



تنسوه من دعائکم ،،،

# RNA Structure & synthesis

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مجهول : Team leader

والشكر لجميع من ساهم في اخراجها بالصورة التي هي عليه وأخص بالشكر:

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وجنودنا المجهولين 😳

## **RNA STRUCTURE & SYNTHESIS**

## <u>OVERVIEW</u>

- Deoxyribonucleotides (DNA) are the <u>genetic</u> master plan of an organism
- DNA serves as template ... thru RNA( working copies )
   ( this process is called transcription )

### $\checkmark$ AND then bigining of the synthesis of :

- a) messenger RNAs are translated into sequence of amino acids,
- b) <u>ribosomal RNA</u>,
- c) transfer RNA.
- SO the RNA are three types

### - the transcription is highly selective (MCQ)

 $\checkmark$  This selectivity is the reason of biochemical differentiation

### highly selective

**Explanation** : many transcripts , are made of some region of DNA . In other region , Few or no transcripts are made .

- Reasons

- **1.** signals sequence in DNA instruct RNA polymerase where & How to Start & stop transcription .
- 2. regulatory proteins.

ultimate result : Biochemical differentiation .

**the RNA transcripts undergo various modifications (**terminal additions, base modification , trimming, internal segmental removal )

then by <u>splicing</u> convert the inactive primary transcripts into a functional molecule . (MCQ)

Q- splicing can make the transcript into functional form (T)

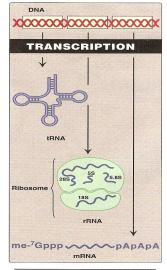


Figure 30.1 Expression of genetic information by transcription. [Note: RNAs shown are eukaryotic.] me-<sup>7</sup>Gppp = <sup>7</sup>-methylguanosine triphosphate "cap," described on p. 414. AAA = poly-A tail, described on p. 414.

## STRUCTURE OF RNA :

- <u>3 types (participate in protein synthesis):</u>
  - 1. ribosomal RNA(rRNA)
  - 2. transfer RNA(tRNA)
  - 3. messenger RNA(mRNA)

In differ from each other in size, function, and structural modification.

Like DNA they are <u>Unbranched polymeric</u> molecules composed of <u>mononucleotie</u> joined together by <u>phosphodiester bonds</u>. (MCQ)(IMP)

DNA	RNA(MCQ)
bigger	smaller
deoxyribose	ribose
thymine	uracil
double	Single strand (capable to folding into complex structure )
More stable	Less stable

## ■ NOTE :

- in eukaryotes small RNA molecules found in the nucleus (snRNAs)

### A. <u>Ribosomal RNA</u> :

- rRNA make up 80% of total RNA in the cell (most)(MCQ)
- Found in <u>ribosomes</u> (sites for protein synthesis) in association with <u>several proteins</u> (not histones)

In prokaryotes there are three rRNA species : (23S, 16S, 5S)
In eukaryotes there are four rRNA species : (28S, 18S, 5.8S, 5S) (there is question on them) (MCQ)

Q-5S are found only in eukaryotes (F)

\*Note: S=Svedberg unit which is related to <u>MW & shape</u> of the compound . (MCQ)

## B. Transfer RNA :

- tRNA make up 15% of total RNA in the cell.

is the <u>smallest RNA molecules</u> (4S) ( always come and he said smallest in amount but the true is smallest in size ), & have (74-95) nucleotides residues .

- at least one specific tRNA molecule for one amino acid  $\rightarrow$  so, at least there are 20 species of tRNA .

### tRNA molecules contain :

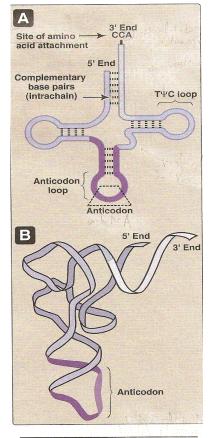
a)unusual bases (e.g. pseudouracil TΨ C loop {not uracil }) b)extensive <u>intrachain</u> base pairing (not interchain) (MCQ)

- each tRNA serve as <u>adaptor molecule</u> (MCQ) that carries its specific amino acid that attached by covalent bond to 3'-end (CCA) to the site of protein synthesis (NOT from nucleus to cytoplasm). there it recognizes the genetic code word on an mRNA, which specifies the addition of its amino acid to the growing peptide chain

### Prokaryotic rRNAs

### Eukaryotic rRNAs

## Figure 30.2 Prokaryotic and eukaryotic rRNAs.



**Figure 30.3** A. Characteristic tRNA structure. B. Folded tRNA structure found in cells.

### C. Messenger RNA :

- mRNA comprises only about <u>5%</u> of RNA in the cell .(smallest in amount not size)
- <u>Most heterogenous & base sequence type</u> (500 to 6000 nucleotide).
- <u>carries information from nuclear DNA to the cytosol where it</u> used as template for protein synthesis . (not like tRNA) .

- <u>Eukaryotic mRNA (</u> NOT prokaryotes ) contains :(always come in exams )

- a. long sequence of Adenine (poly-A tail ) on the 3 –end of RNA (only one P)
- b. one molecule of 7-methyguanosine "cap" on the 5-end attatched " backword " (5' → 5') ( here we have triphosphate linkage )

	3' Untrar trailing se	
	anslated sequence	
Сар	Coding region	Poly-A tail
Gppp-	msm	рАрАрАрАрА-ОН
$\mathcal{L}^{i}$	5'-End	3'-End

Figure 30.4 Structure of eukaryotic messenger RNA.

## TRANSCRIPTION OF PROKARYOTIC GENES :

- eukaryotes & prokaryotes differ in;
- 1) RNA polymerase .
- 2) signals that control trancription
- 3) varieties of modification that RNA transcripts .

## A - Properties of prokaryotic RNA polymerase :

■ In bacteria, one species of RNA polymerase synthesize all of the RNA <u>except</u> for the short RNA primers which synthesize by specialized enzyme ,<u>primease</u>. (MCQ) (very important )

(RNA primer needed for DNA replication)

**RNA polymerase** – <u>multisubunit enzyme(MCQ)</u> that is:

1- recognize a nucleotide sequence (the promoter region) at the beginning of the length of DNA that is to be transcribed.

2- next, makes a complementary RNA copy of DNA template strand.

3- then, recognize the end of DNA sequence to be transcribed (the termination region).

- RNA is synthesized from its **5-end to its 3-end antiparallel** to its DNA template strand. (MCQ)
- the template is copied as in DNA synthesize :

DNA		RNA
G	specifies	С
С	specifies	G
Т	specifies	А
А	specifies	U

But

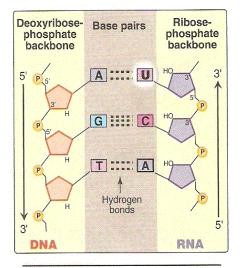


Figure 30.5 Antiparallel, complementary base pairs between DNA and RNA. • <u>transcription unit</u>: extend from the promoter to termination region

• **primary transcript:** product of the process of transcription by RNA polymerase.

Q- Promoter >>> initiation of transcription.

<u>\* transcription by RNA polymerase involves a core enzyme and several</u> <u>auxillary proteins:</u>

### **<u>1-core enzyme :</u>**

- Four enzyme's peptide subunits,  $2\alpha$ ,  $1\beta$ , and  $1\dot{\beta}$ .

- responsible for  $\hat{5} \rightarrow \hat{3}$  RNA polymerase activity

- lacks specificity, that is, it cannot recognize the promoter region on DNA template (MCQ)

## Holoenzyme $\sigma$ $\alpha$ $\alpha$ $\beta$ $\beta'$ Core enzyme

#### Figure 30.6 Prokaryotic *RNA polymerase*.

### 2-holoenzyme :

- holoenzyme =  $\sigma$  (sigma) subunit +core enzyme
- $\sigma$  subunit (sigma factor) function :
- $\checkmark$  Enable RNA polymerase to recognize the promoter region on the DNA

Note : (Different  $\sigma$  factor recognize different groups of genes)



Q- Concerning prokaryotic transcription :

>Sigma ( $\sigma$ ) factor enables RNA polymerase to recognize the promoter region.

Q- Holoenzyme (except)> Its Rho-factor recognizes the termination signal.

### **<u>3-termination factor :</u>**

- Some regions on DNA that signal the termination of transcription are recognize by **RNA polymerase** itself

- others are recognized by specific termination factors e.g. rho ( $\rho$ ) factor of E.coli .

## **B** . Steps in RNA synthesis :

- Three phases :

1) initiation . 2) elongation . 3) termination .

within DNA molecule : both strand serve as template for RNA .
within a specific stretch of double helix : only one strand serve as template .

\_..\_..\_..\_..\_..\_..\_..\_..\_..\_..\_..

\_\_\_\_\_

## 1) Initiation :

- binding of **RNA polymerase holoenzyme** (MCQ) to the promoter region .

- <u>consensus sequence</u> (MCQ) of the promoter region are <u>highly conserved</u> (MCQ) . { so , different promoters contain very similar or identical Sequences }

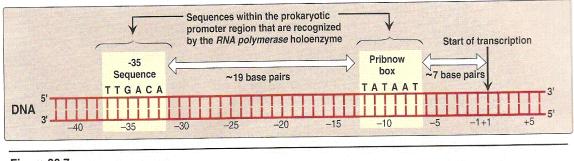


Figure 30.7 Structure of the prokaryotic promoter region.

• <u>Those that are recognized by prokaryotic RNA polymerase σ factor :</u>

## <u>a) Pribnow box :</u>

- stretch of <u>six nucleotides (5 TATAAT- 3)(MCQ)</u> centered about <u>eight</u>
   <u>to ten nucleotide</u> (in the figure he said 7 nucleotide) to the <u>left</u> of the Transcription start site that code for the <u>initial</u> base of the mRNA
  - $\checkmark\,$  The regulatory sequence are in 3 to 5 in template strand & 5 to 3 in nontemplate strand .

• **NOTE :** <u>( Regarding the transcription site ):</u>

- (up stream) (prior) assigned a negative number . e.g : pribnow box -9.
- at & after (downstream) assigned a positive number . e.g : the first base at the transcription site is +1 .

i.e : ( there is no base designated "0") (MCQ)

## B) - 35 sequence :

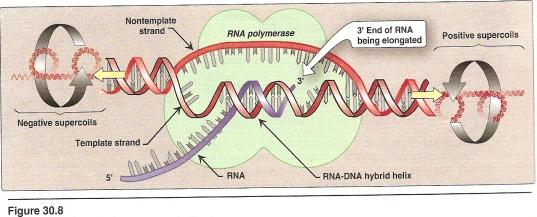
 A consensus sequence (5-TTGACA – 3), which is centered about 35 bases To the <u>left</u> of the transcription start site . (MCQ)

• Note :

✓ A mutation in either Pribnow box or the – 35 sequence can affect the transcription of the gene controlled by mutant promoter .

## 2) Elongation:

- Once the promoter region has been recognized by the holoenzyme, *RNA polymerase* begins to synthesize a transcript of the DNA sequence (usually beginning with purine), & the  $\sigma$  subunit is released. (MCQ).
- Unlike DNA polymerase, <u>RNA polymerase</u>: .(always come in exams)
  - a. <u>does( not)</u> require a primer
  - b. <u>has( no) known endonuclease or exonuclease activity</u>. It, therefore, <u>has( no ) ability to repair</u> mistakes in the RNA, as does *DNA polymerase* during DNA synthesis.(always come in exams )
  - *RNA polymerase* uses **ribonucleoside triphosphats**, & releases pyrophosphate (Tor F) each time a nucleotide is added to the growing chain.



Local unwinding of DNA caused by RNA polymerase.

### • Note :

- As in DNA synthesis, two high-energy bonds are thus used for the addition of each nucleotide.
- The binding of the enzyme to the DNA template result in local unwinding of the DNA helix. (MCQ)

- This process can generate supercoils that can be relaxed by DNA topoisomerases I & II..

Q- Regarding to Prokaryotic transcription >>> Supercoils that relaxed by DNA topoisomerase I & II.

## 3) Termination:

- The process of elongation of the RNA chain continues until a termination signal is reached.
- An additional protein, ρ (rho) factor, may be required for the release of the RNA product (ρ- dependent termination). Alternatively, the tetrameric *RNA polymerase* can, in some instance, recognize termination regions on the DNA template (ρ- independent termination).



- ✓ protein not enzyme (☺MCQ)
- ✓ have some enzymatic activity
- $\checkmark$  requires the participation of an additional protein,  $\rho$  **factor**. (MCQ)
- $\rho$  factor binds to <u>a C-rich region near the 3'-end</u> of the newly synthesized RNA, & migrates along behind the *RNA polymerase* in the <u>5' $\rightarrow$ 3' direction</u> until the termination site is reached.

\_...\_..

### ■ Note :

- Rho factor has <u>ATP- dependent RNA-DNA helicase activity</u> (MCQ) (very important ).that : hydolyzes ATP,& uses the <u>energy to unwind the 3'-end of the transcript</u> from the template.

 $\checkmark$  This facilitates the movement of the protein along the RNA/DNA duplex.

- At the termination site,  $\rho$  factor displace the DNA template strand, facilitating the dissociation of the RNA molecule.

\_..\_..\_..

So, what you should know it : ☺
1) protein not enzyme .
2) bind to <u>a C-rich region near the 3'-end .</u>
3) Rho factor has *ATP- dependent RNA-DNA helicase* activity

## **b. Rho- independent termination :**

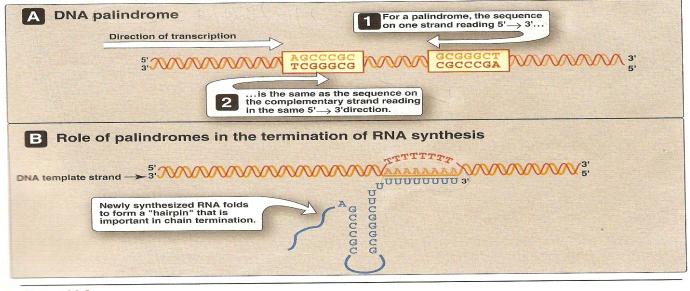


Figure 30.9

ho-independent termination of transcription. A. An example of a palindrome in double-stranded DNA. A transcribed DNA palindrome codes for RNA that can form a hairpin turn.

### \* requires that the newly synthesized RNA have two important structural features:

### First,

### - the RNA transcript must be able to form <u>a staple hairpin turn</u>.(MCQ)

Q- Regarding to termination Prokaryotic transcription >>> RNA form a stable hairpin turn.

• when we ask what is the function of <u>a stable hairpin turn</u>? Answer : it slows down the progress of *RNA polymerase* & causes it to pause temporarily.

• Note : <u>A palindrome</u> is a region of <u>a double-stranded DNA</u> in which each of the two strand contain stretches that have the same nucleotide sequence when read <u>in the same</u> (for example,  $5' \rightarrow 3'$ ) direction

• Note: <u>as a result of the presence of a palindrome</u> The hairpin turn of the RNA is complementary to a region of the DNA template near the termination region exhibits <u>two-fold symmetry(MCQ)</u>

<u>Secondary structure of RNA is stabilizes by a lot of G &C in the</u> <u>base of the stem Of hairpin . (MCQ) ( always come in exams ) (IMP)</u>



beyond the hairpin turn,

- the RNA transcript contains a string of <u>U's</u>. The bonding of <u>U's</u> to the corresponding DNA template <u>A's</u> is <u>weak</u>. This facilitates the separation of the newly synthesized RNA from its DNA template, as the double helix "zips up" behind the *RNA polymerase* 

<u>Rivision</u>: (<u>Rho- independent termination</u>) : -> :
<u>staple hairpin turn</u> \*\* <u>two-fold symmetry</u>
\*\* <u>Secondary structure of RNA is stabilizes by a lot of G &C in the base of the stem Of hairpin</u>
\*\* <u>beyond the hairpin turn</u>.
the RNA transcript contains a string of <u>U's</u>. The bonding of <u>U's</u> to the corresponding DNA template <u>A's</u> is <u>weak</u>

## 4) Action of antibiotics:

- some antibiotics prevent bacterial cell growth by <u>inhibiting</u> <u>RNA synthesis</u>.

### ■ Note : Dactinomycin:

- known to biochemists as actinomycin D.

- It bind to the DNA template & interferes with the movement of the *RNA polymerase* along the DNA.

- was the first antibiotics to find <u>therapeutic</u> application in tumor chemotherapy (MCQ) ■ Note : rifampin :( MCQ) رکز علیه کثیر دائما یجي ورکز انه ما یأثر eukaryotes

- inhibits the initiation of transcription by binding to the  $\underline{\beta}$ -subunit of prokaryotic RNA polymerase (Not eukaryotes) (MCQ) ( always come ), thus interfering with the formation of the first phosphodiester bond .

- Is useful in the treatment of tuberculosis

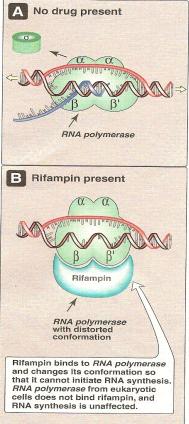


Figure 30.10 Inactivation of *RNA polymerase* by rifampin.

ما أشبه الليلة بالبارحة أتذكر في هذه اللحظة أول مذكرة كتبت سبحان الله كيف تمر الأيام سراعا <u>لا تنسونا من دعائكم</u> <u>المحاضرة الأولى في هذا الباب ------ > Done</u>