

Subject: Genetics Lec no: 8(part1) Done By: Mahmoud Al Qusairi



Gene expression

By Dr. Walaa Bayoumie El Gazzar

Gene expression - The process where agene is used to synthesize proteins is a some sort products.

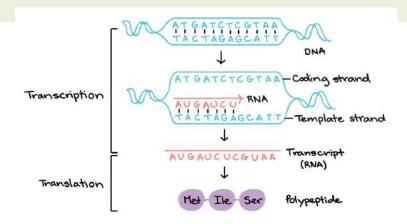
expression = (transcription + transilation)

 Definition: Gene expression can be defined as the gene (DNA) undergoes transcription into mRNA that can translate the encoded genetic information into protein. mRNA سے عند ما مسیری (ransilation و یعملی probeins الآبکون عرفت information خطف mRNA محمد مع مع mRNA محمد المحمد مع مع mRNA محمد المحمد ا

Transcription (RNA synthesis)

Eranscription Quane (gene) strand of DNAL DNA-dependent RNA aide mRNA ender polymenase (RNAP)

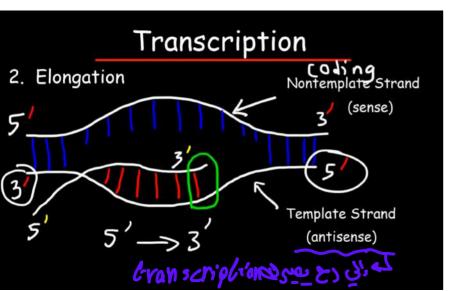
> Definition: Transcription is the synthesis of RNA using DNA as a template by <u>an enzyme</u> <u>DNA –dependent RNA polymerase</u> or RNA polymerase (<u>RNAP</u>)



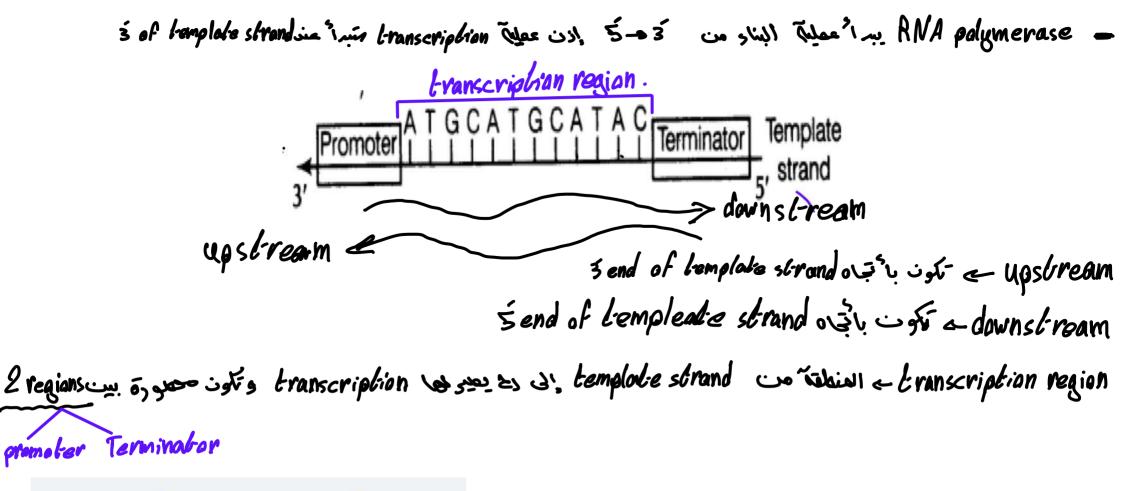
Features of transcription:

 One strand of the two DNA strands is transcribed only, this strand is called **template** strand (anti-sense), because it provides template for ordering the sequence of nucleotides in an RNA transcript, sequence of nucleatides in MA • The other strand (non-transcribed) is called coding strand (sense strand), because its sequence is the same as the newly synthesized RNA transcript (except for thymine is substituted by uracil)

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- The DNA template strand is read in <u>3\to 5\</u> by RNA polymerase enzyme and <u>the new RNA is</u> <u>synthesized in the direction of 5\ to 3\</u>.
- Upstream means in the 3` direction of the template strand.
- Downstream means in the 5` direction of the template strand.
 - A line of the sequence transcribed by the enzyme RNAP. It is the region between the promoter and the terminator.



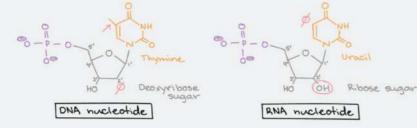
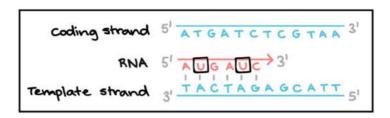
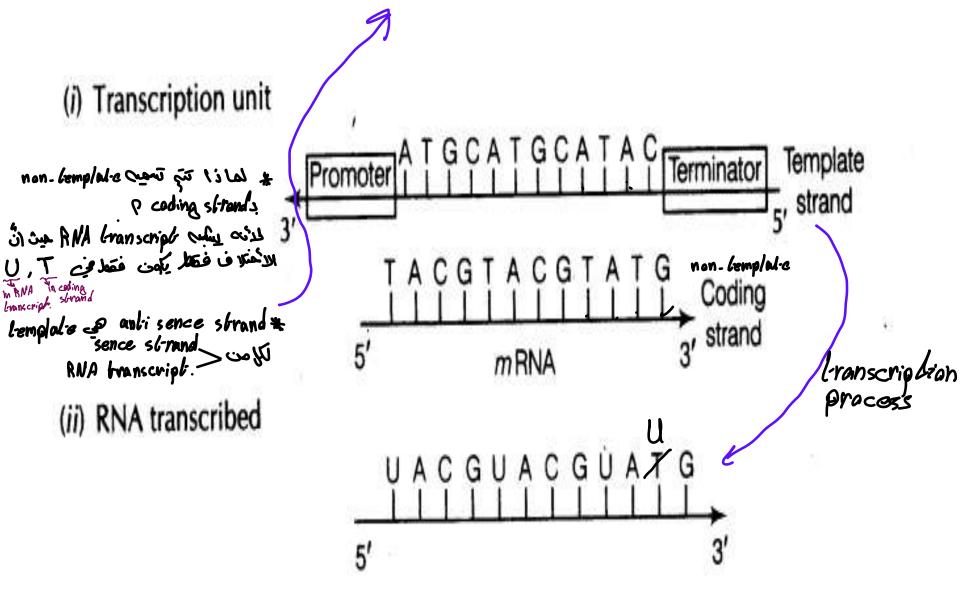


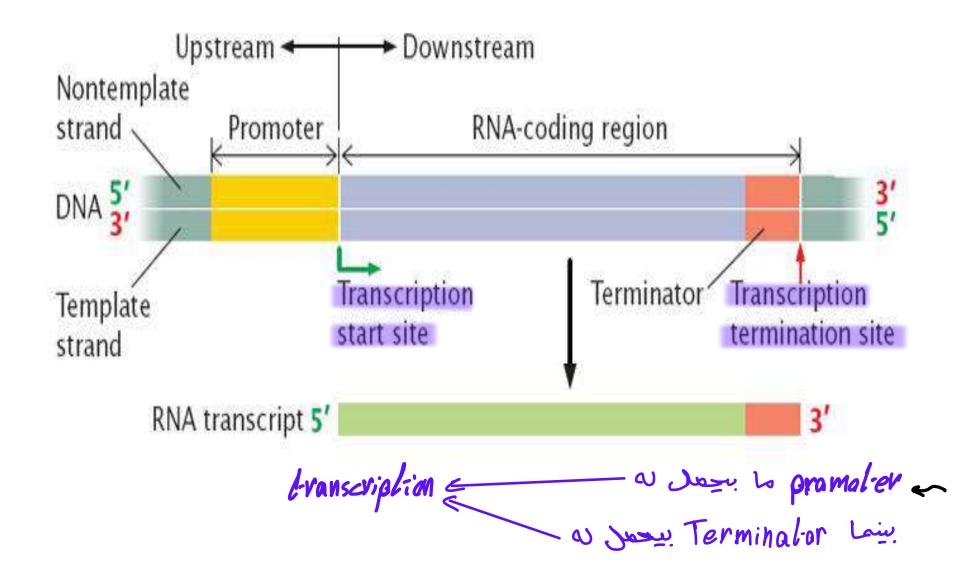
Image based on similar image from CyberBridge ³.

RNA nucleotides are similar to DNA nucleotides, but not identical. They have a ribose sugar rather than deoxyribose, so they have a hydroxyl group on the 2' carbon of the sugar ring. Also, in RNA, there is no T (thymine). Instead, RNA nucleotides carry the base uracil (U), which is structurally similar to thymine and forms complementary base pairs with adenine (A).



The RNA transcript is nearly identical to the **nontemplate**, or **coding**, strand of DNA. However, RNA strands have the base uracil (U) in place of thymine (T), as well as a slightly different sugar in the nucleotide. So, as we can see in the diagram above, each T of the coding strand is replaced with a U in the RNA transcript.





Constant A promoter is the DNA sequence that <u>initially</u> <u>binds</u> the <u>RNA</u> <u>polymerase</u> (together with any initiation factors required). i.e. Nucleotide sequence in DNA to which RNA polymerase binds to begin transcription.

Sequences trigger the elongating polymerase to dissociate from the DNA and release the RNA chain it has made.

of the transcription region <u>" that codes for the</u> <u>initial base of the mRNA"</u>. It is designated +1. Adjacent nucleotides are given positive numbers that increase as we go downstream the transcription unit. • The nucleotide in the promoter adjacent to the +1 nucleotide is designated -1 and adjacent nucleotides are given negative numbers that increase as we go upstream the promoter. Terminator and promober - transkription region Terminator + promober + transkription region & transkription Unittranscription **Unit** Sequence of he nucleotides in DNA that codes for a single RNA molecule, along with the sequences necessary for its transcription; normally contains а promoter, an RNA-coding sequence, and a terminator. (i.e. includes the promoter, the transcription region, and the terminator)

هذا السلايد نفس تمريع side davb side الذي تعن منا أخته ولكن بعينة مختلفة من أخته ولكن بعينة مختلفة من أبغل التدرب على بعض الانشائة التي تأتي بعين مختلفة .

- O The DNA nucleotide encoding the beginning of the RNA chain is called the transcription start site and is designated the "+1" position.
- Sequences in the direction in which transcription proceeds are referred to as **downstream** from the start site. Likewise, <u>sequences preceding the start</u> site are referred to as **upstream** sequences.
- When referring to a specific position in the upstream sequence, this is given a negative value. Downstream sequences are allotted positive values.

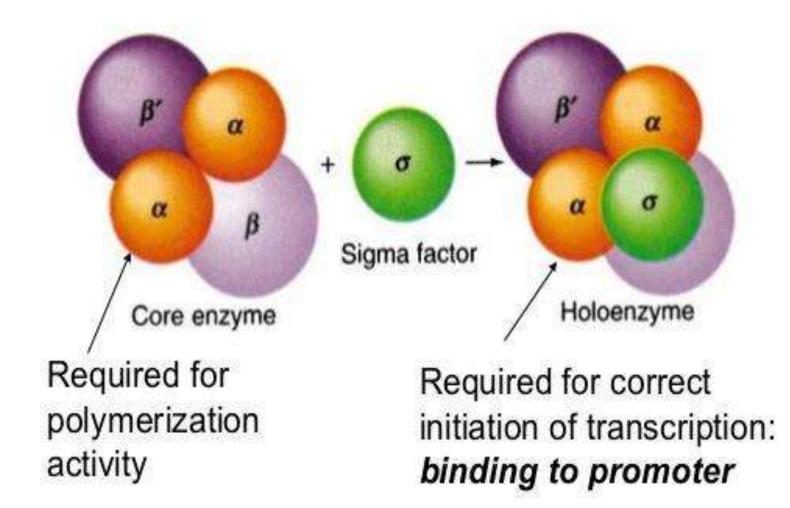
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Transcription in prokaryotes:

- <u>All types of RNA is synthesized by a specific</u> <u>enzyme called RNA polymerase</u> for the short RNA primers needed for DNA replication are synthesized by a primase enzyme.
- Structure of prokaryotic RNA polymerase:
- It is a <u>multi-subunit</u> enzyme formed of <u>core</u> <u>enzyme</u> and <u>sigma factor</u>

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Core enzyme

- Core enzyme: two identical α subunits (regulatory subunits) and two β not identical (β & β') and one ω chain. One of the β subunits (β) binds to the DNA and the other (β') is responsible for the formation of phosphodiester bond. DNA bemplate من والعالي والعالي المعالي ال
- RNA polymerase enzyme <u>lacks specificity</u>, that is, it cannot recognize the promoter region on the DNA template.

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 The σ subunit ("sigma factor"): It enables RNA polymerase to recognize promoter regions on the DNA. The σ subunit plus the core enzyme make up the holoenzyme. [Note: Different σ factors recognize different groups of genes.] (region جند RNA and recognize (جند (an And content of the second s

core enzyme + 6 supunit = holdenzyme

N.B.: The antibiotic binds to the β subunits of RNA polymerase and inhibits RNA synthesis in prokaryotes as it interferes with the formation of the first phosphodiester bond. Rifampicin is useful in the treatment of tuberculosis.

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Steps of RNA synthesis in prokaryotes:

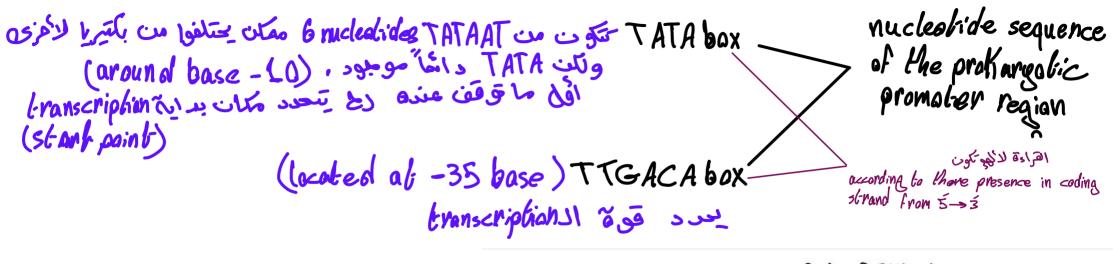
- It is divided into three phases: <u>initiation</u>, <u>elongation</u> and <u>termination</u>.
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 - It involves the binding of RNA polymerase to a specific region on the DNA known as the promoter region formed of specific base sequence. It needs a specific protein factor called sigma factor (σ) that recognizes and sigma factor (σ) that recognizes and specific base sequence.

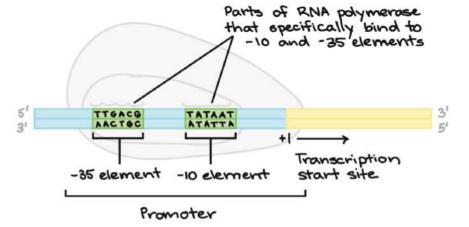
polymerase starts transcription at the TATA box then RNA polymerase starts transcription at the start point (+1) it is the first base transcribed as RNA.

 The characteristic nucleotide sequences of the prokaryotic promoter region (as indicated in the coding strand in the 5 to 3 direction) include:

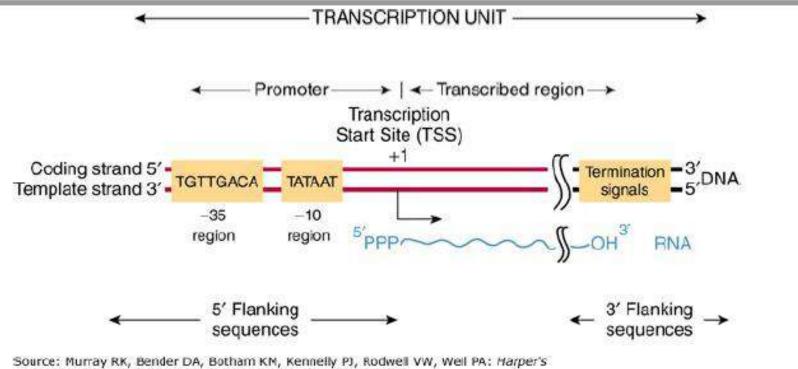
TATA box: It is formed of six nucleotides (TATAAT) and is located 10 bases upstream (i.e. usually occurs around base-10) to the start point (+1 point). It determines where transcription starts.

The (TTGACA) box: this sequence is 35 bases upstream to the start point (located at -35 base i.e. centered about 35 bases to the left of the transcription start site) .<u>It determines the</u> <u>frequency of transcription</u>





The -10 and the -35 elements get their names because they come 35 and 10 nucleotides before the initiation site (+1 in the DNA). The minus signs just mean that they are before, not after, the initiation site.

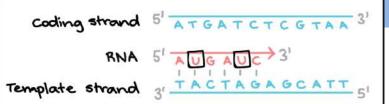


Illustrated Biochemistry, 29th Edition: www.accessmedicine.com

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- In prokaryotes only **one** type of RNA polymerase synthesizes the three types of prokaryotic RNA.
- The binding of RNA polymerase to DNA template produce <u>local unwinding</u> of the DNA double helix to expose the bases.
- The enzyme begins to synthesize RNA in the direction of 5^{\to} 3^{\with} the base sequence complementary to that of the DNA template strand. <u>Sigma factor is</u> released after initiation of transcription.
- The core enzyme moves along the DNA template uses ribonucleoside triphosphate (ATP, GTP, CTP& UTP) and releases pyrophosphate



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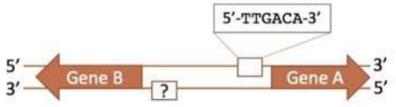
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Unlike DNA polymerase, RNA polymerase does not require a primer and has intrinsic helicase activity, therefore no separate enzyme is needed to unwind the DNA (in contrast to DNA polymerase).

RNAP not only initiates RNA transcription, it also guides the nucleotides into position, facilitates attachment and elongation, has intrinsic proofreading (It doesn't not posses a proof reading feature as efficient as the DNA polymerase but it posses the capability of correct some misadded nucleotide as well) and replacement capabilities, and <u>termination</u> <u>recognition capability</u>. **C18.** Two genes on a bacterial chromosome are transcribed in opposite directions as shown. Transcription of both genes is initiated by RNA polymerase coupled with sigma protein 70. The sequence of a -35 promoter element for gene A exactly matches the consensus sense strand sequence: 5'-TTGACA-3'. Which of these sequences



would you be most likely to find on the indicated strand (?) at the -35 position of gene B?

- A. 5'-TGTCAA-3'
- B. 5'-TTGACA-3'
- C. 5'-ACAGTT-3'
- D. 5'-AACTGT-3'

What is the consensus sequence of the bacterial promoter?

TTGACA ----- 17±1 ----- TATAAT

TAATAT ----- 17±1 ----- ACAGTT