

**BIOLOGY 200**  
**SPRING QUARTER 2015**  
**EXAM 1-PRACTICE QUESTIONS KEY**

**THE GENETIC CODE**

Codon Table →

		SECOND LETTER				
		U	C	A	G	
FIRST (5') LETTER	U	UUU } Phe	UCU } Ser	UAU } Tyr	UGU } Cys	U
		UUC } Phe	UCC } Ser	UAC } Tyr	UGC } Cys	C
		UUA } Leu	UCA } Ser	UAA STOP	UGA STOP	A
		UUG } Leu	UCG } Ser	UAG STOP	UGG Trp	G
	C	CUU } Leu	CCU } Pro	CAU } His	CGU } Arg	U
		CUC } Leu	CCC } Pro	CAC } His	CGC } Arg	C
		CUA } Leu	CCA } Pro	CAA } Gln	CGA } Arg	A
		CUG } Leu	CCG } Pro	CAG } Gln	CGG } Arg	G
	A	AUU } Ileu	ACU } Thr	AAU } Asn	AGU } Ser	U
		AUC } Ileu	ACC } Thr	AAC } Asn	AGC } Ser	C
		AUA } Ileu	ACA } Thr	AAA } Lys	AGA } Arg	A
		AUG } Met (initiator)	ACG } Thr	AAG } Lys	AGG } Arg	G
	G	GUU } Val	GCU } Ala	GAU } Asp	GGU } Gly	U
		GUC } Val	GCC } Ala	GAC } Asp	GGC } Gly	C
		GUA } Val	GCA } Ala	GAA } Glu	GGA } Gly	A
		GUG } (initiator)	GCG } Ala	GAG } Glu	GGG } Gly	G

NOTE: We have included the Bloom's level for each practice question (written in blue after each question). This is a ranking of the type of thinking required to answer a question, which we discussed on the 1<sup>st</sup> day of class. You may find it useful to go through the exam and assess how well you answered the different types of questions to help you focus your studying for the next exam.

Below are the 6 different levels of Bloom's

- Knowledge
- Comprehension
- Application
- Analysis
- Synthesis
- Evaluation

1. You are studying a protein that consists of a single polypeptide. You discover a mutant form of the protein in which the leucine amino acid at the amino terminus of the protein has been replaced by a phenylalanine. Which of the following level(s) of protein structure would be affected by this change? (Circle the best answer)

(COMPREHENSION)

- 1) primary only
- 2) primary and secondary
- 3) primary, secondary and tertiary
- 4) primary, secondary, tertiary and quaternary

Note: this protein does not have any quaternary structure

2.

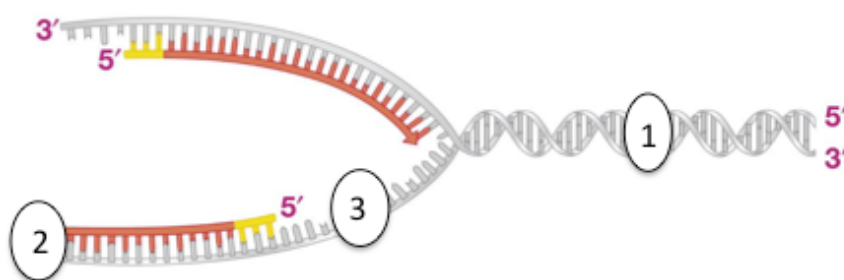


Fig. 1. DNA replication fork.

A. The location of several proteins are indicated by numbered circles on the diagram in Fig. 1. Write the names of the correct proteins in the table from the choices below. Briefly describe the function of the enzyme. Choices: Primase, Ligase, DNA polymerase I, DNA polymerase III, single-stranded DNA binding protein (SSBP), helicase, and topoisomerase. (COMPREHENSION)

Number	Protein	Function of the Protein (7 words Max)
1	<i>Topoisomerase</i>	<i>Relieves pressure of unwinding DNA</i>
2	<i>DNA polymerase III (+I for DNA pol or DNA pol I)</i>	<i>Adds dNTPs</i>
3	<i>Single stranded binding protein or Helicase</i>	<i>SSSBP: Stabilizes single-stranded DNA Helicase: Unwinds ds DNA</i>

B. You have a drug that blocks the activity of Primase. Which of the following would be affected by this drug? (circle one) (APPLICATION)

- a. Synthesis of a complete lagging strand
- b. Synthesis of a complete leading strand
- c. **Synthesis of both a complete lagging strand and a complete leading strand**
- d. No effect, both strands would be synthesized normally

Q2 cont.

C. Looking at the portion of the replication fork shown in Fig.1, which is the leading strand?

Upper strand                  Lower strand

D. You have a drug that blocks the activity of ligase.

Describe what effect this drug would have on replication of the **leading strand**. Explain your reasoning in one sentence or less

*No effect, this strand is synthesized as a continuous piece of DNA, so no ligase is needed*

Describe what effect this drug would have on replication of the **lagging strand**. Explain your reasoning in one sentence or less.

*The Okazaki (short or discontinuous) fragments would be synthesized but would remain as short pieces since there is no "glue" to join them together.*

3. Of the following four 15-bp double-stranded DNA sequences, which will be **most** stable at higher temperatures? In other words, which will most likely remain in a double-stranded form?

(Note: only one strand is shown here) Choose the single best answer. (APPLICATION)

- 1 . CATCCTAGCGACTAT
- 2 . CTATACGACATAGCC
- 3 . AAATGCATACATCTT
- 4 . CCCGCATCGCCATCG

Answer:   4  

4. You have a drug that stops a cell from dividing. Which of the following processes would not be needed for cells treated with this drug to survive? Choose the single best answer. (APPLICATION)

- a. Transcription
- b. Translation
- c. DNA replication
- d. Transcription and translation
- e. Transcription, translation and DNA replication

Answer:   c  

5. Where in a **eukaryotic** cell do you expect to find the enzyme RNA polymerase? (1 word)

(COMPREHENSION)

  Nucleus

6. Below is the sequence of a complete mRNA from a bacterial cell:

(APPLICATION)

5' ACUAGCAGGAGACGUAAGCGAUGUGCCAGAUGCGCAGUCACACAUAACUGCAAG 3'

- A. How many amino acids long is the protein? Answer: 8  
B. How many tRNAs will bind to the ribosome to make this protein? Answer: 8  
C. What is the second amino acid in the protein (counting from N-terminus to C-terminus): Answer: CYS

7. The antibiotic *streptomycin* interferes with prokaryotic translation but not eukaryotic translation. Note: prokaryotes use a different initiating amino acid (f-met) than is found in eukaryotes.

You have a drug that blocks the initiation of prokaryotic translation

List 2 targets that this drug could be blocking. These targets could be molecules or specific parts of a molecule. Be as specific as possible in less than one sentence. (ANALYSIS)

- A. Attachment site for f-met on tRNA OR aminoacyl transferase for f-met tRNA (+3)  
B. anticodon on f-met tRNA (+3)

This question came from the key concept that there are 2 parts of a tRNA that are different from one tRNA to another (the anticodon and the amino acid attachment).

8. Below is a portion of a bacterial chromosome that contains a gene. The promoter region and the +1 base pair are indicated, as well as the polarity of the two DNA strands.

(APPLICATION)

... 3' TTGCATCCGAAACGTACGATCGAT<sup>+1</sup>CGCCGACT<sup>-10</sup>TATTACGATCGGACTACTGCGTCGTAGC5' ...  
... 5' AACGTAGGCTTTGCATGCTAGCTAG<sup>+1</sup>CCGGCTGAATAAT<sup>-10</sup>GCTAGCCTGATGACGCAGCATCG3' ...

a. Write below the letters for the bases of the first 6 nucleotides of the RNA molecule transcribed from this gene. Be sure to indicate the 5' and 3' ends of the strand.

5'-CUAGCU-3' (full credit required correct sequence, and correct labeling of 5' and 3' ends)

You find a mutant with a 10-bp **insertion** between the start site of transcription (+1) and the **ribosome binding site (not shown in the figure)**. This insertion is composed only of C and G nucleotides.

b. (Choose the best answer) This mutation will change:

1. The sequence of the mRNA
2. The sequence of the protein
3. Both the sequences of the mRNA and the protein Answer: 1
4. Neither sequence will be changed

8 (cont.)

c. Explain your reasoning for part b in 2 sentences or less.

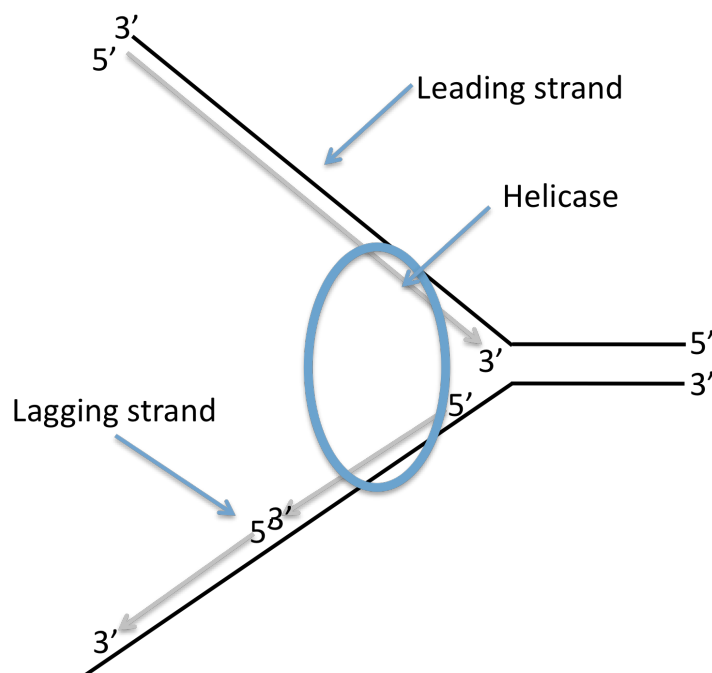
*RNA polymerase will still **initiate transcription in the correct location (+1)**, but it will **now transcribe 10 additional nucleotides (+1)**. The translation start codon will **not be changed** so there will be **no change in the amino acids in the protein (or the reading frame of the protein) (+2)***

9. Name one step in the processing of DNA to protein that can be regulated only in a eukaryote.

(<5 words) (KNOWLEDGE)

*mRNA processing or transporting mRNA out of nucleus....other possibilities*

10.



a) You figure out a way to replicate DNA in a test tube by adding double-stranded DNA template, dNTPs, NTPs and all the proteins needed for replication. However, you forget to add DNA ligase. Fill in the following parts of the growing replication fork shown.

1) Fill in any replicated nucleic acids, using at least 2 Okazaki fragments where appropriate  
2) Label the new strands as “leading” or “lagging”

3) Label the 5' and 3' ends of all nucleic acid strands that you draw

4) Draw a circle representing the location of DNA helicase (do not include any other proteins in your drawing)

APPLICATION

- Labeling both leading and lagging strand
- Labeling 5' and 3' ends correctly
- Continuous DNA on leading strand
- Arrows on nucleic acids showing direction of synthesis

- Okazaki fragments on lagging strand, **not connected**
- Circle showing DNA helicase (could be on either strand or both, but should be at or close to the replication fork (but not past the fork))

b) When you look at the replicated DNA at **the end** of the experiment described in part “a”, do you expect to see any RNA present on either strand? Explain your reasoning (one or two sentences maximum).

**NO, the DNA polymerase I will still be able to remove the RNA primers (laid down by primase), and replace them with DNA.**

Note: for full credit you needed to explain **why** there was no longer any RNA at the replication fork, not simply that the ligase wasn't involved in this step.

c) If you made a mistake and instead of adding dNTPs to your reaction, you added dideoxynucleotide triphosphates (ddNTPs) which lack both a 2' and 3' OH group, which of the following enzymes would be directly affected? (Circle all that apply)

APPLICATION

Primase

**DNA polymerase I** **DNA polymerase III**

Topoisomerase

Helicase

11. For each different mutant cell described below, assume that ONE specific molecule or part of a molecule is mutated in that cell so that the molecule's function has changed. Name as many molecules that could result in the description (but remember that for the mutant phenotype, you are considering each mutation by itself).

(ANALYSIS)

Cell 1: In many different types of proteins, there is the amino acid Thr (threonine) where an Ala (alanine) should be.

*The tRNA with the alanine anticodon has a threonine attached to it instead of an alanine (alternatively, you could say that the amino-acyl tRNA synthetase that normally "charges" the alanine tRNA is mutated so it binds threonine instead)*

Cell 2: Many different types of proteins are much shorter than in a normal cell, but have the correct sequence up to that point. tRNA levels are normal in the cell.

*release factor*

Cell 3: About a third of all new proteins in a mutated cell are not doing their jobs correctly. When you compared to proteins in a healthy cell, these proteins appear much larger overall.

*Some tRNA has changed it's anticodon to recognize one of the three STOP codons, so this is erroneously continuing to elongate all proteins that normally use that STOP codon*

12. You have done a genetic screen looking for mutants in the Compound D synthesis pathway (shown below). Compound D is essential for life. Fill in the table with the expected phenotype (LIVE or DIE) for cells carrying mutations in each of the listed enzymes.



	growth media is supplemented with:		
mutations cause loss of activity in:	A only	B and C	D only
Enzyme 1	DIE	LIVE	LIVE
Enzyme 3	DIE	DIE	LIVE
Both Enzymes 1 & 3	DIE	DIE	LIVE

13. You are studying a plant that grows in the forest and has red flowers. You learn that flower color in this plant is determined by a single gene that codes for red pigment. You discover a different species of this plant in a nearby meadow that has white flowers instead of red. You discover that this meadow species contains a “white allele” with a single nucleotide difference upstream of the start site of transcription of the red pigment gene, as shown in Fig. 1.

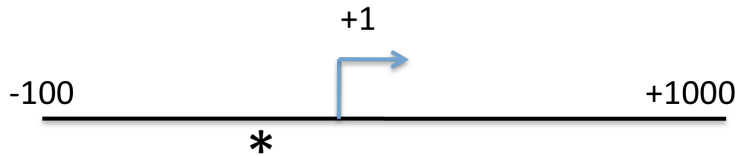


Fig. 1. Red Pigment Gene. The single nucleotide difference found in the white allele is indicated by an asterisk (\*). The start site of transcription is indicated by a +1. Transcription proceeds in the direction of the arrow.

a) What molecular event could have caused this mutation? **DNA damage or DNA polymerase error**

**COMPREHENSION**

0 points for stating "DNA replication", "translation", "insertion", "deletion" or "point mutation"

b) Propose a **hypothesis** for how this nucleotide change could result in white flowers at the molecular level. In your hypothesis, propose specific molecular interactions and cellular processes that would be impacted by the nucleotide change (2 or 3 sentences max). **SYNTHESIS**

The mutation could be in the promoter and prevent the basal/general transcription factors from binding and initiating transcription (partial credit for RNA polymerase). If there is no transcription of the pigment gene there will be no pigment protein and the plant would have white flowers.

+2 points for stating that the mutation is in an upstream noncoding region

+2 points for stating that the gene will not be transcribed

+2 points for stating that the general transcription factors will not be able to bind

*Note: need to connect the idea of no transcription back to the phenotype for full credit*

c) Interestingly you find that the forest species is pollinated by hummingbirds whereas the meadow species is pollinated only by bees. What could explain the continued presence of the white allele in the meadow plant population through several generations? **SYNTHESIS**

There may be fewer hummingbirds and more bees in the meadow. Therefore the flowers that can be pollinated by bees will have increased **reproductive success or fitness**, resulting in **natural selection** for the white allele in meadow grown plants.

*Note: need to connect the idea of the white allele and reproductive success or fitness for full credit*