Problem-solving guideline

- Your first order of business is to understand what exactly is being asked. Read the question carefully! Ask yourself -- do I already have all the information I need in order to answer the question? Is there something I need to figure out before I can answer the question?
- After you have answered the question, check your answer to see if anything that was said in the question contradicts anything you have said in your answer.
- If you can, work with a partner or a few other students. If you get stuck on a problem, figure out where you are stuck.
- If you have trouble with a problem(s), come to office hours.
- Do the problem sets week by week; don't wait until right before an exam.
- Don't do the problems with the posted answers in front of you.
- If you make up allele designations, be very clear on what your allele symbols mean (which allele is associated with which phenotype, and dominant vs. recessive).

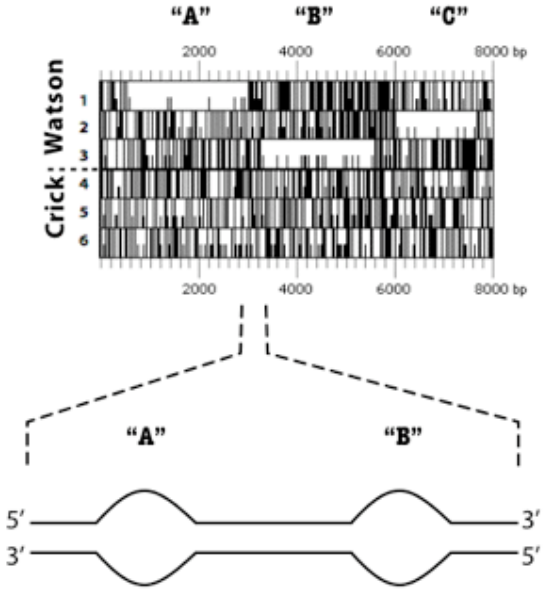
Some common mistakes

- Looking at the question and panicking because the answer is not obvious immediately. In reality, more often than not, there will not be a shortcut--getting to the answer will require a logical progression.
- Answering something that was not asked, and not answering what was really asked (i.e., not reading the question carefully)
- Answers that are not internally consistent -- i.e., answers that contradict themselves. For example, if you identify one parent of a cross as being homozygous dominant, and later on in your answer you say that the progeny of that cross are going to show the recessive phenotype, that's an internally inconsistent answer unless you also explain why the offspring don't express the dominant allele.
- Failing to demonstrate your logic. When we grade your answers, we are more interested in seeing whether you understand how to answer the question, than in whether you got the numerically correct answer. You may have made a mathematical error along the way -- but if you've shown your work, and we can see that your logic was correct, you'll probably get close to full credit. If you didn't show your work, all we can see is the final incorrect answer -- you get NO credit.

1. A 6-frame translation map of a segment of DNA is shown, with three open reading frames (A, B, and C). ORFs A and B are known to be in separate genes.

1a. Two transcription bubbles are shown, one in ORF A and one in ORF B. In the transcription bubble diagram, mark the following:

- the location of RNA polymerase on the appropriate strand in each bubble
- the RNA transcripts to show the relative lengths of RNA made by those two polymerases



1b. Are the promoters for ORFs A and/or B present in the DNA region shown in this diagram?

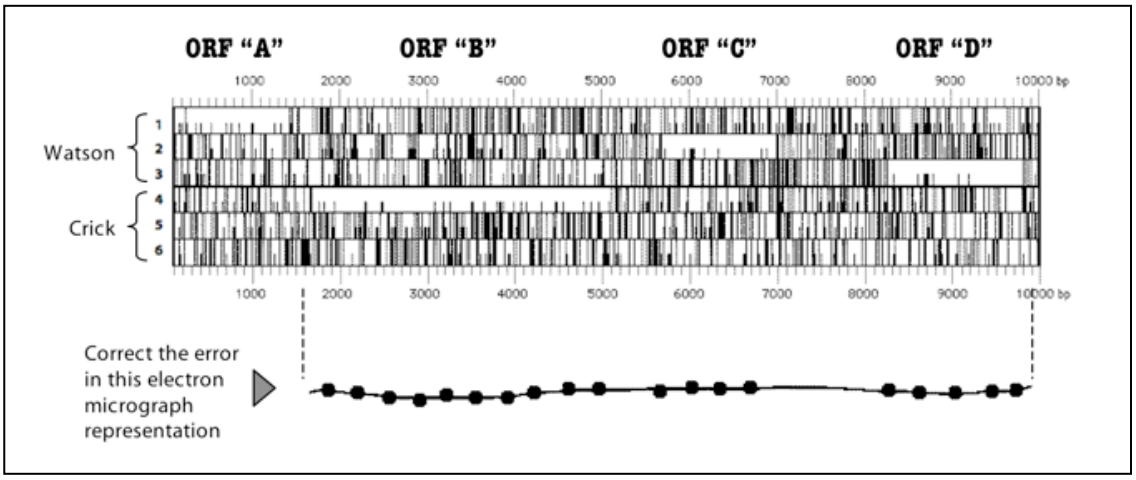
Promoter for A: Present? Yes No (circle one)
If present, mark its location and label it.

Promoter for B: Present? Yes No (circle one)
If present, mark its location and label it.

1c. Electron microscopy experiments failed to show RNA polymerases over the ORF "C" region of DNA. State whether each of the three explanations listed below is valid or not, explaining as necessary:

Explanation	If valid, just write "Valid." If invalid, BRIEFLY explain why.
ORFs B and C are exons of the same gene and a splicing error causes ORF C to be left out.	
ORF C has a mutation in its start (ATG) codon, preventing transcription.	
ORF C has a promoter mutation preventing transcription.	

2. A 6-frame translation map of a portion of a yeast genome is shown. The four potential open reading frames in this region (ORFs A, B, C, D) are indicated; ORFs **C** and **D** are known to be **exons of the same gene.**



2a. The diagram below the ORF map represents an electron micrograph of DNA from the region including ORFs B-D; black dots represent RNA polymerases. You will be asked to draw RNA transcripts next--but first, correct the error in the diagram and explain below why you think it is an error.

Your explanation:

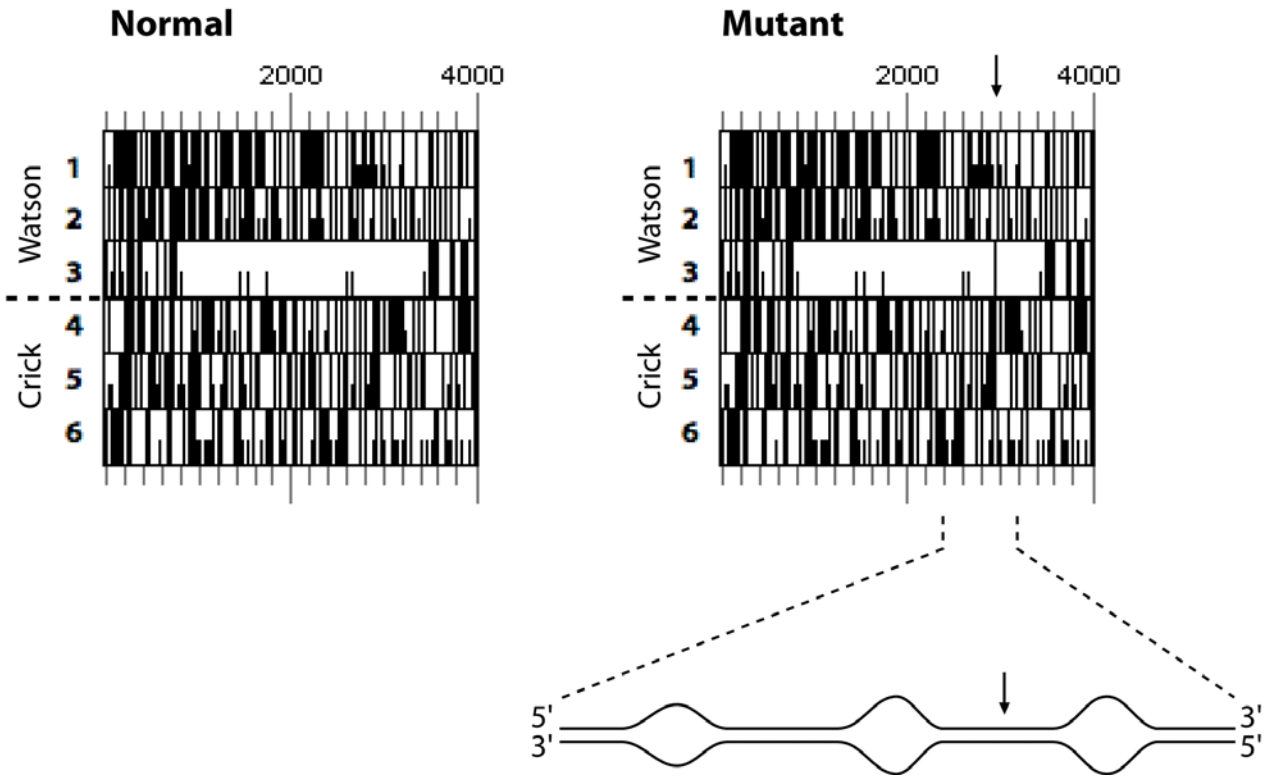
2b. Complete your corrected diagram to show RNA transcripts of relatively correct length on the RNA polymerases.

2c. Several electron micrographs of **ORF "A"** DNA taken at the same time as that in part (a) did not show any RNA polymerases over ORF "A". Of the possible explanations (listed below) for this observation, cross out *all* the ones that you think are not reasonable, and BRIEFLY explain why [just for the unreasonable one(s)]:

Explanation	Why unreasonable (if unreasonable)
The promoter is not included in the region that is shown, so transcription could not occur	
ORF "A" is actually a tRNA gene, so it will never have RNA polymerases on it	

ORF "A" is for a gene that was not being transcribed at the time that the electron microscopy was done.

3. This question concerns a mutation in a gene that creates a premature stop codon. A 6-frame translation map was made of the region containing that gene from normal and from mutant cells as depicted below (arrow marks the location of premature stop codon; assume that the gene does not have an intron):



(**3a**) Three potential transcription bubbles are shown for the region containing the premature stop codon mutation (arrow marks the location of the mutation). In each bubble that you think could contain an active RNA polymerase, draw RNA polymerase and nascent transcripts on the appropriate strand and mark the 5' and 3' ends of the RNA.

(**3b**) Draw an arrow below the diagram to clearly indicate the direction of transcription.

(**3c**) Where is the promoter in relation to the open reading frame of this gene? On the "Normal" 6-frame translation map above, mark the approximate location of the promoter by drawing a box around the appropriate strand or strands.

4. Below is a 22 basepair sequence of DNA that is transcribed to make a 22 base mRNA:

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5′ AGGTAAAATGCATAAATAGCCA 3′
3′ TCCATTTTACGTATTTATCGGT 5′
        |     |     |     |
        5     10    15    20
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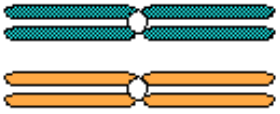
(4a) Write the mRNA sequence that could encode a peptide of 3 amino acids, and indicate with brackets the 3 codons for these amino acids.

(4b) A mutation occurs that adds a T at position 2 on the Watson strand between the A and G. What is the likely consequence on the translation of the peptide indicated in (a)?

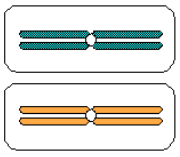
(4c) A different mutation to the original sequence changes base 2 on the Watson strand from G to T. Compared to the original sequence above, would the transcript from this mutant sequence likely have more or fewer associated ribosomes, and why?

(4d) A different mutation to the original sequence changes base 10 on the Watson strand from a G to a C. What is the consequence for translation of the peptide indicated in (a)?

5. Shown here is a pair of homologous chromosomes in a cell soon to undergo division: (only chromosomes are shown; crossovers, if present, are not shown).

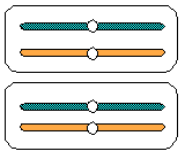


5a. After the ensuing anaphase and telophase, you find that the daughter cells have the following configuration (pretending for the sake of this question that you could actually detect chromosomes in telophase):



Was the division mitosis or meiosis? Explain.

5b. Suppose, instead, that they had this configuration:



Again, was the division mitosis or meiosis? Explain.