1a. Using the single letter amino acid code, give the sequence of the peptide shown below. (4 pts)

1b. In the above diagram, circle all the amino acids that have side chains that are basic. (2 pts)

2. Independent assortment of chromosomes occurs during which of the following? (5 pts)
   a. mitosis
   b. meiosis I
   c. meiosis II
   d. anaphase II
   e. both mitosis and meiosis

3. Crossing over of homologous (non-sister) chromatids has been observed to occur at a very low frequency (usually due to external factors, such as radiation) during which of the following? (5 pts)
   a. mitosis
   b. meiosis I
   c. meiosis II
   d. anaphase II
   e. both mitosis and meiosis

4. Which sequence is the complementary strand of the following strand of DNA? (5 pts)
   5’ GGGAAATTCCCAAACCCTTT3’
   a. 5’-AAAGGGTTTGGGAAAATTTCCC-3’
   b. 3’-AAAGGGTTTGGGAAAATTTCCC-5’
   c. 5’-GGGAAATTTCCCAAACCCTTT-3’
   d. 5’-CCCTTTAAAGGTTTGGGAAA-3’
   e. None of the above
5. Define each of the following terms (3 pts each)
a. Synapsis:

b. DNA primer:

c. Genetic map:

6. Circle True or False. (2 pts each)

T   F   Experimental recombination frequencies between two genes in pea plants can range between 0% and 100%.

T   F   The two terms cM and map unit are interchangeable.

T   F   When two yeast genes both lie close to the centromere on the same chromosome arm, parental ditypes will greatly outnumber nonparental ditypes after sporulation.

T   F   The probability of two or more independent events occurring together is the sum of the probabilities that each will occur by itself.

T   F   DNA polymerase synthesizes DNA strands in the 5’ to 3’ direction.
7. At a given locus, two alleles, 1 and 2, are present in a population in Hardy-Weinberg equilibrium. A third allele is present at a frequency of 10.0%. Homozygotes for allele 1 represent 36% of the population. What percent of the population is homozygous for allele 2? (6 pts)

8a. Each of the following family pedigrees shows the inheritance of a different rare genetic disease. There is one family for each type of inheritance: (A) autosomal recessive, (B) autosomal dominant, (C) X-linked recessive or (D) X-linked dominant. Identify the mode of inheritance for each family by filling in the correct type (A, B, C or D) below each family’s name. Use each letter only once. (8 pts)

b. In the Lee family, what is the probability that the child in the third generation (represented by the open diamond) will have the rare disease, if the child is a boy? (2 pts)

c. In the Lopez family, what is the probability that the child in the third generation (represented by the open diamond) will have the rare disease, if the child is a boy? (2 pts)
9. A haploid yeast strain that cannot grow in the absence of histidine (his-) is mated with a haploid yeast strain that cannot grow in the absence of lysine (lys-). The diploid cells are subsequently sporulated and produce 400 tetrads: 233 PD, 9 NPD and 158 T.

a. What are the genotype(s) of all the spores classified as PD? (3 pts)

b. What are the genotype(s) of all the spores classified as NPD? (3 pts)

c. What are the genotype(s) of all the spores classified as T? (3 pts)

d. Are the two genes above linked? If yes, use the Perkins equation to determine the map distance (in cM) between the his and lys genes. If no, then explain the basis for concluding that the genes are unlinked. (3 pts)
11. Suppose that on the X chromosome of *Drosophila* there are two closely linked recessive genes, Red (X^{r^+}) and Blue (X^{b^+}). When heterozygous females (X^{r^+}X^{b^-} / X^{r^-}X^{b^+}) are backcrossed to X^{r^-}X^{b^-} / Y males, exactly 0.1% of all the resulting progeny are wild type (phenotypically Red+ Green+, X^{r^+}X^{b^+} / X^{r^-}X^{b^-} or X^{r^+}X^{b^-} / Y) and 0.1% of all the resulting progeny are defective for both genes (X^{r^-}X^{b^-} / X^{r^-}X^{b^-} or X^{r^-}X^{b^-} / Y).

a. Suppose that you repeat the same backcross as described above, and you examine 2,000 progeny. What is the probability that you will observe no Red+ Green+ recombinants among the 2,000 progeny? Please write the equation you are using. (5 pts)

b. List all of the possible recombinant genotypes of the male progeny from the backcross. (2 pts)

c. List all of the possible parental genotypes of the female progeny from the backcross. (2 pts)

d. What is the genetic distance in cM units between the Red+ and Green+ loci (without correcting for possible double crossovers)? (3 pts)

11a. If two people who are both carriers for a rare genetic disease marry and have a family of two children, what is the probability that neither of their children have the disease? (3 pts)

11b. Suppose all the 2-child families that have at least one child with the disease form a large support group. Within the support group, what is the expected fraction of families having two children that both have the disease? (3 pts)
12. Consider the following three alignments: (3 pts)

1. QDKLDPRASLTRTRYRTRR
   QDKLDPASLTRDRSRFRSK
2. QDKLDPRASLTRTRYRTRR
   QDKLDP---ASLTRDRSFRSK
3. QDKLDPRASLTRTRYRTRR
   QDKLDP---ASLTRDRSFRSK

How many identities are there in:

a. Alignment 1?

b. Alignment 2?

c. Alignment 3?

13. Which one of the following statements (a – f) is true? (3 pts)

a. Of these alignments, 1 will always score highest (regardless of the parameters used)

b. Of these alignments, 2 will always score highest (regardless of the parameters used)

c. Of these alignments, 3 will always score highest (regardless of the parameters used)

d. Either alignment 1 or alignment 2 could have the highest score (depending on the parameters used), but 3 could not.

e. Either alignment 2 or alignment 3 could have the highest score (depending on the parameters used), but 1 could not.

f. Any one of the three alignments could have the highest score (depending on the parameters used)

14. Explain your answer to question 13. (6 pts)