

12 two part questions (as before): 4 points for the correct multiple choice, 3 points for a coherent and correct explanation of why a particular wrong response is wrong.



1. If genetic information were encoded in the living structure of cells, rather than in the sequence of DNA molecules, Griffith's studies on transformation in bacteria ...

- ☐ would not have been effected
- ☐ would not have worked
- ☐ would have identified proteins as the genetic material
- ☐ would have proved that evolution was impossible
- ☐ no idea

_____ is wrong because

2. A mutation occurs that leads to higher rates of mutation in actively dividing cells, but has no obvious effect in non-dividing cells. You would be justified in assuming that the mutation ...

- ☐ inactivated the DNA-dependent DNA polymerase
- ☐ inactivated the proof-reading activity associated with DNA polymerase
- ☐ inactivated DNA-dependent, RNA polymerase
- ☐ inactivated DNA repair enzymes
- ☐ no idea

_____ is wrong because

3. Non-sense suppressor mutations ...

- ☐ alter a tRNA's anti-codon
- ☐ alters the rate that DNA-dependent, RNA polymerase synthesizes RNA
- ☐ alter the ability of a ribosome to recognize an messenger RNA
- ☐ alters the specificity of an aminoacyl-tRNA synthetase
- ☐ no idea

_____ is wrong because

4. To say that a protein has a short half-life means....

- ☐ it is rarely synthesized
- ☐ it is inactive except in the presence of an allosteric effector
- ☐ it is short
- ☐ it is rapidly degraded
- ☐ no idea

_____ is wrong because

5. A mutation occurs in the region of a gene that is recognized by a negatively-acting transcription factor; such a mutation would most likely

- ☐ increase the rate of transcription in all genes
- ☐ decrease the rate of transcription of the mutant gene
- ☐ decrease the rate of translation of the mutant mRNA
- ☐ increase the rate of transcription in the mutant gene
- ☐ no idea

_____ is wrong because

6. You have two genes, *aya* and *bub*. Both encode cytoplasmic polypeptides (AYA and BUB). The rates of transcription and translation are similar. The BUB polypeptide is 10 times longer than the AYA polypeptide. PREDICT the overall rate of AYA synthesis (# of polypeptides made per minute) compared to the BUB synthesis.

- ☐ both rates are similar
- ☐ AYA synthesis is 10 time faster than BUB synthesis
- ☐ AYA synthesis is more than 10 time faster than BUB synthesis
- ☐ the BUB synthesis rate is faster than that for AYA
- ☐ no idea

_____ is wrong because

7. A mutation occurs in the region of a polypeptide that, in the normal case, is buried within the molecule's interior. The mutation replaces a hydrophobic amino acid with a positively charged amino acid. You would be justified in predicting that such a mutation would ...

- ☐ alter the polypeptide's location within the cell
- ☐ have little effect on the polypeptide's three dimensional structure
- ☐ function normally since it only effects the polypeptide's primary structure
- ☐ produce a dramatic change in protein folding and activity
- ☐ no idea

_____ is wrong because

8. Mutations can occur throughout the sequence of gene. Consider a non-sense mutation that occurs at codon 42 of a 544 amino acid long polypeptide, and consider a similar mutation that occurs at codon 536 of a the same polypeptide. You would be justified in predicting that ...

- ☐ both mutations would have similar effects on polypeptide function
- ☐ the mutation at codon 42 would have a more severe effect
- ☐ the mutation at codon 536 would have a more severe effect
- ☐ more information is required to answer this question
- ☐ no idea

_____ is wrong because

9. Assume an organism used single-stranded DNA (rather than double stranded DNA) as its genetic material. If you knew the percentage of A in the DNA of that organism, you would know

- ☐ the percentage of T
- ☐ the percentage of G
- ☐ the percentage of C
- ☐ the percentage of C + G
- ☐ nothing else (or rather the percentage of T + C + G)
- ☐ no idea

_____ is wrong because

10. Assume that mutations in a single gene, encoding a polypeptide, are responsible for the change from the disease causing (virulent) S strain of Streptococcus to avirulent R strains. Based on this information you would predict that

- ☐ the rate of S to R mutation are more frequent than R to S mutations
- ☐ the rate of R to S mutation are more frequent than S to R mutation
- ☐ R to S and S to R mutations occurs with equal frequency
- ☐ only nonsense mutations at the start of the gene's coding region can explain the S to R phenotype
- ☐ no idea

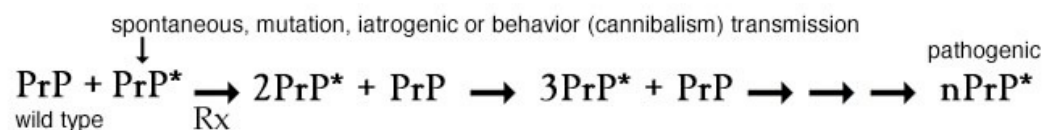
_____ is wrong because

11. Through the studies of Avery et al, it became clear the molecules that carried genetic information in cells were nuclease sensitive. Knowing what we now know about prion disease, which type of enzyme would be most likely to destroy the “infectious” activity of a disease sample?

- ☐ protease
- ☐ nuclease
- ☐ lipase
- ☐ reverse transcriptase
- ☐ no idea

_____ is wrong because

12. In prion disease wild type PrP is converted into the pathogenic PrP*



form. This reaction can be influenced by mutation; alternatively the formation of PrP* can be initiated by surgical or behavioral “infection”. Once present PrP* drives the transformation of PrP into PrP* (Rx). In the case of cannibalism-based disease vast majority of the PrP* found in the sick person differs from PrP...

- ☐ in its primary structure
- ☐ in its secondary and tertiary structure
- ☐ in the sequence of the gene that encodes PrP
- ☐ no idea

_____ is wrong because

