Prokaryotes	Eukaryotes
• Single DNA	• Multiple DNA
• Circular "loop of DNA"	• "Linear non-looped chromosomes"
• No nucleus	• Have a nucleus
• There are 5 DNA polymerases • DNA repair: DNA polymerase II, IV and V • DNA polymerase III: DNA polymerization at growing fork in E.coli (formation of newly synthesized DNA) • The complex of primosome (Helicase + primase) and polymerase III is known as replisome • DNA polymerase I: 5' to 3' exonuclease activity Fills the gaps between okazaki fragment	• There are 9 DNA polymerases • most of them for DNA repair • DNA polymerase Alpha (α) has high fidelity and low processivity also "the only one has primase" • Delta (δ) and Epsilon (ε) both have high processivity and fidelity and have proofreading mechanism (3' → 5' exonuclease) • Gamma (γ) has profreading mechanism and is located in mitochondria. • The polymerases do not have 5' to 3' exonucleas • DNA polymerase δ fills in the gaps
Oric: 9-mer: binding site for initiator protein called DnaA. 13-mers: AT-rich region - it facilitates separation of the double strand DNA	Oric: Several autonomously replicating sequences, each containing an 11-base-pair ARS consensus sequene (ACS) and (B1/B2/B3)
• Contain a single type of RNA polymerase • The core polymerase consists of 2 α, 1 β, 1 β' and 1 omega subunits (ω) • σ subunit guide the RNA polymerase to the promoter region "important in efficiency of RNA polymerase Not in RNA synthesis (not required for the basic catalytic activity of the enzyme) • The do not require help to initiate transcription	• Contain 3 RNA polymerase • RNA polymerase I: transcribes rRNA genes • RNA polymerase III: transcribes tRNA genes and one rRNA gene. • RNA polymerase II: transcribes protein encoding genes (mRNA) and microRNA • They require help from general transcription factors

σ subunit ← (help position the RNA polymerase correctly at the promoter) → general transcription factors

RNA polymerase ← (aid in pulling apart the 2 strands of DNA) "like helikase" → general transcription factors

Consensus sequences (The promoter):

- Prokaryotes ← (−35); TATA box (−10)
- Eukaryotes → BRE (−37 to −32); TATA box (−31 to −26); Initiator (Inr) (−2 to +4); DPE (+28 to +32)

*A promoter is "upstream" of the transcription initiation (start) site.

"اللي بكون عنده موجود بعضهم أو كلهم"

Prokaryotes	Eukaryotes
• Genes can be monocistronic or polycistronic	• Genes must be monocistronic

Operons ← (In order to coordinate the expression of all genes that share similar pathways) → Promoter proximal elements (PPE)

Prokaryotes	Eukaryotes
• mRNAs are very unstable (having a half-life of about 3 minutes)	• mRNAs are more stable (up to 10 hours, average of 30 minutes)

Mechanism of Transcription

Prokaryotes

Eukaryotes

1 Initiation

- The RNA polymerase binds to the promoter by help σ subunit and form closed promoter complex
- RNA polymerase act as helicase and form open promoter complex
- Transcription is initiated by the joining of two NTPs.
- After addition of about 10 nucleotides, σ is released from the polymerase and binds to another RNA polymerase

- TFIID binds to the promoter recruiting other proteins and forming the transcription pre-initiation complex.
- A member of this complex is TFIIH, which contains a DNA helicase
- TFIIH creates an open promoter exposing the DNA template to the RNA polymerase

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2 Elongation

- As the polymerase moves forward, it :-
  - unwinds the template DNA ahead of it
  - elongates the RNA
  - rewinds the DNA behind it

- Movement of the polymerase is activated by the addition of phosphate groups to the "tail" of the RNA polymerase
- This phosphorylation is also catalyzed by TFIIH, which also possess a protein kinase subunits.

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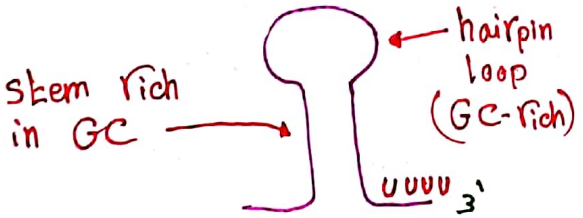
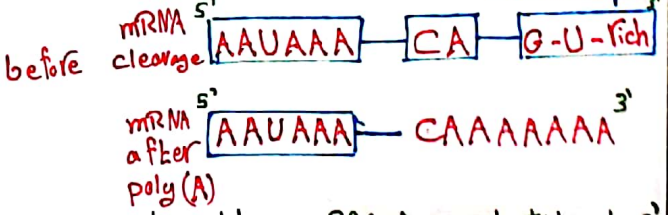
3 Termination

- Symmetrical inverted repeat of a GC-rich sequence followed by A residues
- Transcription of the GC-rich inverted repeat results in the formation of a stable stem-loop structure



- Termination is determined by a consensus sequence for termination in mRNA, which is AAUAAA followed 10-30 nucleotide downstream by a GU-rich sequence
- Termination is coupled to the process that cleaves and polyadenylates the 3'-end of the transcript



↳ adds ~200 A nucleotides to 3'