UC Extension Mol Biol X107A Test #1, 10/12/00. Name:
(Please print)

Total points: 18 ARE YOU REGISTERED? _____

General

- Closed book. You may use one page of your own notes.
- If in doubt about what a question means, please ask.
- Your reasons are as important as your answers. If in doubt, say more, not less, about what you do and why. (Some questions request a simple answer and an explanation. It's the explanation that is important. No credit for answer without a requested explanation.)
- If you change your mind, please make clear what I'm supposed to read.
- Extra paper is available. Just put your name and the question number on it.

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1. (4 pts.; 2 pts. per part) Hamsters kept in the lab with a normal light-dark cycle (like a day) will start to exercise about 15 min after dark. In the absence of a light-dark cycle (for example, if kept in constant darkness), they will start to exercise about every 24 hr. Thus they have an internal clock, which appears to be set to 24 hr. All discussion below refers to this internal clock, whose operation is apparent in the absence of the light-dark cycle.

In a lab population, one hamster was found which exercised every 22 hr. Breeding of this hamster led to some hamsters which exercised every 20 hr. These observations could be explained by postulating a "clock" gene, which is called τ (tau) and behaves as an ordinary Mendelian gene. (Assume that only one kind of defective allele is relevant here.)

a. What is the genotype for each of the three hamster phenotypes discussed above?

Phenotype	Genotype

b. The original observation involved only one "22 hr" hamster. It took two successive crosses to get a "20 hr" hamster. Describe the first of these. Who are the parents (for the cross)? What will be the progeny, and what are the (statistically) expected percentages of each kind? Include a gamete matrix in your explanation. (Note: part b depends heavily on your answer to part a. If you are having trouble with both, please see me during the test.)

2. (6 pts.; continues on next page) In this question the individual DNA strands that are mentioned are all single-stranded (SS), and about 40 nucleotides (nt) long. The exact length is not critical for us; however, it is short enough that longer DS regions are significantly more stable than short DS regions.

Assume that strand directions are what you need. One part will ask about strand direction, but otherwise don't worry about it.

Consider, to start, three DNA strands, called 1, 2, and 3. One end (nearly half of the sequence) of strand 2 is complementary to one half of strand 1. One end of strand 3 is complementary to the other half of strand 1.

⇒ Space for answers is on the next page.

a. (1 pt.) Sketch the structure that these three strands will form. The key point is to show SS and DS regions. Align the strands so that strands 2 and 3 each have a "tail", extending beyond strand 1 -- in opposite directions. Labels the three strands (1, 2, 3).

> This is somewhat confusing! I suggest that you have me check your answer to this part, to see that you are on the right track.

b. (1 pt.; probably no partial credit) Label the two ends of each strand (# 1, 2, 3) as to whether they are 5′ or 3′. To start, label any one end whichever you want. Then label all the other ends to be consistent with that. Do this by labeling your sketch in part a. (Again, the strand polarities are not relevant to any other part of this question. In the other parts, we will simply assume that all polarities are "ok".)

> Parts c and d are closely related, and must agree with each other. You may want to think about them together.

c. (1/2 pt.) Look at the structure from part a, and consider strand 1. Which part(s) of strand 1 is/are in a relatively rigid structure, and which is/are in a relatively flexible structure? Label the sketch in part a, to show the rigid and flexible parts of strand 1.

d. (1/2 pt.) Fold the structure from part a so that the two SS tails are both pointing in (approximately) the same direction -- say, to the right of your sketch. (In folding the part a structure, be sure to make use of what you said in part c.)

e. (1 pt.) Now add strand 4. One end of strand 4 is "approximately" complementary to the tail of strand 2 (part d); the other end of strand 4 is "approximately" complementary to the tail of strand 3. Show the structure that results from strand 4 being added to what you already had in part d. (Label all the strands, 1-4.)

f. (1 pt.) Now add strand 5 -- which is the precise complement of strand 4. Draw the resulting product(s) (hint!) of adding strand 5 to what you formed in part e. (Label all the strands, 1-5.)

parts a, b, c:	part d:
part e:	part f:

g. (1 pt.) You now continue to add, alternating… strand 4 and then strand 5, and then strand 4 and then strand 5, etc. What happens? In particular what happens to the distance between the two ends of strand 1 as you successively add strand 4 and then strand 5, etc? (Hint: can you use the word "tweezers" in your explanation?)

3. (3 pts., 1 pt. per part) Consider a protein molecule. What kind of bonding force is primarily responsible for each of the following: [It is sufficient to name the bond type, using standard chemical terminology, such as covalent, hydrogen bond, London forces, etc. (However, the term "van der Waals force" requires an explanation, since it has two distinct meanings.) Or you may describe the bonding forces.]

a. The general shape of an alpha helix region of the protein?

b. The fact that the side chains of amino acids such as alanine (R = $-CH_3$) and leucine (R = $-C_4H_9$ tend to be buried deep inside a folded protein?

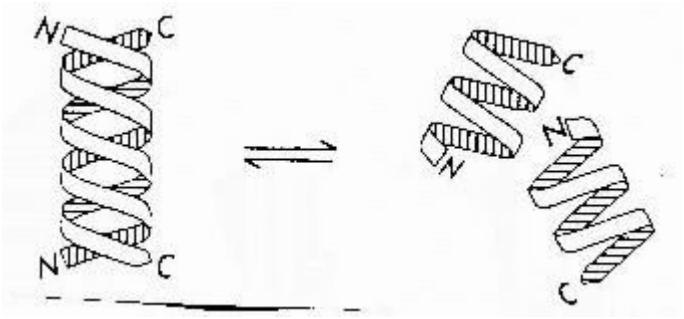
c. The attachment of one amino acid to the next along a single peptide chain?

4. (1 pt.; no credit without explanation) Some viruses have SS RNA as their genetic material (instead of DS DNA). There are two general strategies used by such RNA viruses for replicating…

1. SS RNA (that is, the viral RNA) → DS RNA → more DS RNA → SS (viral) RNA.
2. SS RNA → RNA-DNA hybrid (DS, 1 strand of each) → DS DNA → SS (viral) RNA.

Is there any logical difference between these two pathways, in terms of information flow? That is, do we need to learn any new principles of biological information to deal with one or the other of them? Explain.

5. (2 pts.) Gramicidin A is a peptide antibiotic. It can exist in various forms, as shown at the right. [N and C refer to the amino terminus and carboxyl terminus of the peptide chain.]



a. (1 pt.) What is the handedness of the DS gramicidin helix?

b. (1/2 pt.) The handedness of the DS gramicidin helix is the same as for which DNA structure (B or Z)? Choose correct term from parentheses. (Use your answer to part a as the starting point for this.)

c. (1/2 pt.) The two strands shown here are (parallel OR antiparallel).

6. (2 pts.; no credit without relevant sketch) *Alphabeticus romanus* is particularly convenient for genetics problems (even though no living specimens are available, thus precluding experimental work). Chromosome 3 contains the genes P through T (in alphabetical order, of course -- and equally spaced). Consider a cross between two alphies, one with the "a" allele for each gene (i.e., $P^aQ^a…T^a$) and one with the "b" allele for each gene.

How many crossover events are required to produce a $P^bQ^aR^bS^bT^a$ recombinant chromosome? Sketch the two chromosomes, and show all the genes and their alleles. Show the crossovers that give the desired event. [Show the minimum number required. Obviously, many larger numbers would also work.]

Any comments/suggestions/gripes on the course, either content or form?? (Or turn in any comments separately next time -- or any time.)