

AAB MOLECULAR DIAGNOSTICS PRACTICE TEST (SAMPLE)

STUDY GUIDE



**SAMPLE STUDY GUIDE
WITH LIMITED QUESTIONS**

**VISIT US ONLINE FOR
THE FULL VERSION STUDY GUIDE**

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Introduction

Preparing for a certification exam can feel overwhelming, but with the right tools, it becomes an opportunity to build confidence, sharpen your skills, and move one step closer to your goals. At Examzify, we believe that effective exam preparation isn't just about memorization, it's about understanding the material, identifying knowledge gaps, and building the test-taking strategies that lead to success.

This guide was designed to help you do exactly that.

Whether you're preparing for a licensing exam, professional certification, or entry-level qualification, this book offers structured practice to reinforce key concepts. You'll find a wide range of multiple-choice questions, each followed by clear explanations to help you understand not just the right answer, but why it's correct.

The content in this guide is based on real-world exam objectives and aligned with the types of questions and topics commonly found on official tests. It's ideal for learners who want to:

- Practice answering questions under realistic conditions,
- Improve accuracy and speed,
- Review explanations to strengthen weak areas, and
- Approach the exam with greater confidence.

We recommend using this book not as a stand-alone study tool, but alongside other resources like flashcards, textbooks, or hands-on training. For best results, we recommend working through each question, reflecting on the explanation provided, and revisiting the topics that challenge you most.

Remember: successful test preparation isn't about getting every question right the first time, it's about learning from your mistakes and improving over time. Stay focused, trust the process, and know that every page you turn brings you closer to success.

Let's begin.

How to Use This Guide

This guide is designed to help you study more effectively and approach your exam with confidence. Whether you're reviewing for the first time or doing a final refresh, here's how to get the most out of your Examzify study guide:

1. Start with a Diagnostic Review

Skim through the questions to get a sense of what you know and what you need to focus on. Your goal is to identify knowledge gaps early.

2. Study in Short, Focused Sessions

Break your study time into manageable blocks (e.g. 30 – 45 minutes). Review a handful of questions, reflect on the explanations.

3. Learn from the Explanations

After answering a question, always read the explanation, even if you got it right. It reinforces key points, corrects misunderstandings, and teaches subtle distinctions between similar answers.

4. Track Your Progress

Use bookmarks or notes (if reading digitally) to mark difficult questions. Revisit these regularly and track improvements over time.

5. Simulate the Real Exam

Once you're comfortable, try taking a full set of questions without pausing. Set a timer and simulate test-day conditions to build confidence and time management skills.

6. Repeat and Review

Don't just study once, repetition builds retention. Re-attempt questions after a few days and revisit explanations to reinforce learning. Pair this guide with other Examzify tools like flashcards, and digital practice tests to strengthen your preparation across formats.

There's no single right way to study, but consistent, thoughtful effort always wins. Use this guide flexibly, adapt the tips above to fit your pace and learning style. You've got this!

Questions

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- 1. Which is NOT a characteristic of membrane-bound SSP-PCR?**
 - A. Utilizes a solid phase
 - B. May use Luminex technology
 - C. Results in negative readings
 - D. Is performed on immobilized target
- 2. What does QA for surgical pathology aim to identify?**
 - A. The function of the assay
 - B. "Floaters" in surgical pathology specimens
 - C. Presence of donor alleles
 - D. Contamination in reagents
- 3. What characterizes dual-color probes used in FISH?**
 - A. They cover part of a chromosome
 - B. They allow multiple target detections
 - C. They are used for single-copy detection
 - D. They identify centromeres
- 4. Which of the following best describes the method for visualizing fragments in Maxam-Gilbert Sequencing?**
 - A. Polymerase chain reaction
 - B. Fluorescence microscopy
 - C. Autoradiography yields a series of dark bands
 - D. Gel electrophoresis without labeling
- 5. Which of the following is NOT a stop codon?**
 - A. UAA
 - B. UAG
 - C. AUG
 - D. UGA
- 6. Which of the following bases are classified as purines?**
 - A. Adenine and Cytosine
 - B. Adenine and Guanine
 - C. Cytosine and Thymine
 - D. Guanine and Uracil

- 7. Which enzymes are involved in restoring the correct sequence during mismatch repair?**
- A. DNA polymerase I and helicase
 - B. DNA polymerase III and ligase
 - C. DNA ligase and topoisomerase
 - D. DNA polymerase I and RNA polymerase
- 8. What type of chromosomes are responsible for genetic traits linked to gender?**
- A. Autosomes
 - B. Sex chromosomes
 - C. Euchromatin
 - D. Nucleosomes
- 9. Which of the following sequences is not characteristic of a eukaryotic polymerase II promoter?**
- A. TATAAA
 - B. TTGACA
 - C. CAAT box
 - D. GC-rich box
- 10. How can Hepatitis C Virus (HCV) be identified?**
- A. Using qualitative and quantitative PCR tests
 - B. Only through liver biopsy
 - C. By observing symptoms only
 - D. Through chest X-rays

Answers

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

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Explanations

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1. Which is NOT a characteristic of membrane-bound SSP-PCR?

- A. Utilizes a solid phase
- B. May use Luminex technology
- C. Results in negative readings**
- D. Is performed on immobilized target

Membrane-bound SSP-PCR, which stands for Sequence-Specific Primer Polymerase Chain Reaction, has distinct characteristics that set it apart from other PCR methods. One key aspect of this technique is the use of a solid phase, which provides a stable environment for the reaction and allows for greater control over the conditions. Therefore, utilizing a solid phase is a defining feature of membrane-bound SSP-PCR. In addition to this, the method can incorporate advanced technologies such as Luminex, which utilizes color-coded beads for detecting different nucleic acid sequences effectively. This capability enhances the multiplexing ability of the assay, allowing simultaneous detection of multiple targets. Another essential characteristic is the performance of the assay on immobilized targets, which aids in the specificity of the reaction. This immobilization helps ensure that the amplification occurs only in the presence of the specific target sequences, which is crucial for the method's reliability and accuracy. The statement regarding negative readings is not a characteristic of the technique, as SSP-PCR is designed to produce positive results when the target sequence is present. Negative readings may be related to the absence of the target sequence or technique failure, but they do not inherently define the characteristics of membrane-bound SSP-PCR. Thus, the option regarding negative readings correctly identifies something that is

2. What does QA for surgical pathology aim to identify?

- A. The function of the assay
- B. "Floaters" in surgical pathology specimens**
- C. Presence of donor alleles
- D. Contamination in reagents

Quality Assurance (QA) for surgical pathology primarily focuses on verifying and maintaining high standards in diagnostic practices to ensure accurate and reliable results. One of the critical aspects of QA is the identification of "floaters" in surgical pathology specimens. "Floaters" refers to non-specific materials or artifacts that can appear in tissue samples, which may obstruct the interpretation of the pathology results. Recognizing these artifacts is crucial because they can mislead pathologists and potentially result in incorrect diagnoses. QA processes in surgical pathology involve various checks and balances, including the review of specimens to ensure that all components are representative of the tissue being analyzed and that no extraneous materials interfere with the analysis. The other options provided relate to different aspects of laboratory quality and procedures but do not directly address the specific aims of QA in surgical pathology. For example, the function of the assay may relate more to laboratory tests than to the pathological evaluation of tissues. The presence of donor alleles is relevant in transplant scenarios, while contamination in reagents pertains to broader laboratory quality issues rather than the specific challenges faced within surgical pathology specimens.

3. What characterizes dual-color probes used in FISH?

- A. They cover part of a chromosome
- B. They allow multiple target detections**
- C. They are used for single-copy detection
- D. They identify centromeres

Dual-color probes used in fluorescence in situ hybridization (FISH) are specifically designed to allow the detection of multiple targets simultaneously within the same specimen. This characteristic is essential for applications such as the identification of chromosomal abnormalities, where the simultaneous visualization of different genomic regions can reveal insights into structural rearrangements, duplications, or deletions. When dual-color probes are employed, each probe emits a distinct fluorescent signal, enabling researchers to differentiate between the two targets. This method enhances the capability to study the spatial organization of genes and their interactions in a single analysis, providing a more comprehensive understanding of the genetic landscape. The ability to detect multiple targets in one experiment is particularly useful in complex analyses, such as those involving cancer genomics, where multiple genetic alterations may be present. While it's true that some other options may describe certain features of probes in FISH, they do not accurately characterize the unique functionality of dual-color probes. For instance, while some probes could be designed to cover part of a chromosome or identify centromeres, these characteristics do not necessarily pertain to the dual-color aspect, which is fundamentally about detecting multiple targets concurrently.

4. Which of the following best describes the method for visualizing fragments in Maxam-Gilbert Sequencing?

- A. Polymerase chain reaction
- B. Fluorescence microscopy
- C. Autoradiography yields a series of dark bands**
- D. Gel electrophoresis without labeling

Maxam-Gilbert Sequencing is a method used for DNA sequencing that relies on the selective cleavage of DNA at specific bases. After the DNA is subjected to chemical reactions that cleave the strands at various nucleotide positions, the resulting fragments need to be visualized to determine the sequence. The most effective way to visualize these fragments is through autoradiography, which captures the radioactive signals emitted by the cleaved DNA fragments. In this context, the statement that autoradiography yields a series of dark bands is particularly accurate. Each band represents fragments of DNA that are the result of the cleavage process, corresponding to the locations of the bases. The dark bands on the autoradiograph indicate the length of these fragments, allowing researchers to deduce the sequence of the original DNA strand by analyzing the positions of the bands. Other methods mentioned, such as polymerase chain reaction, fluorescence microscopy, and gel electrophoresis without labeling, do not provide the same direct visual representation of the specific fragment sizes and sequences produced in Maxam-Gilbert Sequencing. Each of these methods serves different purposes in molecular biology but is not directly applicable to visualizing the results of this specific sequencing technique.

5. Which of the following is NOT a stop codon?

- A. UAA
- B. UAG
- C. AUG**
- D. UGA

The correct answer is C, AUG, which is not a stop codon. Instead, AUG serves a critical role in the process of protein synthesis as it is recognized as the start codon. In the genetic code, AUG not only specifies the amino acid methionine but also signals the beginning of translation, where the ribosome assembles around the mRNA strand to start synthesizing a protein. In contrast, the other options—UAA, UAG, and UGA—are all recognized as stop codons. Stop codons play a crucial role in the termination of protein synthesis. When any of these codons are encountered during translation, they signal the ribosome to stop adding amino acids, leading to the release of the complete polypeptide chain. Understanding the function of start and stop codons is essential in molecular biology, particularly in the context of gene expression and protein synthesis.

6. Which of the following bases are classified as purines?

- A. Adenine and Cytosine
- B. Adenine and Guanine**
- C. Cytosine and Thymine
- D. Guanine and Uracil

Purines are one of the two classes of nitrogenous bases found in nucleic acids, the other being pyrimidines. The purines are characterized by their two-ring structure, which distinguishes them from pyrimidines, which have a single-ring structure. In this context, adenine and guanine are the only two nitrogenous bases that are classified as purines. Adenine is a fundamental component of DNA and RNA and plays a critical role in energy transfer through ATP (adenosine triphosphate). Guanine, similarly, is a key component of both DNA and RNA, contributing to the coding of genetic information and the regulation of cellular metabolism. Cytosine and thymine, as well as cytosine and uracil, are classified as pyrimidines. These bases have a single-ring structure, differing from purines in their chemical makeup and properties. This structural distinction helps to categorize them properly within the framework of molecular biology and genetics. Thus, the identification of adenine and guanine as purines is correct because they share the necessary two-ring structure characteristic of purines, making option B the correct choice.

7. Which enzymes are involved in restoring the correct sequence during mismatch repair?

- A. DNA polymerase I and helicase
- B. DNA polymerase III and ligase**
- C. DNA ligase and topoisomerase
- D. DNA polymerase I and RNA polymerase

The role of DNA polymerase III in mismatch repair is crucial because this enzyme is responsible for synthesizing new DNA strands. When a mismatch is identified, DNA polymerase III can remove the incorrectly paired nucleotide and replace it with the correct one, ensuring the accuracy of the DNA sequence. Additionally, DNA ligase plays a significant role in joining the newly synthesized DNA segment back to the existing strand after the mismatch has been corrected. This sealing action is necessary to maintain the integrity of the DNA molecule and ensure that the new and old DNA strands are properly linked. While other enzymes listed do participate in various DNA repair and replication processes, they do not specifically address the sequence restoration during mismatch repair as directly as DNA polymerase III and ligase do. For example, helicase unwinds the DNA, but it does not contribute to the correction of mismatches. Therefore, the combination of DNA polymerase III for synthesis and ligase for sealing is essential for effectively restoring the correct DNA sequence during the mismatch repair process.

8. What type of chromosomes are responsible for genetic traits linked to gender?

- A. Autosomes
- B. Sex chromosomes**
- C. Euchromatin
- D. Nucleosomes

Sex chromosomes are the specific type of chromosomes responsible for genetic traits linked to gender. In humans, there are two sex chromosomes: X and Y. Females typically have two X chromosomes (XX), while males have one X and one Y chromosome (XY). This distinction directly influences the development of sexual characteristics and the inheritance of gender-linked traits. For example, the presence of the Y chromosome triggers the development of male physical traits, while the absence of it (having two X chromosomes) aligns with female development. Various traits, such as certain types of color blindness or hemophilia, are linked to genes located on the X chromosome, demonstrating how sex chromosomes can influence gender-specific genetic traits. Other options like autosomes (which are non-sex chromosomes) carry the majority of genetic information unrelated to gender. Euchromatin is a form of chromatin that is involved in gene expression, while nucleosomes are the structural unit of chromatin that packages DNA, neither of which directly relate to the inheritance of gender-specific traits.

9. Which of the following sequences is not characteristic of a eukaryotic polymerase II promoter?

- A. TATAAA
- B. TTGACA**
- C. CAAT box
- D. GC-rich box

A eukaryotic polymerase II promoter typically comprises several key elements that are important for the initiation of transcription. Among the options provided, the sequence that is not characteristic of this type of promoter is indeed the TTGACA sequence. The TATAAA box, commonly referred to as the TATA box, is a well-known core promoter element found in many eukaryotic promoters that helps position the RNA polymerase II enzyme for transcription initiation. It is usually located about 25 to 30 base pairs upstream of the transcription start site. The CAAT box is another important sequence element that can be found in eukaryotic promoters. It is generally located further upstream and plays a role in enhancing the transcriptional activity of that promoter. Similarly, a GC-rich box is associated with many eukaryotic promoters, particularly those that are constitutively active. This element contains a high frequency of guanine (G) and cytosine (C) residues, which can also contribute to the regulation of gene expression. In contrast, the TTGACA sequence is a characteristic sequence found in prokaryotic promoters, specifically as part of the -35 region recognized by sigma factors in bacterial RNA polymerase. This sequence does not typically appear

10. How can Hepatitis C Virus (HCV) be identified?

- A. Using qualitative and quantitative PCR tests**
- B. Only through liver biopsy
- C. By observing symptoms only
- D. Through chest X-rays

Identifying Hepatitis C Virus (HCV) primarily involves laboratory testing methods that directly detect the virus or its components. Qualitative and quantitative PCR (Polymerase Chain Reaction) tests are critical for this purpose. Qualitative PCR tests detect the presence of HCV RNA in the blood, confirming an active infection. Quantitative PCR provides the viral load information, measuring the amount of HCV RNA present, which can be crucial for monitoring the effectiveness of treatment and disease progression. In contrast, liver biopsy, while useful for assessing liver damage caused by HCV, does not directly identify the virus itself. Observing symptoms alone is insufficient, as many individuals with HCV can be asymptomatic, leading to potential delays in diagnosis. Chest X-rays are not applicable for the diagnosis of HCV, as they are used mainly for visualizing lung conditions and other thoracic issues, not viral infections. Thus, the use of PCR testing is the most accurate and effective approach to identify HCV.

Next Steps

Congratulations on reaching the final section of this guide. You've taken a meaningful step toward passing your certification exam and advancing your career.

As you continue preparing, remember that consistent practice, review, and self-reflection are key to success. Make time to revisit difficult topics, simulate exam conditions, and track your progress along the way.

If you need help, have suggestions, or want to share feedback, we'd love to hear from you. Reach out to our team at hello@examzify.com.

Or visit your dedicated course page for more study tools and resources:

<https://aabmoleculardiagnosics.examzify.com>

We wish you the very best on your exam journey. You've got this!

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