

**1** Regulatory transcription factors bind with a DNA sequence called an **enhancer**.

**2** Binding of regulatory transcription factors recruits the general transcription factors to the promoter of the gene.

**3** The general transcription factors recruit the components of the RNA polymerase complex, and transcription takes place.

Operons are a cluster of genes (multiple coding regions) that share a common promoter and termination sequence. One mRNA is produced yet multiple proteins are translated.

When the DNA in a loop is nicked, the supercoils in that loop unwind and the DNA duplex forms a relaxed double helix.

**1** DNA double strand

**2** Nucleosome fiber 10 nm in diameter

**3** Chromatin fiber 100 nm in diameter

**4** Colloid fiber 700 nm in diameter

**5** Metaphase chromosome 1400 nm in diameter

**6** Core region

**7** Protein

**8** Supercoiled DNA

**9** Coiled chromatin fiber

**10** Nucleosome

**11** Histone proteins

**Phosphate group**

**Deoxyribose sugar**

**Base (A)**

**Deoxyribose sugar**

**Phosphate group**

**Base (A)**

**Next tRNA binds with the A site.**

**Ribose has a hydroxyl (-OH) group where deoxyribose has a hydrogen (-H).**

**Bas** Deoxyribose

**Uracil (U)** Ribose

**Thymine (T)** Deoxyribose

**Adenine (A)** Deoxyribose

**Guanine (G)** Deoxyribose

**Cytosine (C)** Deoxyribose

**Free amino acids**

**Uncharged tRNA**

**Charged tRNA**

**Aminoacyl tRNA synthetase**

**Each enzyme binds to one uncharged tRNA.**

**The enzyme also binds to the corresponding amino acid.**

**There is a specific enzyme for each amino acid.**

**The enzyme attaches the amino acid to the 3' end of the tRNA.**

**1** Incoming ribonucleotides are accepted if they correctly base pair with the template DNA.

**2** The 3'-OH of the growing strand attacks the high-energy phosphate bond of the incoming ribonucleotide, providing the energy to drive the reaction.

**3** The two phosphates of the incoming ribonucleotide are released as pyrophosphate.

**Not translated! s-RNA assembled with ribosomal proteins.**

**Not translated! Exhibit ds feature within a single molecule.**

**Translated into a protein during translation (protein synthesis)**

**5'**

**3'**

**mRNA**

**0.1 μm**

**5'**

**3'**

**This end of the DNA is...**

**nd of the**

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Compare/contrast...	Eukaryotes	Bacteria
Chromosome structure	Contains histones (nucleosomes)	Does not contain histones
Site of transcription	Nucleus	Cytoplasm
What is the promoter structure?	TATA box, 30 bp upstream	-35 box and -10 box
What are the proteins involved contacting the promoter?	General/basal transcription factors	Sigma
Is splicing (removal of introns) required?	Yes	No
Capping and tailing of mRNA?	Yes	No
Site of translation	Cytoplasm	Cytoplasm
Can translation occur while transcription is still occurring?	No	Yes

**T or F? Statement**

- T a. The direction of transcription for both gene 1 and gene 2 is 3' → 5' on the template strand.  
 T b. The template strand for gene 2 is represented by the bottom strand.  
 F c. The +1 site (start of transcription) for gene 2 is downstream of its "T" (terminator).  
 T d. For gene 2, the top strand sequence is identical to its mRNA except T's will be U's.  
 F e. If the two genes above (gene 1, gene 2) were being transcribed simultaneously, the RNA polymerases would be moving towards each other (convergent).  
 F f. The coding strand for gene 1 is the top strand (5' → 3').  
 T g. When considering the direction of transcription for gene 1, the promoter for gene 2 (P2) is upstream from the promoter (P1) for gene 1.  
 F h. The top strand will always be the coding strand for all genes in this bacterium.  
 T i. The -10 box of the promoter sequence for gene 1 will be located closer to the 3' end of the bottom strand than its 5' end.  
 T j. The +1 site for gene 2 can be found upstream of T2 considering direction of transcription for gene 2.  
 F k. Both genes would share a ribosomal binding site.  
 T l. The template strand for gene 1 is represented by the top strand.  
 T m. For both genes 1 and 2, movement of RNA polymerase depends on the orientation of two different consensus sequences (-35 box and -10 box) on the promoter.

**T or F? Statement**

- T The template strand for this operon is the bottom strand.  
 F Each protein coding region within the operon will have its own +1 site.  
 T Each protein coding region within the operon will have its own start codon.  
 F The terminator sequence will stop translation for all 4 proteins.  
 F One ribosomal binding site is shared by all 4 protein coding regions.  
 F Four different RNA polymerases are required to transcribe the operon.  
 F Translation of the proteins further downstream (e.g. proteins 3 and 4) depends on the successful translation of the upstream proteins 1 and 2.  
 T All four proteins can be translated simultaneously as each have their own ribosomal binding site.

Gene structure	Bacterial Gene? v	Eukaryotic Gene? v	Description and Function
<b>Promoter</b>	v	v	Binds the RNA Polymerase
<b>Introns</b>		v	Sequence that are cut out in RNA processing/splicing
<b>Stop codon</b>			Does not function in transcription, only TRANSLATION! Codes for the end of protein synthesis.
<b>5' CAP</b>		v	Added to mRNA once the 5' end is synthesized
<b>TATA box</b>		v	sequence on Euk promoter, TBP/general transcription factors bind here
<b>-10 and -35 box</b>	v		sequence on Bac promoter, sigma binds here
<b>Template strand</b>	v	v	DNA strand that Codes for the mRNA
<b>Transcription start site</b>	v (+1 site)	v	First base that is transcribed into mRNA Bac = ~10 bases from -10 box Euk = ~25 bases from TATA box
<b>Terminator</b>	v (hairpin)	v	Terminates transcription – Bac = hairpin loop, Euk – multiple repeat sequences

<b>+1 site</b>	v	v	First base that is transcribed into mRNA
<b>Start codon</b>			Does not function in transcription, only TRANSLATION!
<b>Exons</b>		v	Coding regions that may be spliced out or kept in a mRNA transcript.
<b>Ribosomal binding site</b>			Does not function in transcription, only TRANSLATION!
<b>Non-template /coding</b>	v	v	Opposite strand of the template but often used to read the code! (Same sequence as the mRNA except with T's instead of U's.
<b>Poly A tail</b>		v	Added after mRNA made in Euk.

