BIOL 1550
Unit 4
Problem Set 4A

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This problem set has short answer, problem solving, fill in the blank, and multiple-choice questions. All multiple-choice questions have only 1 correct answer unless you are specifically asked to "select all that apply."

For all short answer and problem-solving questions, please show your work/reasoning to get full credit.

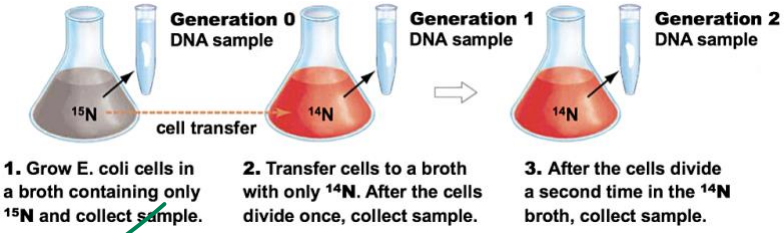
You are welcome to work with colleagues, but all work must be your own. You cannot copy others. You must be in accordance with Webster's academic honesty policy.

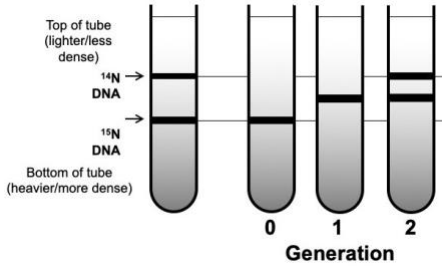
You must submit your answers as one document. You can edit this PDF on your computer or provide hand-written responses. If you choose the hand-written route, please be sure to compile your images into one document via a scanning app such as CamScanner or utilizing a word doc.

This problem set is worth 40 pts.

- ALL THE BEST & HAVE FUN! –

1. After the structure of DNA was discovered, three different models for how DNA could be replicated were proposed (shown above). Meselson and Stahl (1958) performed a classic experiment to test these models by growing E. coli bacteria in the presence of ^{15}N and ^{14}N nitrogen isotopes (nitrogen atoms that have a different number of neutrons and therefore different densities). Because DNA contains a lot of nitrogen, the density of the bacteria's DNA would be impacted by which isotope was present in the DNA. Generation 0 refers to DNA before replication, generation 1 after one round of replication, and generation 2 after two rounds. DNA samples were placed in test tubes and then spun in a centrifuge to separate DNA based on density (heavier DNA will settle toward the bottom), and results are shown below.





a. Why is the DNA band for Generation 1 shifted relative to the band for Generation 0? [1 pt]

Because the parental dna (heavy) splits and binds to the newly created (light) dna strand that causes the resulting double strand to take on the avg. of the 2.

b. Based on results, which model can you rule out after one round of replication? Why? [2 pts]

Conservation replication b/c the resulting dna strands would retain their original heavy & light weights

c. Why are there two DNA bands for Generation 2? [1 pt]

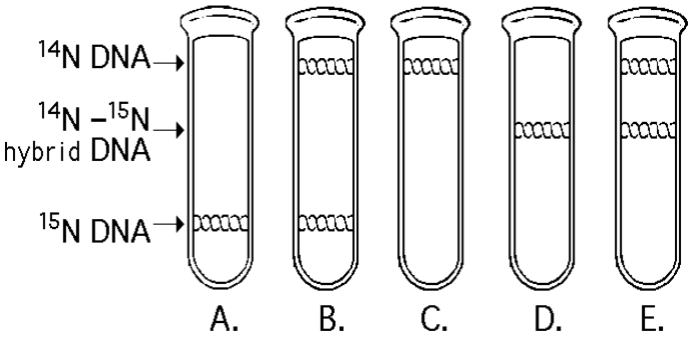
The light strand from the blended double helix binds w/ another light strand and the heavy strand binds w/ another light strand. Resulting in some light double helixes and some blended-weight double helixes.

newly created

d. Based on results, which model can you rule out after two rounds of replication? Why? [2 pts]

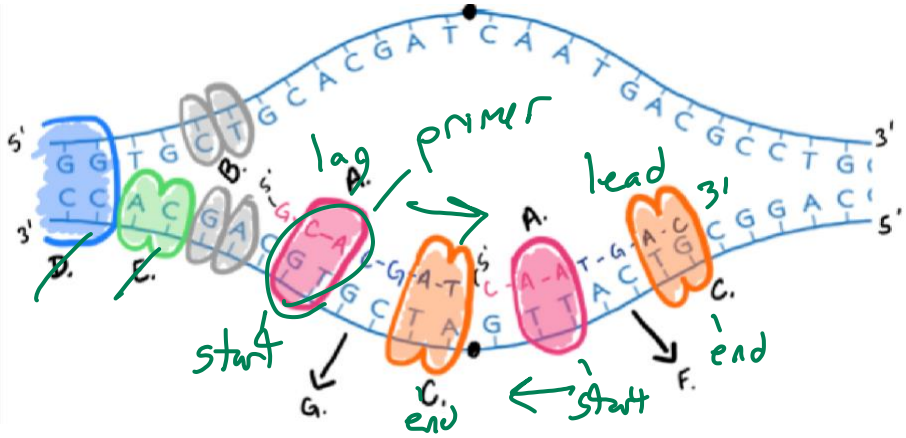
Dispersion. Because the weights would stay blended and the dna would get progressively lighter → 14N.

2. A space probe returns with a culture of a microorganism found on a distant planet. Analysis shows that it is a carbon-based life-form that has DNA. You grow the cells in ^{15}N medium for several generations and then transfer them to ^{14}N medium for one generation. Which pattern in figure would you expect if the DNA was replicated in a conservative manner? [1 pt]



Write the letter of your answer here: B

For questions 3-4, use the drawing of the replication bubble to the right. Fill in your answers to question 3 on the table below and write your responses to question 4 in the boxes provided.



3. Match the protein functions listed below (numbers 1-7) AND the location on the image of the replication bubble (letters A-G) with the correct protein.
***Note**: Some proteins are not pictured on the replication bubble. [0.5 pt for each correct box= 7 pts total]

Possible functions:

1. joins DNA fragments together
2. untwists and separates strands
3. holds DNA strands apart
4. synthesizes RNA primer
5. adds DNA nucleotides to new strands
6. relieves strain caused by unwinding
7. removes RNA primer and replaces it with DNA

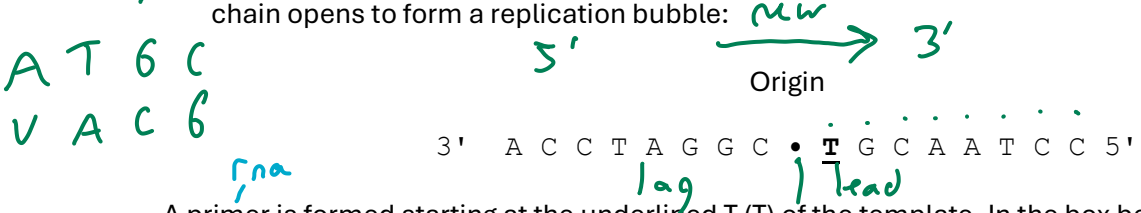
Protein	Protein Function Number	Location on Replication Bubble
Helicase	2	E
Single-strand binding proteins	3	B.
Primase	4	/
Topoisomerase	6	D
Ligase	1	/
DNA polymerase I	7	A
DNA polymerase III	5	C.

4. Using the replication bubble, write whether you agree or disagree with the following statements [1 pt each= 2 pts total]:

   a. The lagging strand is labeled with the letter G. Agree

   b. The leading strand is labeled with the letter F. Agree

5. At a specific area of a chromosome, the sequence of nucleotides below is present where the chain opens to form a replication bubble:



A primer is formed starting at the underlined T (T) of the template. In the box below, write out the sequence of the primer deposited by primase. This primer is **8 nucleotides long**. Make sure to indicate the 5' and 3' end of the sequence. [2 pts]

5'-ACGUUAGG-3'

6. A student isolates, purifies, and combines in a test tube a variety of molecules needed for DNA replication. When she adds some DNA to the mixture, replication occurs, but each DNA molecule consists of a normal strand paired with numerous segments of DNA a few hundred nucleotides long. What has she probably left out of the mixture? [1 pt]

   ○ DNA polymerase

   ● DNA ligase – leaves okazaki fragments unattached.

   ○ Okazaki fragments

   ○ primase

   Briefly explain your answer in a maximum of 2-3 sentences. [2 pts] (lead + okazaki fragments)

   Can't be primase b/c there are numerous segments of dna attached. Okazaki fragments wouldn't be added to the mixture. DNA polymerase is required to build any segment.

7. For number 7, please download and use the "HBB alignment" to answer these questions. This PDF shows an alignment of the Hemoglobin B (HBB) DNA sequence (non-template strand), the pre-mRNA sequence, and the RNA sequence of the HBB gene. Write your responses in the boxes below each question.

   a. Locate the transcription start site, what base is found at this position? [1 pt]

   A

   b. Where would you expect to find the promoter for the HBB gene? (Hint: provide a location using nucleotide numbers, not sequence) [1 pt]

   Just before the pre-rna sequence starts.

   ~130

   c. How many exons are in the HBB gene? How many introns? [2 pts]

   Exons: 3 Introns: 2

8. Fill in the following table to summarize each process. [0.5 pt for each correct box= 3 pts total]

Process	Template	Product	Synthesized Location in Eukaryotic Cell
Transcription	DNA	mRNA	Nucleus
Translation	mRNA	Proteins	Ribosome

B, E, R.

9. The short segment of double-stranded DNA shown below contains a very small gene. Write your responses to each question in the boxes below.

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5'-TACGCCGACATGGTTTTATACACCGCGCTCTAGTCTAATGA-3'
3'-ATGCGGCTGTACCAAAATATGTGGCGCGAGATCAGATTACT-5'
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a. The promoter for this gene is 3'-CGGC-5' and the terminator is 3'-ATTA-5'. Write the pre-mRNA produced during transcription in the box below. [2 pts]

5'-ACAUGGUUUUAUACACCGCGCUCUAGUCUAAU-3'

b. The introns for this gene are 5'-UAUA-3' and 5'-GCGC-3'. Write the mature mRNA that would be generated during mRNA processing in the box below. [2 pts]

5'-ACAUGGUUUCACCUCUAGUCUAAU-3'

c. Now translate this gene. Write the amino acid sequence of the protein coded for by this gene in the box below using the codon table at the end of the problem set. [2 pts]

Met, Val, Sec, Pro, Leu, Val, Stop

10. This mRNA sequence was transcribed from a small gene:

5'-GCGAUGCCUCAUCGAUAACCG-3'

How many amino acids does this mRNA code for? Use the codon table at the end of the problem set. [3 pts]

4

Met, Pro, His, Arg, stop

11. A gene has five exons. Exons #1 and #5 contain the start and stop codons, respectively. The RNA sequence below is for exon #3. The correct reading frame for exon #3 should not contain a stop codon. What is the amino acid sequence most likely coded for by this mRNA? Write the RNA sequence with corresponding amino acids. [3 pts]

mRNA

start

5' - UUAGUUAUUUACUGAAA - 3'

~~AGU, UAU, UUA, CUG, AAA~~

UAA
UAG
UGA

amino acids = Ser, Tyr, Leu, Leu, Lys

rna = 3'-AGU, UAU, UUA, CUG, AAA-5'

on mRNA

Second base in codon

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

UAC rna