

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:**
 - 1- Both processes use DNA as the template.
 - 2- Phosphodiester bonds are formed in both cases.
 - 3- Both synthesis directions are from 5' to 3'.
- **Differences between replication and transcription:**

| | replication | transcription |
|-----------|----------------|----------------|
| template | double strands | single strand |
| substrate | dNTP | NTP |
| primer | yes | no |
| Enzyme | DNA polymerase | RNA polymerase |
| product | dsDNA | ssRNA |
| base pair | A-T, G-C | A-U, T-A, G-C |

- The requirements for transcription

Template and Enzymes:

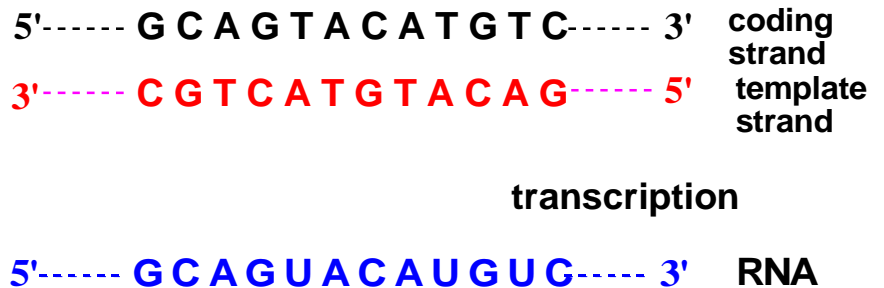
- The whole genome of DNA needs to be replicated, but only small portion of genome is transcribed in response to the development requirement, physiological need and environmental changes.

1.1 Template

The template strand is the strand from which the RNA is actually transcribed. It is also termed as antisense strand.

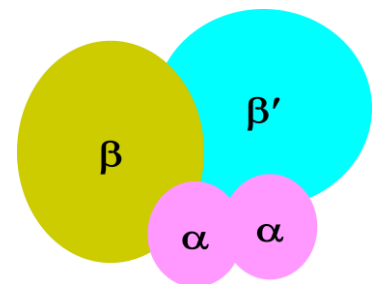
The coding strand is the strand whose base sequence specifies the amino acid sequence of the encoded protein. Therefore, it is also called as sense strand.

-DNA regions that can be transcribed into RNA are called structural genes.



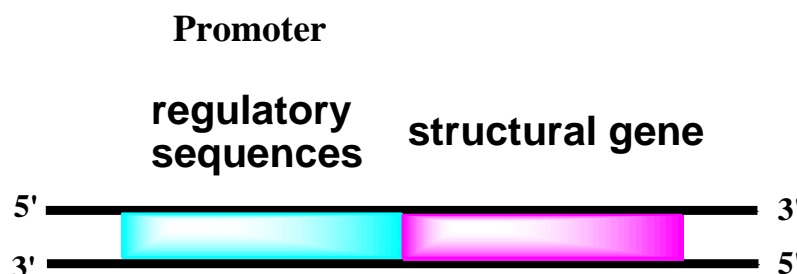
2-RNA Polymerase:

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



4- Recognition of Origins

- Each transcriptable region is called operon.
- The promoter is the DNA sequence that RNA-pol can bind. It is the key point for the transcription control.

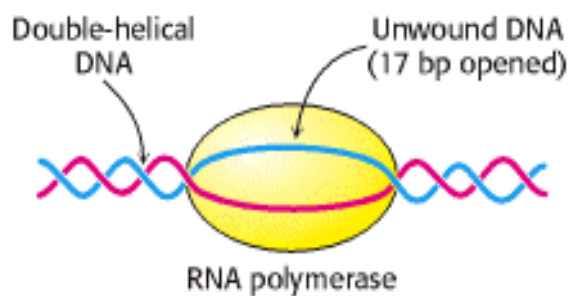


The steps of Transcription:

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

a. Initiation

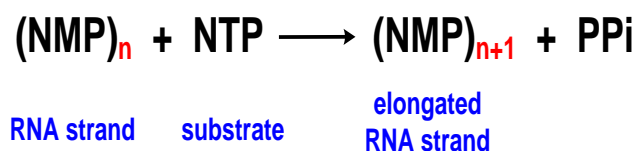
- RNA-pol recognizes the TTGACA region, and slides to the TATAAT region, then opens the DNA duplex.



b. Elongation

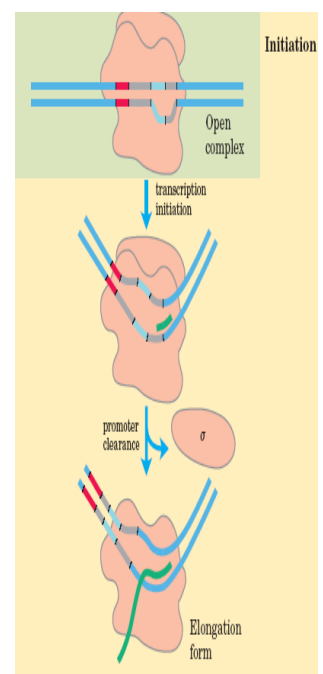
- The release of the σ subunit causes the conformational change of the core enzyme. The core enzyme slides on the DNA template toward the 3' end.

Free NTPs are added sequentially to the 3' -OH of the nascent RNA strand



c. Termination

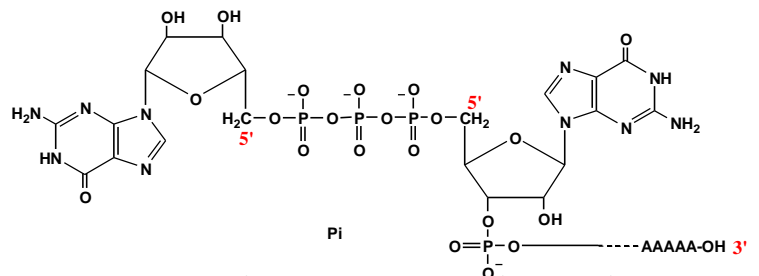
- The RNA-pol stops moving on the DNA template. The RNA transcript falls off from the transcription complex.
- **Post-Transcriptional :**
- **Modification**
- The nascent RNA, also known as primary transcript, needs to be modified to become functional tRNAs, rRNAs, and mRNAs.
- The modification is critical to eukaryotic systems.



Modification of hnRNA

- Primary transcripts of mRNA are called as heteronuclear RNA (hnRNA).
- hnRNA are larger than matured mRNA by many folds.
- Modification includes
 - 1- Capping at the 5'- end
 - 2- Tailing at the 3'- end
 - 3- mRNA splicing

1 . Capping at the 5'- end



- The 5'- cap structure is found on hnRNA 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.

2 . 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.

2 . mRNA splicing

The matured mRNAs are much shorter than the DNA templates

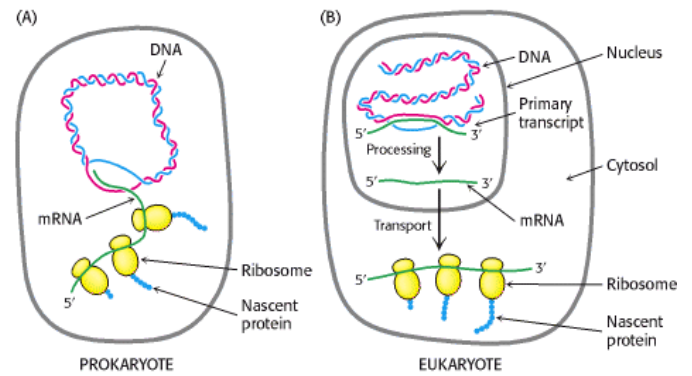
- Split gene :

The structural genes are composed of coding and non-coding regions that are alternatively separated.

- 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.



PROKARYOTE

EUKARYOTE

PROKARYOTE

EUKARYOTE