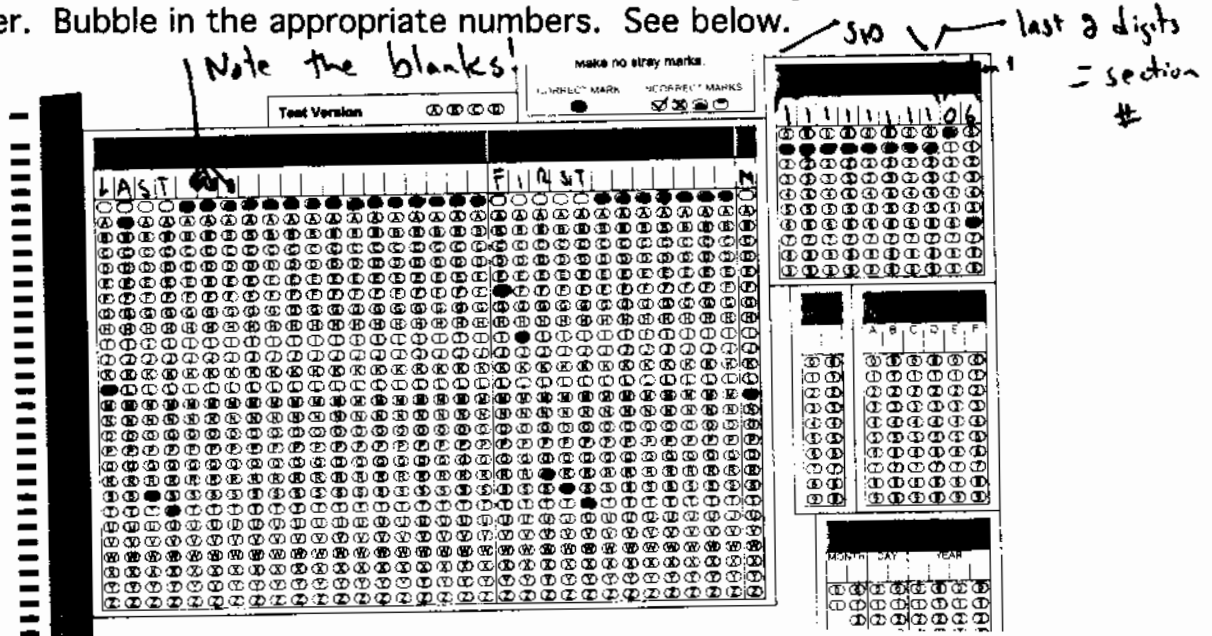


1. Sit every other seat and sit by section number. Place all books and paper on the floor. Turn off all phones, pagers, etc. and place them in your backpack. They cannot be visible. No calculator is permitted.

Instructions for Scantron

2. Use a #2 pencil. ERASE ALL MISTAKES COMPLETELY AND CLEARLY.
3. On the front and top of the scantron write in your name and under subject write in your GSI's name. Write in your SID #AND the last two digits of your section number. Bubble in the appropriate numbers. See below.

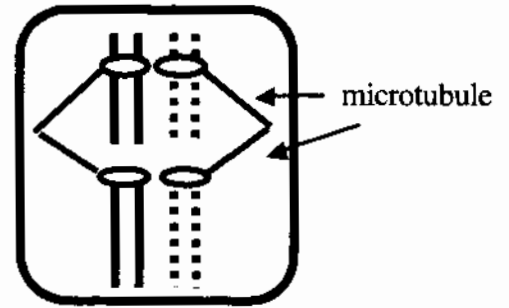


EXAM Instructions:

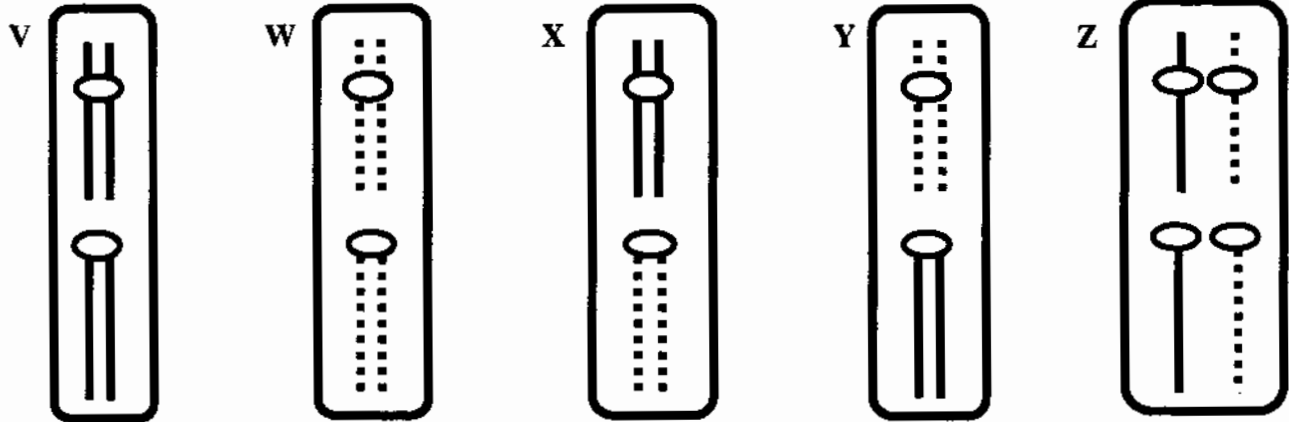
5. Print your name on THIS COVER SHEET. (otherwise, you will get a ZERO).
6. Leave your exam **face up**. When told to begin, check your exam to see that there are **8 numbered pages**, 45 multiple choice questions.  
The exam is worth 100 pts. Each multiple choice question is worth 2 points unless otherwise indicated. You are NOT PENALIZED for guessing on **multiple choice questions!**
7. It is extremely important that you read all questions and choices carefully before bubbling in your response.
8. Do not talk during the exam. The exam is closed book. You can not use a calculator. If you have a question, raise your hand; a GSI will help you. They will not give you the answer or explain scientific terms.
9. LOCATE YOUR GSI. Turn in your SCANTRON and EXAM to your GSI. YOU MUST TURN IN **BOTH** or else you will get a ZERO.
10. WHEN TOLD TO STOP- STOP! Bubble in guesses **BEFORE THIS TIME!**

1. The cell on the right is most likely

- A. A diploid cell at metaphase in the first meiotic division.
- B. A diploid cell at metaphase in the second meiotic division.
- C. A diploid cell at metaphase during mitosis.
- D. A haploid cell at metaphase in the first meiotic division.
- E. A haploid cell at metaphase in the second meiotic division.



2. What are the progeny of the cell in question 1 immediately after that cell divides?



- A. Only Z.
- B. Only V.
- C. Only V and W.
- D. Only V, W, and Z.
- E. All (V, W, X, Y, and Z).

3. For Arabidopsis,  $2N = 10$ . How many chromosomes are in Arabidopsis gametes?

- A. 2
- B. 5
- C. 10
- D. 20
- E. The number of chromosomes in gametes is variable.

4. (3 pts) Jane's mother and father are carriers for a severe genetic disease observed in individuals homozygous for a recessive mutant allele. Jane shows no symptoms of the disease. Jane's husband, John is a carrier for the same severe genetic disease. Assuming that this genetic disease is not sex linked, what is the probability that John and Jane's child will display the genetic disease?

- A. 1/12
- B. 1/6
- C. 1/4
- D. 1/3
- E. 1/2

5. (3 pts) A plant with genotype  $A/a B/b C/c$  was crossed to a plant with genotype  $a/a B/B C/c$ . What is the probability of obtaining  $A/a B/b C/c$  progeny?

- A. 1/64
- B. 1/32
- C. 1/16
- D. 1/8
- E. 1/4

6. **During meiosis recombination commonly occurs between**
- non-homologous portions of the X and Y chromosomes.
  - chromatids of homologous chromosomes (non-sister chromatids) but only within the centromere
  - chromatids of homologous chromosomes (non-sister chromatids).
  - chromatids of non-homologous chromosomes
  - Both B and C
7. (3 pts) **Two true breeding pea lines have been generated that have a mutant phenotype in that the plants are very tall. The lines were crossed and all the F1 progeny were normal size. We can conclude from these results that**
- Each line has a mutation in the same gene. That is, the mutations represent different alleles.
  - Each line has a mutation in a different gene.
  - The mutations in the two lines are linked.
  - The mutations in the two lines are dominant.
  - None of the above.
8. (3 pts) **Fruit color (red versus yellow), stem width (skinny versus fat), and leaf shape (broad versus narrow) are three genetically unlinked characters of tomato plants. Suppose you cross two true breeding lines (red fruit, fat stem, broad leaf) X (yellow fruit, skinny stem, narrow leaf). All of the F1 progeny have red fruit, fat stems, and broad leaves. We can conclude from this experiment that**
- The allele for Red fruit color (R) is dominant to the allele for yellow fruit (r).
  - The allele for fat stems (F) is dominant to the allele for skinny stems (f).
  - The allele for broad leaves (B) is dominant to the allele for narrow leaves (b).
  - None of the above are true.
  - A, B, and C are true.
9. (3 pts) **Suppose that the F1 progeny in question 8 above are crossed. What fraction of the F2 progeny will have red fruit, skinny stems, and broad leaves?**
- 1/64
  - 3/64
  - 9/64
  - 27/64
  - all of the progeny.
10. (3 pts) **Among the F2 plants in question 9 what fraction will be heterozygous R/r, heterozygous F/f, and heterozygous B/b?**
- 1/32
  - 1/16
  - 1/8
  - 1/4
  - 1/2

R F B  
 Rr Ff Bb  
 R F B  
 Rr Ff Bb  
 R F B  
 Rr Ff Bb

$P(R) = \frac{3}{4}$   
 $P(F) = \frac{1}{4}$   
 $P(B) = \frac{3}{4}$

$\frac{1}{4} \times \frac{1}{4} = \frac{1}{16}$

WORK AREA: (If needed)

11. Which enzyme simultaneously copies both strands of DNA?

- A. DNA polymerase I
- B. DNA polymerase III
- C. RNA polymerase II
- D. Primase
- E. Both (A) and (B) are correct.

12. (3 pts) In *Drosophila*, the *lb* (large body) allele is recessive to the wild type *lb+* (normal body size) allele. Also, the *sw* (slender wing) allele is recessive to the *sw+* (normal size wing) allele. Suppose a wild type female from a true breeding population was crossed to a large body, slender wing male. An F1 female was crossed to a wild type male. If the large body gene and the slender wing gene are separated by 10 centimorgans on the X chromosome (and are not on the Y chromosome) what F2 progeny would you expect to see?

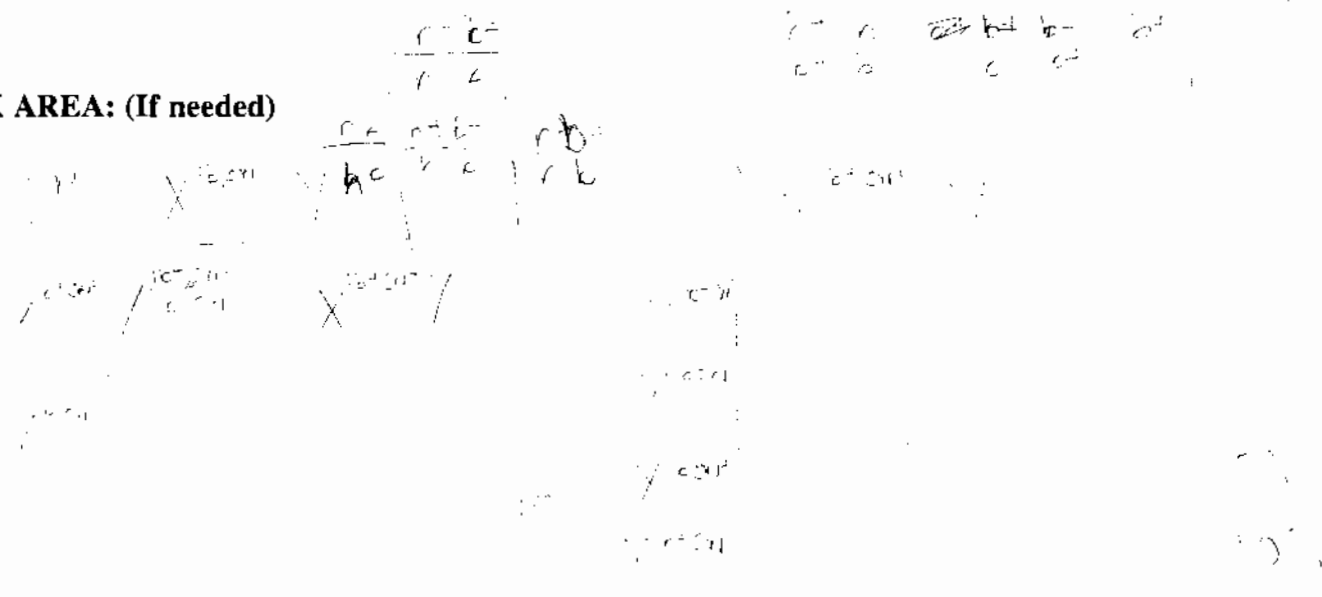
- A. All males are wild type. Among the females, 450 are large body and slender, 450 are wild type for both traits, 50 are normal body and slender wings, 50 are large body and normal wings.
- B. All males are wild type. Among the males, 400 are large body and slender, 400 are wild type for both traits, 100 are normal body and slender wings, 100 are large body and normal wings.
- C. All females are wild type. Among the males, 450 are large body and slender, 450 are wild type for both traits, 50 are normal body and slender wings, 50 are large body and normal wings.
- D. All females are wild type. Among the males, 400 are large body and slender, 400 are wild type for both traits, 100 are normal body and slender wings, 100 are large body and normal wings.
- E. Male and female F2 progeny show the same distribution of progeny. Among 1000 F2 progeny (half male and half female), 450 are large body and slender, 450 are wild type for both traits, 50 are normal body and slender wings, 50 are large body and normal wings.

13. (3 pts) In *Drosophila*, the *h* (hairy) allele is recessive to the wild type *h+* (normal amount of hair) allele. Also, the *b* (black body) allele is recessive to the wild type *b+* (normal tan body color) allele. A wild type female from a true breeding population was crossed to a hairy, black body male. An F1 female was crossed to a hairy, black body male. Among the F2 population there were approximately equal numbers of all four possible phenotype combinations: i) hairy, black body, ii) hairy and wild type body color, iii) wild type hair and body color and iv) wild type hair and black body color. Female and male flies showed the same distribution of phenotypes. You can conclude from this experiment that---. Please read all choices.

- A. *b+* and *h+* are tightly linked (less than 10 centimorgans) on an autosome.
- B. *b+* and *h+* are on different chromosomes.
- C. *b+* and *h+* are tightly linked (less than 10 centimorgans) on the X chromosome.
- D. *b+* and *h+* are on the same chromosome and are separated by at least 50 centimorgans.
- E. Both (B) and (D) could be true and they cannot be distinguished by this experiment.

Handwritten notes:  $h^+ h^-$ ,  $b^+ b^-$ ,  $h^+ b^+$ ,  $h^- b^-$

WORK AREA: (If needed)



14. **What statement is FALSE regarding the structure of DNA?**
- A. The charged phosphodiester linkages are on the outside and the aliphatic base pairs are on the inside.
  - B. The amount of dA equals dT, and the amount of dG equals dC.
  - C. The two strands have a major groove and an minor grove.
  - D. DNA is a double-stranded helix.
  - E. The two strands in the DNA double helix are parallel (both are oriented in the same direction, 5' to 3')
15. **During gene transcription, a ribonucleotide is added to the 3'-end of an RNA molecule, the reaction involves**
- A. Nucleophilic attack of the electrons of the 3'-hydroxyl group on the innermost ( $\alpha$ ) phosphate.
  - B. Nucleophilic attack of the electrons of the 3'-hydroxyl group on the middle ( $\beta$ ) phosphate.
  - C. Nucleophilic attack of the electrons of the 2'-hydroxyl group on the innermost ( $\alpha$ ) phosphate.
  - D. Nucleophilic attack of the electrons of the 2'-hydroxyl group on the middle ( $\beta$ ) phosphate.
  - E. Nucleophilic attack of the electrons of the 2'-hydroxyl group on the outermost ( $\gamma$ ) phosphate.
16. **What process insures that during replication the correct bases are incorporated in the newly synthesized strand of DNA?**
- A. Each aminoacyl tRNA synthase only binds to the correct base.
  - B. DNA polymerase correctly reads the sugar-phosphate backbone.
  - C. Bases on the outside of the double strand DNA helix interact with DNA polymerase.
  - D. Formation of H-bonds and steric considerations only allow "A" to base pair with "T", and "C" to base pair with "G".
  - E. Formation of H-bonds, and steric considerations, only allow "A" to base pair with "G", and "C" to base pair with "T".
17. **What process insures that a newly synthesized protein contains the correct sequence of amino acids?**
- A. Each aminoacyl tRNA synthase only binds the correct amino acid to the correct tRNA. S
  - B. Base pairs are formed between the codon of the mRNA and the anti-codon of the tRNA.
  - C. Base pairs are formed between the ribosomal RNAs and the ribosomal proteins.
  - D. Base pairs are formed between the ribosomal RNAs and the proper tRNA.
  - E. Both (A) and (B) are true.
18. **Which of the following is true of a codon?**
- A. It consists of two nucleotides.
  - B. It never codes for the same amino acid as another codon does.
  - C. It may code for more than one amino acid.
  - D. It codes for the same amino acid when mRNAs are translated in the cytoplasm of E. coli, Drosophila, and humans.
  - E. It correctly base pairs with the anticodon in rRNAs.
19. **Peptide bond formation is catalyzed**
- A. when ATP and the amino acid bind to the aminoacyl tRNA synthase.
  - B. by the enzyme activity associated with a protein in the ribosome.
  - C. when the amino acid is covalently attached to the tRNA.
  - D. by the activity of translation termination factor.
  - E. by a ribosomal RNA.
20. **A "missense" mutation**
- A. always causes premature translation termination resulting in a truncated polypeptide.
  - B. when transcribed, causes a change in a single base of the mRNA so that the insertion of the wrong amino acid may occur when the mRNA is translated.
  - C. causes a change in the reading frame so that all amino acids downstream from the mutation will be wrong.
  - D. is a mutation that never has an effect on translation.
  - E. Both A and C.

21. **The large subunit (50S) of the ribosome**  
 A. binds the mRNA and initiates translation by binding a tRNA with the amino acid methionine.  
 B. binds the mRNA and initiates translation by binding a tRNA with the amino acid glycine.  
 C. attaches the amino acid methionine to the proper tRNA.  
 D. contains the catalytic component for peptide bond formation  
 E. Both A and C are true.
22. **Which statement about the methionine tRNA is FALSE?**  
 A. has the anticodon for methionine.  
 B. binds to all aminoacyl tRNA synthases.  
 C. interacts with a methionine – AMP intermediate when it is bound to the correct aminoacyl tRNA synthase  
 D. can be involved in the initiation of translation.  
 E. Only binds to methionine.
23. **A typical prokaryote mRNA**  
 A. has a 5' - monophosphate.  
 B. has a 5' - CAP structure.  
 C. has introns.  
 D. has a 3' - polyA tail.  
 E. is transcribed and translated in the same compartment of the prokaryote cell.
24. **If splicing is inaccurate and three intron bases are left in the translated portion of the mRNA then which of the following would you expect knowing that the three intron bases do not encode a translation termination signal?**  
 A. There will be little damage because the spliceosome checks the splicing reaction and degrades all RNAs that are not spliced properly.  
 B. The spliceosome will splice the RNA a second time and remove the three intron bases.  
 C. There will be little damage because the RNA with the extra bases will not be exported to the cytoplasm for translation.  
 D. The reading frame will be altered and many of the amino acids incorporated into the protein will be wrong.  
 E. A single extra amino acid will be inserted when the extra 3 bases are translated by the ribosome.
25. **Bacteriophage**  
 A. often lyse their host.  
 B. do not need E. coli enzymes to replicate their DNA.  
 C. do not need E. coli enzymes to transcribe their genes.  
 D. do not need E. coli enzymes to translate their mRNAs.  
 E. All of the above are true.
26. **Which statement is the most correct about retroviruses?**  
 A. RNA genomes and reverse transcriptase proteins are inside the virus.  
 B. DNA genomes and reverse transcriptase proteins are inside the virus.  
 C. Retroviruses do not need a genome because they have reverse transcriptase.  
 D. The integrated retrovirus DNA is transcribed by reverse transcriptase to make mRNA.  
 E. A retrovirus is always inserted into the same site of the host cell genome.
27. **The best definition of the P site in the lac operon is**  
 A. The DNA sequence that binds the lac repressor.  
 B. The DNA sequences that binds the CRP protein.  
 C. The DNA sequence that binds RNA polymerase.  
 D. An RNA sequence in the lac mRNA where the ribosome binds  
 E. The DNA sequence where RNA polymerase terminates transcription of the lac operon.

**28. Retrotransposons**

- A. are packaged into viral protein coats and move from cell to cell.
- B. use reverse transcriptase to create new copies of themselves that insert in their host genome.
- C. are composed of inverted repeats that flank a transposase gene.
- D. always kill their host cell.
- E. both B and C are true.

**29. In the trp operon, tryptophan**

- A. binds the repressor so that the repressor cannot bind to the operator and tryptophan biosynthesis genes are transcribed.
- B. binds the repressor so that the repressor can bind to the operator so that tryptophan biosynthesis genes are not transcribed.
- C. binds the CRP protein so that RNA polymerase can bind to the promoter and the tryptophan biosynthesis genes are transcribed.
- D. binds the CRP protein so that RNA polymerase cannot bind to the promoter and the tryptophan biosynthesis genes are not transcribed.
- E. None of the above are correct.

In question 30 – 32, all bacterial plates have X-gal and also glycerol as an energy and carbon source. All bacteria have a functional  $\beta$ -galactosidase gene (Z+) in the lac operon. The rest of the genotype of the bacteria, and whether the plates have inducer (IPTG) and/or glucose, are indicated in each question.

**30. The plates have no IPTG, no glucose, and the colony is blue. Which of the following could be true regarding the genotype of the colony?**

- A. wild type for all genes.
- B. mutation in the I gene (I-).
- C. mutation in the operator (O-).
- D. mutation in the CRP gene (CRP-).
- E. both B and C could be true.

*blue  $\rightarrow$   $\beta$ -gal  $\rightarrow$  transcription*  
*mutation*  
*CRP-  $\rightarrow$  no CRP  $\rightarrow$  no transcription*

**31. The plates have IPTG, no glucose, and the colony is white. Which of the following could be true regarding the genotype of the colony?**

- A. wild type.
- B. mutation in the I gene (I-).
- C. mutation in the operator (O-).
- D. mutation in the CRP gene (CRP-).
- E. both A and C could be true.

*no glucose  $\rightarrow$  no transcription*  
*no CRP  $\rightarrow$  no transcription*  
*no IPTG  $\rightarrow$  no transcription*

**32. The plates have IPTG, have glucose, and the colony is white. Which of the following could be true regarding the genotype of the colony?**

- A. wild type.
- B. mutation in the I gene (I-).
- C. mutation in the operator (O-).
- D. mutation in the CRP gene (CRP-).
- E. all of the above could be true.

*all of the above could be true*  
 *$\rightarrow$  no transcription*

**WORK AREA: (If needed)**

33. (3 pts) What statement about transposons, if any, is **FALSE**?
- A. They increase their number of copies in the genome by jumping ahead of DNA polymerase III as it replicates the genome.
  - B. They increase their number of copies in the genome by jumping ahead of RNA polymerase II that transcribes genes. .
  - C. They create repeated sequences that facilitate the process of gene duplication.
  - D. They insert themselves randomly in the genome.
  - E. If all of the above are true, please select E
34. **Interspersed repeated DNA sequences in the genome are primarily caused by**
- A. mistakes by DNA polymerase.
  - B. failure to transcribe certain regions of the genome.
  - C. Movement of transposons studied by Barbara McClintock.
  - D. Movement of retrotransposons.
  - E. Both C and D are true.
35. **What is the process that most likely resulted in the duplication of the ancestral hemoglobin gene?**
- A. equal (normal) recombination at meiosis.
  - B. unequal recombination at meiosis.
  - C. failure of chromosomes to properly segregate at meiosis.
  - D. Unequal recombination at mitosis.
  - E. Both C and D are true.
36. **In eukaryotes, the DNA is wrapped around**
- A. DNA polymerases
  - B. ribosomes
  - C. nucleosomes
  - D. RNA polymerases
  - E. spliceosomes
37. **When DNA is replicated, patterns of DNA methylation (5-methylcytosine) are maintained in the genome by**
- A. DNA polymerase III which inserts a 5-methylcytosine when it replicates past a 5-methylcytosine in the template DNA strand.
  - B. A DNA methyltransferase that methylates cytosine at the 5-carbon position in the newly synthesized DNA strand when the template strand is 5'-C<sup>m</sup>G-3'.
  - C. DNA polymerase I that converts the cytosine into 5-methylcytosine after DNA polymerase III is finished replicating the genome.
  - D. All of the above are correct.
  - E. None of the above are correct.
38. **Nucleosomes are composed of**
- A. Histone proteins
  - B. Ribosomal proteins
  - C. Spliceosome proteins
  - D. Histone RNAs
  - E. tRNAs

**EXAM CONTINUES**



39. (3 pts) DNA methylation causes histone deacetylation at a transposon promoter region that causes the
- A. transposon RNA to be improperly spliced.
  - B. transposon to be transcribed.
  - C. transposon to not be transcribed.
  - D. nucleosomes to compress and make the DNA inaccessible to RNA polymerase and transcription factors.
  - E. Both C and D are correct.
40. The primary reason our neuron cells differ from our skin cells is they
- A. transcribe different genes.
  - B. have transposons inserted in different sites of the genome.
  - C. have different kinds of genes.
  - D. have different kinds of ribosomes that utilize different genetic codes.
  - E. have different numbers of chromosomes.
41. What enzymes are used to construct a genomic library?
- A. Reverse transcriptase
  - B. Ligase
  - C. DNA polymerase 1
  - D. Restriction endonuclease
  - E. Both B and D are correct.
42. What sequences are most likely to be included in a cDNA library?
- A. Introns
  - B. Promoters
  - C. Exons
  - D. Centromeres
  - E. Telomeres
43. Screening a library by hybridization to a labeled probe works because
- A. The radioactive probe only forms base pairs with clones containing its complementary sequence.
  - B. The radioactive probe will form base pairs with every clone in the library.
  - C. The radioactive probe covalently binds to the clone containing its complementary sequence.
  - D. The radioactive probe enters and kills only the E. coli host with a clone that is complementary to the probe sequence.
  - E. None of the above is correct.
44. The AGAMOUS amino acid sequence can most easily be deduced from the sequence of the
- A. wild type *AGAMOUS* genomic clone.
  - B. wild type *AGAMOUS* cDNA clone.
  - C. mutant *ag(transposon)* genome clone
  - D. wild type *AGAMOUS* hnRNA.
  - E. none of the above.
45. The best reason why we know that AGAMOUS is necessary for reproductive organ development in flowers is
- A. The *AGAMOUS* gene encodes a transcription factor.
  - B. The *AGAMOUS* protein is related to other important transcription factors.
  - C. The *AGAMOUS* gene is transcribed in the reproductive organs of flowers.
  - D. Plants that are homozygous *ag(transposon)/ag(transposon)* do not make reproductive floral organs.
  - E. None of the above are good reasons.