BIOL 112: Unit 2 Practice Questions – PART I

This document contains some questions for you to practice. The questions are grouped by topic along with the learning objectives associated with each of the topics. We encourage you to use the learning objectives to guide your studying; ask yourself if you could answer each objective if it was in the form of a question. There are different levels of questions provided:

1. **Study questions**: these are questions on your direct knowledge of the topics, so essentially 'drills' on the basics – practice to make sure you get the fundamentals. Work with these questions first to build up your skills.
2. **Exam-type questions, of which there are two types:**
    a. **Multiple choice:** these are the types of questions you are likely to see on the exam – various levels of application of the fundamental knowledge and skills for each topic area.
    b. **Open response questions (ORQs):** a few examples to give you an idea of the kinds of short answer questions you will see on the exams.

Topic:
Biological Information flow

This topic describes the major functions of DNA as the hereditary genetic material that can be copied and inherited; DNA is transcribed to generate an RNA molecule, and that a subset of RNA called messenger RNA are read/translated into proteins.

- **Describe** the biological information flow from DNA to proteins in cells, and the role of transcription and translation in this process.
- **Distinguish** between the processes of replication, transcription, and translation.
- **Describe** the role of RNA molecules as a link between genes and proteins.
- **Compare and contrast** the different types of RNA molecules: rRNA, tRNA, mRNA.

Transcription

This topic describes the general mechanisms of how DNA is transcribed to generate an RNA molecule. We will compare and contrast this process in both bacteria and eukaryotes.

Gene structure

- **Draw** the structure of transcription units (a gene) in both bacteria and eukaryotes, clearly differentiating between regulatory and transcribed regions.
- **Identify** a promoter region on a transcription unit (gene).
- **Explain and Identify** upstream and downstream regions of the genome when used to describe relative location of gene structures.
- **Explain** the difference between the template strand and the non-template (coding) strand in DNA.
- **Compare and contrast** the structure of the transcription units in bacteria and eukaryotes.

Mechanism of transcription

- **Define** consensus sequences and their role in transcriptional control.
- **Determine** a consensus sequence from a simple data set.
- **Describe** the role of RNA polymerase in transcription, and initiation of transcription.
- **Predict** the RNA sequence transcribed from the DNA sequence of a transcription unit.
- **Predict** the types of non-covalent interactions likely to form between DNA and a protein involved in transcription**.**
- **Describe** the role of the important DNA sequences (TATA box, promoter proximal elements) in regulation of eukaryotic transcription and how that compares to bacteria. '
- **Compare** how proteins involved in transcription in bacteria and eukaryotes recognize a promoter.
- **List** the various eukaryotic mRNA processing events – 5'-capping, splicing, and poly-adenylation (polyA tails).
- **Compare and contrast** the different types of RNA molecules: rRNA, tRNA, mRNA.

Study questions:

1. Transcription is the process of copying _____to _____.

2. _____is the synthesis of _____from mRNA.

3. **Transcription comparison:**

Compare/contrast…	**Eukaryotes**	**Bacteria**
Chromosome structure		
Site of transcription		
How many RNA polymerase?		
What is the promoter structure?		
What are the proteins involved contacting the promoter?		
Is splicing (removal of introns) required?		
Capping and tailing of mRNA?		
Site of translation		
Can translation occur while transcription is still occurring?		

4. **Transcript initiation and processing comparison:**

Compare and contrast	**Eukaryotes**	**Bacteria**
Type of RNA polymerase		
Splicing (yes or no)		
Site of initiation for transcription (promoter structure)		
RNA has 5'cap (yes or no)		
RNA has 3' poly A tail (yes or no)		

Exam Type Questions:

5. The following is a list of regulatory sites that are partly identified by looking at nucleic acid sequences. Which of them are coded in RNA as well as DNA?

    1) Promoter
    2) Ribosome binding site
    3) Start codon

    A. 1 only.
    B. 2 and 3.
    C. 1 and 2.
    D. 1 and 3.
    E. All of the above.

6. What determines where the *E. coli* RNA Polymerase initiates transcription?
    A. The binding of the RNA Pol to the single unique origin of transcription downstream on the *E. coli* chromosome.
    B. The binding of the sigma subunit to the consensus sequences upstream of the transcription start site.
    C. The binding of the sigma subunit to the consensus sequences downstream of the transcription start site.
    D. At the RNA stem loop that forms at a consensus sequence 5' of the transcription start site.
    E. RNA Pol initiates transcription at the first AUG codon of each gene.

7. How do DNA-binding proteins (such as sigma or transcription factors) **specifically** recognize the correct binding site on DNA? (Choose any/all that are true)
    A. Through ionic interactions with the phosphodiester backbone of the DNA at the binding site.
    B. Part of their tertiary structure is similar (in size, shape, and charge/polarity) to the major or minor groove of that DNA sequence
    C. They make specific covalent interactions with the DNA
    D. They interfere with the base-pair hydrogen bonds and stacking interactions to stabilize the DNA.

8. You have found that a particular protein binds to a specific sequence of bases in the DNA of a bacterial cell. There are six possible sequences for this binding site.

    The sequences where it binds are shown at right:

    Which of the following is the consensus base in position 4?
    A. A
    B. G
    C. C
    D. T
    E. There is no consensus.

Position	123456
	TAGTCA
	AAGACA
	TTAAGA
	TGTCAT
	CTGAAC
	TAATCA
	TCGGCA
	TTTACA

9. Shown at right is the interaction between an amino acid side chain (Arginine) in the bacterial DNA-binding protein, sigma, and a nucleotide base (guanine) within the promoter of a gene.

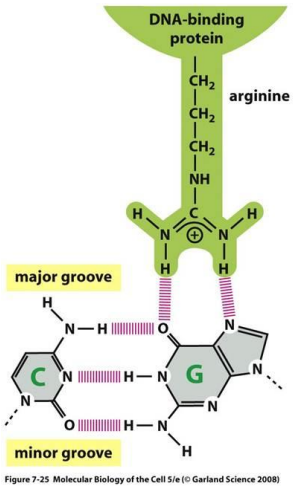
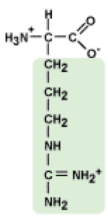


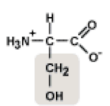
Figure 7-25 Molecular Biology of the Cell 5/e (© Garland Science 2008)

If Arginine were replaced with by Serine in the protein (both shown below) **predict** what would be the effect on the protein-DNA binding. See next page…

Arginine

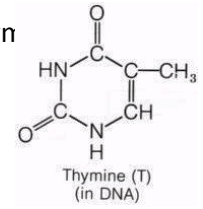


Serine



Could this replacement have an effect on transcription of this gene? **Explain** your reasoning for your prediction.

Compared to the original situation: In the DNA sequence, if guanine were replaced by thym
(shown at right), **predict** what would be the effect on the protein-DNA binding.
Could this replacement have an effect on transcription of this gene?
Explain your reasoning for your prediction.



Thymine (T)
(in DNA)

10. **The diagram below represents part of a genome of a bacterial cell.** The light blue lines represent double stranded DNA. The boxed areas represent two different genes (gene 1, gene 2) that code for two different proteins. Recall in BIOL 112, a "gene" is defined as the DNA sequence from the promoter to the terminator.

For each statement, indicate true or false (T or F).

T or F?	Statement
	a. The direction of transcription for both gene 1 and gene 2 is 3' –> 5' on the template strand.
	b. The template strand for gene 2 is represented by the bottom strand.
	c. The +1 site (start of transcription) for gene 2 is downstream of its "T" (terminator).
	d. For gene 2, the top strand sequence is identical to its mRNA except T's will be U's.
	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. The coding strand for gene 1 is the top strand (5' –> 3')
	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.
	h. The top strand will always be the coding strand for all genes in this bacterium.
	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.
	j. The +1 site for gene 2 can be found upstream of T2 considering direction of transcription for gene 2.
	k. Both genes would share a ribosomal binding site.
	l. The template strand for gene 1 is represented by the top strand.
	m. For both genes 1 and 2, movement of RNA polymerase depends on the orientation of two different consequences sequences (-35 box and -10 box) on the promoter.

11. Which of the following *correctly* describes the comparison of typical bacterial and eukaryotic mRNAs?
    A. Eukaryotic mRNAs have 5' untranslated regions, but bacterial mRNAs do not.
    B. Eukaryotic mRNAs are spliced before translation but bacterial mRNAs are not.
    C. Eukaryotic mRNAs have several open reading frames, but bacterial mRNAs have only one.
    D. Bacterial RNA polymerases are the same as RNA polymerases in eukaryotes.
    E. Eukaryotic mRNAs can accommodate several ribosomes, but bacterial mRNAs cannot.

12. Which of the following components come together to form the initiation complex so that transcription can begin in eukaryotic cells?

    1) Regulatory Transcription Factors.
    2) Activators.
    3) Basal transcription factors.
    4) RNA Polymerase II.
    5) TATA Binding Protein.
    6) Histones.

    A. 1, 3, and 4.
    B. 1, 2, 3 and 5.
    C. 1, 2, 3, 4 and 5.
    D. 2, 4, 5 and 6.
    E. 3 and 4.

13. Which of the following statements about alternative splicing are true?
    1) introns are spliced out and exons are joined together.
    2) exons are spliced out and introns are joined together.
    3) is a form of post-translational control of gene expression.
    4) reduces the number of genes needed to express different proteins.

    A. 2 only.
    B. 1, 3 and 4.
    C. 3 and 4.
    D. 1 and 4.
    E. 1 and 3.

14. What would happen to an mRNA strand in a eukaryotic cell if during RNA processing the poly A tail is not added?

    A. Nothing. The tail is just a way to mark the 3' ends of the mRNA strand.
    B. The mRNA strand would not be able to leave the nucleus as the tail is necessary to pass through the nuclear membrane.
    C. The mRNA strand would no longer be protected by the poly A tail and would be more easily degraded by ribonucleases.
    D. The mRNA strand would be transported into the mitochondria where poly A tails are not required from translation.
    E. The mRNA would be translated in the nucleus.

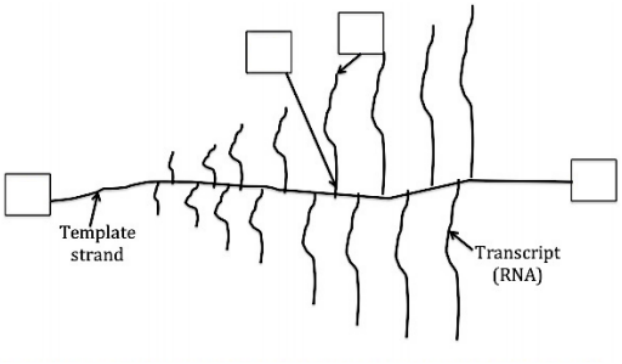
15. An intron is _____; and an exon is typically _____.

A. RNA that is removed during the processing of an mRNA molecule and leaves the nucleus; part of an intact, mature mRNA that stays in the nucleus.
B. a peptide sequence that is spliced out post-transcriptionally; a peptide sequence spliced out post-translationally.
C. RNA that is removed during the processing of an mRNA molecule and degraded in the nucleus; part of an intact, mature mRNA that leaves the nucleus.
D. part of a tRNA that binds to the codon during translation; part of mRNA that has the ORF.
E. part of an rRNA that becomes part of the ribosomes; part of the mRNA that has the ORF.

16. The fact that translation is not simultaneous with transcription in eukaryotes is primarily due to:

A. the fact that introns are spliced from eukaryotic mRNAs before translation.
B. the fact that eukaryotic mRNAs need a polyA tail to be translated.
C. the fact that eukaryotic mRNAs need a 5' cap to be translated.
D. the fact that the processed mRNA needs to be exported to the cytoplasm for translation.
E. the fact that the DNA must be decondensed in the nucleus before transcription.

17. The cartoon below represents the process of transcription as observed in an electron micrograph.
On the diagram below indicate the directionality (5’ or 3’) in the boxes against the structure.



Translation

- **List** RNAs involved in the process of translation, and describe their roles.
- **Describe** the features of the genetic code ("universal", "redundant" and "non-overlapping").
- **Explain** the function of amino acyl tRNA synthetase enzymes and why they are described as "the translators" of the genetic information.
- **Describe** the roles of the ribosome binding sites (rbs) in bacteria, the start codon, and stop codons on a mRNA.
- **Identify** the structural features of the ribosome and their importance in the process of translation.
- **Explain** what is meant by "wobble" in tRNA binding.
- **Describe** the general events in the three-step process of translation (initiation, elongation, and termination) and the directionality of translation.
- **Predict** the anticodon of a tRNA for a given amino acid using the codon table.
- **Translate** a stretch of DNA coding sequence into its polypeptide product.

Study Questions:

1. How is translation initiated in bacteria? What part of the mRNA transcript does the ribosome bind to? How does this differ in Eukaryotes?

2. What specific sequence or region leads to transcription termination and translation termination?

3. If a given tRNA has an anticodon of 5'-ACU-3', what is the mRNA codon, what is the template strand DNA sequence, and which amino acid does it carry? (3points)

4. Interaction between which two macromolecules sets the translation frame in bacteria?
    A. The ribosome and the tRNA.
    B. The mRNA and the tRNA.
    C. The ribosome and the rRNA.
    D. The ribosome and the mRNA.
    E. The tRNA and the initiation amino acid methionine.

Exam Type Questions:

5. Given that there are 61 codons for the 20 amino acids, which of the following is good evidence for the wobble hypothesis?
    A. The genetic code is a triplet.
    B. There are three different termination codons but only one start codon.
    C. The tRNAs are the main translators of protein synthesis.
    D. Wobble controls the number of proteins translated from each mRNA.
    E. The fewer than 60 different types of tRNA in a cell.

6. The DNA sequence below (the template strand) is part of the coding region of a gene. What would be the sequence of amino acids for this portion of DNA? (the reading frame is indicated by the vertical lines)

   3' – ACG|ATT|CTT|TGC - 5'

   A. N - alanine - lysine - asparagine - arginine - C
   B. N - cysteine - asparagine - valine - serine - C
   C. N - threonine - isoleucine - leucine - cysteine - C
   D. N - cysteine – C
   E. More information is needed to answer this question.

7. A region of DNA is transcribed and the mRNA is translated into a sequence of amino acids. The sequence of amino acids that is encoded by this strand is:

   NH_2 - serine - alanine - lysine - leucine - COOH.

   What is/are the possible sequence(s) of the corresponding template DNA?

   1. 3′–CAATTTAGCAGA–5′
   2. 3′–AGTCGGTTCGAT–5′
   3. 3′–AGACGATTTAAC–5′
   4. 3′–GTTAAATCGTCT–5′
   5. 3′–TCTGCTAAATTG–5′
   6. 3′–AGACGATTCGAC–5′

   A. 1 only
   B. 4 only
   C. 1, 4 and 5 only
   D. 2 and 3 only
   E. 2, 3, and 6 only

8. Shown below is a portion of an mRNA stretch, starting at the start codon:

   AUG GGG AGU AAA UUU

   The DNA encoding this region would be correctly written as:

   A. 3′ ATGGGGAGTAAATTT 5′
      5′ TACCCCTCATTTAAA 3′

   B. 5′ ATGGGGAGTAAATTT 3′
      3′ TACCCCTCATTTAAA 5′

   C. 5′ TTTAAATGAGGGGAT 3′
      3′ AAATTTACTCCCCTA 5′

   D. 3′ TTTAAATGAGGGGAT 5′
      5′ AAATTTACTCCCCTA 3′

9. What is the function of aminoacyl-tRNA synthetases?
    A. They catalyze the folding of the tRNA into a cloverleaf structure.
    B. They catalyze the modification of the bases in tRNAs.
    C. They catalyze the correct alignment of the mRNA codon with a tRNA anticodon.
    D. They catalyze peptide-bond formation between two amino acids.
    E. They catalyze the covalent attachment of an amino acid to the correct tRNA.

10. Which of the following describes what happens *during* peptide bond formation on the ribosome?

    A. The amino acid attached to the tRNA in the P site is transferred to the amino acid attached to the tRNA in the E site.
    B. The amino acid attached to the tRNA in the P site is transferred to the amino acid attached to the tRNA in the A site.
    C. The amino acid attached to the tRNA in the p site is covalently linked to the amino acid attached to the tRNA in the E site.
    D. The amino acid attached to the tRNA in the P site is covalently linked to the amino acid attached to the tRNA in the A site.

11. Which of the following statements about translation in bacteria are true?

    1. Proteins called initiation factors contribute to the interaction between the RNA in ribosome small subunit and the ribosomal binding site on the mRNA.
    2. Both the small and large subunits of the ribosome bind together at the 5' cap on the mRNA.
    3. During elongation, tRNAs enter at the A site, move to the P site, then exit from the E site.
    4. The RNA in the ribosome catalyzes formation of peptide bonds.
    5. A release factor ends protein synthesis by binding to the stop codon and preventing the ribosomes from moving on the mRNA anymore.

    A. 1, 3 and 5.
    B. 1, 3 and 4.
    C. 2 and 4.
    D. 2, 3 and 5.
    E. 2, 3, 4 and 5.

12. Cells use a two-step process (transcription and translation) to synthesize proteins from the information carried in the DNA, instead of directly translating information in the DNA to proteins. Which of the following features result from the two-step process?

    1) There are more places to control protein synthesis.
    2) More proteins can be produced in a given time period.
    3) Resolves the problem of the ribosomes being too large to interact with DNA.
    4) DNA does not need to have the sequence for the ribosome binding sites (RBS).

    A. 1 and 2.
    B. 2 and 3.
    C. 3 and 4.
    D. 1, 2 and 3.
    E. 2, 3 and 4.

13. Not all mutations in a protein coding region cause a change in phenotype. Explain giving 2 examples.

14. Each of the statements below is false. Re-write the statements to make them factually correct. You must re-write the statements for full points. Examples of changes we were looking for:

    A. The nitrogenous base thymine is present in DNA and RNA, while uracil is present only in RNA. (F)

    B. A hydrogen atom is present on the 3' carbon of the ribose of DNA nucleotides, whereas a hydroxyl group is present at the same position on RNA nucleotides. (F)

    C. The DNA and RNA molecules in a cell are copied by replication before a cell divides. (F)

15. The antibiotic called streptomycin is known to bind to the ribosome. Streptomycin distorts the ribosome structure so the ribosome does not stabilize the correct codon-anticodon base pairs. Instead, the ribosome stabilizes incorrect codon-anticodon base pairs.

    Consider a ribosome where streptomycin is present during translation. Compared to normal translation, do you predict that the proteins being translated by the streptomycin-bound ribosome will have: ***(circle one)***

    fewer mistakes **the same number of mistakes** **more mistakes**

    Explain your choice in one short sentence.

16. The following DNA sequence is part of a transcribed region of a gene, and has a start codon in one of the strands only:

```
5′ GCGTAATTGCCGCATTTCAATAA 3′
3′ CGCATTAACGGCGTAAAGTTATT 5′
```

a. Which is the template strand?
b. Which is the coding strand?
c. Write out the mRNA sequence that will be synthesized from this sequence.

d. Translate the mRNA sequence to protein:

e. In the above sequence, if the underlined cytosine on the top strand is changed to G, what would happen to the product of transcription, and what would happen to the product of translation?

f. What is meant when we say the genetic code is redundant? Explain with an example of a specific codon.

17. The following nucleotide sequence encodes the C terminus region of a wild type (also called “native” or “normal”) protein. The stop codon is underlined.

Native:
```
5'–GCCTCTAAAATCAGGAGAACACACGCCGCCATGTAA–3'
3′–CGGAGATTTTAGTCCTCTTGTGTGCGGCGGTACATT–5'
```

The highlighted bases are mutated to the form below:

Mutant:
```
5'–GCCTCTTAAATCAGGAGAACACACGCCGCCATGTAA–3'
3′–CGGAGAATTTAGTCCTCTTGTGTGCGGCGGTACATT–5'
```

Predict the consequence of this base change from A to T on the protein produced.

A. The mutation would result in a shorter protein.
B. The mutation would result in a different amino acid being inserted into the protein.
C. The mutation would result in a longer protein.
D. The mutation would not change the amino acid sequence of the protein.
E. The mutation would change all the amino acid sequence in this region.

Regulating gene expression: *the bacterial mal* and *lac* operons as examples

This topic provides a general overview of gene regulation in prokaryotes, with a focus on that which occurs in bacteria. We will apply this information to two cases of specific gene regulation in bacteria focusing on the mal and lac operons.

General principles in gene regulation and the structure of a bacterial operon

- **Explain using examples** of how gene expression may be regulated at the transcriptional and post-transcriptional levels.
- **Contrast** the general mechanisms of positive and negative transcriptional regulation
- **Describe** what is meant by basal level (constitutive) transcription and how the cell regulates this transcription.
- **Explain** how promoter binding strength and operator location (upstream vs. downstream) affects the expression of a positively or negatively regulated operon.
- **Identify** the structural components of a bacterial operon, and define the roles of each component in operon regulation

Gene regulation in bacteria - mal operon:

- **Explain** the logic of the function and regulation of the *mal* operon relative to the availability of maltose.
- **Draw** a correct representation of the *mal* operon that includes the genes, the promoter and operator regions, and that of its regulator, *malT* gene with its promoter.
- **Describe** "strong" vs. "weak" promoters as related to the *mal* operon.
- **Explain** how the presence of maltose results in the induction of the *mal* operon.
- **Predict** the binding of MalT regulator protein to the operator region of the *mal* operon based on the presence and absence of maltose.
- **Predict** the effects of mutations in the DNA sequences of the *mal* operon and the genes and promoters for *malT.*
- **Apply** the principles of gene expression learned from *mal* operon to explain other examples of transcriptional regulation.

Gene regulation in bacteria - lac operon:

- **Explain** the logic of the function and regulation of the *lac* operon relative to the availability of lactose.
- **Draw** a correct representation of the *lac* operon that includes the *lacZYA* genes, the promoter and operator regions, the *lacI* gene with its promoter.
- **Describe** "strong" vs. "weak" promoters as related to the *lac* operon.
- **Explain** how the presence of lactose results in the induction of the *lac* operon.
- **Explain** the mechanisms of repression/blocking of transcription of *lac* operon by the negative regulator LacI.
- **Predict** the effects of mutations in the DNA sequences of the lac operon and the genes and promoters for *lacI.*
- **Use** the lac operon example to explain other examples of negative regulation in operons.

1. Operons allow bacteria to express genes that encode proteins with related functions quickly at the same time and in the same amounts. Which of the following would explain why eukaryotes don't employ operons?
   A. Eukaryotes don't express genes with related functions.
   B. In eukaryotes, genes with related functions are translated from one mRNA by alternate splicing.
   C. Translation of a coding region requires a 5'cap structure.
   D. Genes with related functions are likely to be found on different chromosomes.
   E. Translation and transcription take place separately in eukaryotes.

2. The diagram below represents an operon found on the genome of a bacterial cell. The light blue lines represent double stranded DNA. The boxed areas represent 4 different protein coding regions (protein 1, protein 2, protein 3 and protein 4).

   P = promoter (orange)
   T= terminator (green)

Considering the operon shown above, for each statement, indicate true or false (T or F)

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

3. Consider the basic structure of an operon. Each protein coding sequence within that operon would have:

    1. Its own promoter.
    2. Its own transcription terminator.
    3. Its own start codon.
    4. Its own stop codon.

    A. All of the above.
    B. 3 only.
    C. 2 and 3.
    D. 3 and 4.
    E. 1 and 2.

4. The genes for the arginine operon are located on a bacterial chromosome. The proteins produced by the operon are used to synthesize the amino acid, arginine. If the operon is controlled negatively by a regulatory protein ArgR, what would be the role of <u>arginine</u>?

    A. to bind to ArgR which will then bind to the operator region in the operon.
    B. to bind to the ArgR which will then not bind to the operator region in the operon.
    C. to bind to the operator region and block RNA polymerase from binding to the Promoter region of the operon.
    D. to bind to RNA polymerase to make it capable of binding to the promoter region of the operon.
    E. None of the above.

5. MalT is a _____ regulator of the *malPQ* operon

    A. Positive
    B. Negative

6. Consider the *mal* operon. What happens if maltose levels are high? Put the following list in order of when they occur (1-4).

	"MalT-maltose" complex– binds the operator with a greater affinity.
	Maltose binds to MalT and this changes the conformation of MalT .
	RNA polymerase binds more effectively to the *malPQ* promoter, leading to high levels of *malPQ* transcription.
	Maltose is transported into the cell from the environment.

7. Assume that there is a mutation in *malT* gene, such that it is unable to bind maltose.

    a. Compared to the wild type cells (cells that have no mutation in the *malT* gene), what is the effect of this mutation on MalPQ levels in mutant cells in the ABSENCE of maltose in the environment? Why?

    b. Compare to the wild type cells, what is the effect of this mutation on MalPQ levels in mutant cells in the PRESENCE of maltose in the environment? Why?

8. A mutation in MalT protein (the regulator) caused a change in its tertiary structure. The mutated protein can bind to the operator without binding maltose. What would be the result?

    A. The mutated protein would prevent MalPQ from ever being expressed.
    B. There would be a decrease in expression of MalPQ but maltose would need to be present to cause expression of MalPQ.
    C. There would be expression of MalPQ all the time.
    D. There would be an increase expression of MalPQ but only when maltose is present.
    E. This mutation would have no effect on MalPQ expression.

9. Which of the following statements is an accurate description of regulation of the *lac* operon?

    A. When lactose is present in the growth medium, LacI binds to the DNA with very low affinity and the operon is transcribed at high level.
    B. When lactose is present in the growth medium, LacI binds to the DNA with high affinity and the operon is transcribed at high level.
    C. When lactose is present in the growth medium, LacI binds to the DNA with high affinity and the operon is not transcribed.
    D. When lactose is absent from the growth medium, LacI binds to the DNA with high affinity and the operon is transcribed at high level.
    E. When lactose is absent from the growth medium, LacI binds to the DNA with very low affinity and the operon is not transcribed.

10. Compare these two gene expression systems.

	lac operon	*mal* operon
Regulates breaking down of:		
What binds to the operator & when does this occur?		
High levels of what substance affects the operon, and how?		
Is this positive regulation or negative regulation? Why?		

11. Consider the *lac* operon. What happens if lactose levels are low? Put the following list in order of when they occur (1-6).

	Lactose from the environment enters the cell and binds to LacI, which leads to a conformational change in LacI.
	When RNA polymerase tries to bind to the promoter, it cannot get past the LacI repressor protein, therefore RNA polymerase is mostly blocked from transcribing the genes for the lactose metabolizing enzymes.
	The enzymes β-galactosidase and permease, coded for by *lacZ* and *lacY*, are not required by the cell at low levels of lactose, hence they are transcribed at low levels.
	Without LacI bound to the operator, RNA polymerase is able to bind to the promoter and transcribe the lac operon.
	LacI bound to lactose is no longer able to bind to the operator with high affinity.
	The LacI protein binds to the operator with high affinity.

12. Assume that there is a mutation in the *lacI* gene such that it is unable to bind lactose.
    a. Compared to the wild type cells (where *lacI* gene is not mutated) what is the effect of this mutation on LacZY levels in the ABSENCE of lactose in the environment? Why?

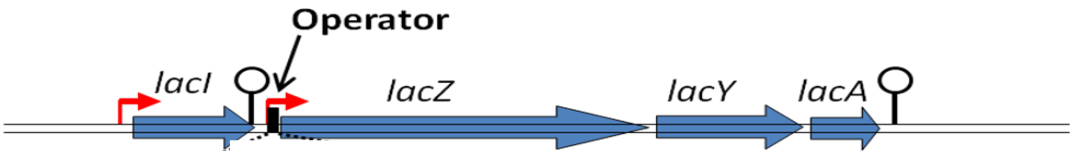
    b. Compared to the wild type cells (where *lacI* gene is not mutated) what is the effect of this mutation on LacZ levels in the PRESENCE of lactose in the environment? Why?

13. Which of the following statements about regulation of the *lac* operon of *E. coli* is NOT correct? Choose all that apply.

    A. The LacI protein binds to the operator and inhibits transcription of the *lac* operon.
    B. When grown in media with no lactose, *E. coli* produce high levels of *lacZY* mRNA.
    C. The LacI protein will change shape in the presence of lactose.
    D. Cells that contain a mutant LacI protein that cannot bind lactose are unable to metabolize lactose.
    E. When cells are grown in medium that contains lactose, the LacI protein, after binding to lactose, will bind near the promoter for the *lac* operon.

14. In the presence of the signal molecule that binds to the regulatory protein, the fundamental difference between the regulatory proteins LacI and MalT can be stated as:
    A. LacI will bind downstream of the promoter and MalT will not bind to the operator upstream of the promoter.
    B. LacI will bind upstream of the promoter and MalT will bind downstream of the promoter.
    C. LacI binds DNA efficiently and MalT does not.
    D. LacI prevents transcription of the genes in the operon, but MalT promotes the transcription of the genes in the operon.
    E. MalT binds DNA efficiently and LacI does not.

15. A well-characterized mutant of *E. coli* has a deletion in LacI gene starting at the +1 site of LacI, up to/including its terminator sequence. The LacI promoter is intact but the rest of the gene has been deleted. Which of the following statements describes what will happen in this mutant?



A. The cells will be unable to use lactose to grow.
B. The cells will produce high levels of LacZ, LacY, and LacA, but only when grown in medium with lactose.
C. The cells will produce LacZ, LacY and LacA even when there is no lactose in the medium.
D. The absence of the LacI protein will prevent the expression of the *lac* operon.
E. The mutation will have no effect at all on the regulation of the lac operon.

16. A mutant of *E. coli* is isolated such that the lac operon is always expressed at high levels whether lactose is present or not. This could be due to a mutation in:

1. the signal molecule
2. *lacI*
3. the *lac* terminator
4. the *lac* operator

A. Only 1.
B. 2 and 4.
C. 1 and 2.
D. 3 and 4.
E. All of the above.