Tips for Genetics Problems

1. Write down symbols for the alleles. Remember, capital letters for dominant alleles, lower case for recessive alleles.
2. Write down the possible genotypes, as determined by the phenotype. Keep alleles for each gene together and always write dominant alleles first.
   a. If the phenotype is that of the dominant trait (for example, purple flowers), then the genotype is either homozygous dominant or heterozygous (*PP* or *Pp* in this example).
   b. If the phenotype is that of the recessive trait, the genotype must be homozygous recessive (for example, *pp*).
   c. If an intermediate phenotype or blending of phenotypes is observed, expect incomplete dominance or codominance.
   d. If a trait expresses itself disproportionately in males or females, suspect sex-linkage.
   e. If the problem says "true-breeding," the genotype is homozygous.
3. Determine what the problem is asking for. If asked to do a cross, write it out in the form [genotype]×[genotype], using the alleles you've decided on.
4. To figure out the outcome of a cross, set up a Punnett square.
   a. To determine the allele(s) in each gamete, set up a systematic way to list all the possibilities. (Remember, each gamete has one allele of each gene.) Remember there are 2^n possible types of gametes, where *n* is the number of genes that are heterozygous. For example, an individual with genotype *AaBbCc* would produce $2^3=8^3$ types of gametes. Remember that each parent makes their own gametes. Also, each gamete has to get one allele of each gene (*i,e,* one letter from each trait).
   b. Fill in the Punnett square as if each possible sperm were fertilizing each possible egg, making all of the possible offspring (*i.e.*, random fertilization). Count genotypes and phenotypes to obtain the genotypic and phenotypic ratios. Because the Punnett square is so large, this method is not the most efficient. See tip 5.
   c. Monohybrid crosses result in 3:1 phenotypic ratios and dihybrid crosses result in 9:3:3:1 phenotypic ratios. Incomplete dominance and codominance result in 1:2:1 phenotypic ratios.
5. You can use the rules of probability if a Punnett square would be too big. You can consider each gene separately.
6. If the problem gives you the phenotypic ratios of offspring but not the genotypes of the parents in a given cross, the phenotypes can help you deduce the parents' unknown genotypes.
   a. For example, if 1/2 of the offspring have the recessive phenotype and 1/2 the dominant, you know that the cross was between a heterozygote and a homozygous recessive.
   b. If the ratio is 3:1, the cross was between two heterozygotes.
   c. If two genes are involved and you see a 9:3:3:1 ratio in the offspring, you know that each parent is heterozygous for both genes. Caution: Don't assume that the reported numbers will exactly equal the predicted ratios. For example, if there are 13 offspring with the dominant trait and 11 with the recessive, assume that the ratio is one dominant to one recessive.
7. For pedigree problems, you'll have to use some deduction to determine what kind of trait is involved.
   a. If parents without the trait have offspring with the trait, the trait must be recessive and the parents both carriers.
   b. If the trait is seen in every generation, it is most likely dominant (see the next possibility, though).
   c. If both parents have the trait, then in order for it to be recessive, all offspring must show the trait.

d. To determine the likely genotype of a certain individual in a pedigree, first label the genotypes of all the family members you can. Even if some of the genotypes are incomplete, label what you do know. For example, if an individual has the dominant phenotype, the genotype must be *AA* or *Aa*; you can write this as *A–*. Try different possibilities to see which fits the results. Use the rules of probability to calculate the probability of each possible genotype being the correct one.