

## EXAMPLE QUESTIONS AND ANSWERS

1. Topoisomerase does which one of the following?

- (a) Makes new DNA strands.
- (b) Unties knots in DNA molecules.**
- (c) Joins the ends of double-stranded DNA molecules.
- (d) Is required for making recombinant DNA molecules *in vitro*.

2. Which one of the following general properties of the genetic code makes it impossible for sequence information to be transferred from protein to RNA or DNA?

- (a) It is a triplet code.
- (b) It is commaless.
- (c) It is degenerate.**
- (d) It includes start and stop codons.

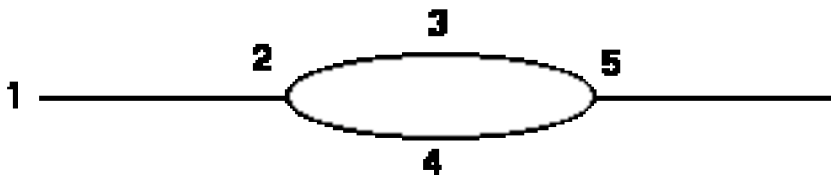
3. The following enzymes or enzyme activities are involved in DNA replication and repair:

- A. DNA polymerase
- B. endonuclease
- C. exonuclease
- D. ligase
- E. helicase
- F. single-strand binding protein
- G. topoisomerase

- (a) Which enzyme(s) make 5' - 3' phosphodiester bonds?   A, D, G
- (b) Which enzyme(s) untie knots in DNA molecules?   G
- (c) Which enzyme(s) make single-strand breaks in DNA backbones?   B, G
- (d) Which enzyme(s) join the ends of double-stranded DNA molecules?   D

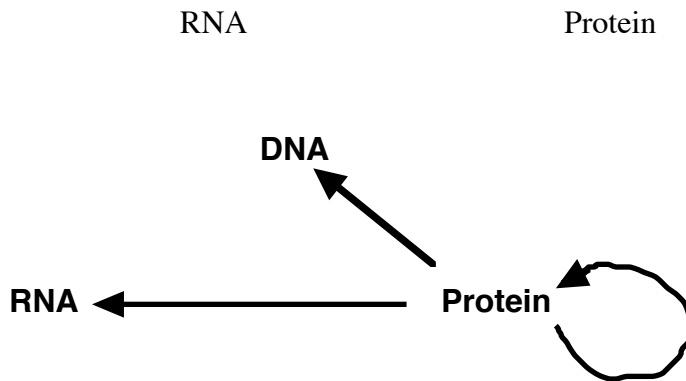
4. The drawing below represents a replicating DNA molecules from an animal seen in the electron microscope. Which number(s) represent the origin(s) of replication?

  3, 4  



5. Draw one or more arrows to show the direction(s) in which sequence information can *NOT* flow.

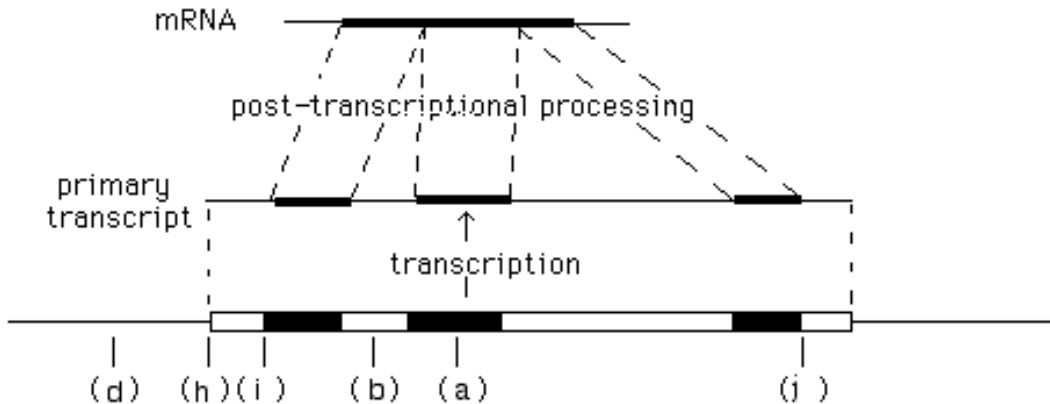
DNA



6. What is the N-terminal amino acid in  $\beta$ -globin? Methionine

The N-terminal amino acid is the first amino acid with which translation begins. Translation of all mRNAs begins at the 5' end of the mRNA with the AUG start codon which codes for Met.

7. Below is a diagram of a segment of DNA and its RNA products. Identify some of the regions by writing the letter corresponding to the name of each in the parentheses.



- a exon   b intron   c 3' UTR   d 5' flanking region   e operon   f 3' flanking region  
g 5' UTR   h transcription start   i ATG   j TAG   k transcription stop

8. In the blank nest to the name of each kind of mutation on the left, write the number(s) from the list on the right that tell what effect the mutation will most likely have on a polypeptide.

- |              |              |   |
|--------------|--------------|---|
| (a) missense | <u>  3  </u> | 1 polypeptide is longer                         |
| (b) nonsense | <u>  2  </u> | 2 polypeptide is shorter                        |
|              |              | 3 polypeptide has one amino acid substitution   |
|              |              | 4 polypeptide has many amino acid substitutions |

(c) frameshift 4, 1, 2

9. Recall that in peas, G and g determine yellow and green peas, respectively, and T and t determine tall and short plants. The genes are unlinked. A plant of genotype G g T t is crossed to a short plant that developed from green seeds.

(a) Write the genotype of the second parent. g g t t

(b) Out of 100 progeny seeds, how many do you expect to be yellow and produce tall plants?

G g T t X g g t t --> 1/4 G g T t   1/4 G g t t   1/4 g g T t   1/4 g g t t

1/4 X 100 = 25

10. Martian dragons are normally green, but a recessive mutation makes them white. The alleles are  $w^+$  and  $w$ . This mutation is due to a 500-bp insertion. Suppose you took a few cells from the tail of a sleeping green Martian dragon (very gently!), then isolated DNA from the cells, used PCR to amplify the region containing the insertion, and separated the PCR fragments on an agarose gel by electrophoresis. You got two bands, one of size 400 bp and the other 900 bp.

(a) Circle the genotype of this dragon:  $w^+ w^+$     $w^+ w$     $w w$

(b) If this green dragon mated with a white dragon, what would be the genotypes and genotypic ratios in the offspring? (Assume no sex linkage.)

$w^+ w$  X  $w w$  --> 1/2  $w^+ w$  1/2  $w w$

11. A three-factor test cross was done between a *Drosophila* female heterozygous for black body (*b*), purple eye (*pr*), and engrailed (*en*) and a homozygous recessive male. The numbers and phenotypes of the progeny were:

+ + +	431	<b>P</b>
b en pr	437	<b>P</b>
+ + pr	1	<b>D</b>
+ en +	37	
b en +	2	<b>D</b>
+ en pr	28	
b + pr	35	
b + +	<u>29</u>	
	1000	

(a) Write P next to each parental genotype and D next to each double crossover type.

- (b) Which gene is in the middle? *Pr* \_\_\_\_\_
- (c) What is the map distance between the *en* and *pr* loci? **7.5 map units or cM**  
7 pts

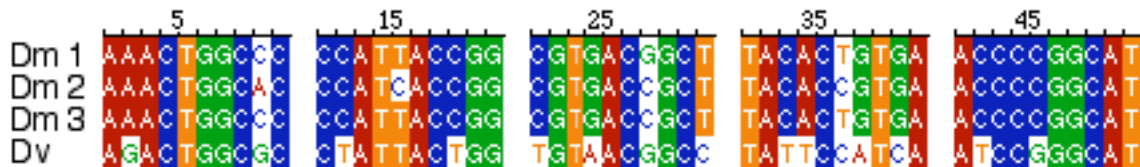
Show your calculations.

$$\frac{1}{37} \times \frac{75}{1000} = 0.075$$

12. In *Drosophila*, the *e* (for *ebony*) gene is on chromosome III. On what chromosome would you find the  $e^+$  allele? Circle the correct number:

I (X)      II      **III**      IV

13. Below are partial sequences (50 bp) of the *Adh* gene from three different individuals of *Drosophila melanogaster* (Dm 1, 2, 3) and one copy from *Drosophila virilis* (Dv).



(a) Calculate the sequence difference between each of the following pairs of genes:

Dm 1 and Dm 2  $4/50 = 0.08$

Dm1 and Dm 3  $1/50 = 0.02$

Dm2 and Dm 3  $3/50 = 0.06$

(b) Calculate the nucleotide diversity in *D. melanogaster*.

$(0.08 + 0.02 + 0.06)/3 = 0.0533$

or

$(4 + 1 + 3)/3 \times 50 = 0.0533$

14. In the preceding question, the three copies of the *Adh* gene from *D. melanogaster* are more similar to each other than they are to the *D. virilis* gene. The best explanation is:

- (a) The *D. melanogaster* sequences have a more recent common ancestor.
- (b) The mutation rate is lower in *D. melanogaster*
- (c) The population size is larger in *D. melanogaster*.
- (d) Balancing selection is operating in both species.

THE (ALMOST) UNIVERSAL GENETIC CODE

	U	C	A	G
U	UUU phe F	UCU ser S	UAU tyr Y	UGU cys C
	UUC phe F	UCC ser S	UAC tyr Y	UGC cys C
	UUA leu L	UCA ser S	UAA och Z	UGA opa Z
	UUG leu L	UCG ser S	UAG amb Z	UGG trp W
C	CUU leu L	CCU pro P	CAU his H	CGU arg R
	CUC leu L	CCC pro P	CAC his H	CGC arg R
	CUA leu L	CCA pro P	CAA gln Q	CGA arg R
	CUG leu L	CCG pro P	CAG gln Q	CGG arg R
A	AUU ile I	ACU thr T	AAU asn N	AGU ser S
	AUC ile I	ACC thr T	AAC asn N	AGC arg R
	AUA ile I	ACA thr T	AAA lys K	AGA arg R
	AUG met M	ACG thr T	AAG lys K	AGG arg R
G	GUU val V	GCU ala A	GAU asp D	GGU gly G
	GUC val V	GCC ala A	GAC asp D	GGC gly G
	GUA val V	GCA ala A	GAA glu E	GGA gly G
	GUG val V	GCG ala A	GAG glu E	GGG gly G