

Name/ID: _____

1. Describe at least three different ways that gene expression can be regulated in eukaryotic cells.

Gene expression can be regulated anywhere along the pathway of the central dogma, including transcription (such as chromatin structure or transcription factors), mRNA processing (such as alternative splicing), translation (such as blocking the process), and even after translation (such as modifying proteins). External signals (such as hormones) can also regulate gene expression.

2. Which eukaryotic structures could be interfered with to prevent translation of mature mRNAs?

Translation could be interrupted by interfering with the mature mRNAs, tRNAs, or ribosomes.

3. Which of the major molecules involved in gene expression (DNA, pre-mRNA, mature mRNA, protein) would change if a mutation that does not impact splicing occurs in an intron? Explain.

Mutations are permanent changes in DNA, and introns are transcribed into pre-mRNA, so both of those molecules would have different sequences. Because the spliceosome removes introns from pre-mRNA during processing, the mature mRNA and resulting protein would not change.

4. A small gene codes for Met-Phe-Tyr-Ile-Thr-Val-Ala, but following a single point mutation, the product becomes Met-Phe-Ser-Leu-Arg. What type of point mutation occurred? Explain.

If the changes are due to a single point mutation, it had to be a frameshift (addition or deletion of nucleotides). For example, a deletion in the codon for tyrosine would explain these changes.

5. If leucine replaces tryptophan as the fifth amino acid in a protein due to a single point mutation in the associated gene, can you determine which nucleotide was mutated in the codon? Explain.

Tryptophan has one codon (UGG), and leucine has six codons (UUA, UUG, CUU, CUC, CUA, and CUG). There is only one way for this amino acid substitution to occur by changing a single nucleotide (UGG replaced by UUG), so the second nucleotide was mutated in the DNA codon.

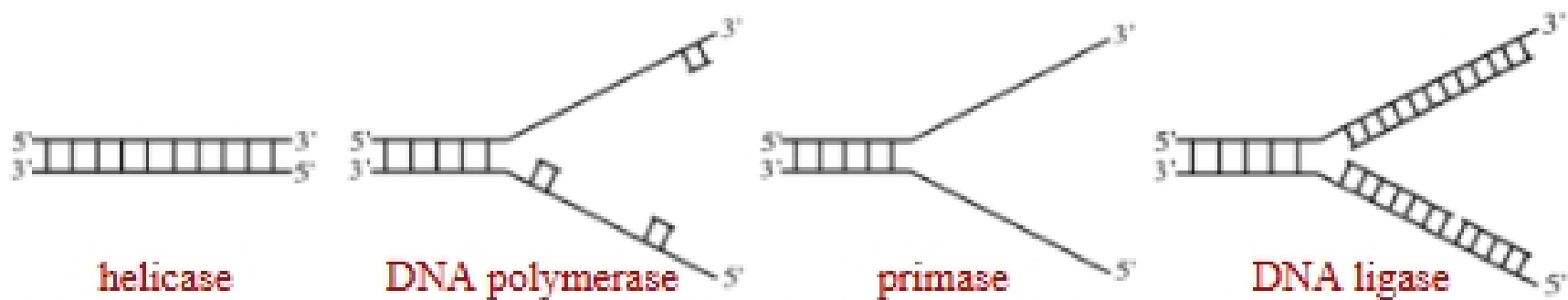
6. Which point mutations that affect the coding regions of genes (missense, nonsense, frameshift, silent mutations) are the most predictable in terms of their impact on protein function? Explain.

Silent mutations are the most predictable, since the resulting protein does not change. Nonsense and frameshift mutations usually result in a nonfunctional protein, unless only the amino acids at the end of a protein are affected. Missense mutations are the least predictable, since changing one amino acid for another could have negative, neutral, or positive effects on protein function.

7. Which genetic code property creates the possibility of frameshift mutations in genes? Explain.

Frameshift mutations are caused by an addition or deletion of nucleotides in the coding region of a gene. Such a change would only impact a few amino acids if codons overlapped with each other, but because the genetic code is nonoverlapping, the result is a shift in the reading frame.

8. Determine which replication enzyme was not functional at each replication fork shown below.

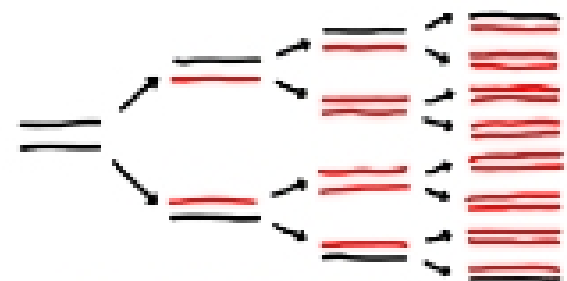


9. Which of the major replication enzymes (DNA polymerase, helicase, primase, topoisomerase, DNA ligase, telomerase) is not required to replicate the circular DNA of prokaryotes? Explain.

Replication is a very similar process in prokaryotes and eukaryotes, but because circular DNA has no ends, telomerase is not required to finish replicating the lagging strands in prokaryotes.

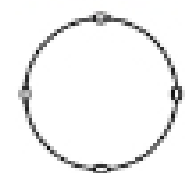
10. If a nonradioactive DNA molecule is replicated three times when only radioactive nucleotides are available, how many of the eight DNA molecules will contain nonradioactive nucleotides?

Replication is semiconservative (strands separate and are used as templates to make complementary strands). After three replications, two DNA molecules will have original nucleotides that are nonradioactive (black in the picture).



11. Four replication bubbles form in the circular DNA of a bacterium, and a replication fork moves 450 base pairs per second. How long would it take to replicate 5.4 million base pairs of DNA?

There are eight replication forks in this case, so the time calculation would be:
 $5,400,000 \text{ bp} / (8 \times 450 \text{ bp per second}) / (60 \text{ seconds per minute}) = 25 \text{ minutes}.$



12. Explain why the replication enzymes other than DNA (Taq) polymerase are not used for PCR.

primase: Primers are DNA rather than RNA and are designed for PCR.

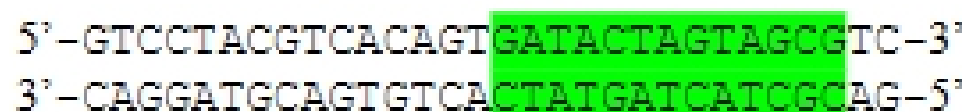
telomerase: PCR does not have lagging strands produced in fragments.

topoisomerase: Heat can separate the DNA strands without unwinding.

DNA ligase: Primers are DNA instead of RNA and cannot be removed.

helicase: Heat is used to separate the DNA strands without unwinding.

13. If you perform a polymerase chain reaction (PCR) on the DNA shown below using the primers 5'-GATAC-3' and 5'-CGCTA-3', you would produce up to a billion copies of what product?



PCR amplifies target regions bracketed by the two primers (which are included in the product).

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Explain or provide examples for each.
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