

1. The base composition of a virus was found to be 11% A, 32% G, 18% U and 39% C. Is this a DNA or RNA virus? Is it single-stranded or double-stranded?

The presence of Uracil shows that it is RNA. The base composition is unequal, so it must be single stranded.

2. Which of these DNA fragments will have a higher melting temperature? (circle one)

A) GCATTGACCGGAGGGACT
CGTAACTGGCCTCCCTGA

B) GGATTTCAATTACTTAAT
CCTAAAGTTAATGAATTA

A has a higher melting temperature. The triple hydrogen bonds between G and C are harder to break, so fragments with higher GC content will have a higher melting temperature.

3. Here is a very short chromosome of a eukaryotic cell *that lacks telomerase*. Replication starts near x. One strand of the DNA has been labeled with heavy (15) N, hence the capital letters, but all newly synthesized DNA will have normal N.

5' aaaggg x ccctttggg 3'
3' TTTCCC X GGGAAACCC 5'

That cell divides to make two daughters, which in turn divide to make two granddaughter cells.

Draw the cell pedigree, showing this chromosome in the two daughter and four granddaughter cells. (*For the purposes of this question, assume that replication uses a primer that is only 3 bases long. Also, real chromosomes would have specific sequences at the ends- I just used these because they are easy to write down.*)

This question required you to put together two different concepts: semi-conservative replication and the function of telomerase.

Semi-conservative replication means that heavy N would be present in only one of the four granddaughter chromosomes.

The lack of telomerase meant that the new strands would be shorter at the 5' end each generation, leaving a 3' overhang. Because it is semi-conservative, the original strand is unchanged, however. So at the end you have a mix of short and long strands.

Assuming the primer is 3 bases long, the chromosomes will get shorter in multiples of 3.

Daughters

5' aaaggg x ccctttggg 3'
3' tttccc x gggaaa 5'

5' ggg x ccctttggg 3'
3' TTTCCC X GGGAAACCC 5'

Granddaughters

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5' aaaggg . . . . . x . . . . . ccctttggg 3' (P)
3' tttccc . . . . . x . . . . . gggaaa 5'

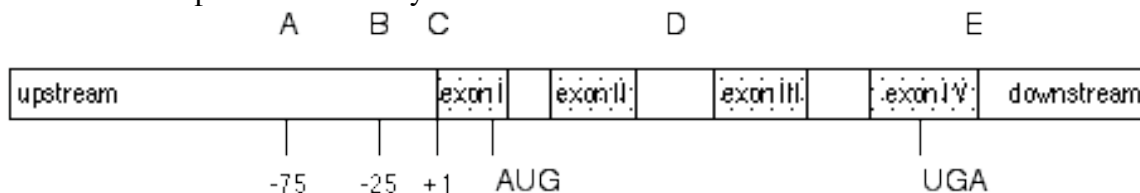
3' tttccc . . . . . x . . . . . gggaaa 5'
5'    ggg . . . . . x . . . . . aaattt 3'

5'    ggg . . . . . x . . . . . ccctttggg 3'
    ccc . . . . . x . . . . . gggaaa 5'

3' TTTCCC . . . . . X . . . . . GGGAAACCC 5'
5'    ggg . . . . . x . . . . . ccctttggg

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4) This diagram represents regions around a gene encoding an mRNA. Exon I of the mRNA contains the translation initiation AUG codon. Exon IV contains the UGA termination codon. The letters A through E above the diagram refer to areas of the gene and its transcript located directly below them.



- What region of the primary transcript is removed by a spliceosome? D
- What region of the DNA contains the TATA box? B
- Where is the poly (A) tail added to the transcript? E
- Where is the 5' cap added to the transcript? C

5) A eukaryotic structural gene has two introns and three exons:

exon1-intron1-exon2-intron2-exon3

The GU at the 5' end of intron2 has been mutated so it is no longer recognized. What would the mature mRNA look like in the wild type and in the mutant?

Wild type: 5'cap-exon1-exon2-exon3-poly(A) tail

Mutant: 5'cap-exon1-exon2-intron2-exon3-poly(A) tail

6) A geneticist isolates a gene that contains five exons. She then isolates the mature mRNA produced by this gene. After making the DNA single stranded, she mixes the single-stranded DNA and RNA. Some of the single-stranded DNA hybridizes (pairs) with the complementary mRNA. Draw a picture of what the DNA-RNA hybrids would look like under an electron microscope. Keep the drawing simple (i.e. a single line for

DNA and for RNA). *Hint:* think about how DNA and RNA might pair and where the complementary bases are.

Note that the DNA has introns, but the mRNA does not. Therefore the exons (of the template strand) can pair -with the mRNA but there is nothing for the introns to pair with. The result will be a DNA-RNA hybrid with paired exons and 4 loops of single strand DNA coming out (one for each intron).

7) Complete the following table:

Label the 5' and 3' ends of DNA and RNA and the amino and carboxyl ends of the protein. Assume it is read left to right and the columns represent transcriptional and translational alignments. (a copy of the codon table is on the last page of this exam)

DNA double helix	c	g	t	a	c	c	g	c	a	a	c	t
	g	c	a	t	g	g	c	g	t	t	g	a
mRNA	g	c	a	u	g	g	c	g	u	u	g	a
tRNA anticodon	c	g	u	a	c	c	g	c	a	a	c	u
Amino acid	Ala			trp			Arg			(stop)		

Note that the T:U alignment shows that row 2 must be the coding strand and row 1 must be the template. Also the codon table shows the sequence in the mRNA, not the tRNA.

8) An anticodon of a tRNA has the sequence 5'GCA3'.

a. What amino acid does this tRNA carry? Codon = 5'UGC3' = Cysteine

b. What would be the effect of a mutation that changes the C to an A?

The anticodon would then recognize UUC = Phenylalanine. However the tRNA that mutated still carries a Cysteine at the 3' end. The mutated tRNA will recognize Phe sites, but put a Cys onto the growing polypeptide. The resulting protein will have incorrect amino acids.

At the same time, there will be some normal Phe tRNAs, so a mixture of polypeptides will be produced, some with incorrect amino acids and some with the correct amino acids.

9) One phrase is enough for these:

a. How do prokaryotic ribosomes recognize the 5' end of the messenger RNA?

Shine delgarno sequence and the AUG start codon

b. How do eukaryotic ribosomes recognize the 5' end of the messenger RNAs?

They start at the 5' methylG cap and "scan" down the message until they get to the AUG.

10) The antibiotic erythromycin disrupts protein synthesis by preventing ribosomal translocation – movement of the ribosome relative to the mRNA. It *does not affect any other step* in protein synthesis. Suppose you are doing a translation reaction *in vitro* and you add erythromycin just before the 3rd bond is about to be made. You wait a few minutes and look at the ribosome.

- a. The carboxyl end of AA #3 should now be covalently bonded *directly* to (tRNA #2) (tRNA #3) (tRNA #4) (AA #2) (AA #3) (**AA #4**) (none of these).

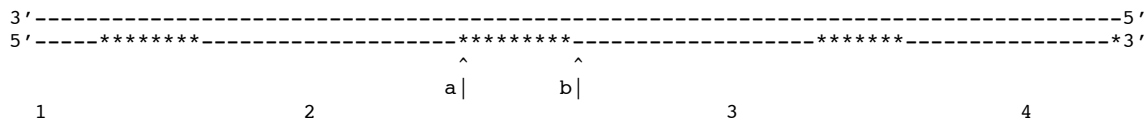
It starts out attached to tRNA#3, but is transferred to AA#4 as soon as it arrives.

- b. Which tRNA will you find in the A site? (tRNA #1) (tRNA #2) (tRNA #3) (**tRNA #4**) (tRNA #5).

- c. The tRNA in the A site will carry (an amino acid) (**a polypeptide**) (neither) (either one).

Initially, the tRNA simply carries an amino acid, but then the growing polypeptide is transferred to the A site before translocation. That peptide bond can still be formed in the presence of erythromycin.

11. Here is a short stretch of replicating DNA from the bacterium *E. coli*. The top strand is the template. Assume the ***** are the RNA primers. This shows parts of four Okazaki fragments.



Which was made first, the Left or the Right fragment? **RIGHT**_____

Which primer will be the first to be removed, Left, Middle, or Right? **RIGHT**_____

When the primer in the middle is removed and filled in with DNA, the fragments must then be joined.

Which enzyme removes the RNA primer? **DNA polymerase I**_____

Which enzyme joins the fragments? **ligase**_____

Where is the final connection made? (a or b?) **B**_____