THE TRANSCRIPTION CYCLE IN BACTERIA

A) Bacterial Promoters vary in strength and sequence, but Have certain Defining Features

- The enzyme RNA polymerase catalyzes the process of transcription.

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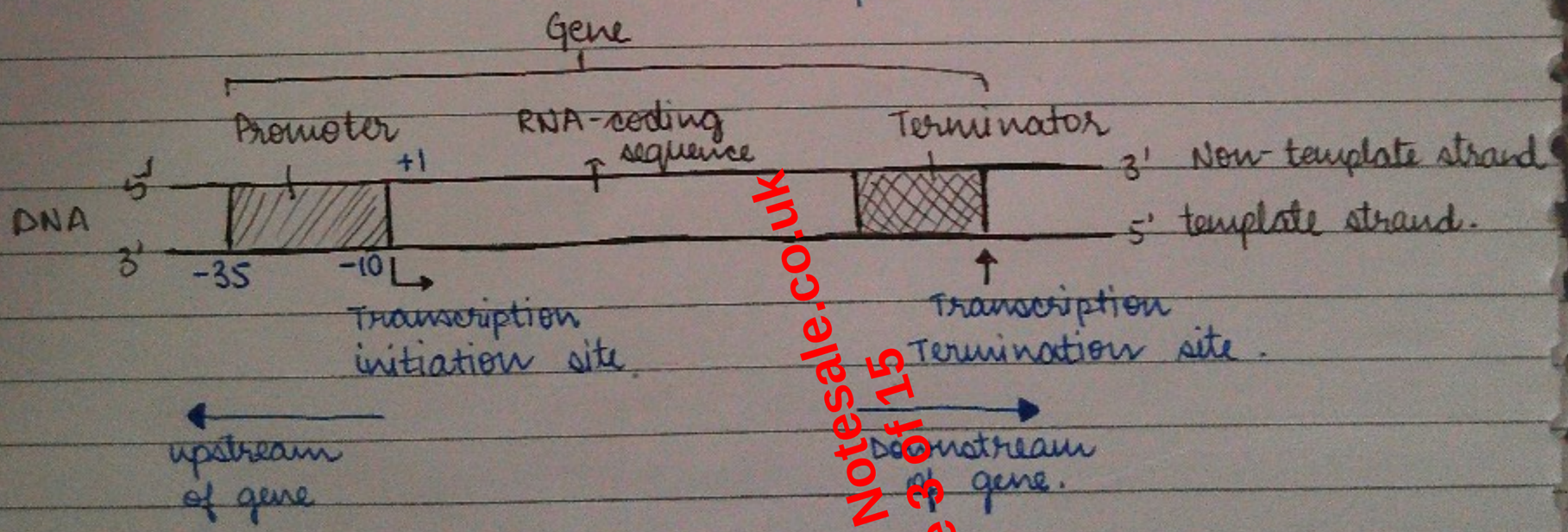
DNA-dependent RNA polymerase

(because it uses a DNA template for the synthesis of an RNA chain).

- In bacteria, RNA pol. is responsible for unwinding.
- In Euk., unwinding is done by other proteins that bind to DNA near the start point for transcription

- Unlike DNA polymerases, RNA polymerases can initiate new RNA chains; in other words, no primer is needed.



- The promoter is upstream of the coding sequence, the terminators downstream.
- The coding sequence begins at nucleotide +1.
- Promoter consists of two conserved sequence, each of six nucleotides, are separated by a non-specific stretch of 17-19 nucleotides.

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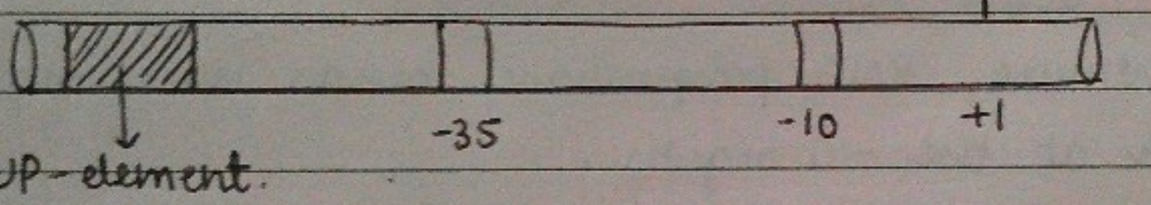
- In case of E.Coli, the predominant σ factor is called σ^{70}.
- Vast majority of σ^{70} promoters contain recognizable -35 and -10 regions.

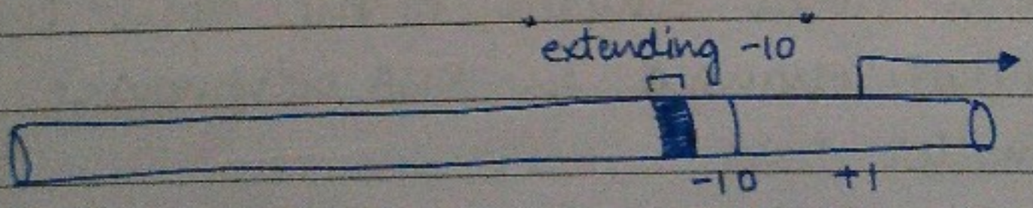
→ The correlation b/w promoter strength and sequence explains why promoters are so heterogeneous: some genes need to be expressed more highly than others and their promoters are likely to have sequences closer to the consensus

- **UP-element.**



→ An additional DNA element that binds RNA polymerase is found in some strong promoters, for eg- those directing expression of the ribosomal RNA (rRNA) genes. This is called UP-element.

→ It increases polymerase binding by providing an additional specific interaction b/w the enzyme and the DNA.



→ Another class of σ^{70}- promoters lacks a -35 region and instead has a so-called "**extending -10**" element. This comprises a standard -10 region with an additional short sequence element at its upstream end.

→ Extra contacts made b/w polymerase and this additional sequence element compensate for the absence of a -35 region.