DNA Transcription

Transcription, is the process of creating an equivalent RNA copy of a sequence of DNA.

Transcription is the first step leading to gene expression.

Transcription is the first of several steps of DNA based gene expression in which a particular segment of DNA is copied into RNA by the enzyme RNA polymerase. Both DNA and RNA are nucleic acids.

into Single stranded RNA Double stranded DNA must be TRANSCRIBED

1. mRNA "messenger

made from DNA in nucleus…travels out of nucleus and finds a ribosome.

2. tRNA "transfer

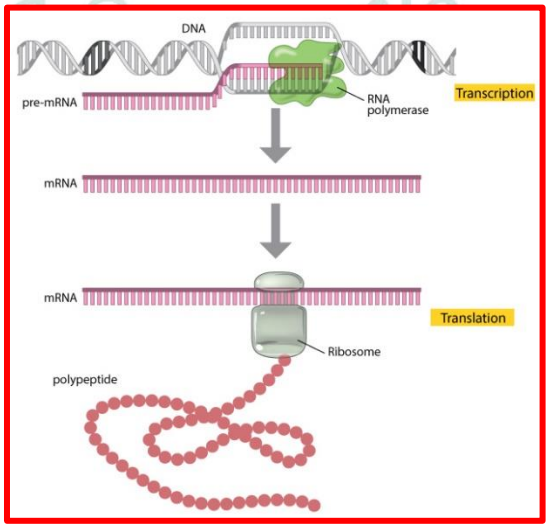
brings amino acids to the ribosomes; found in cytoplasm

3. rRNA "ribosomal

part of the ribosome; this is where proteins are made.

How does the DNA get made into RNA and that made into Protein?

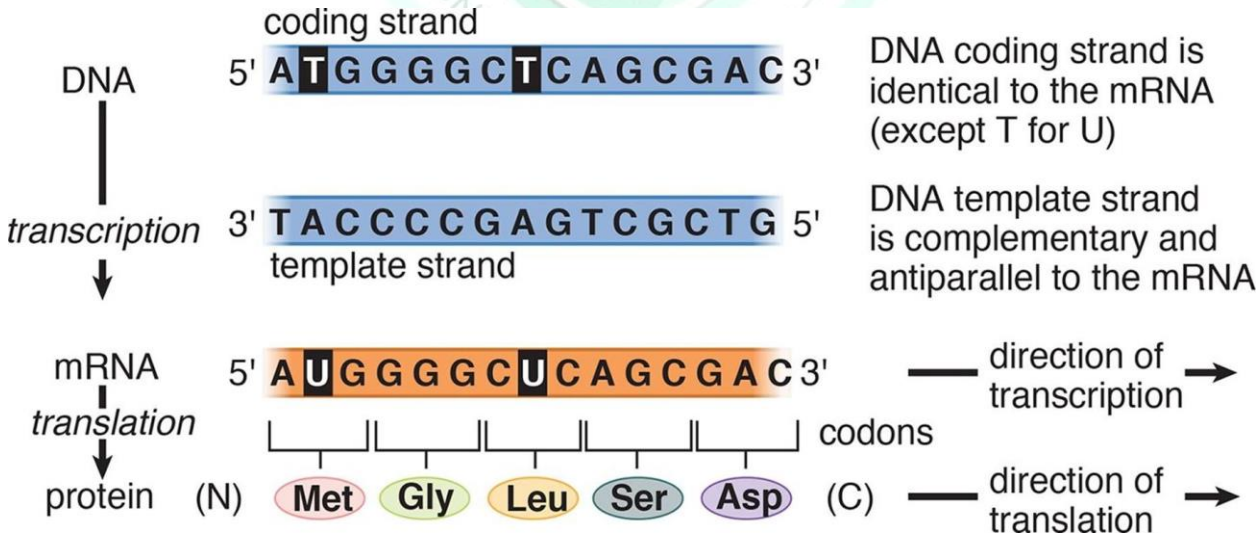
During transcription, the enzyme RNA polymerase (green) uses DNA as a template to produce a pre-mRNA transcript (pink). The pre-mRNA is processed to form a mature mRNA molecule that can be translated to build the protein molecule (polypeptide) encoded by the original gene



Transcription in prokaryote

- RNA molecules are produced by copying part of a nucleotide sequence of DNA into a complementary sequence in RNA. This Process is called transcription.
- Transcription requires the enzyme RNA polymerase.
- During transcription, a DNA sequence is read by RNA polymerase, which produces a complementary, antiparallel RNA strand.
- Transcription results in an RNA complement that includes Uracil (U) instead of thymine (T).

Coding and Non-Coding Strands



Stages of Transcription in Prokaryote

• Initiation

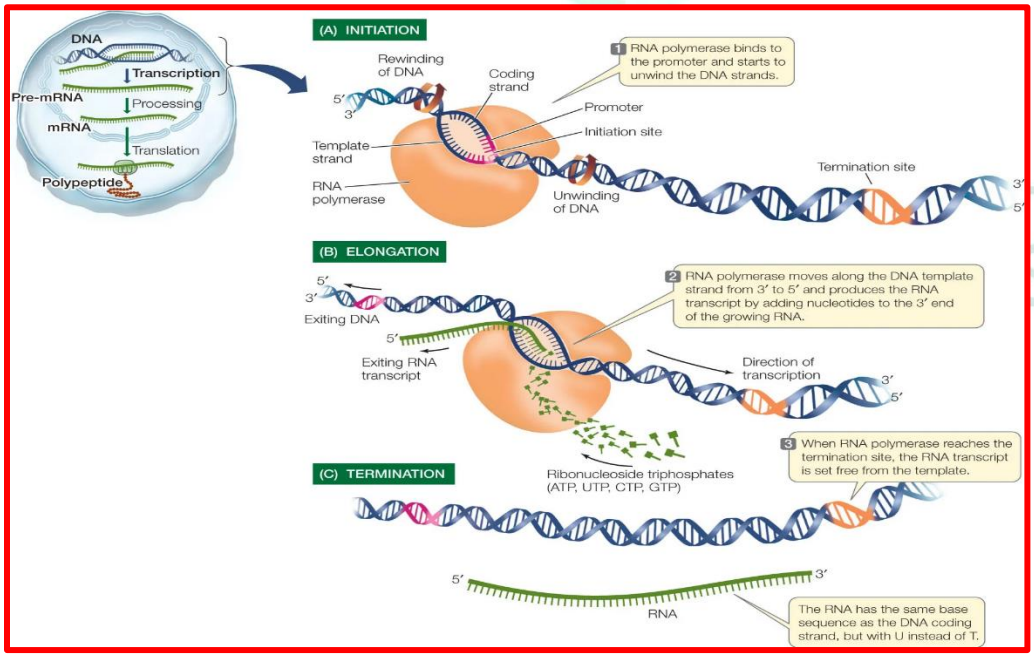
RNA polymerase attaches to the DNA molecule and moves along the DNA strand until it recognizes a promoter sequence(Sequence on DNA 10 and 35 bases upstream of start site). These are known as the transcription start sites. The DNA double helix then unwinds and all the bases on each of the DNA strands are exposed. This acts as a template for a new mRNA strand.

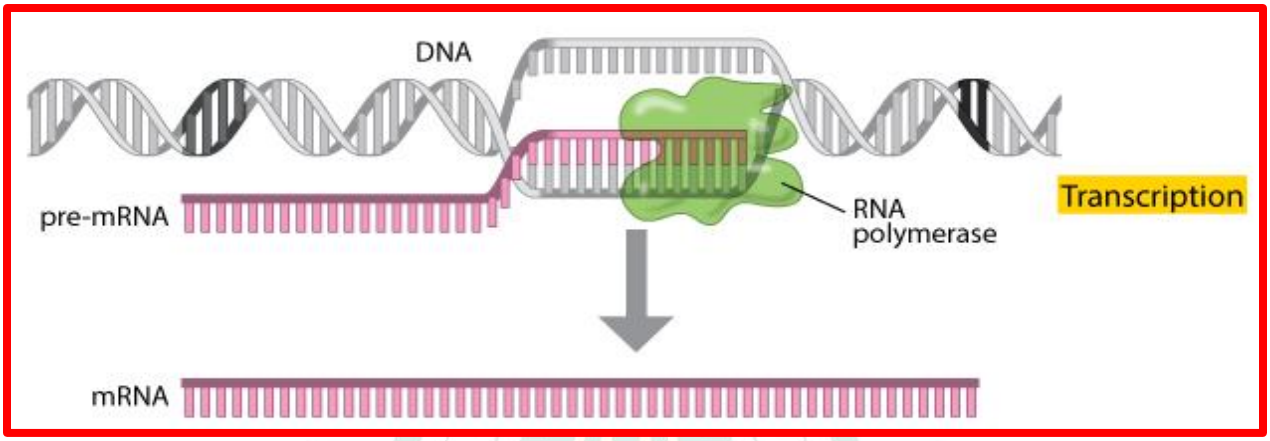
• Elongation

- Ribonucleotides are added to the template strand that enables the growth of mRNA growth.

• Termination

- RNA polymerase encounters a terminator sequence and the transcription stops. RNA polymerase then releases the DNA template.





(5′) C G C T A T A G C G T T T (3′) DNA nontemplate (coding) strand

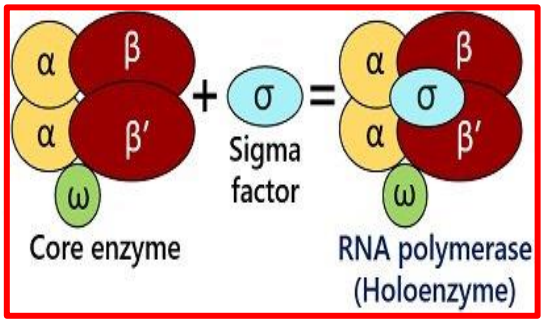
(3′) G C G A T A T C G C A A A (5′) DNA template strand

(5′) C G C U A U A G C G U U U (3′) RNA transcript

Figure 26-2
Lehninger Principles of Biochemistry, Fifth Edition

RNA polymerase in prokaryotic

- In most prokaryotes, a single RNA polymerase species transcribes all types of RNA. RNA polymerase "core" from E. coli consists of five subunits: two alpha (α) subunits of 36 kDa, a beta (β) subunit of 150 kDa,
- a beta prime subunit (β′) of 155 kDa,
- and a small omega (ω) subunit.
- Sigma (σ) factor



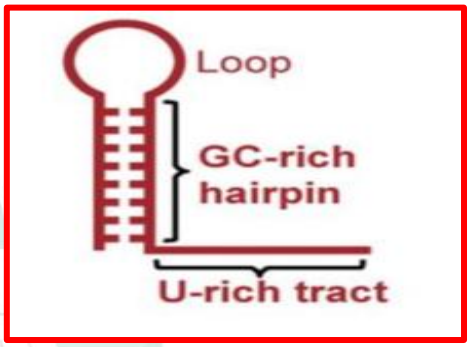
*Smaller protein

*Guides RNA polymerase to target DNA sequence

* Sigma factor released after open complex (unwinds DNA at promoter).

Transcription Termination

- **Rho-dependent termination**



- Rho (ρ) factor binds to mRNA
- Slides along mRNA to polymerase
- Breaks polymerase, mRNA off of DNA
- The ρ factor, a hexamer, is a ATPase and a Helicase

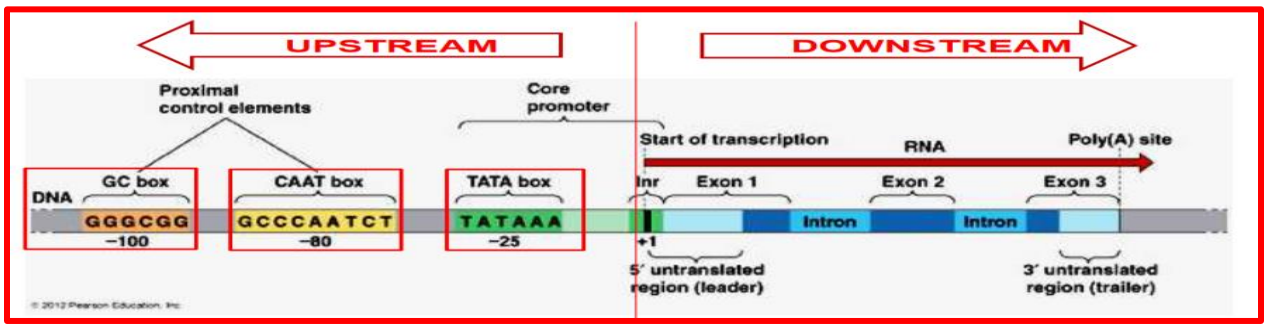
- **Rho-independent termination**

- The termination signal is a stretch of 30-40 nucleotides on the RNA
- transcript, consisting of many GC followed by a series of U.
- • The sequence specificity of this nascent RNA transcript will form
- particular stem-loop structures to terminate the transcription.

Promoters

TATA box (Hogness Box)

Sequence of nucleotides (TATAAA) is found centered about 25 nucleotides upstream of the transcription start site. This core promoter consensus sequence is called the TATA, or Hogness, box.

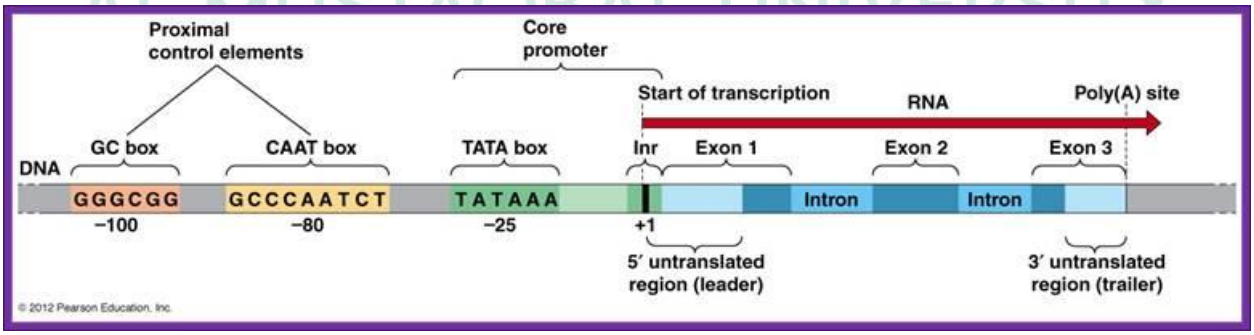


Transcription factors:

- RNA-pol II does not bind to the promoter sequences directly.
- RNA-pol II associates with six transcription factors.
- TFII A, TFII B, TFII D, TFII E, TFII F and TFII H.

Eukaryotic Transcription

- Promoters
- Much more complex than those found in bacteria.
- These are consensus sequences located at the upstream regions of Coding strand.
- **1) TATA box (Hogness Box)**
- Very similar to the prokaryotic TATA box,except the sequence is slightly different (TATAAA) and it is located in between25 to -30.
- **2) CAAT box**
- Located in between -70 to -80.
- Always contains CCAAT.
- **3) GC box**
- Usually has the sequence GGGCGG and is typically found at -110.



Enhancers:

- Enhancers elements are the sequences located in a variety of regions of a gene both upstream and downstream of the transcription start site and even within the transcribed portions of some genes.
- Enhancers increases the transcription rate by several folds.

Elongation

- During elongation, **the transcription machinery needs to move histones out of the way every time it encounters a nucleosome**.
- TFIIF remains associated with RNA Pol-II throughout elongation.
- The activity of the RNA poly-II is greatly enhanced by proteins called Elongation factors

Termination

- When the RNA Polymerase transcribes the terminator region of the DNA, the polymerase releases the mRNA
- The termination sequence is AATAAA followed by GT repeats.

RNA polymerase in Eukaryote

Name	Can be found in	Transcribes
RNA Polymerase I	All Eukaryotes	Large rRNAs
RNA Polymerase II	All Eukaryotes	mRNA, snoRNAs, some snRNAs and miRNAs
RNA Polymerase III	All Eukaryotes	tRNAs, small rRNAs, some snRNAs and miRNAs
RNA Polymerase IV	Plants	some siRNAs
RNA Polymerase V	Plants	RNAs important in heterochromatin formation