

Biol 505

EXAM 1 (100 points): Due Wed 10/14/09 at the beginning of class. Hard copy only.

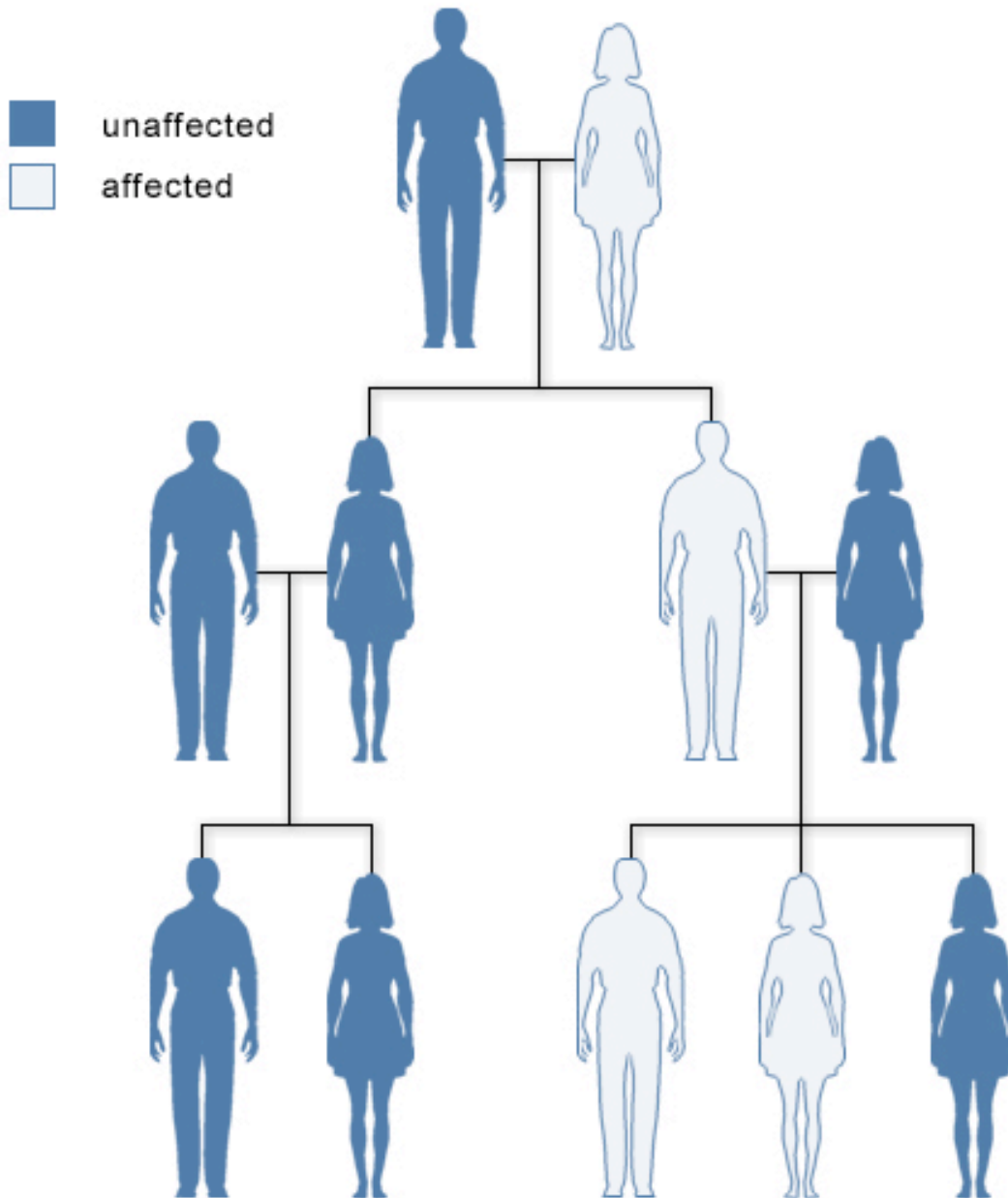
Although this is an open book/open note exam, you are taking this exam under the honor system, which requires that you refrain from sharing any information regarding the exam with any of your classmates. The honor system also requires that you report any infractions of this code to me. Even the appearance of academic dishonesty (e.g., identical wrong answers) will be taken seriously and dealt with accordingly. Please use your own words when answering questions and do not plagiarize from texts or the internet.

Part I: Molecular Genetics (60 points)

1. Outline the relations between genes, DNA, and chromosomes.
2. Compare and contrast genotype and phenotype.
3. What is semiconservative replication?
4. Draw a molecule of DNA undergoing eukaryotic linear replication. On your drawing, identify (1) origin, (2) polarity (5' and 3' ends) of all template strands and newly synthesized strands, (3) leading and lagging strands, (4) Okazaki fragments, and (5) location of primers.
5. What are the major classes of RNA? Where would you expect to find each class of RNA within eukaryotic cells?
6. Compare and contrast transcription and DNA replication. How are these processes similar and how are they different.
7. The following sequence of nucleotides is found in a single-stranded DNA template: A T T G C C A G A T C A T C C C A A T A G A T. Assume that RNA polymerase proceeds along this template from left to right. Which end of the DNA template is 5' and which end is 3'? Give the sequence and label the 5' and 3' ends of the RNA copied from this template DNA. As far as you are able determine the amino acid sequence using the single letter amino acid code.
8. Differentiate between an intron and exon.
9. Chromosome mutations come in two basic forms, those that change the number of chromosomes (individual number and number of whole sets) and those that change the organization of the gene loci on the chromosome. Describe the different types of mutations that change the organization of the gene(s) on the chromosome.

10. Determine which modes of inheritance are possible in the following pedigree.

Condition affecting members of a family



Part II: NCBI Questions. (40 Points)

1. Below is the partial nucleotide sequence of a gene associated with a genetic disorder.

```
TCCTGGCATCAGTTACTGTGTTGACTCACTCAGTGTGGGATCACTCACTTTCCCCCTACAGGACTCAGA  
TCTGGGAGGCAATTACCTTCGGAGAAAAACGAATAGGAAAAACTGAAGTGTTACTTTTTTTAAAGCTGCT  
GAAGTTTGTGGTTTCTCATTGTTTTTAAGCCTACTGGAGCAATAAAGTTTGAAGAAGTTTTACCAGGTT  
TTTTTTATCGCTGCCTTGATATACACTTTTCAAATGCTTTGGTGGGAAGAAGTAGAGGACTGTT
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- a. What is the name of the gene?
- b. On which chromosome and arm is it found.
- c. What is the name of the disorder associated with variant forms of this gene?
- d. How big is this gene (exons + introns)...how many nucleotides? How big (in number of amino acids) is the resulting protein?
- e. When you blast the sequence, how many significant alignments result? What is the expect score for the first significant alignment? Define the expect score?
- f. Provide the entire classification/taxonomy for the organism.
- g. Using ENTREZ, how many total pubmed entries are associated with this disorder?
- h. Blast the nucleotide sequence (above) against the mouse genome. For the most significant alignment: what is the identity? Expect score? How many gaps had to be inserted into the alignment to match up the nucleotides?

2. Below is the partial amino acid sequence of an unknown gene and organism.

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SGPVCVRERLIEKLTYPKAGSIPETQPKKVLILGSGGLSIGQAGEFDYSGSQAIKALREEKIQTILINPN  
IATVQTSKGLADKVYFLPLTKEYVEQVIKAERPNGALLTFGGQTALNCGVELEKAGVFSKYNVKILGTPIT  
SIIETEDRKIFADRVAEIG
```

Using the best expect score: what is the gene? What is the organism? List the citation where this sequence was published.

