Chapter 2: Protein Synthesis

Multiple Choice
Identify the choice that best completes the statement or answers the question.

____ 1. What is the relationship among genes, DNA, and proteins?
A. DNA is composed of a series of amino acids that provide the directions for synthesizing proteins.
B. Protein is composed of DNA that is organized into specific gene sequences called amino acids.
C. A gene is a section of DNA that provides the directions for synthesizing a specific protein.
D. Proteins are the nitrogenous bases that form double strands of DNA in its helical shape.

____ 2. What is the difference between DNA transcription for DNA synthesis and DNA transcription for protein synthesis?
A. Transcription for DNA synthesis is rapidly followed by the process of translation.
B. Transcription for protein synthesis has "greater fidelity" than does transcription for DNA synthesis.
C. Transcription for protein synthesis occurs only in cells undergoing mitosis, and transcription for DNA synthesis occurs in both dividing and nondividing cells.
D. Transcription for DNA synthesis occurs with both the "sense" and the "antisense" strands, while transcription for protein synthesis occurs with only the "sense" strand.

____ 3. Which mature messenger RNA strand correctly reflects the accurate transcription of the following segment of DNA, in which large letters represent introns and small letters represent exons?

tTGCGaAccaGaCTtaaAAtTAAA

A. AUGGUUAUUA
B. ACGCTCGATTATTT
C. ACGCUCGAUUAUUU
D. AACGCUUGGUCUGAAUUUUAAUUU

____ 4. What is the function of ribosomes (also known as ribosomal RNA) in protein synthesis?
A. Allows interpretation of the two strands of DNA to determine which is the "sense" strand and which is the "antisense" strand
B. Serves as the coordinator mechanism to allow proper reading of the mRNA and placement of the correct amino acid in the sequence by the tRNAs
C. Allows further processing of synthesized proteins (post-translational modification in order to ensure that the final product is physiologically active)
D. Serves as a transport molecule able to move a specific amino acid to the site of protein synthesis (peptide chain elongation) in the correct sequence

____ 5. A strand of recently transcribed messenger RNA contains the following components: exon (1), intron (2), intron (3), exon (4), intron (5). Which sequence represents the mature messenger RNA?
A. 1, 4
B. 2, 3, 5
C. 2, 3, 4
D. 1, 2, 3, 4, 5

____ 6. After a protein is synthesized during translation, what further process or processes is/are needed for it to be fully functional?
A. No further processing beyond the linear arrangement of amino acids is required.
B. Although minimal function can occur in the linear form, the protein is more active when it undergoes mitosis.
C. The protein first twists into a secondary structure and then "folds" into a specific tertiary structure for activation and function.
D. The initial protein produced is a "preprotein" that requires a series of depolarizations by electrical impulses for conversion to an active protein.

____ 7. How does an "anticodon" participate in protein synthesis?
A. Splicing out the introns to form a functional and mature messenger RNA
B. Identifying which DNA strand is the "sense" strand to transcribe into RNA
C. Ensuring the appropriate tRNA places the correct amino acid into the protein
D. Interpreting the correct "stop" triplet or codon that signals for translation termination

____ 8. The protein glucagon contains 29 amino acids in its active linear form. What is the minimum number of bases present in the mature messenger RNA for this protein?
A. 29
B. 58
C. 87
D. 116

____ 9. Which feature or characteristic is most critical for protein function or activity?
A. The number of amino acids
B. The sequence of amino acids
C. Deletion of all active exons
D. Transcription occurring after translation

____ 10. How does replacement of thymine with uracil in messenger RNA help in the process of protein synthesis?
A. Allowing messenger RNA to leave the nucleus
B. Ensuring only the "sense" strand of DNA is transcribed
C. Determining the placement of the "start" signal for translation
D. Promoting post-translational modification for conversion to an active protein

____ 11. How does the process of *polyadenylation* affect protein synthesis?
A. Binding to the antisense DNA strand to prevent inappropriate transcription
B. Promoting attachment of ribosomes to the correct end of messenger RNA
C. Linking the exons into the mature messenger RNA

D. Signaling the termination of mRNA translation

____ 12. Why are ribonucleases that digest mature messenger RNA a necessary part of protein synthesis?
A. These enzymes prevent overexpression of critical proteins.
B. Without ribonucleases, messenger RNA could leave one cell type and lead to excessive protein synthesis in a different cell type.
C. When ribonucleases degrade RNA, the degradation products are recycled, making protein synthesis more energy efficient.
D. The activity of these enzymes promotes increased translation of individual messenger RNAs so that fewer RNA molecules are needed for protein production.

____ 13. Which statement about the introns within one gene is correct?
A. These small pieces of DNA form microRNAs that regulate gene expression.
B. They are part of the desert DNA composing the noncoding regions.
C. When expressed, they induce post-translational modifications.
D. The introns of one gene may be the exons of another gene.

____ 14. Which DNA segment deletion would cause a frameshift mutation?
A. TCT
B. GAGTC
C. TACTAC
D. GCATGACCC

____ 15. What is the expected result of a "nonsense" point mutation?
A. Total disruption of the gene reading frame, no production of protein
B. Replacement of one amino acid with another in the final gene product
C. Replacing an amino acid codon with a "stop" codon, resulting in a truncated protein product
D. No change in amino acid sequence and no change in the composition of the protein product

____ 16. What makes a frameshift mutational event more serious than a point mutational event?
A. Frameshift mutations occur primarily in germline cells, and point mutations occur only in somatic cells.
B. Frameshift mutations result in the deletion or addition of whole chromosomes (aneuploidy), and point mutations are undetectable at the chromosome level.
C. The rate of frameshift mutations increases with aging because DNA repair mechanisms decline, whereas the rate of point mutations is unchanged with age.
D. When the mutations occur in expressed genes, frameshift mutations always result in disruption of the gene function, whereas a point mutation can be silent.

____ 17. What is the expected outcome when a person (twin A) experiences a large deletion of DNA in one of his noncoding region and his monozygotic twin (twin B) does not?
A. DNA identification of each twin will be more specific.
B. Only their somatic cells will remain identical at all loci.
C. Only their germline cells will remain identical at all loci.
D. They will now be dizygotic twins instead of monozygotic twins.

____ 18. Which statement about single nucleotide polymorphisms (SNPs) is true?

A. SNPs can change an exon sequence into an intron sequence.
B. SNPs can change an intron sequence into an exon sequence.
C. SNPs are generally responsible for frameshift mutations.
D. SNPs are generally responsible for point mutations.

____ 19. Why are people who have poor DNA repair mechanisms at greater risk for cancer development?
A. Their cancers are usually resistant to chemotherapy.
B. Their somatic mutations are more likely to be permanent.
C. They have greater exposure to environmental carcinogens.
D. They have sustained a mutational event in all cells and tissues.

____ 20. How does an acquired mutation in a somatic cell gene leading to cancer development affect a person's ability to pass on a predisposition for that cancer type to his or her children?
A. The predisposition can only be passed on if the person with the somatic cell mutation is female.
B. There is no risk of passing on a cancer predisposition to one's children from a somatic cell mutation.
C. The risk for predisposition is dependent upon which tissue type experienced the somatic mutation.
D. Multiple somatic mutations are required for passing on a predisposition to cancer development.

Chapter 2: Protein Synthesis
Answer Section

MULTIPLE CHOICE

1. ANS: C
   The correct sequence and relationships are listed in option *C*. A gene is a section of a specific DNA sequence that encodes the instructions for the amino acid sequence of a specific protein. The DNA is "read" and transcribed into messenger RNA, which is translated as a series of amino acids. When these amino acids are joined together in the correct sequence encoded by the DNA, it is a protein.

   PTS: 1
2. ANS: D
   Transcription is the process of making a strand of RNA that is complementary to the DNA sequence that contains the gene for the protein needed. During DNA replication, both of the double strands of DNA within one cell are entirely copied resulting in the total synthesis of two new complete strands. During protein synthesis, only the segment of DNA that contains the actual gene for the protein needed is involved in the process, not the entire genome. This means that only a segment of *one* DNA strand is read and transcribed into RNA.

   PTS: 1
3. ANS: A
   The introns are not part of the gene and must be spliced out to form the mature messenger RNA that contains only the information encoded in the exons (expressed regions of a gene). In RNA, which is complementary to the DNA of the "sense strand," thymine is replaced with uracil. Therefore, response *B* is incorrect because it contains thymine. Response *C* is incorrect because it shows the segments corresponding to the introns and not the exons. Response *D* is incorrect because it shows retention of both the exons and the introns.

   PTS: 1
4. ANS: B
   A ribosome is a cytoplasmic adapter molecule containing a complex of proteins and some RNA that essentially decodes the mRNA and places the proper individual amino acid into the growing peptide chain during protein synthesis. It does not have anything to do with double-stranded DNA, nor does it perform any post-translational modification. The transport molecules are the transfer RNAs (tRNAs), not the ribosomes.

   PTS: 1
5. ANS: A
   Converting the early transcript of messenger RNA into mature messenger RNA requires splicing out the introns, which are the intervening sequences that are not part of the gene encoding for a specific protein. Only the exons (expressed regions) of the initial transcript should remain in the mature messenger RNA that is then ready for translation.

   PTS: 1
6. ANS: C

Proteins are not in their final forms for active function when they are first synthesized and require post-translational modification, the further processing of the newly translated primary protein structure into at least its secondary and tertiary structures to make it fully functional. Secondary protein structure is a twisting of the primary structure as a result of the interaction of amino acids located near each other. Tertiary structure is the folding of the linear structure and occurs as a result of remote amino acids interacting with each other. Folding often creates a "pocket" within the protein that becomes an "active site," able to interact with other structures or substances.

PTS: 1

7. ANS: C
The amino acid attachment site is the location that a specific amino acid can attach to and be carried by any one tRNA. Which amino acid attaches depends on the tRNA's anticodon, which is the tRNA complementary code for an amino acid codon. Thus, for every RNA codon, there is a corresponding complementary anticodon on the tRNA that can attach and carry the correct amino acid. (Every single amino acid has its own specific tRNAs.)

PTS: 1

8. ANS: C
Each amino acid is coded for by a triplet of bases in the DNA, which corresponds to the complementary triplet of bases composing the codon in RNA for each amino acid. Because each amino acid codon has three bases, the minimum number of bases needed in the mature messenger RNA for glucagon is 29 multiplied by 3, or 87.

PTS: 1

9. ANS: B
Every active protein has a specific amount of the amino acids and a unique sequence in which they are connected together. The exact sequence is critical for protein function. It is possible for two separate proteins to have the same total number of amino acids and perhaps even the same numbers of individual amino acids (so response *A* is incorrect). However, the sequencing order of the amino acids is what makes one protein different in structure and function from another protein. The exons are the actual directions for the sequence of amino acids. Deleting these would not result in a functional protein. Transcription always occurs *before*, not after, translation in the process of protein synthesis.

PTS: 1

10. ANS: A
RNA does not contain the pyrimidine base thymine. The base uracil is used in place of thymine because it is a pyrimidine base with a structure that does not contain the methyl group (CH_3) that thymine has. This difference between thymine and uracil is important because molecules in the nucleus that contain a methyl group remain trapped inside the nucleus. Because the remaining phases of protein synthesis occur outside the nucleus, the newly transcribed RNA must be able to exit the nucleus.

PTS: 1

11. ANS: D

The addition of a poly-A tail to the newly transcripted RNA, known as polyadenylation, results in a segment of RNA that contains mostly adenine and is not translated into part of the protein. Thus, it serves as a signal to stop translation.

PTS: 1

12. ANS: A
Once in the cytoplasm, mRNA molecules have a very short life span, only seconds before they are degraded by enzymes known as ribonucleases (RNases). This rapid degradation of mRNA is important in preventing an inadvertent overproduction of specific proteins. The idea is to make just enough active protein as is needed at that time and no extra. This makes protein synthesis less wasteful and more efficient. It also prevents too much of a specific protein from being present and exerting effects that are not needed.

PTS: 1

13. ANS: D
Introns are the sectional parts of DNA within a gene coding region that do not belong to the gene coding sequence of the protein being synthesized. However, because these introns are in gene coding regions, they are parts of another gene. In that other gene, they would be considered exons for that gene. Thus, they are not part of the desert DNA and have no role in synthesis of the gene product for which they are introns.

PTS: 1

14. ANS: B
Because an amino acid is encoded in the DNA by a "triplet" of bases, deletion of any number of bases which is not a multiple of three will alter the reading frame and result in a frameshift mutation. Although deletion of "triplet" bases can result in a change in some areas of the amino acid sequence and have an influence on protein function, the essential reading frame is not disrupted.

PTS: 1

15. ANS: C
A nonsense point mutation results in an inappropriate placement of a stop signal, which has a negative effect on protein function. This type of mutation prevents the completion of a protein. The protein may not be synthesized at all, if the stop signal is present early in the reading sequence. If it is present later in the sequence, protein synthesis stops prematurely and results in a short or truncated protein that usually has little if any function.

PTS: 1

16. ANS: D
Frameshift mutations are disruptions of the DNA reading frame (not the chromosome) as a result of having a whole base or group of bases added or deleted. They can occur in somatic cells or germline cells. When this type of mutation occurs in gene coding regions, it always disrupts the reading frame from the start of the mutation to the end of the gene. The result is complete alteration of amino acid position and prevention of synthesis of a functional protein. A normal protein cannot be made from a gene with a frameshift mutation. Although mutations may accumulate over a lifetime, frameshift mutations do not occur more often than point mutations as a person ages.

PTS: 1

17. ANS: A
Mutations of any type that occur in noncoding regions are responsible for making one person's DNA different from and identifiable from another person's DNA. Even identical twins (monozygotic twins) do not have absolutely identical DNA by the time they are born, although they probably did when the embryo first split into two embryos. By the time identical twins are born they usually have at least 100 base pairs different from each other in the noncoding regions. As they live their lives, each twin continues to accumulate more and different mutations so that as they age, these identical twins become less identical in their DNA.

PTS: 1

18. ANS: D
Point mutations are substitutions of one base for another and can occur in DNA or RNA. This type of change does not result in an extra base or a lost base, just a substitution. This type of base change is known as a single nucleotide polymorphism (SNP). Frameshift mutations are deletions or insertions of DNA bases, not one-for-one substitutions. SNPs do not interconvert introns and exons.

PTS: 1

19. ANS: B
Everyone experiences some mutational events as a result of spontaneous DNA replication error or exposure to mutagens or carcinogens in the environment. Many of these mutational events are correctly repaired and have no lasting consequences. However, when they remain unrepaired and occur in a gene coding region for cell growth regulation, they can have permanent consequences for the individual, including a greater risk for cancer development.

PTS: 1

20. ANS: B
Somatic cell mutations occur only in ordinary body cells, not in germline cells (eggs or sperm). Thus somatic mutations cannot be passed on to one's children. The presence of somatic mutations is a major cause of sporadic cancer in a person, but this predisposition cannot be inherited by his or her children.

PTS: 1