

AAB MOLECULAR DIAGNOSTICS PRACTICE TEST (SAMPLE)

STUDY GUIDE



Prepare with structure. Pass with confidence



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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. When does an analyte run through a gel matrix at constant velocity, according to Stokes Law?**
 - A. When the sample is diluted
 - B. When electrophoretic driving force equals frictional force
 - C. When the gel concentration is low
 - D. When the electric field is turned off
- 2. Which syndrome is an example of an imprinting disorder?**
 - A. Turner syndrome
 - B. Angelman syndrome
 - C. Klinefelter syndrome
 - D. Cystic fibrosis
- 3. What resolution is achieved by the changes introduced in DNA sequences during bisulfite conversion?**
 - A. Single-molecule resolution.
 - B. Single-nucleotide resolution.
 - C. Single-cell resolution.
 - D. Single-gene resolution.
- 4. Which mutation occurs in 80-85% of most hemochromatosis cases?**
 - A. C282Y mutation
 - B. H63D mutation
 - C. S65T mutation
 - D. R572W mutation
- 5. Which DNA repair mechanism specifically addresses mispaired bases in DNA?**
 - A. Base excision repair
 - B. Mismatch repair
 - C. Nucleotide excision repair
 - D. Single-strand repair

- 6. What is the main effect of bisulfite conversion in methylation analysis?**
- A. It amplifies DNA for sequencing purposes.
 - B. It alters cytosine residues to Uracil.
 - C. It converts all DNA into RNA.
 - D. It enhances the binding of primers.
- 7. How are STR alleles identified?**
- A. By sequencing base pairs
 - B. By PCR product size
 - C. Through direct observation under a microscope
 - D. Using fluorescent dyes
- 8. Which type of mutation does not alter the resulting amino acid sequence?**
- A. Missense mutation
 - B. Nonsense mutation
 - C. Silent mutation
 - D. Frameshift mutation
- 9. What genetic disorder is an example of a point mutation?**
- A. Cystic fibrosis
 - B. Sickle cell anemia
 - C. Turner syndrome
 - D. Down syndrome
- 10. A ratio greater than 2 in OD260/OD280 suggests what type of contamination?**
- A. Protein contamination
 - B. DNA contamination
 - C. RNA contamination
 - D. Water contamination

Answers

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

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Explanations

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1. When does an analyte run through a gel matrix at constant velocity, according to Stokes Law?

- A. When the sample is diluted
- B. When electrophoretic driving force equals frictional force**
- C. When the gel concentration is low
- D. When the electric field is turned off

The correct choice focuses on the balance between the electrophoretic driving force and the frictional force acting on the analyte when it travels through a gel matrix. According to Stokes Law, the velocity of a particle moving through a viscous medium is determined by the balance between the forces acting on it. When an analyte is subjected to an electric field, it experiences a driving force that propels it forward. Simultaneously, as it moves through a gel matrix, it encounters resistance in the form of friction from the gel. For the analyte to run through the gel matrix at a constant velocity, these two forces must be equal. This means that the force pushing the analyte forward due to the electric field must precisely counteract the resistance caused by the gel. If this balance is achieved, the analyte will move at a steady speed, indicating a dynamic equilibrium between the opposing forces. Other options imply scenarios that do not facilitate the condition for constant velocity. For instance, dilution of the sample or changing the conditions of the gel concentration or electric field may affect the interactions but do not address the critical balance of forces as described by Stokes Law.

2. Which syndrome is an example of an imprinting disorder?

- A. Turner syndrome
- B. Angelman syndrome**
- C. Klinefelter syndrome
- D. Cystic fibrosis

Angelman syndrome is indeed an example of an imprinting disorder, which arises from the concept of genomic imprinting. This phenomenon occurs when certain genes are expressed in a parent-of-origin-specific manner. In the case of Angelman syndrome, which is typically caused by the loss of function of the UBE3A gene located on chromosome 15, the paternal allele is usually silenced while the maternal allele is expressed. If the maternal copy is deleted or mutated, it leads to the symptoms associated with Angelman syndrome, such as severe developmental delay, seizures, and problems with movement and balance. In contrast, Turner syndrome, Klinefelter syndrome, and cystic fibrosis result from other genetic mechanisms and do not involve genomic imprinting. Turner syndrome is characterized by the absence of one X chromosome in females and is primarily associated with developmental issues and infertility. Klinefelter syndrome involves the presence of an extra X chromosome in males, which leads to features such as reduced testosterone levels and infertility. Cystic fibrosis is caused by mutations in the CFTR gene and is an autosomal recessive disorder, affecting the respiratory and digestive systems. Hence, the distinct mechanisms underlying these other conditions set them apart from imprinting disorders like Angelman syndrome.

3. What resolution is achieved by the changes introduced in DNA sequences during bisulfite conversion?

- A. Single-molecule resolution.
- B. Single-nucleotide resolution.**
- C. Single-cell resolution.
- D. Single-gene resolution.

The process of bisulfite conversion specifically targets the methylation status of cytosine residues in DNA. During this treatment, unmethylated cytosines are converted to uracils, while methylated cytosines remain unchanged. This alteration allows researchers to determine the methylation pattern at the single-nucleotide level, meaning they can identify whether each individual cytosine in the sequence is methylated or not. The precision of this method is what gives it single-nucleotide resolution. Consequently, analysis that follows bisulfite conversion, such as sequencing or PCR, can reveal detailed information about the methylation status of DNA down to the level of individual nucleotides, making it a powerful tool for epigenetic studies. This level of detail is crucial for understanding the role of DNA methylation in gene expression and regulation. The other resolutions mentioned, such as single-molecule, single-cell, or single-gene, do not capture the specificity and detail of the information derived from bisulfite conversion regarding methylation at every cytosine position.

4. Which mutation occurs in 80-85% of most hemochromatosis cases?

- A. C282Y mutation**
- B. H63D mutation
- C. S65T mutation
- D. R572W mutation

The C282Y mutation is the most prevalent mutation associated with hereditary hemochromatosis, accounting for 80-85% of cases. This mutation involves a substitution of tyrosine for cysteine at position 282 of the HFE protein, which is involved in iron regulation in the body. Individuals who are homozygous for the C282Y mutation have a significantly higher risk of developing iron overload and related complications due to impaired regulation of dietary iron absorption. Given the high prevalence of this particular mutation in affected individuals, it reflects the genetic basis of the disease and its commonality in specific populations, particularly those of Northern European descent, where the mutation is more frequently observed. The other mutations listed, while they may contribute to hemochromatosis, do not occur with the same frequency or have as significant an impact on the overall disease presentation.

5. Which DNA repair mechanism specifically addresses mispaired bases in DNA?

- A. Base excision repair
- B. Mismatch repair**
- C. Nucleotide excision repair
- D. Single-strand repair

Mismatch repair is the mechanism specifically designed to identify and correct mispaired bases in DNA. During DNA replication, errors can occur, leading to the incorporation of the wrong nucleotide. Mismatch repair proteins recognize these mismatches and work to remove the erroneous section of DNA. After excising the mispaired region, the DNA polymerase synthesizes the correct DNA sequence, followed by ligation to restore the DNA strand. Base excision repair is primarily involved in correcting small-scale damage such as modified or damaged bases rather than addressing mismatched pairs. Nucleotide excision repair handles bulky DNA adducts and lesions that distort the DNA helix, such as those caused by UV light or chemical exposure. Single-strand repair mechanisms are generally related to the repair of single-strand breaks induced by radiation or chemicals. Hence, the specific role of mismatch repair in correcting mispaired bases distinctly positions it as the correct answer.

6. What is the main effect of bisulfite conversion in methylation analysis?

- A. It amplifies DNA for sequencing purposes.
- B. It alters cytosine residues to Uracil.**
- C. It converts all DNA into RNA.
- D. It enhances the binding of primers.

Bisulfite conversion is a critical step in methylation analysis, particularly when assessing DNA methylation patterns. The primary effect of bisulfite conversion is to specifically alter cytosine residues by converting them to uracil. This chemical reaction happens when bisulfite is applied to DNA; unmethylated cytosines are converted into uracils, while methylated cytosines remain unchanged. This distinction allows researchers to identify where methylation is present in the DNA strand. Subsequent amplification and sequencing of the converted DNA enable comparison of the original sequence to the converted sequence, revealing which cytosines were methylated. This process is foundational for understanding gene regulation and epigenetic modifications. The unique conversion pattern ultimately provides insights into various biological processes and disease states associated with aberrant methylation.

7. How are STR alleles identified?

- A. By sequencing base pairs
- B. By PCR product size**
- C. Through direct observation under a microscope
- D. Using fluorescent dyes

Short Tandem Repeats (STR) alleles are primarily identified by analyzing the size of the PCR products that are generated from specific regions of the DNA containing these repeats. During the Polymerase Chain Reaction (PCR), primers that flank the STR regions amplify the DNA. The resulting PCR products vary in length depending on the number of repeat units present in each allele. Once the PCR amplification is complete, the size of these products can be determined using gel electrophoresis or capillary electrophoresis. This method allows for the visualization and comparison of the lengths of the PCR products, which correspond to the number of repeats in the STR locus. The size differences are typically measured in base pairs (bp), enabling the identification of specific alleles based on their unique length. While sequencing could provide detailed information about the exact nucleotide composition of the STRs, it is not the primary method used for allele identification in forensic and clinical contexts due to its complexity and cost. Similarly, direct observation under a microscope does not provide precise measurements of PCR product size, and the use of fluorescent dyes is typically part of the detection process in PCR but does not directly identify the alleles themselves without analyzing the size of the products.

8. Which type of mutation does not alter the resulting amino acid sequence?

- A. Missense mutation
- B. Nonsense mutation
- C. Silent mutation**
- D. Frameshift mutation

A silent mutation is a specific type of genetic alteration that does not change the amino acid sequence of the protein produced. This happens because the mutation occurs in the DNA sequence but still results in the same codon due to the redundancy of the genetic code. In the genetic code, multiple codons can encode for the same amino acid, which allows for some mutations to be 'silent' in terms of their effect on the protein. For example, if a DNA sequence undergoes a change from GGT to GGC, both codons still code for glycine, meaning that the resulting protein remains unchanged despite the mutation at the DNA level. This is significant in molecular diagnostics and genetics, as such silent mutations can sometimes be overlooked in analyses because they do not affect the phenotype or function of the organism in the way that other types of mutations might. In contrast, missense mutations result in a different amino acid being incorporated into the protein, potentially altering its function. Nonsense mutations lead to the introduction of a premature stop codon, resulting in truncated proteins that can be nonfunctional. Frameshift mutations, caused by insertions or deletions that shift the reading frame, typically result in a completely different amino acid sequence downstream of the mutation. Thus, silent mutations

9. What genetic disorder is an example of a point mutation?

- A. Cystic fibrosis
- B. Sick cell anemia**
- C. Turner syndrome
- D. Down syndrome

Sickle cell anemia is indeed an example of a point mutation. This condition arises from a single nucleotide substitution in the beta-globin gene, where adenine (A) is replaced by thymine (T). This subtle change results in the alteration of one amino acid in the hemoglobin protein—specifically, it changes glutamic acid to valine. This seemingly minor modification has significant consequences for the structure and function of hemoglobin, leading to the characteristic sickling of red blood cells in affected individuals. In contrast, cystic fibrosis is typically caused by a deletion of three nucleotides in the CFTR gene, which results in the loss of a phenylalanine residue, rather than a point mutation. Turner syndrome and Down syndrome are chromosomal abnormalities where the entire chromosomes are affected—Turner syndrome involves a missing X chromosome, while Down syndrome results from an extra copy of chromosome 21 (trisomy 21). Thus, the nature of the mutations in these conditions distinctly differs from the point mutation found in sickle cell anemia.

10. A ratio greater than 2 in OD260/OD280 suggests what type of contamination?

- A. Protein contamination
- B. DNA contamination
- C. RNA contamination**
- D. Water contamination

A ratio greater than 2 in OD260/OD280 indicates significant RNA contamination in a sample. The OD260/OD280 ratio is a common method used to assess the purity of nucleic acids. In this context, the absorbance at 260 nm primarily correlates with nucleic acids, while the absorbance at 280 nm is indicative of proteins. When analyzing nucleic acids, a pure sample of DNA or RNA typically has an OD260/OD280 ratio around 1.8 to 2.0. If the ratio is significantly higher than 2, it suggests that there is more RNA present in the sample than DNA or that the sample is contaminated with additional substances influencing the absorbance readings – in this case, RNA. This ratio, therefore, provides insight into the composition of the sample and highlights the presence of contaminating RNA, which can interfere with applications such as quantitative PCR or other downstream molecular biology techniques where the purity of DNA is crucial. Other types of contamination such as protein or water typically present different absorbance characteristics, leading to lower ratios for protein contamination or unaffected ratios for water, which does not significantly interfere with the nucleic acid absorbance measurements.

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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