In each of the following questions there are two or more statements. One is true (generally, it is taken directly from your text or another source). The other(s) have been modified so as to be untrue or misleading. Circle or otherwise designate the correct statement.

1. A region of DNA unwound by RNA polymerase is called the transcription bubble.
   a) Within the transcription bubble, the nascent RNA chain remains base paired with the DNA template, forming a DNA-RNA hybrid.
   b) Within the transcription bubble, the nascent RNA chain is immediately released from the DNA, displaced by the DNA duplex.

2. When geneticists refer to the sequence of a gene, they usually mean
   a) the sequence of the RNA-like strand.
   b) the sequence of the template strand.

3. How do cells make a mature RNA from a gene whose mature mRNA sequence is interrupted by introns?
   a) carry out discontinuous transcription whereby the RNA polymerase skips introns, transcribing only exons.
   b) make a primary transcript containing both introns and exons and then remove introns by RNA splicing.

4. a) A strategy of splicing carried out by some eukaryotes, trans-splicing, joins the exon of one gene with the exon of another gene.
   b) All RNA splicing is cis-splicing, whereby exons of the same primary transcript are joined together.

5. The effective concentration of transcription factor (as sensed by RNA polymerase at a promoter) is greatest when it is bound:
   a) About 2,000 nucleotides from the promoter.
   b) About 500 nucleotides from the promoter.
   c) About 200 nucleotides from the promoter.

6. Exposed regions of DNA recognized by their hypersensitivity to DNase digestion
   a) are associated with inactive genes.
   b) are associated with active genes.

7) In the case of genomic imprinting
   a) the expression of a gene depends on stochastic fluctuations
   b) the copy of a gene inherited by one parent but not the other is transcriptionally inactive.
Name ________________________________

8) RISC
   a) stands for RNA-induced silencing complex and mediates RNA interference
   b) stands for ribosome-initiated stable complex and is a storage form of masked mRNAs

9) In contrast to transcriptional regulation, ubiquitination
   a) swiftly acts to remove specific proteins in response to a regulatory signal
   b) slowly alters the activity of specific proteins in response to a regulatory signal

10. The *Drosophila* autoregulatory protein Sxl (Sex-lethal)
    a) **promotes** its own synthesis through RNA splicing, resulting in a productive mRNA, thereby acting as a self-reinforcing on/off switch.
    b) **inhibits** its own synthesis through RNA splicing, resulting in less productive mRNA, thereby acting to finely tune its level and activity

11. Autozygosity is a term used to refer to homozygosity
    a) by descent from a common ancestor.
    b) that results from mitotic recombination.

12. In classical genetics
    a) A null allele is usually recessive to wild-type.
    b) A null allele is usually dominant to wild-type.
    c) The null allele is usually wild-type.

13. The modern concept of dominant negative most closely resembles the classic
    a) neomorphic allele.
    b) antimorphic allele.
    c) hypermorphic allele

14. A mutant hypomorphic allele (*m*) over a deficiency (*m/Df*) is expected to be
    a) **more severe** in phenotype than *m/m* homozygotes.
    b) **equivalent** in phenotype to *m/m* homozygotes.

15. If an *Arabidopsis* mutation causes narrow leaves, a genetic enhancer would
    a) enhance the mutant phenotype, causing the leaves in the double mutant (*narrow, enhancer*) to be even more narrow.
    b) enhance expression of the gene, thereby alleviating the phenotype, causing less narrow leaves in the double mutant (*narrow, enhancer*).

16. Haploinsufficiency is a rare form of
    a) sterility in which germ cells die following meiosis.
    b) dominance in which an individual heterozygous for a wild-type allele and a null allele shows an abnormal phenotype.
17. The 5' UTR of \textit{NAT2} is derived from  
\textbf{a)} a noncoding \textit{exon} and six nucleotides of exon 2.  
\textbf{b)} a noncoding \textit{intron} and six nucleotides of exon 2.

18.  
\textbf{a)} Linkage and association are relations between loci.  
\textbf{b)} Linkage and association are relations between alleles.  
\textbf{c)} Linkage is a relation between alleles, but association is a relation between loci.  
\textbf{d)} Association is a relation between alleles, but linkage is a relation between loci.

19. Autozygosity is a term used to refer to homozygosity  
\textbf{a)} that results from mitotic recombination.  
\textbf{b)} for markers identical by descent and inherited from a recent common ancestor.

20. Small regulatory RNAs like \textit{lin-4} RNA  
\textbf{a)} are a novel feature of gene regulation in nematodes.  
\textbf{b)} play a much larger role in development than originally suspected, and not only in nematodes.

Examine the following pedigree.

21. (2 points) The A\textsubscript{1} alleles in the two brothers are identical by state (this just means that they are both A\textsubscript{1}). Can you infer that they are also identical by descent?  
\textbf{a)} You don't know whether or not A\textsubscript{1} is identical by descent.  
\textbf{b)} You can conclude that A\textsubscript{1} is identical by descent.  
\textbf{c)} You can conclude A\textsubscript{1} is not identical by descent.

22. (2 points) The B\textsubscript{1} alleles in the two brothers are identical by state (this just means that they are both B\textsubscript{1}). Can you infer that they are also identical by descent?  
\textbf{a)} You don't know whether or not B\textsubscript{1} is identical by descent.  
\textbf{b)} You can conclude that B\textsubscript{1} is identical by descent.  
\textbf{c)} You can conclude B\textsubscript{1} is not identical by descent.
You are studying Elbonian population in order to test whether hairlessness is genetic. You examine 100 males and observe the following haplotype counts for this X-linked region.

27 A1 B1 C1
27 A1 B1 C2
3 A1 B2 C1
3 A1 B2 C2
2 A2 B1 C1
2 A2 B1 C2
18 A2 B2 C1
18 A2 B2 C2

The following questions are worth 0.5 point each:

23. What is the frequency of A1 in the Elbonian population?
24. What is the frequency of A2 in the Elbonian population?
25. What is the frequency of B1 in the Elbonian population?
26. What is the frequency of B2 in the Elbonian population?
27. What is the frequency of C1 in the Elbonian population?
28. What is the frequency of C2 in the Elbonian population?

For each of the following, indicate true or false (2 points each)

29. ___ Loci A and B are in linkage disequilibrium.
30. ___ Loci A and C are in linkage disequilibrium.
31. ___ Loci B and C are in linkage disequilibrium.

32. T/F (1 pt. each):
   ___ A LOD score is the logarithm of the ratio of two likelihoods.
   ___ A LOD score of 3 is classically used to infer linkage
   ___ Negative LOD scores are impossible
   ___ Negative LOD scores (below -2) are classically used to reject linkage
   ___ The value of θ that give the highest LOD score will normally be the observed recombination frequency.
Consider a mapping cross between two inbred strains of venus flytrap that you are trying to develop as a pest control product for apartment dwellers. You have identified a collection of indel markers (these are primer pairs that give differently sized PCR products when used to amplify DNA from each of the two strains). The following are depictions of a gel used to examine PCR products from three such indel markers. Strain S (for "sugar") attracts cockroaches but does not trap them. Strain K (for "killer") can capture cockroaches but they show no interest. Your plan is to combine those traits, but for now you are just trying to map markers with respect to each other. Consider the following results:

33. What is the observed recombination frequency between 2345 and 2087?
34. What is the observed recombination frequency between 2345 and 8799?
35. What is the observed recombination frequency between 2087 and 8799?
36. (2 points) Which F2 individuals, if any, must carry a double crossover?
37. (2 points) Draw a genetic map for this data showing the order of 2345, 2087 and 8799 and the map units between them (you do not need to correct for double crossovers).
Define genetic heterogeneity (5 points)

Define phenocopy (5 points)

Define neomorphic allele (5 points)