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

Study Guide

BY EXAMZIFY

Everything you need from our exam experts!

Questions

1. **What is the primary function of eukaryotic DNA Polymerase ε?**
   - A. Replication of the lagging strand
   - B. Base excision repair
   - C. DNA replication and repair, mainly for the leading strand
   - D. Primase activity for initiating replication

2. **Which EWSR1 gene fusion accounts for 80% of Ewing sarcoma cases?**
   - A. EWSR1 with ERG gene
   - B. EWSR1 with FLI-1 gene
   - C. EWSR1 with ETV1 gene
   - D. EWSR1 with FEV gene

3. **Which genetic alteration is noted as AML-ETO?**
   - A. t(15;17)
   - B. t(16;16)
   - C. t(8;21)
   - D. inv(16)

4. **What is the full name of SDS?**
   - A. Sodium Dodecyl Sulfate
   - B. Sustained Dodecane Sulfate
   - C. Sodium Dodecane Solution
   - D. Sodium Decyl Sulfate

5. **What determines the optimal binding conditions of a probe and target during hybridization?**
   - A. Temperature only
   - B. Probe concentration only
   - C. Stringency
   - D. Salt concentration only

6. What is the repeat expansion associated with Huntington's Disease?

A. CGG repeats

B. CAA repeats

C. CAG repeats

D. GTG repeats

7. Which application was one of the first for LCR technology?

A. Detection of viral infections

B. Screening for genetic diseases

C. Detection of mutations in beta globulin associated with sickle cell disease

D. Genetic mapping of chromosomes

8. What is the average rate of eukaryotic DNA replication?

A. 25 nucleotides per second

B. 50 nucleotides per second

C. 75 nucleotides per second

D. 100 nucleotides per second

9. Which chromosome contains the HLA genes?

A. Chromosome 1

B. Chromosome 6

C. Chromosome 12

D. Chromosome 15

10. What is the result of the actions taken during the primer annealing phase in LCR?

A. Only full-length products are created

B. Even single nucleotide mismatches can prevent ligation

C. Detectable amounts of RNA are generated

D. Multiple different primers are ligated together

Answers

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

Explanations

1. What is the primary function of eukaryotic DNA Polymerase ε?

A. Replication of the lagging strand

B. Base excision repair

C. DNA replication and repair, mainly for the leading strand

D. Primase activity for initiating replication

Eukaryotic DNA Polymerase ε plays a critical role in the replication of DNA, primarily focusing on the leading strand. During DNA replication, the leading strand is synthesized in a continuous manner, as opposed to the lagging strand, which is synthesized in discontinuous fragments known as Okazaki fragments. DNA Polymerase ε is specifically responsible for this continuous synthesis as it has a high processivity and is essential for accurately and efficiently elongating the leading strand. In addition to its primary role in leading strand replication, DNA Polymerase ε is also involved in the repair mechanisms of DNA, contributing to the overall integrity of the genetic material. This dual functionality emphasizes its importance in maintaining both the replication process and the response to DNA damage. Understanding the specific activities of different polymerases, including DNA Polymerase ε, allows for a more profound insight into eukaryotic cellular processes related to DNA replication and repair mechanisms.

2. Which EWSR1 gene fusion accounts for 80% of Ewing sarcoma cases?

A. EWSR1 with ERG gene

B. EWSR1 with FLI-1 gene

C. EWSR1 with ETV1 gene

D. EWSR1 with FEV gene

The EWSR1 gene fusion that accounts for approximately 80% of Ewing sarcoma cases is the fusion between EWSR1 and the FLI-1 gene. This specific fusion results in the production of a chimeric transcription factor that plays a critical role in the pathogenesis of Ewing sarcoma by driving oncogenesis through the dysregulation of target genes. EWSR1, which stands for Ewing Sarcoma Breakpoint Region 1, is involved in several gene fusion events in Ewing sarcoma, but the EWSR1-FLI1 fusion is the most prevalent and is considered a hallmark of the disease. The presence of this particular fusion is often utilized in diagnostic testing to confirm the diagnosis of Ewing sarcoma, alongside other clinical and histological features. In contrast, other gene fusions involving EWSR1, such as with ERG, ETV1, and FEV, are less common and do not represent the majority of cases. While they may be relevant in specific contexts, they do not account for the overwhelming majority of Ewing sarcoma cases as the EWSR1-FLI1 fusion does. Hence, recognizing the significance of the EWSR1-FLI1

3. Which genetic alteration is noted as AML-ETO?

A. t(15;17)

B. t(16;16)

C. t(8;21)

D. inv(16)

The correct genetic alteration noted as AML-ETO is the translocation t(8;21). This specific translocation is typically associated with acute myeloid leukemia (AML) and results in the fusion of the AML1 gene (also known as RUNX1) on chromosome 21 and the ETO gene (also known as RUNX1T1) on chromosome 8. This fusion gene plays a significant role in the pathogenesis of this subtype of AML by disrupting normal hematopoiesis and promoting leukemogenesis. In contrast, the other options refer to different genetic alterations associated with other types of leukemias or distinct transformations. For instance, the translocation t(15;17) is characteristic of acute promyelocytic leukemia (APL), related to the fusion of the promyelocytic leukemia (PML) gene and the retinoic acid receptor alpha (RARA) gene. The t(16;16) translocation is commonly associated with acute myeloid leukemia with abnormal eosinophils, leading to a specific type of AML labeled as acute myeloid leukemia with inv(16). The inversion inv(16), also linked to acute myeloid leukemia, involves a rearrangement of chromosome 16

4. What is the full name of SDS?

A. Sodium Dodecyl Sulfate

B. Sustained Dodecane Sulfate

C. Sodium Dodecane Solution

D. Sodium Decyl Sulfate

The full name of SDS is Sodium Dodecyl Sulfate. This compound is a detergent commonly used in biochemistry and molecular biology laboratories, particularly in the process of protein denaturation and in the SDS-PAGE technique, where it helps to unfold proteins and impart a negative charge to them. Sodium Dodecyl Sulfate consists of a long hydrophobic tail (dodecyl) that interacts with lipid membranes and a hydrophilic head (sodium sulfate) that interacts with water, making it effective in solubilizing proteins. This characteristic allows for the separation of proteins based on their size during electrophoresis, as they will migrate through a gel matrix under an electric field according to their molecular weight. The other options do not correctly describe the compound. For instance, "Sustained Dodecane Sulfate" and "Sodium Dodecane Solution" do not accurately reflect known chemical structures or the common use of SDS in molecular biology. "Sodium Decyl Sulfate" also misrepresents the alkyl chain length, as decyl refers to a ten-carbon chain, whereas dodecyl refers to a twelve-carbon chain, making option A the only accurate choice.

5. What determines the optimal binding conditions of a probe and target during hybridization?

A. Temperature only

B. Probe concentration only

C. Stringency

D. Salt concentration only

The optimal binding conditions of a probe and target during hybridization are primarily determined by stringency. Stringency refers to the conditions that affect the specificity of the hybridization process, including temperature, salt concentration, and the presence of other factors that influence the stability of the probe-target complex. High stringency conditions generally promote the formation of only highly complementary hybrids between the probe and target, whereas lower stringency conditions may allow for more mismatched hybrids to form. This balance is crucial in molecular techniques, such as PCR, microarray analysis, and in situ hybridization, where achieving the right match between probe and target influences the accuracy and sensitivity of the detection. While temperature, probe concentration, and salt concentration play important roles in the hybridization process, they are all aspects that can affect stringency. For example, increasing temperature typically increases stringency because it can lead to the dissociation of less stable, mismatched hybrids. Similarly, changes in salt concentration can affect the stability of the hybrid DNA, thus influencing hybridization conditions. Hence, a comprehensive understanding of stringency encompasses these factors, making it the central determinant for optimal probe-target binding.

6. What is the repeat expansion associated with Huntington's Disease?

A. CGG repeats

B. CAA repeats

C. CAG repeats

D. GTG repeats

Huntington's Disease is caused by a specific type of mutation known as a repeat expansion in the HTT gene, which encodes for the protein huntingtin. The pathological feature of this mutation is the expansion of CAG trinucleotide repeats within this gene. Normally, the number of CAG repeats in the HTT gene ranges from about 10 to 35. However, in individuals with Huntington's Disease, this number can expand to 36 repeats or more, leading to the development of neurological symptoms associated with the disorder. The CAG repeat is translated into a polyglutamine stretch in the huntingtin protein; as the number of repeats increases, the protein can misfold and aggregate, which is thought to play a critical role in the neurodegenerative process of the disease. Understanding the mechanism behind this repeat expansion is crucial for diagnosing Huntington's Disease and furthering research into potential therapies.

7. Which application was one of the first for LCR technology?

A. Detection of viral infections

B. Screening for genetic diseases

C. Detection of mutations in beta globulin associated with sickle cell disease

D. Genetic mapping of chromosomes

The detection of mutations in beta globulin associated with sickle cell disease represents one of the pioneering applications of LCR (Ligase Chain Reaction) technology. This method is particularly suited for identifying specific genetic mutations due to its high sensitivity and specificity. Sickle cell disease is caused by a single nucleotide mutation in the beta-globin gene; therefore, LCR's ability to detect very small amounts of DNA is critical for diagnosing this condition effectively. LCR technology operates by leveraging the ligation of probes that are hybridized to the target DNA, allowing for the amplification and detection of sequences that might differ due to mutations. When applied to beta globulin, it can accurately identify whether an individual has the mutation responsible for sickle cell disease, aiding in both diagnosis and carrier screening. This application laid the groundwork for the broader use of LCR technology in molecular genetics and diagnostics. While other options, such as the detection of viral infections, screening for genetic diseases, and genetic mapping, are significant applications of various molecular biology techniques, they are not as closely linked to the foundational use of LCR technology as the detection of mutations associated with sickle cell disease.

8. What is the average rate of eukaryotic DNA replication?

A. 25 nucleotides per second

B. 50 nucleotides per second

C. 75 nucleotides per second

D. 100 nucleotides per second

The average rate of eukaryotic DNA replication is typically around 50 nucleotides per second per replication fork. This rate allows for efficient duplication of the complex eukaryotic genome, which contains multiple origins of replication to facilitate faster copying of the large amount of DNA contained within eukaryotic cells. While the replication rate in prokaryotes can be significantly higher, eukaryotic cells face additional challenges, such as higher complexity and the presence of histones. This contributes to their relatively moderate pace of replication. The other options indicate higher rates than what is typically observed in eukaryotic systems. For instance, a replication rate of 75 or 100 nucleotides per second, while potentially applicable in different contexts or under specific conditions, does not align with the average observed in standard eukaryotic replicative mechanisms. The choice of 50 nucleotides reflects a well-established understanding of the average dynamics of DNA synthesis in eukaryotic organisms during the S phase of the cell cycle.

9. Which chromosome contains the HLA genes?

- A. Chromosome 1
- B. Chromosome 6
- C. Chromosome 12
- D. Chromosome 15

The HLA (human leukocyte antigen) genes are located on chromosome 6. This chromosome houses a critical region known as the Major Histocompatibility Complex (MHC), which plays a vital role in the immune system by helping the body distinguish between self and non-self entities. The HLA genes are particularly important for the regulation of the immune response and are involved in the presentation of antigens to T cells. The MHC is divided into several classes, with class I molecules (such as HLA-A, HLA-B, and HLA-C) presenting antigens to CD8+ cytotoxic T cells, whereas class II molecules (such as HLA-DP, HLA-DQ, and HLA-DR) present antigens to CD4+ helper T cells. The diversity of HLA genes is crucial for the immune system's ability to recognize different pathogens, and variations in these genes can influence individual susceptibility to various diseases. The incorrect choices pertain to chromosomes that do not contain the HLA gene cluster. Chromosome 1, 12, and 15 have different sets of genes and genetic markers that do not directly pertain to the HLA complex. Thus, identifying chromosome 6 as the location for H

10. What is the result of the actions taken during the primer annealing phase in LCR?

- A. Only full-length products are created
- B. Even single nucleotide mismatches can prevent ligation
- C. Detectable amounts of RNA are generated
- D. Multiple different primers are ligated together

During the primer annealing phase in Ligase Chain Reaction (LCR), the importance of primer specificity is emphasized. The correct choice reflects that even a single nucleotide mismatch between the primer and the target DNA can prevent the ligation step from occurring. This is crucial because the efficiency of the ligation reaction heavily relies on the perfect complementarity of the primers to their target sequences. If a mismatch occurs, the ligase enzyme is unable to form a stable bond between the primers, leading to a failed reaction. This specificity is particularly significant in applications such as diagnostics, where accurate detection of specific sequences is essential. The rigorous requirement for exact matching during the annealing phase ensures high fidelity in the amplification process, contributing to the overall reliability and accuracy of the LCR technique. In contrast, the other statements do not accurately reflect the principles of LCR. While ligation of multiple primers can occur in a broader context, it is not a defining feature of the primer annealing phase itself, focusing instead on the thermal stability and compatibility of the annealed primers. Additionally, the generation of detectable RNA or the creation of only full-length products is not characteristic of the primer annealing phase, as these outcomes depend on various factors beyond primer annealing alone.