Molecular Biology Midterm 5

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Base in anticodon, 1st position.	Base(s) in codon, 3rd position.
G	CU
C	G
A	U
U	AG
I	AUC

1. (1 pt.) Consider a single tRNA that can read both glutamine (Gln) codons. What is the anticodon? Make sure the sequence direction is clear. Assume that the E. coli wobble rules (above) are used.

2. (2 pts.) In discussing the roles of proteins in biological systems, a common point is that enzymes catalyze reactions -- speed them up. Yet we spent considerable time on a case where a role of a protein is to slow a reaction down. What is the "purpose" of this? That is, why is it "good" to slow down the reaction? Discuss a specific example: what is slowed down, by what, and why? [In grading this, I will look for two key points: a meaningful discussion of the biological advantage of slowing the reaction down, and a recognition of where this occurs. I do not need much detail about how the slowing down occurs, so long as the other points are made. The question is not intended to be semantic (e.g., about the meaning of the word "enzyme"), but to address a substantive biological issue.]

3. (2 pts., 1 pt. per part) Consider one codon in a coding sequence. It codes for some amino acid X. You mutate this codon. Each mutant carries a single base change (not addition or deletion); the collection of mutants contains all possible such single base changes.

⇒ As noted more specifically below, the intent is that you do part a without looking at the code, and part b using the code.

a. In principle, what is the maximum possible number of new amino acids that you could get at this position. Explain, in terms of the general nature of the genetic code. [This part is intended to deal with a logical argument about the code, not with any specific codons. That is, you should do this part without looking at the code; quoting anything from the code is likely to hurt your answer here.]

b. In practice, you are likely to get fewer new amino acids than the "theory" (part a) allows. Why? Give a specific example; state the starting codon and its amino acid, and give the specific changes that result in fewer new amino acids than predicted in part a.

4. (2 pts.; 1 pt. per part) You have a bacterial strain (#1) that carries a point mutation in the *lacZ* gene. As a result, the strain is Lac^-. You construct two derivatives of strain #1. Each carries a plasmid. In strain #2, the plasmid codes for a glutamine tRNA that recognizes the "amber" termination codon, UAG. In strain #3, the plasmid codes for a serine tRNA that recognizes the amber codon. (Assume that both of these tRNAs are made at the same level, which is "ok".) You find that strain #2 is Lac^+, whereas #3 remains Lac^-.

> [The only significance of "Lac" in this question is that the phenotype is easy to detect. You need not know anything specific about the Lac system.]

a. What do you conclude about the original *lacZ* mutation -- based on strain #2 being Lac^+? (That is, what is at the mutated site?) Explain.

b. What do you conclude about the protein -- based on strain #3 being Lac^-? Explain.

5. (5 pts.) The following parts deal with an ordinary DNA replication fork. The general plan of the question is to draw a replication fork, and then describe individual features of it. Read over all the parts before drawing part a; that will help you to include the appropriate level of detail the first time around.

a. (No points for this, per se; features of it will be scored for the following parts.) Sketch a replication fork. The level of detail needed is defined by what follows; that is, the sketch here must be adequate for the following parts.

Each of the following parts is 1 pt. Each requires some labeling of your sketch in part a. Some also require an explanation.

b. Label the 5′ end of each DNA strand (new and parental). (Be sure it is clear.)

c. Label the leading and lagging strands.

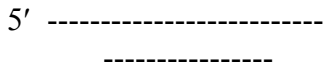
d. Label the DNA helicase. Briefly explain what it does (and, therefore, why it is where it is at the fork).

e. Label the “sliding clamps”. Briefly explain what they do.

f. Label a DNA ligase. Briefly explain what it does (in this context).

6. (1 pt.; no credit without explanation) As a public service, you are trying to develop a process to degrade chad. You isolate the key enzyme for degrading chad (probably a cellulase), and find that the first amino acid (N-terminus) is serine. What is the one codon that is most likely used for initiation when the mRNA for this protein is translated? Explain. (Note: There is only one acceptable answer, and it is clearly defined by the statement of the problem.)

7. (3 pts.; 1 pt. per part; no partial credit in parts a or b) The piece of DNA sketched below is mostly double stranded, but it has single stranded tails.



The following parts focus on the four chain ends in the sketch above.

⇒ In parts a and b, "which" may mean any number from none to all; mark all that apply, and be sure your answers are well-labeled. Show your answer(s) by putting a labeled arrow at each relevant end. No explanation required. (Assume that the ends are suitable for polymerase action, i.e., OH-group or phosphate as required. Do not assume any specific DNA sequences.) As noted above, no partial credit for parts a and b.

a. At which of these ends can (ordinary) DNA polymerase extend the chain?

b. At which of these ends can telomerase act?

c. How is it that telomerase can act at an end at which ordinary DNA polymerase cannot act? That is, what feature of the telomerase enzyme allows it to act here?

8. (1 millipoint) The shape of the state of Florida is "similar" to the shape of which common macromolecule (from current chapters)?