ASCP Molecular Biology (MB) Technologist Practice Exam (Sample)

Study Guide

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Questions

1. What type of control ensures that the enzyme is active and the thermal cycler functions properly?

A. Negative control

B. Positive control

C. Amplification control

D. Internal control

2. What does Northern Blotting primarily analyze?

A. DNA sequences

B. Proteins

C. RNA sequences

D. gene mutations

3. What is the definition of heteronuclear RNA (hnRNA)?

A. RNA with only exons

B. Uncapped RNA

C. Newly transcribed mRNA with unremoved introns

D. Mature mRNA ready for translation

4. What characterizes an oncogene?

A. A gene that inhibits cell growth

B. A normal gene that can become mutated

C. A gene that only promotes apoptosis

D. A gene that leads to normal cell function

5. Which of the following oncogenes have tyrosine kinase activity?

A. EGFR

B. ALL of the above

C. BCR-Abl

D. HER2

6. Which type of organisms contain introns in their genes?

A. Eukaryotes

B. Prokaryotes

C. Both Eukaryotes and Prokaryotes

D. Nobody contains introns.

7. What initiates protein synthesis in cells?

A. Activation of amino acids by covalent attachment to tRNA

B. DNA unwinding

C. Assembly of the ribosomal subunits

D. Binding of mRNA to ribosome

8. In pulsed field gel electrophoresis, what is the minimum number of bands that must differ between two organisms for them to be considered unrelated?

A. 2

B. 3

C. 6

D. 7

9. Which of the following is a signal amplification method?

A. Branched DNA Amplification (bDNA)

B. Polymerase Chain Reaction (PCR)

C. Real-Time PCR

D. Restriction Fragment Length Polymorphism (RFLP)

10. How many RNA polymerases do eukaryotes have?

A. One

B. Two

C. Three

D. Four

Answers

1. B
2. C
3. C
4. B
5. B
6. A
7. A
8. C
9. A
10. C

Explanations

1. What type of control ensures that the enzyme is active and the thermal cycler functions properly?

A. Negative control

B. Positive control

C. Amplification control

D. Internal control

The positive control is utilized in molecular biology experiments to confirm that the experimental setup, including the enzyme activity and the functionality of the thermal cycler, is operating as expected. In this context, a positive control would involve using a known template with a target sequence to ensure that the polymerase enzyme can successfully amplify the DNA and that the thermal cycler can efficiently manage the temperature changes necessary for the reaction. When a positive control is included in a reaction mix, it should yield a clear, interpretable result, indicating that the conditions required for enzyme activity and cycling processes are indeed functioning correctly. This allows for confidence in the experimental results, as any failure to amplify the positive control sample would suggest issues with the reagents or the machine being used. Given this understanding of positive controls, it ensures that both the enzyme and the thermal cycler are operating correctly during the reaction, thus validating the entire experimental process. In contrast, other types of controls, like negative controls, focus more on confirming that no non-specific amplification occurs, rather than validating the performance of the reaction itself.

2. What does Northern Blotting primarily analyze?

A. DNA sequences

B. Proteins

C. RNA sequences

D. gene mutations

Northern Blotting is a laboratory technique specifically designed to detect and analyze RNA molecules within a sample. This method involves the separation of RNA by gel electrophoresis, followed by transfer to a membrane and hybridization with a complementary labeled probe. The primary application of Northern Blotting is to assess the size, abundance, and expression levels of specific RNA transcripts, which provides valuable information regarding gene expression. By focusing on RNA rather than DNA or proteins, Northern Blotting enables researchers to study various aspects of RNA biology, including alternative splicing, developmental regulation, and responses to environmental signals. The technique is particularly useful for investigating gene expression profiles in different tissues or under varying conditions, thereby shedding light on the functional roles of specific genes.

3. What is the definition of heteronuclear RNA (hnRNA)?

A. RNA with only exons

B. Uncapped RNA

C. Newly transcribed mRNA with unremoved introns

D. Mature mRNA ready for translation

Heteronuclear RNA (hnRNA) refers to the primary transcript produced from a gene before it undergoes any processing, which includes splicing and the removal of introns. This type of RNA contains both exons (the coding regions) and introns (the non-coding regions) immediately after transcription. The defining characteristic of hnRNA is that it includes unspliced transcripts, which means that it has not yet been modified to remove the introns. This modification is essential for the RNA to become mature mRNA, which is subsequently translated into proteins. Only after the introns are removed and the exons are spliced together does the RNA become a mature form that is ready for translation. Thus, the correct characterization of hnRNA as the newly transcribed mRNA that still retains introns makes it distinct from other forms of RNA that are fully processed and ready for translation.

4. What characterizes an oncogene?

A. A gene that inhibits cell growth

B. A normal gene that can become mutated

C. A gene that only promotes apoptosis

D. A gene that leads to normal cell function

An oncogene is characterized by its potential to promote uncontrolled cell growth and division, which can lead to cancer. In its normal state, an oncogene is referred to as a proto-oncogene, which is involved in regular cellular functions such as growth and division. However, when this gene undergoes mutations or is expressed at higher levels than normal, it can lead to a gain of function that contributes to the transformation of a normal cell into a cancerous one. The choice that identifies an oncogene as a normal gene that can become mutated accurately captures this critical aspect of its function. Mutations in proto-oncogenes can result in proteins that are hyperactive or constitutively active, leading to the promotion of malignancy. This is why understanding the transformation of proto-oncogenes to oncogenes is essential in the study of cancer biology and therapy. Other choices do not encapsulate the essence of what an oncogene represents: inhibiting growth is contrary to the defining characteristics of oncogenes, while the promotion of apoptosis does not align with the fundamental role of oncogenes in driving cellular proliferation rather than cell death. Finally, a gene that leads to normal cell function does not typically classify as an oncogene since oncogen

5. Which of the following oncogenes have tyrosine kinase activity?

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The correct answer is that all of the mentioned oncogenes exhibit tyrosine kinase activity. Tyrosine kinases are crucial players in cellular signaling pathways, particularly those related to growth and differentiation. Each of the oncogenes listed is known for its role in cancer through mechanisms involving tyrosine kinase activity. EGFR (epidermal growth factor receptor) is a receptor tyrosine kinase that, when activated by binding to its ligand, undergoes autophosphorylation. This phosphorylation activates several downstream signaling pathways that promote cell proliferation and survival, connecting it to various cancers. BCR-Abl is a fusion protein resulting from the Philadelphia chromosome translocation associated with chronic myeloid leukemia (CML). This fusion combines the breakpoint cluster region (BCR) gene with the Abelson murine leukemia viral oncogene (Abl), creating a constitutively active tyrosine kinase that leads to uncontrolled cell division. HER2 (human epidermal growth factor receptor 2) is another receptor tyrosine kinase that, when overexpressed, is implicated in breast cancer. Like EGFR, HER2 can trigger signaling cascades promoting cell division and survival through its tyrosine kinase activity. The presence of ty

6. Which type of organisms contain introns in their genes?

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Eukaryotes are the type of organisms that are characterized by having introns in their genes. Introns are non-coding sequences found within genes that are transcribed into precursor mRNA but are removed during RNA processing before translation. This process of splicing is a critical step in the expression of eukaryotic genes and allows for the possibility of alternative splicing, which can lead to the production of different protein isoforms from a single gene. In contrast, prokaryotes, which include bacteria and archaea, typically do not contain introns in their genes. Their genes are often organized in operons and lack the complex gene architecture seen in eukaryotes, leading to a more streamlined process of transcription and translation. This fundamental difference in genetic organization and expression is one of the key distinctions between eukaryotic and prokaryotic organisms.

7. What initiates protein synthesis in cells?

A. Activation of amino acids by covalent attachment to tRNA

B. DNA unwinding

C. Assembly of the ribosomal subunits

D. Binding of mRNA to ribosome

The initiation of protein synthesis begins with the activation of amino acids, where they become covalently attached to their corresponding transfer RNA (tRNA). This crucial step ensures that the amino acids are correctly matched to the codons present on the mRNA template during translation. Activation of amino acids is catalyzed by enzymes called aminoacyl-tRNA synthetases, which facilitate the binding of the specific amino acid to its tRNA, forming an aminoacyl-tRNA complex. Once the amino acids are attached to their tRNAs, the next steps in protein synthesis can proceed, including the binding of the mRNA to the ribosome and the assembly of the ribosomal subunits. However, these processes cannot occur without the prior activation of the amino acids. Therefore, the activation of amino acids is a fundamental and initial step in the overall process of protein synthesis, making it a critical component in the pathway that leads to the formation of proteins.

8. In pulsed field gel electrophoresis, what is the minimum number of bands that must differ between two organisms for them to be considered unrelated?

A. 2

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In pulsed field gel electrophoresis (PFGE), the resolution of DNA fragments allows for detailed analysis of the genetic differences between organisms. The practice of using PFGE is particularly important in distinguishing between strains of bacteria, especially in epidemiological studies. To consider two organisms as unrelated, there must be enough genetic variation to indicate distinct genetic lineages or backgrounds. The presence of a minimum number of different bands indicates that there are significant differences in the DNA fragments being analyzed. In this context, the idea is that 6 bands represents a threshold of genetic divergence that suggests the organisms do not share a recent common ancestor. Having fewer than this threshold of differing bands may suggest that the organisms are more closely related or could potentially be variations of the same strain. Contrarily, demonstrating 6 or more differing bands establishes a more definitive genetic distinction, making it unlikely that the two organisms share significant genetic material. Therefore, the requirement of differing bands in PFGE is a quantitative measure of genetic diversity and distance, and a minimum of 6 bands is crucial to support the conclusion that the organisms in question are indeed unrelated.

9. Which of the following is a signal amplification method?

A. Branched DNA Amplification (bDNA)

B. Polymerase Chain Reaction (PCR)

C. Real-Time PCR

D. Restriction Fragment Length Polymorphism (RFLP)

Branched DNA Amplification (bDNA) is a signal amplification method that allows for the detection of specific nucleic acid sequences with increased sensitivity. This technique utilizes a structure where the initial probe hybridizes to the target nucleic acid, followed by the binding of additional probes, creating a branched structure. Each branch can then further attach to additional labeled probes, effectively amplifying the signal rather than the target DNA itself. This form of signal amplification is particularly useful in situations where the target nucleic acid is present in very low quantities, as it enhances the detection capabilities without requiring multiple rounds of amplification of the target DNA. In contrast, Polymerase Chain Reaction (PCR) and Real-Time PCR are methods primarily used for targeted amplification of DNA, increasing the amount of the target sequence rather than amplifying the signal directly. While PCR is excellent for amplifying specific DNA sequences, it does not inherently involve the same kind of signal enhancement that bDNA does. Additionally, Restriction Fragment Length Polymorphism (RFLP) is a technique used to analyze the variability in DNA sequences by cutting them with specific restriction enzymes, which does not include a signal amplification aspect. In summary, the key distinction of bDNA as a signal amplification method lies in its

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Eukaryotes contain three distinct RNA polymerases, each responsible for synthesizing different types of RNA. RNA polymerase I primarily synthesizes ribosomal RNA (rRNA), which is a key component of ribosomes, the cellular machinery for protein synthesis. RNA polymerase II is responsible for synthesizing messenger RNA (mRNA), which conveys genetic information from DNA to the ribosome for protein production. Finally, RNA polymerase III synthesizes transfer RNA (tRNA), as well as other small RNAs like 5S rRNA and various nuclear RNA molecules. This specific categorization allows eukaryotic cells to compartmentalize and efficiently manage gene expression and RNA processing in a more complex way compared to prokaryotic organisms, which generally rely on a single RNA polymerase for all types of RNA production. Thus, recognizing that eukaryotes have three different RNA polymerases is fundamental to understanding their transcriptional mechanisms and the intricacies of gene regulation.