promoter Access

Core histone proteins



(a) **Histone acetylation**



ATP-dependent chromatin remodeling complex



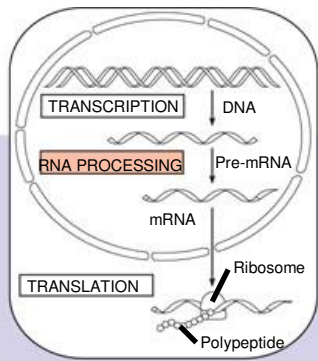
Change in the relative positions of a few nucleosomes



Change in the spacing of nucleosomes over a long distance

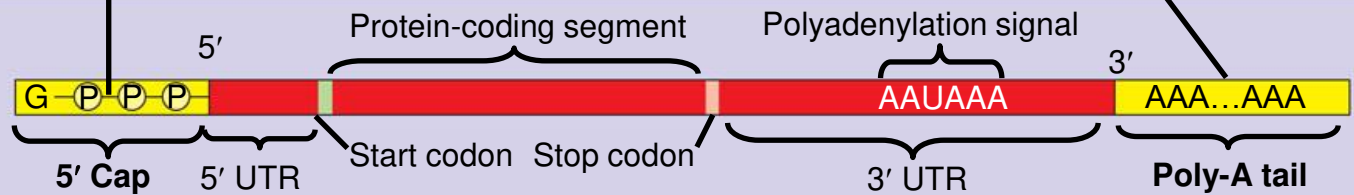
(b) **Chromatin remodeling**

RNA processing: addition of the 5' cap and poly-A tail

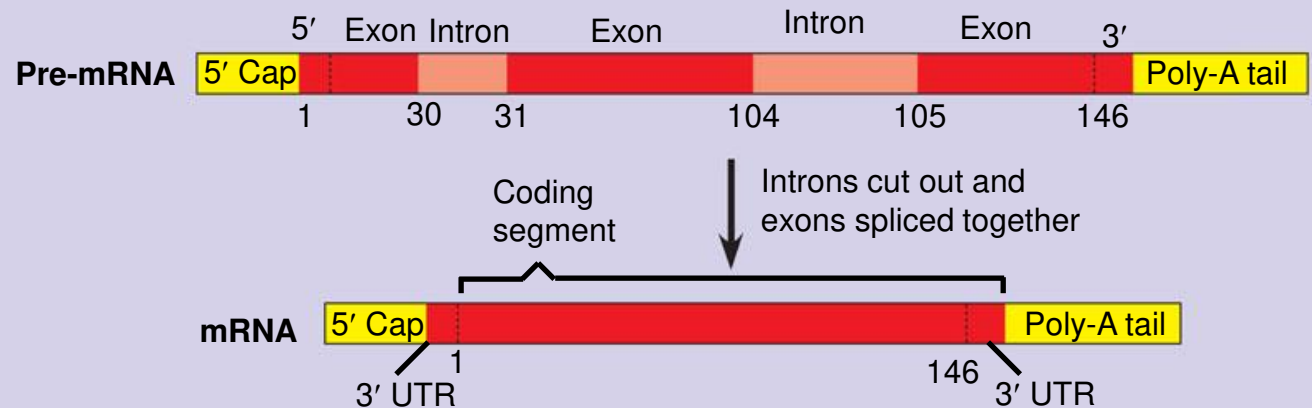
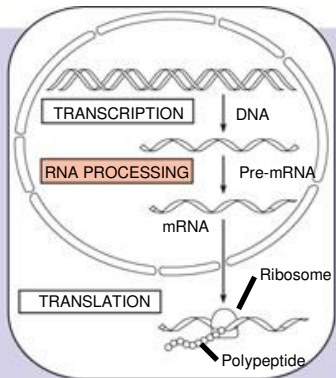


A modified guanine nucleotide added to the 5' end

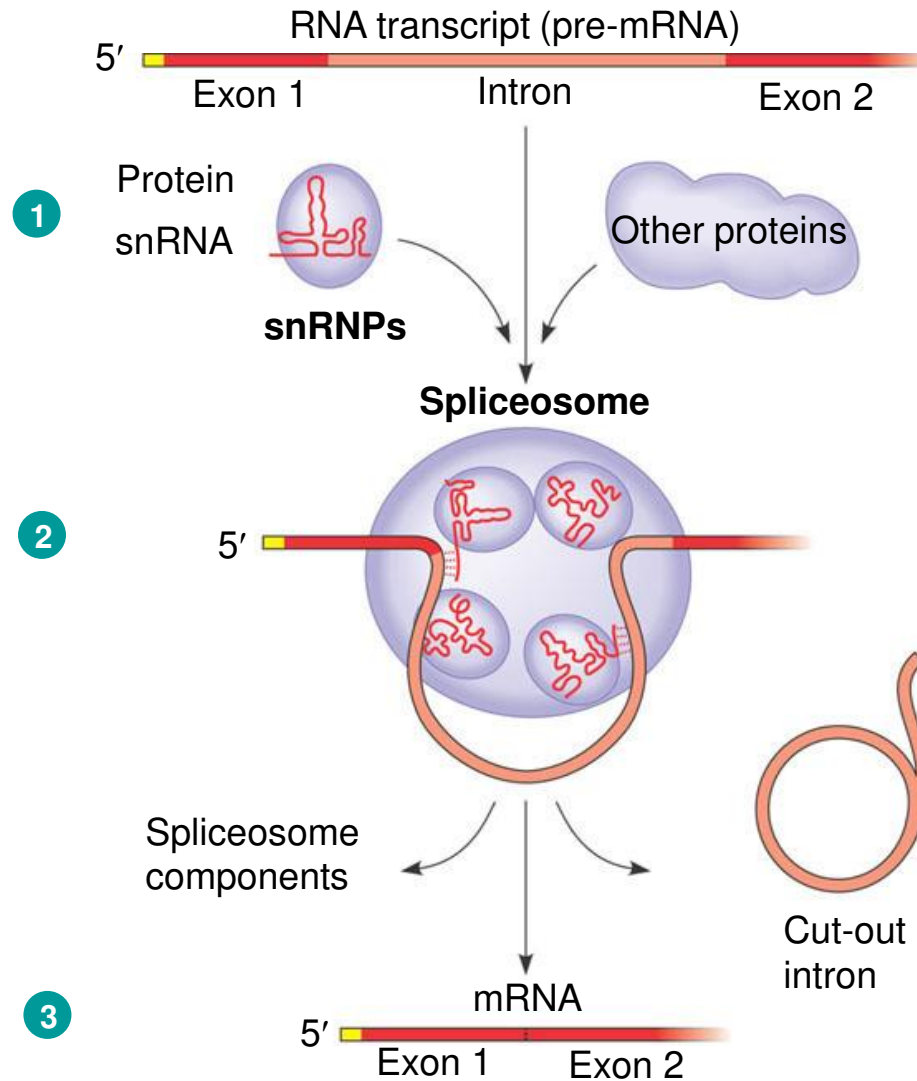
50 to 250 adenine nucleotides added to the 3' end



RNA processing: RNA splicing



The roles of snRNPs and spliceosomes in pre-mRNA splicing



Regulation of Translation