

Please show all of your work in answering the questions below.

1. F⁻ bacterial cells of genotype met⁻ thi⁻ pur⁻ were conjugated with F⁺ cells with the genotype met⁺ thi⁺ pur⁺. After the conjugation reaction was interrupted, cells containing met⁺ were selected and tested for the unselected markers thi and pur. The number of met⁺ colonies with the following genotypes determined:

thi ⁺ pur ⁺	400
thi ⁺ pur ⁻	0
thi ⁻ pur ⁺	8
thi ⁻ pur ⁻	52

(a) What is the gene order?

(b) Draw a genetic linkage map showing map distances between met, thi, and pur.

2. Three testcrosses with combinations of three linked genes were performed. The crosses and the inferred gametes produced by the tested parent were as follows:

AB/ab X ab/ab: 40% AB, 40% ab, 10% Ab, 10% aB

AD/ad X ad/ad: 46% AD, 46% ad, 4% Ad, 4% aD

BD/bd x bd/bd: 44% BD, 44% bd, 6% bD, 6% Bd

What is the probable genetic map of the three genes? Show your work.

3. Crosses were made between two strains of yeast. Each strain carried a different allele of the *a* gene. While most of the tetrads formed as a product of this cross were normal, one unusual tetrad was observed. Explain (using figures) how this tetrad could have been generated.

Cross: $a1 a3^+ \times a1^+ a3$

Abnormal tetrad:
 $a1^+ a3$
 $a1^+ a3$
 $a1^+ a3^+$
 $a1 a3^+$

4. If a woman and a man are heterozygous for a gene, and if they have three children, what is the chance that all three will also be heterozygous?

5. In *Drosophila*, the three gene pairs for red eyes (cn^+) vs. cinnabar (cn), normal bristle number (rd^+) vs. reduced (rd), and long wings (vg^+) vs. vestigial (vg) are known to map to X chromosome. A female heterozygous for all three genes was crossed against a male fly with cinnabar eyes, reduced bristle number and vestigial wings. Map the position of these three genes to one another draw a map. Show your work.

cinnabar, reduced, vestigial	406
cinnabar, reduced, long	46
cinnabar, normal vestigial	28
cinnabar, normal, long	3
red, normal, long	438
red, normal, vestigial	45
red, reduced, long	33
red, reduced vestigial	1

a) Calculate the map distances between the genes, and construct a linkage map of these loci. Show your work.

b) Determine the coefficient of coincidence for this set of loci.

6. Draw the banding pattern you would expect to see on a DNA-sequencing gel if you annealed the primer 5'-CTAGG-3' to the following single-stranded DNA fragment and carried out a dideoxy sequencing reaction.

3'-G-A-T-C-C-A-A-G-T-C-T-A-C-G-T-A-T-A-G-G-C-C-5'

7. Use the supplied figure of the genetic code to complete the following table. Assume that reading is from left to right and that the columns represent transcriptional and translational alignments.

	C		T		DNA
	T		T		double helix
A		U	C		mRNA
			A C G		tRNA anticodon
	Trp				amino acid

8. Consider the inducible regulation of the lac operon. For both for β -galactosidase (z) and permease (y), is enzyme production by each of the following genotypes constitutive, uninducible or inducible?

β -galactosidase permease

a) $I^+ p^+ o^c z^+ y^+$

b) $I^+ p^+ o^+ z^- y^- / i^- p^+ o^c z^- y^+$

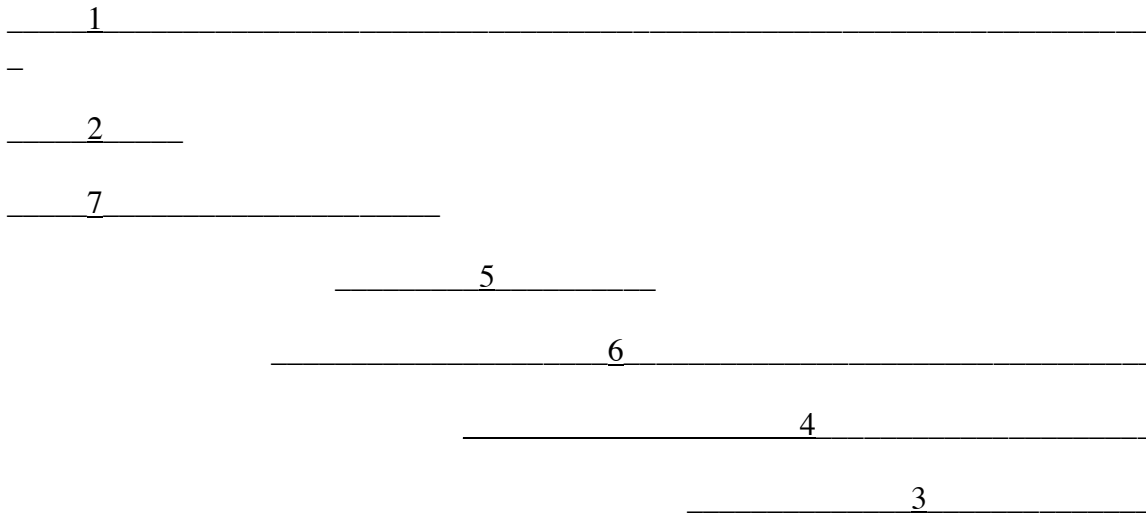
c) $I^+ p^+ o^+ z^+ y^- / i^- p^+ o^c z^- y^+$

d) $I^+ p^+ o^c z^+ y^- / i^s p^+ o^+ z^- y^+$

e) $i^s p^+ o^+ z^+ y^- / I^+ p^+ o^+ z^- y^+$

9. The molecule 2-aminopurine is an analog of adenine that pairs with thymine. It also occasionally pairs with cytosine. What types of mutations will be induced by 2-aminopurine after two rounds of replication? (Show your reasoning)

10. A set of seven different rII deletion mutants of bacteriophage T4, 1-7, were mapped, with the following result: (the lines indicate the extent of the deletion)



Five rII point mutants were crossed with each of the deletions, with the following results, (+ = r⁺ recombinants and 0 = no r⁺ recombinants)

Point Mutants	Deletion Mutants						
	1	2	3	4	5	6	7
a	0	+	+	+	0	0	0
b	0	0	+	+	+	+	0
c	0	+	+	0	0	0	+
d	0	+	0	0	+	0	+
e	0	+	+	+	+	0	0

Map the locations of the point mutations.

11. In the Meselson and Stahl experiment, ^{15}N -labeled bacterial cells were shifted to ^{14}N medium, at what we can designate as generation 0. What proportion of ^{15}N - ^{15}N , ^{15}N - ^{14}N and ^{14}N - ^{14}N DNA would you expect to find at generations 1, 2 and 3?