

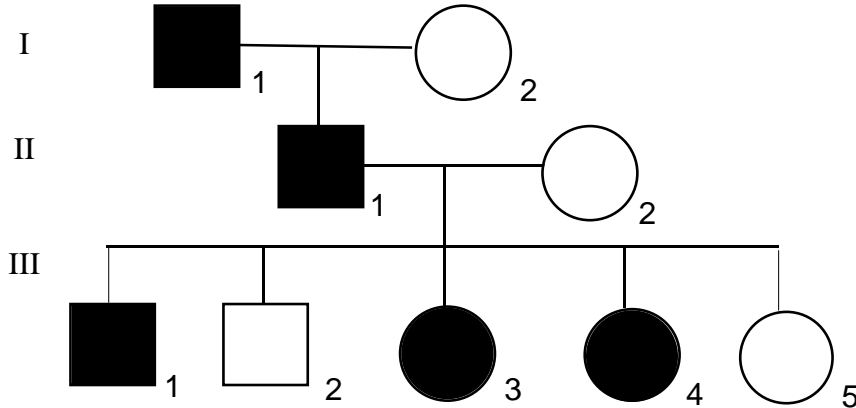
Your name:

1. (10 points). Compare and contrast the initiation of translation in prokaryotes and eukaryotes. Your answer should incorporate information about differences in gene organization and cellular structure.

2. (10 points) Discuss mechanisms for the elimination of aberrant mRNAs that contain misplaced in-frame translation stop codons. Once again, contrast eukaryotes and prokaryotes, mentioning the role of splicing and mRNA export in this process.

This pedigree shows a family affected by an autosomal dominant genetic disease.

Genotypes for three markers, A, B and C, are shown



The genotypes are:

- | | | | |
|------|--|-------|--|
| I-1 | A _{1,3} B _{1,2} C _{1,2} | III-1 | A _{1,4} B _{1,4} C _{1,4} |
| I-2 | A _{1,3} B _{3,3} C _{3,3} | III-2 | A _{3,4} B _{3,4} C _{3,4} |
| II-1 | A _{1,3} B _{1,3} C _{1,3} | III-3 | A _{1,4} B _{1,4} C _{3,4} |
| II-2 | A _{4,4} B _{4,4} C _{4,4} | III-4 | A _{1,4} B _{1,4} C _{1,4} |
| | | III-5 | A _{3,4} B _{3,4} C _{3,4} |

3. (8 points). Indicate the haplotypes of individual II-1 by checking which of the following are possible (check all that apply):

- a) A₁ B₁ C₁ / A₃ B₃ C₃
- b) A₁ B₁ C₃ / A₃ B₃ C₁
- c) A₁ B₃ C₁ / A₃ B₁ C₃
- d) A₃ B₁ C₁ / A₁ B₃ C₃

4. (6 points; two points per pair of markers) For each individual in the third generation (III-1, III-2, III-3, III-4 and III-5) indicate whether they are **recombinant**, **nonrecombinant** or **indeterminate** for each pair of **markers** in this pedigree (Fill in each of the 15 squares with **yes**, **no** or **maybe**).

individual	A B recombinant	B C recombinant	A C recombinant
III-1			
III-2			
III-3			
III-4			
III-5			

5. (4 pt.) Considering only the data for marker locus A (i.e. ignoring B and C), what is the approximate lod score for linkage **between A and the disease gene** with $\theta = 0$?

6. (4 pt.) Considering only the data for marker locus **B**, what is the approximate lod score for linkage **between B and the disease gene** with $\theta = 0$?

7. (4 pt.) Considering only the data for marker locus **C**, what is the **approximate** lod score for linkage **between C and the disease gene** with $\theta = 0$?

8. (16 points) This question concerns amorphic (null), neomorphic, hypermorphic and antimorphic dominant alleles. I'm asking you to consider how the mutant phenotype caused by each type of dominant allele is affected by an extra dose of the normal allele (duplication) or by reduced activity (a hypomorphic allele) at the other allele. In the following table, label each of the eight empty squares as **unchanged**, **enhanced** (a more extreme mutant phenotype) or **suppressed** (a less severe mutant phenotype – more like wild-type).

	Dominant/+ The typical situation	Dominant+/+ <i>i.e.</i> an extra dose of the wild-type allele	Dominant/hypomorphic (in trans to a hypomorph)
amorphic	unchanged (compare to this)		
neomorphic	unchanged (compare to this)		
hypermorphic	unchanged (compare to this)		
antimorphic	unchanged (compare to this)		

(4 points each). In each of the following there are two or more statements. One is true (generally, it is taken directly from your textbook) and the others have been modified so as to be untrue or misleading. Circle, check or otherwise designate the correct statement.

9. a) It is only when Myc and Max come together in a heterodimer that a transcriptional activator is formed.
b) Max homodimers are transcriptional activators, but the Myc-Max heterodimer activates a distinct set of genes involved in cell proliferation.
10. a) Autozygosity is a term used to refer to homozygosity by descent from a common ancestor.
b) Autozygosity is a term used to refer to homozygosity that results from mitotic recombination.
11. a) In forward genetics, one starts with the mutant phenotype.
b) In reverse genetics, one starts with the mutant phenotype.
12. a) The relation between physical and genetic distances is remarkably constant across the human genome; the approximation 1 cM = 1 Mb. is a useful rule of thumb in the case of humans, and variation is typically less than experimental error.
b) The relation between physical and genetic distances is not constant across the genome; the approximation 1 cM = 1 Mb. is a useful rule of thumb in the case of humans, but the actual value varies widely for different chromosomal regions.

-
13. a) Alleles at separate loci that are associated with each other at a frequency significantly higher than expected by chance are said to be in linkage disequilibrium.
b) Alleles at separate loci that are physically linked and common in a given population are said to be in linkage disequilibrium in that population.
14. a) Recombinant progeny can result from either the recombination of genes or markers on the same chromosome or by independent assortment of genes on nonhomologous chromosomes.
b) Progeny are described as recombinant only if they result from the recombination of genes or markers on the same chromosome.
15. a) Epigenetic imprints generally persist throughout the life of a mammal, but are erased during the passage of a gene through the germ line into the next generation.
b) Epigenetic imprints gradually decay during the life of a mammal and are rarely transmitted through the germ line into the next generation.
c) Epigenetic imprints generally persist throughout the life of a mammal, and are often transmitted through the germ line into the next generation.
16. (10 points)
Define, compare and contrast siRNAs and miRNAs. Spell out the abbreviations, explain what they do, how they work and what species have them. Include a definition of the RISC complex.