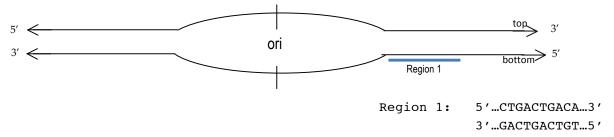
Molecular Biology Unit Exam

Question 1

Consider the following origin of replication that is found on a chromosome. The sequence of region 1 is shown below.



a) Within Region 1, which strand will be the template for leading strand synthesis, the top or the bottom?

b) If we assume that a lagging strand fragment is made from region 1, what will be its sequence?

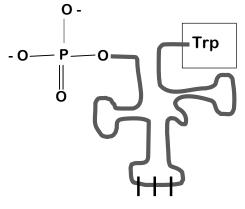
c) You examine DNA replication in an *E. coli* mutant, which has a partially defective DNA polymerase. In vitro experiments using the mutant DNA polymerase gives an error rate of 10^{-3} , as compared to the expected error rate of 10^{-6} . Which of the following activities is the mutant polymerase likely to be missing, as compared to the normal polymerase? Circle all that apply.

5'→3' polymerase	$3' \rightarrow 5'$ exonuclease
5'→3' exonuclease	3′ → 5′ polymerase
5'→3' recombinase	3'→5' recombinase

d) Below is a schematic of the molecule that inserts the fourth amino acid (a trytophan) into the mutant polymerase. A codon chart is found on the final page of the exam.

This schematic represents a ______

ii) On the schematic, give the nucleotides of the anticodon.



Below are 210 consecutive base pairs of DNA that includes only the beginning of the sequence of gene X. The underlined sequence (from position 20-54) represents the promoter for gene X and the underlined and italicized sequence (from position 71-90) encodes the gene X ribosome binding (RBS) site. Transcription begins at and includes the T/A base pair at position 60 (bold)

	1	10	20	30	40	50	60	70
	I	I	I	I	I	I	I	I
5′	ATCGGI	CTCGGCTAC	TACA <u>TAAACGO</u>	CGCGCATATAT	CGATATCTAC	<u>GCTAGCTAT</u> CO	GTC T AGGCTA	ACTAC
3′	TAGCCA	GAGCCGATG	ATGTATTTGCC	GCGCGTATATA	GCTATAGATO	CGATCGATAGO	CAGATCCGAT	GATG
				Promoter				
		80	90	100	110	120	130	140
		I	I	I	I	I	I	I
5'	CAGGTA	TCGGTCTGA	<i>TCTAG</i> CTAGCT	гтст с ттстст	CTCTCCCCC	GCGGGGGGCTG	TACTATCATGO	CGTCG
3′	<u>GTCCA1</u>	AGCCAGACT	A <i>GATC</i> GATCGA	AAGA G AAGAGA	GAGAGGGGGG	CGCCCCCGAC	ATGA T AGTACO	GCAGC
	F	RBS						
		150	160	170	180	190	200	210
		I	I	I	I	I	I	I
5′	TCTCGG	CTACTACGT	AAACGCGCGC	ATATATCGATA	TCTAGCTAGO	CTATCGGTCTC	CGGCTACTAC	STAAA
3′	AGAGCC	GATGATGCA	TTTGCGCGCG	TATATAGCTAT	AGATCGATCO	GATAGCCAGAG	GCCGATGATGC	CATTT

a) What are the first 6 nucleotides of the mRNA from gene X?

b) What are the first 4 amino acids encoded by gene X? (A codon chart is found on the final page)

You have found two different mutations of gene X, mutation 1 and mutation 2.

c) In mutation 1, there is an insertion of the following three base pairs immediately after the C/G base pair at position 100 (shown in bold).

5' TGT 3' 3' ACA 5'

i) Would the mRNA expressed from this version of gene X be longer, shorter, or the same as that produced from the normal gene X? Explain and if longer or shorter, indicate by how many in bases.

ii) If the mRNA can be translated, ...

- ...would you expect the protein to be longer, shorter, or the same as that produced from the normal gene X? If longer or shorter, indicate by how many in amino acids.
- ...do you expect that the protein produced will have the same function as the normal protein X? Explain your thinking.

Question 2, continued

This is the same sequence as shown on the previous page. It is repeated for your convenience. Below are 210 consecutive base pairs of DNA that includes only the beginning of the sequence of gene X. The underlined sequence (from position 20-54) represents the promoter for gene X and the underlined and italicized sequence (from position 71-90) encodes the gene X ribosome binding (RBS) site. Transcription begins at and includes the T/A base pair at position 60 (bold)

	1	10	20	30	40	50	60	70
	I	I	I	I	I	I	I	I
5′	ATCGGT	CTCGGCTAC	TACA <u>TAAACGO</u>	CGCGCATATAT	CGATATCTAC	<u>GCTAGCTAT</u> CO	GTC T AGGCTA	ACTAC
3′	TAGCCA	GAGCCGATG	ATGT <u>ATTTGCC</u>	GCGCGTATATA	GCTATAGATO	CGATCGATAGO	CAGATCCGAT	GATG
				Promoter				
		80	90	100	110	120	130	140
		I	I	I	I	I	I	I
5′	CAGGTA	TCGGTCTGA	<i>TCTAG</i> CTAGC1	гтст с ттстст	CTCTCCCCC	GCGGGGGGCTG	ACTATCATGO	CGTCG
3′	GTCCAT	AGCCAGACT	A <i>GATC</i> GATCGA	AAGA G AAGAGA	GAGAGGGGGG	CGCCCCCGACA	ATGA T AGTACO	GCAGC
	R	BS						
		150	160	170	180	190	200	210
		I	I	I	I	I	I	I
5′	TCTCGG	CTACTACGT	AAACGCGCGC	ATATATCGATA	TCTAGCTAGC	CTATCGGTCTC	CGGCTACTACO	STAAA
3′	AGAGCC	GATGATGCA	TTTGCGCGCG	TATATAGCTAT	AGATCGATCO	GATAGCCAGAG	GCCGATGATGC	CATTT

d) In mutation 2, there is an insertion of the following four base pairs immediately after the A/T base pair at position 130 (shown in bold).

5' ATGT 3' 3' TACA 5'

i) Would the mRNA expressed from this version of gene X be longer, shorter, or the same as that produced from the normal gene X? Explain and if longer or shorter, indicate by how many in bases.

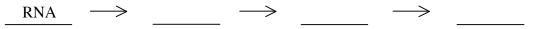
ii) If the mRNA can be translated,...

- ...what are the first four amino acids produced?
- ...would you expect the protein to be longer, shorter, or the same as that produced from the normal gene X? If longer or shorter, indicate by how many in amino acids.
- ...do you expect that the protein produced will have the same function as the normal protein X? Explain your thinking.

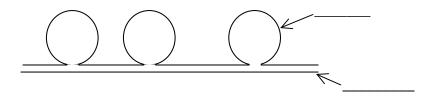
You have discovered a new virus that contains only RNA as its genetic material. Curious as to how this virus works, you infect host cells with this virus and discover that after infection, you find that the host cell makes lots of viral RNA molecules and various viral proteins. Upon further examination, you discover that the host genome now encodes viral proteins.

a) What type of virus you have discovered.

b) Outline the steps of the information flow for this virus by filling in the blanks below. Each arrow represents a process, for example, copying of DNA from a DNA template. Circle the arrow that represents a process not found naturally in the host cell.



c) There is a human gene that encodes a protein identical to one of the proteins produced by the virus. You isolate a fragment of DNA that includes the shared gene, heat the fragment to separate the two DNA strands and allow the human DNA to base pair with the viral RNA. You find the following hybrid molecule using electron microscopy.



i) Label which strand is human DNA and which is viral RNA in the picture.

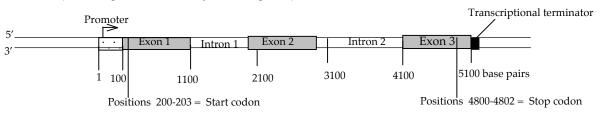
ii) Why can some regions form complementary base pairs, while other regions cannot?

iii) If you were to isolate mature mRNA from the human cell and allow it to base pair with the viral RNA, would you see the same type of hybrid molecule? Explain your thinking.

d) In an actively dividing, normal cell, indicate whether the following statements are true or false for the virus discussed above.

True	False	RNA-dependent RNA polymerase is used at some point during the viral life cycle to copy the viral genome.
True	False	RNA-dependent DNA polymerase is used at some point during the viral life cycle to copy the viral genome.
True	False	DNA-dependent DNA polymerase is used at some point during the viral life cycle to copy the viral genome.
True	False	The polymerase used by the virus to copy its genome forms a covalent bond between a 5' phosphate and a 3' hydroxyl.
True	False	The polymerase used by the virus to copy its genome forms a covalent bond between an N-terminal amine and a C-terminal carboxyl.
True	False	Polymerization of the viral genome would be $5' \rightarrow 3'$.
True	False	Polymerization of the viral genome would be $3' \rightarrow 5'$.
True	False	Deoxyribonucleotides would be incorporated into the packaged viral genome.
True	False	Di-deoxyribonucleotides would be incorporated into the packaged viral genome.

a) Below is a schematic of gene Y, which encodes protein Y. The promoter region is indicated by the dotted box. Transcription begins immediately following the promoter.



- The transcript first produced by this gene would be approximately how many nucleotides long?
- Two different transcripts are produced from this gene, one is approximately 2000 nucleotides long, the other is approximately 3000 nucleotides long. Explain how two different transcripts can be produced from this gene.
- Assume each transcript produces a protein. Given your answer above and the diagram, what is the approximate size of the two proteins produced from this gene?

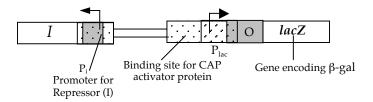
b) Assume gene Y was mutated such that the base pair found at position 200 was changed from an A/T to a G/C. Transcription and translation of the altered gene Y still occurs.

- Would the first transcript be the same length, shorter or longer than the first transcript produced from the wild type gene Y? Give all possible answers and explain your thinking.
- Would the protein produced be the same length, shorter or longer than the protein produced from the wild type gene Y? Give all possible answers and explain your thinking.

c) Now assume gene Y was mutated such that only the base pair found at position 2100 was changed from a C/G to an A/T. Transcription and translation of gene Y still occur.

- Would the first transcript be the same length, shorter or longer than the first transcript produced from the wild type gene Y? Give all possible answers and explain your thinking.
- Would the protein produced be the same length, shorter or longer than the protein produced from the wild type gene Y? Give all possible answers and explain your thinking.

You design a summer class where you recreate experiments studying the lac operon in E. coli (see schematic below). In your experiments, the activity of the enzyme β -galactosidase (β -gal) is measured by including X-gal and IPTG in the growth media. X-gal is a lactose analog that turns blue when metabolized by β -gal, but it does not induce the lac operon. IPTG is another analog of lactose that is an inducer of the lac operon but is not metabolized by β -gal.



a) Which of the following would you expect to bind to b -galactosidase? Circle all that apply.

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Lactose (or allolactose) X-gal IPTG
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b) Which of the following would you expect to bind to the lac repressor? Circle all that apply.

Lactose (or allolactose) X-gal IF	allolactose)	X-gal	IPTG
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After mutagenesis you find 7 mutants that never turn blue as shown in the table below. Each mutant has a single loss-of-function mutation.

Cell Type	Media			
	+ glucose	+ glucose	No glucose	No glucose
	No lactose + X-gal	+ lactose + X-gal	No lactose + X-gal	+ lactose + X-gal
Wild type	White colonies	White colonies	White colonies	Dark blue colonies
Mutants 1-7	White colonies	White colonies	White colonies	White colonies

c) A single loss-of-function mutation in which component or components could produce the phenotype seen in these mutants? List all that apply. Choose from:

I, P_i, CAP binding site, O, lacZ, or Pl_{ac}

You also find three mutants with the following phenotype. Each mutant has a single loss-of-function mutation.

Cell Type			Media	
	+ glucose No lactose + X-gal	+ glucose + lactose + X- gal	No glucose No lactose + X-gal	No glucose + lactose + X-gal
Wild type	White colonies	White colonies	White colonies	Dark blue colonies
Mutants	White colonies	White colonies	Dark blue colonies	Dark blue colonies

d) A single loss-of-function mutation in which component or components could produce the phenotype seen in these mutants? List all that apply. Choose from:

I, P_i, CAP binding site, O, lacZ, or Pl_{ac}

7.01SC Fundamentals of Biology Fall 2011

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