

(e) Selling only male knockouts.

4. Scientists produce large quantities of RNA by transcription *in vitro* rather than by expression of cloned genes *in vivo* primarily because

- (a) *in vitro* transcription removes the need to clone the gene for the RNA into a DNA vector.
- (b) the viral RNA polymerases used for *in vitro* transcription are not active *in vivo*.
- (c) RNA molecules are present in only a few copies per cell and thus only small amounts of RNA can be prepared *in vivo*.
- (d) *in vitro* transcription eliminates the need to purify the RNA produced from the cell's RNA molecules.

5. A mutation engineered *in vitro* introduces a mismatch into the DNA. When the mismatched DNA is introduced into cells, its replication would be expected to generate an equal mixture of parental and mutant genomes. Would you expect that the mismatched DNA would be reorganized and repaired by DNA mismatch repair enzymes? Would you expect mismatch repair to increase, reduce, or not affect the frequency of mutants? Explain your answer.

6. Which of the following is a substrate for β -galactosidase?

- A. lacZ
- B. chloramphenicol
- C. X-gal
- D. acetyl-CoA
- E. both lacZ and acetyl-CoA

7. Site-directed mutagenesis is used for which of the following purposes?

- A. to insert fragments of more than 100 pairs into a specific DNA site
- B. to induced site-specific recombination
- C. to make changes to specific bases in DNA
- D. to remove large segments of a DNA sequence
- E. Both to induce site-specific recombination and to make changes to specific bases in DNA are correct.

8. It is suspected that a novel histone protein only interacts with the promoter region of β -globin genes. Which of the following techniques should be used to confirm this suspicion?

- A. EMSA
- B. DNase footprinting
- C. filter binding
- D. gel mobility shift assay
- E. all of the choices are correct.

9. A bacterium that you can culture secretes a protein into the growth medium. Your hypothesis is that this protein is a protease. You can recover the protein from a sample of growth medium, and you already have a genomic library from the bacterium (constructed in a lambda replacement vector). How will you determine the sequence of the gene for the putative protease, to compare it