SOS in Biochemistry, Jiwaji University, Gwalior M.Sc. II Semester (2019-20) Paper BCH 205: Fundamentals of Molecular Biology (Unit II)

➤The information for making proteins is stored in DNA.

➤There is a process (transcription and translation) by which DNA is converted to protein.

➢By understanding this process and how it is regulated we can make predictions and models of cells.

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Replication m	RNA (protein synthesis)
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Transcription (RNA synthes	is)
	Protein



Gene expression refers to a process by which information(s) encoded in DNA structure is read out into a gene product (that may be a RNA or a proteín).

# **Gene Expression**

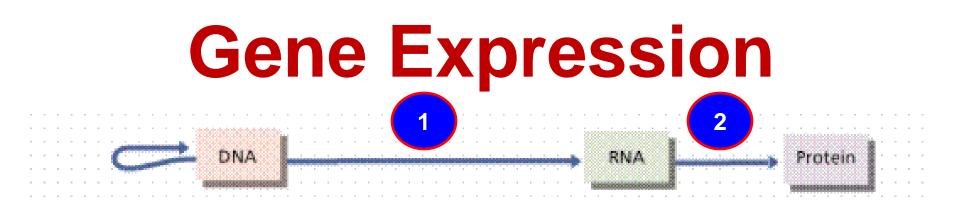
➢Gene differs from other forms of genetic information because they are expressed.

➢Gene expression involves taking the information from the gene and using it to generate a gene product which may be RNA or protein.

≻In its simplest form, gene expression can be summarized by the Central Dogma of molecular biology, which states that genetic information flows unidirectionally from DNA through RNA to proteins.

>Only Gene found over the genome possess the capability to get expressed. **Rest** part of the genome plays more or less some role in regulation.

Gene expression involves taking the information from the gene and using it to generate a gene product (RNA or protein).



# There are 4 major events that occur during the process of gene expression

- Transcription major
- RNA processing (for fine tuning)
- Translation major
- Protein processing (for fine tuning)

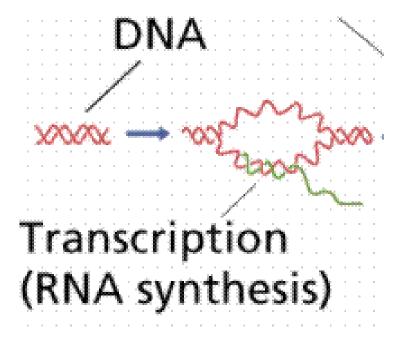
# WHY THE PROCESS IS NAMED AS TRANSCTIPTION?

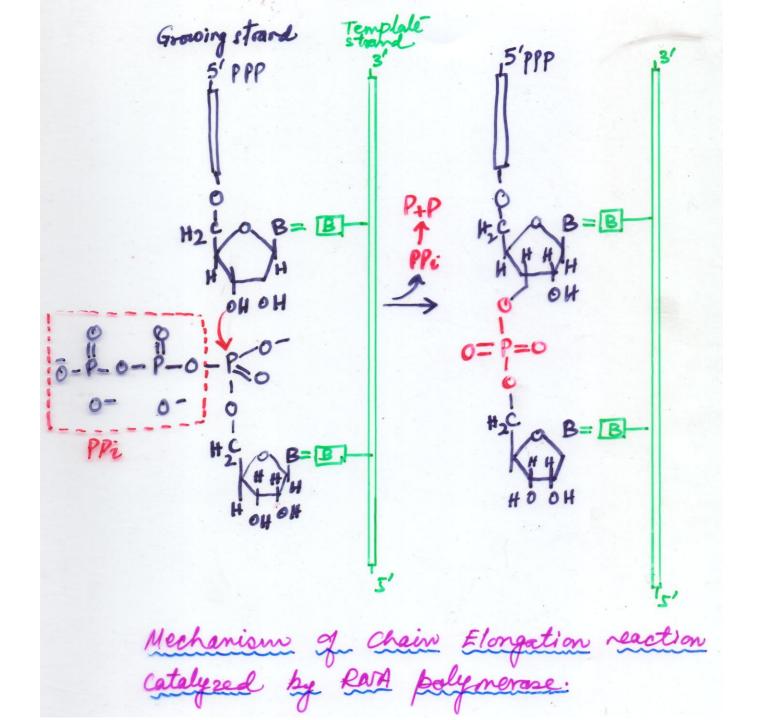
# प्रतिलेखन

1.किसी आलेख, पत्र या पुस्तक आदि से कोई चीज़ ज्यों का त्यों उतारने की क्रिया या भाव

 भाषण या संकेत लिपि में अंकित तथ्यों या टिप्पणियों के आधार पर पढ़ने योग्य लिखित प्रति तैयार करना;
(ट्रांसक्रिप्शन)।

# **BASIC FEATURES**

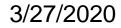




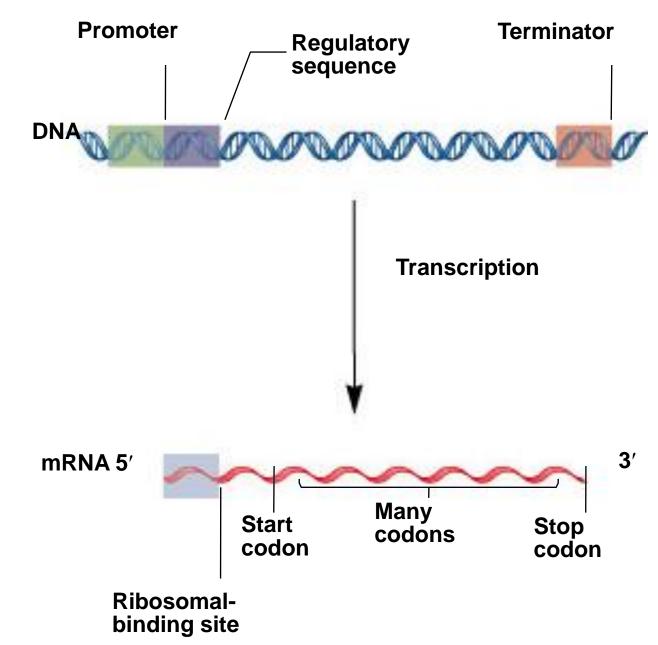
# $nNTP + XTP \qquad \xrightarrow{DNA, RNA Polymerase} (NMP)_n - XTP + nPPi$ $Mg^{++}$



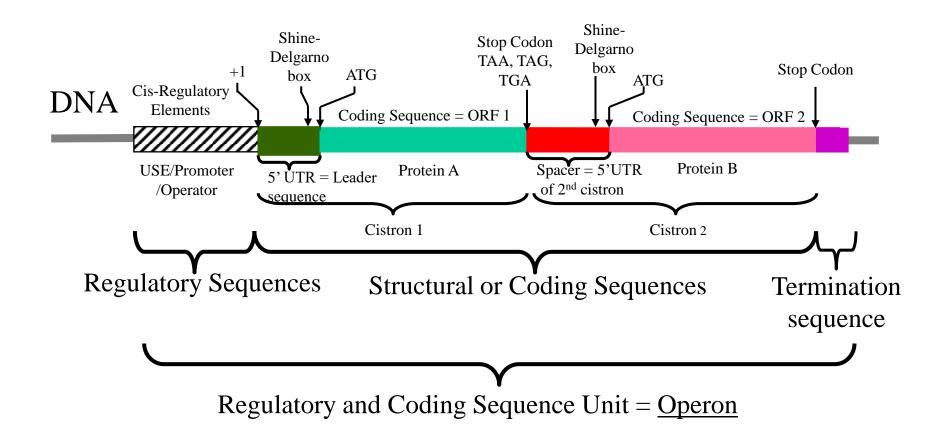
### **Gene = Transcription Unit + Regulatory Sequences**



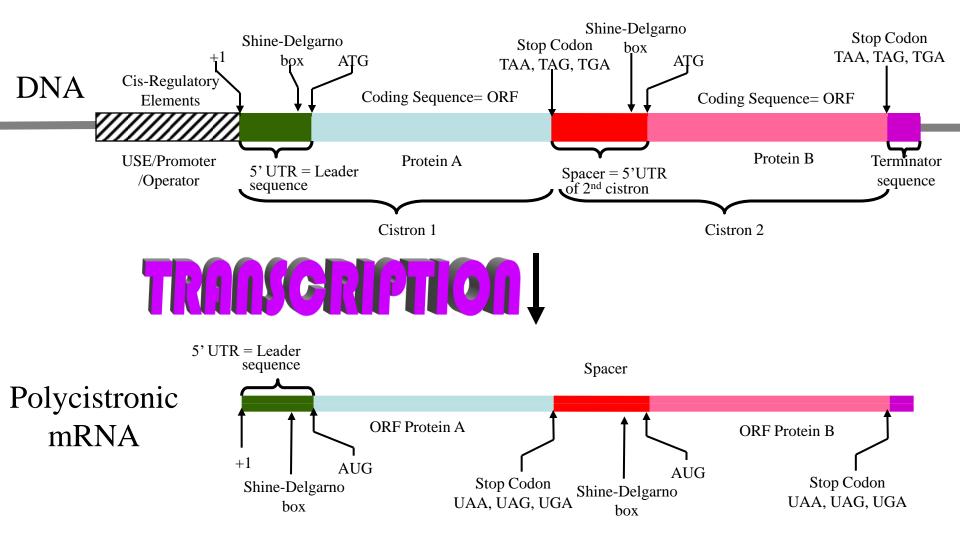
## **A Gene is a Transcription Unit**



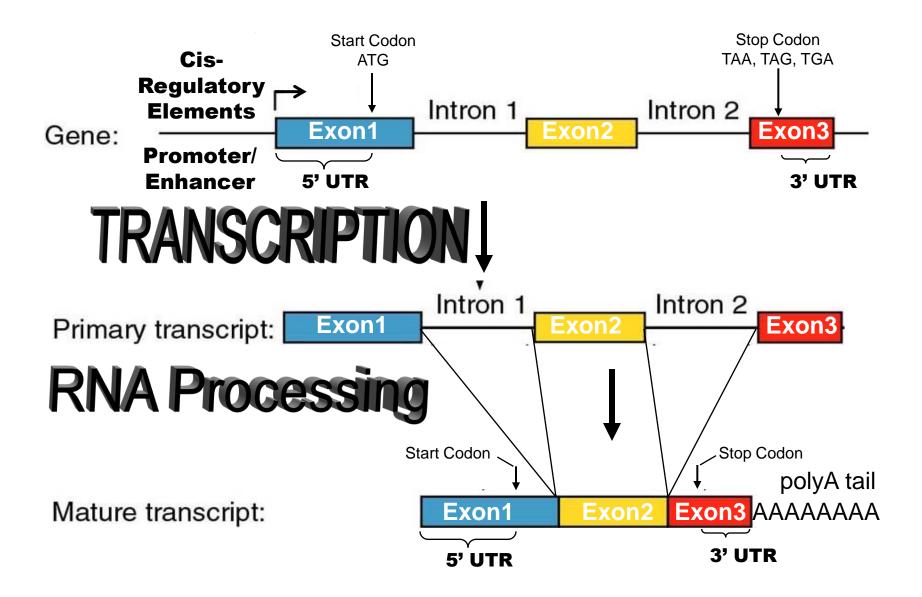
## **Prokaryotic Gene Structure**



## **Prokaryotic Gene Structure**



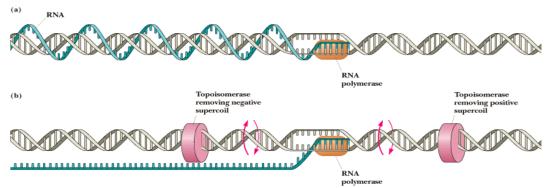
### **Eukaryotic Gene Structure**

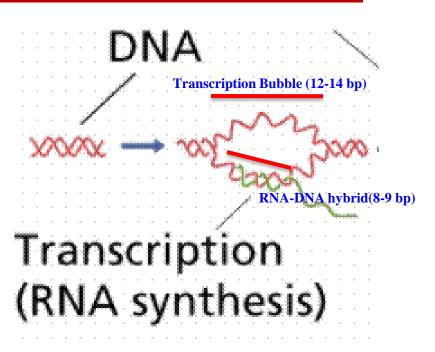


# STEPS OF TRANSCRIPTION

#### <u>STEPS</u>

- **1. Binding of RNA Polymerase to DNA template to a specific site (Promoter)**
- 2. Initiation of RNA synthesis
- 3. RNA chain elongation
- 4. Chain termination & release from the machinery





# Remember!!!!!!!

Transcription unit extends from the promoter to the terminator.

A transcription unit may encode more than one gene.

# **RNA Polymerases**

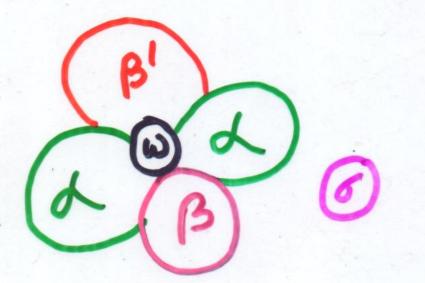
# **Bacterial RNA Polymerases**

# **RNA Polymerases**

Only one polymerase in bacteria (transcribes all types of bacterial RNA)

Three types in eukaryotes RNAP I – transcribes 28S, 18S an 5.8S rRNA RNAP II – transcribes mRNA & snRNA RNAP III – transcribes tRNA & 5S rRNA

Bacterial RNA Polymerase



~ 90 × 95 × 160 p

2 BB670

Holoenzyne

(~460 kD)

(~400 kD)

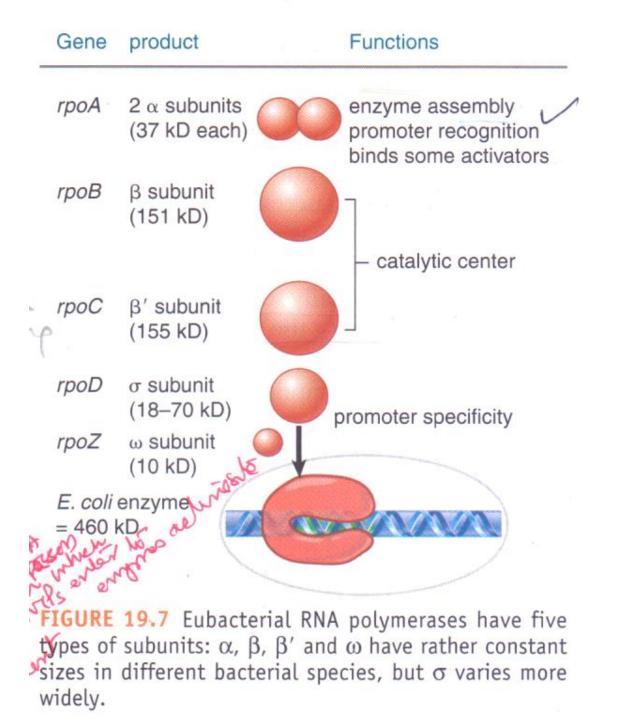
azBB +

Sigma-70

70

(70kD)

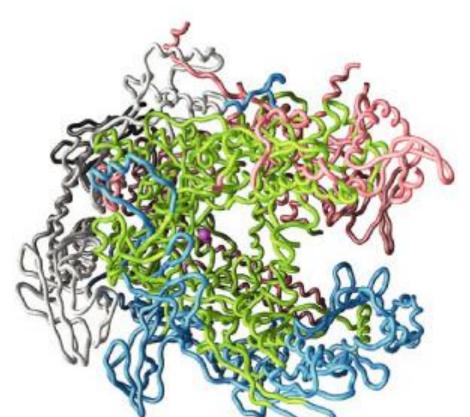
Subunit/protein	Gene Name	Map position	MW (rd)	# g Emyme	Function	Proprilies
B	трос	90	155	1	DNA Binding	Basic
ß	rpoB	90	151	1	Active site (nucleolide Binding)	Acidic
¢	rþoA	73	36.5	2	Enzyminis tom all amalysis in locals well porte agulato	"
w	rpoz	?	10	1	smilmer assimply	.17
670	poD	67	70	(	Promoter recognition and initiation	"
54	mtrA	70	54	- 1	"	"
632	htpR.	76	32	L	27	"



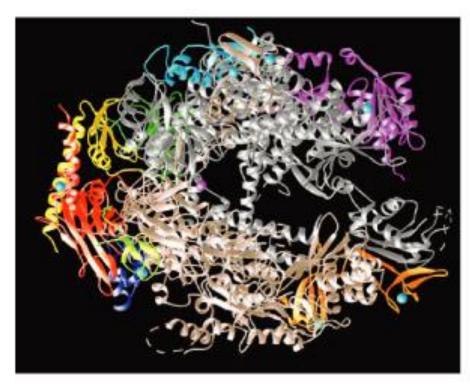
# **RNA** Polymerases

- Differences between eukaryotes & prokaryotes
- Prokaryotes
  - 1 enzyme with 4 subunits
    - 2 α's, 1 β, & 1 β'
    - actual polymerase function
  - Sigma factors ( $\sigma$ )
    - recognize & bind promoter DNA sequence
- Eukaryotes
  - 3 separate holoenzymes each has ~12 subunits
    - RNA Pol I 28S, 18S, 5.8S rRNA
    - RNA Pol II mRNA, snRNA
    - RNA Pol III tRNA, 5S rRNA
  - 3 sets of basal transcription factors
    - recognize promoter DNA sequences

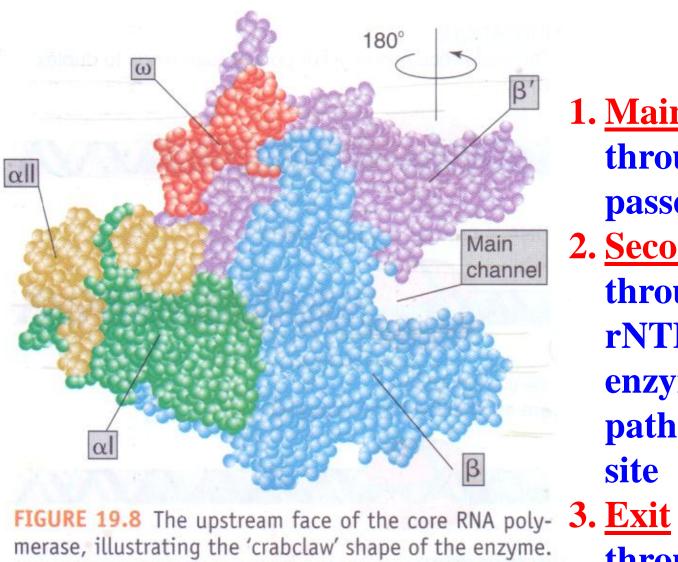
## **RNA** Polymerases



Structure of a bacterial RNA polymerase



# Structure of a eukaryotic RNA polymerase II



**FIGURE 19.8** The upstream face of the core RNA polymerase, illustrating the 'crabclaw' shape of the enzyme.  $\beta$  (cyan) and  $\beta$ ' subunit (pink) of RNA polymerase have a channel for the DNA template.  $\alpha$  I is shown in green and  $\alpha$  II in yellow,  $\omega$  is red. Adapted from K. M. Geszvain and R. Landick (ed. N. P. Higgins). *The Bacterial Chromosome*. American Society for Microbiology, 2004.

1. Main Channel, through which DNA passes 2. Secondary Channel, which through rNTPs enter to their enzyme on path to the active site Channel, which through nascent RNA leaves enzyme

#### B& B' together **Bacterial RNA Polymerase**

- 1. ~13,000 RNA polymerase molecules are present per *E. coli* cell.
- 2. Although the precise number varies with the growth conditions.
- 3. Not all RNA polymerases are actually engaged in transcription at any given time.
- 4. Almost all are bound either specifically or non-specifically to DNA.
- 5. A very little fraction remain in cytosol.

2 BB 670 Holdenzyme (~460 kD)

polymerare,

(~400 kD)

d2BB

Form the entyme's

brimarily responsible

for promotet

active centre

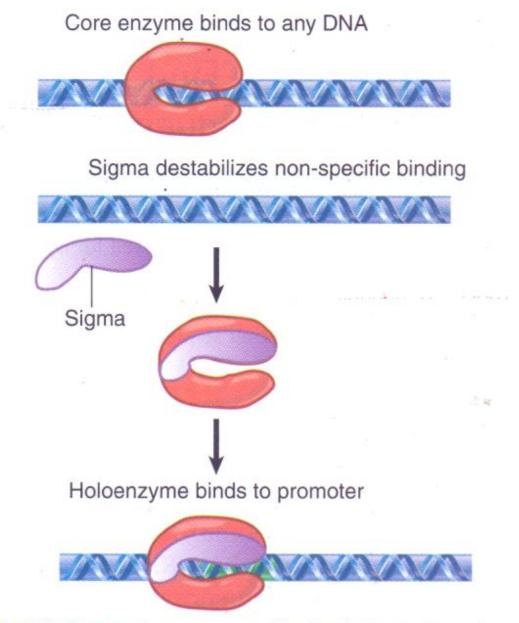
(70kD)

# SIGMA (o) FACTOR

# **Dual Functions:**

1. Reduces the affinity of holoenzyme for non-specific DNA & increases its affinity for specific DNA (promoter)

**2. In accurate initiation** 



**FIGURE 19.10** Core enzyme binds indiscriminately to any DNA. Sigma factor reduces the affinity for sequence-independent binding and confers specificity for promoters.

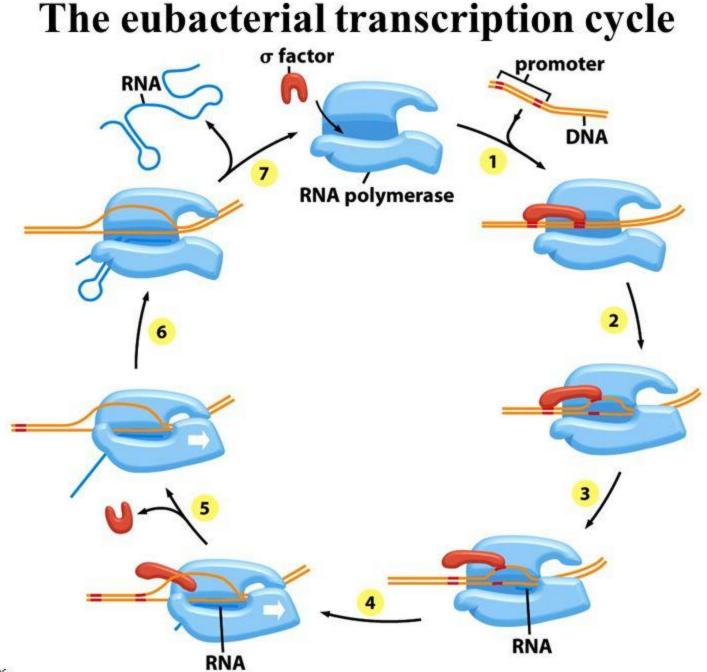
#### SIGMA (o) FACTORS

- 1. A sigma factor is a protein needed only for initiation of RNA synthesis.
- 2. Sigma factor changes the DNA binding properties of RNA polymerase so that its affinity for general DNA is reduced and its affinity for promoters is increased.
- **3.** It is a bacterial transcription initiation factor that enables specific binding of RNA polymerase to gene promoters.
- 4. The specific sigma factor used to initiate transcription of a given gene will vary. It depends on following two factors:
  - a) On gene itself
  - b) On the environmental signals needed to initiate transcription of that gene.
- 4. Every molecule of RNA polymerase holoenzyme contains exactly one sigma factors .
- 5. The number of sigma factors varies between bacterial species.

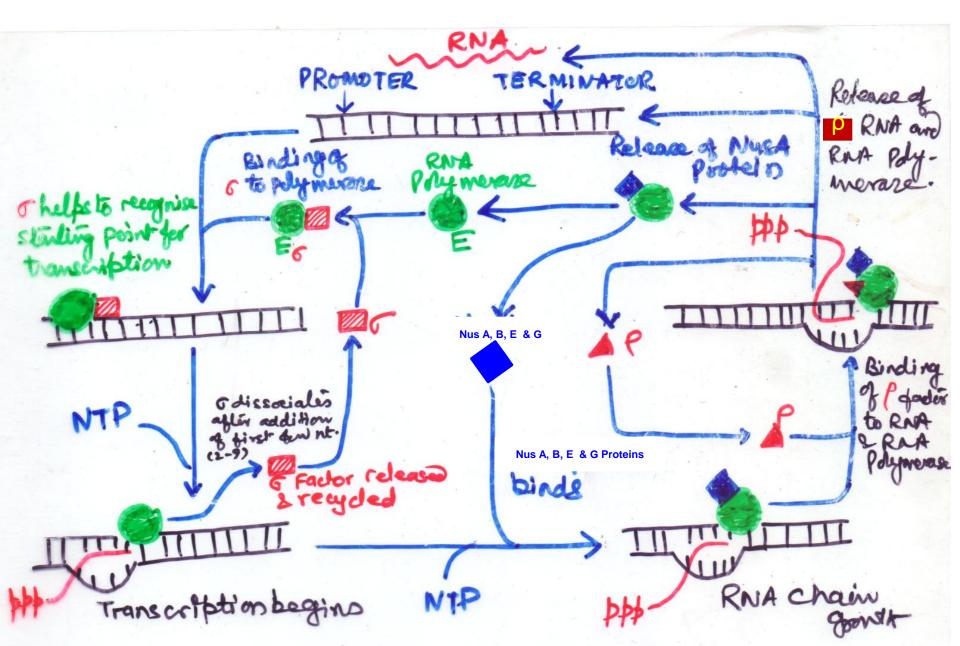
#	Species	Types of sigma factors
1	E. coli	07
2	B. subtilis	18
3	Streptomyces coelicolor	60

# **FUNCTIONS OF SIGMA (σ) FACTOR**

- 1. There is a wide variation in the rate at which the holoenzyme binds to different promoter sequences.
- 2. This is an important parameter in determining 'promoter strength (the efficiency of an individual promoter in initiating transcription).
- 3. Frequency of initiation varies (from ~1/sec to <1/30 min.)
- 4.  $\sigma$  factor is usually released when the RNA chain reaches less than ~10 nt in length, leaving the core enzyme responsible for elongation.



# **SIGMA (σ) CYCLE**

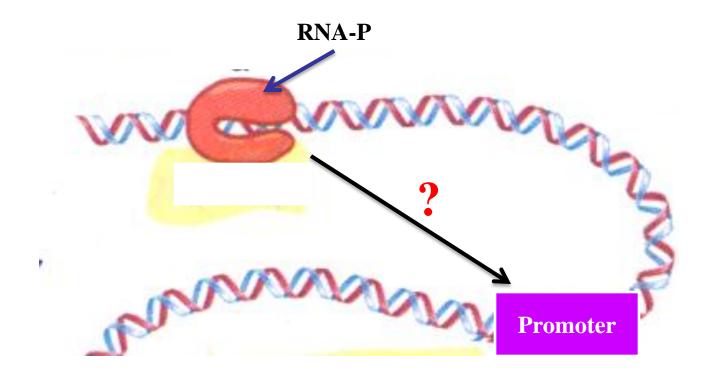


### **How does RNA Polymerase**

#### finds

### a Promoter Sequence on DNA?

(*E. coli* genome size is ~4 x  $10^6$  bp, where ~ 2,000 promoters are found).



Ans.: RNA Polymerase finds a Promoter Sequence by three mechanisms?

- a) By Sliding Mechanism
- **b) By Intersegment Transfer Mechanism**
- c) By Intrasegment Transfer Mechanism [intra domain Association or dissociation (hopping)]

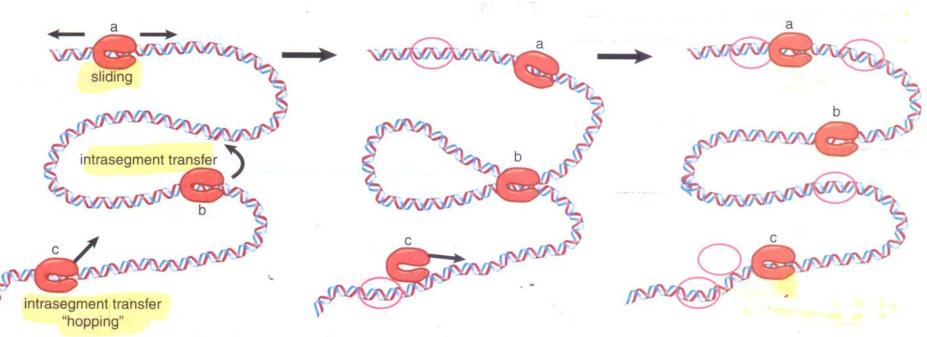
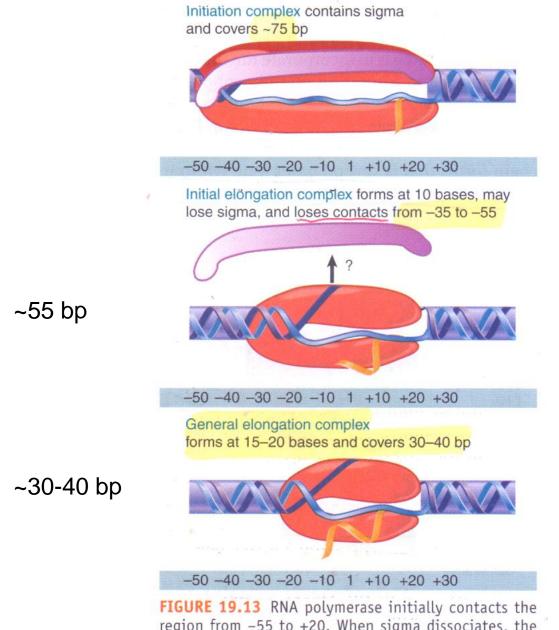


FIGURE 19.11 Proposed mechanisms for how RNA polymerase finds a promoter. (a) sliding (b) intersegment transport (c) intradomain association and dissociation or hopping. Adapted from C. Bustamante, et al., J. Biol. Chem. 274 (1999): 166665–166668.

Holoenzyme goes through transitions in the process of recognizing and escaping from promoter



region from -55 to +20. When sigma dissociates, the core enzyme contracts to -30; when the enzyme moves a few base pairs, it becomes more compactly organized into the general elongation complex.

Description Birding & RNA-P to Bonder Description I englis (bp) earend Regions en DAA carend 1. Closed binany complex 55 bp -55 to +1 position (ds DNA opens from -11 to +3 region when RAAP birds to Bornder DNA) 2. open complex (Initializer complex) 75 bp (Initializer complex) (Initializer complex) (Initializer complex) one momente of organe Signa 10 discreto 3. Initial elongation complex -35 65 120 position SSPD 4. General elementation complex - 20 15 + 20 prostom 30- 40 bp sugne cetually succeed in excerping the prompter after oddition of 20 outs.