Molecular Basis of Inheritance Practice Test (Sample)

Study Guide

Everything you need from our exam experts!

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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

1. **What is the result of alternative RNA processing?**
    - **A. Different mRNA variants from the same gene**
    - **B. No effect**
    - **C. Production of tRNA**
    - **D. Degradation of mRNA**

2. **Which statement describes Chargaff's base-pairing rule?**
    - **A. A=C and T=G**
    - **B. A=T and C=G**
    - **C. A=T and C=A**
    - **D. A=G and C=T**

3. **Which statement best describes the central dogma?**
    - **A. DNA is transcribed to RNA in the nucleus, RNA carries the message to the cytoplasm where ribosomes translate it into protein.**
    - **B. Proteins are transcribed into DNA, which is then translated into RNA.**
    - **C. RNA is replicated into DNA, which directs protein synthesis in mitochondria.**
    - **D. Lipid signals regulate gene expression.**

4. **How many nucleotides comprise a codon in the genetic code?**
    - **A. Three nucleotides**
    - **B. One nucleotide**
    - **C. Two nucleotides**
    - **D. Four nucleotides**

5. **Which statement correctly describes replication origins in eukaryotes?**
    - **A. There is only one origin per chromosome.**
    - **B. Origins can be hundreds or thousands in a chromosome.**
    - **C. Origins are randomly located and do not form bubbles.**
    - **D. Origins are the sites where replication begins.**

6. Which statement is true about RNA and genes?

- **A. Only a single type of RNA is encoded by genes.**
- **B. RNA is not encoded by genes.**
- **C. Three major RNA types (mRNA, tRNA, rRNA) are each encoded by their own genes.**
- **D. RNA is produced by protein-coding genes.**

7. In DNA, which base pairs with Adenine?

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

8. What is the process called when RNA is used to synthesize a protein?

- **A. Splicing**
- **B. Replication**
- **C. Transcription**
- **D. Translation**

9. Which sequence correctly describes the flow of genetic information in cells?

- **A. DNA -> RNA -> Protein**
- **B. RNA -> DNA -> Protein**
- **C. DNA -> Protein -> RNA**
- **D. Protein -> RNA -> DNA**

10. Which process involves mismatch repair after DNA replication?

- **A. Mismatch repair system**
- **B. Nucleotide excision repair**
- **C. Base excision repair**
- **D. Double-strand break repair**

Answers

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

Explanations

1. What is the result of alternative RNA processing?

- **A. Different mRNA variants from the same gene**
- **B. No effect**
- **C. Production of tRNA**
- **D. Degradation of mRNA**

Alternative RNA processing can generate multiple mature mRNA transcripts from a single gene by including or skipping different exons, or by using different transcription start or polyadenylation sites. This creates distinct mRNA variants that may encode different protein isoforms or have different regulatory properties, increasing the diversity of the gene's output without adding new genes. It's the transcript-level variety that's being produced, not a lack of effect, not production of tRNA, and not an automatic degradation outcome.

2. Which statement describes Chargaff's base-pairing rule?

- **A. A=C and T=G**
- **B. A=T and C=G**
- **C. A=T and C=A**
- **D. A=G and C=T**

DNA base pairing is highly specific: adenine pairs with thymine, and cytosine pairs with guanine. Chargaff's rules show that in any double-stranded DNA, the amount of A equals T and the amount of C equals G. So the statement that A pairs with T and C pairs with G directly reflects both the pairing rules and the equal-base composition observed in both strands. If you tried to pair A with C or A with G, or claimed that A equals C or T equals G, you'd break the actual complementary pairing pattern and the equalities that Chargaff reported. This complementary pairing is what lets each strand serve as a template for the other during replication.

3. Which statement best describes the central dogma?

- **A. DNA is transcribed to RNA in the nucleus, RNA carries the message to the cytoplasm where ribosomes translate it into protein.**
- **B. Proteins are transcribed into DNA, which is then translated into RNA.**
- **C. RNA is replicated into DNA, which directs protein synthesis in mitochondria.**
- **D. Lipid signals regulate gene expression.**

The central idea is that genetic information flows from DNA to RNA to protein. In eukaryotic cells, transcription copies DNA into RNA in the nucleus, and the resulting RNA molecule—usually messenger RNA—carries the message to the cytoplasm, where ribosomes translate it into a protein. This description matches the standard flow of information: DNA → RNA → protein, with transcription in the nucleus and translation in the cytoplasm. The other scenarios describe processes that either reverse the direction of information flow or involve regulatory signals that don't represent how genetic information is typically used to build proteins. Small exceptions exist (like reverse transcription in certain viruses), but the stated path is the canonical description.

4. How many nucleotides comprise a codon in the genetic code?

A. Three nucleotides

B. One nucleotide

C. Two nucleotides

D. Four nucleotides

Three nucleotides. Using triplets gives 4^3 = 64 possible codons, which is enough to encode the 20 amino acids plus start and stop signals. With only two nucleotides, there would be 4^2 = 16 codons—insufficient to cover all amino acids and termination signals. If codons were four nucleotides long, there would be 4^4 = 256 possibilities, adding unnecessary complexity to the reading frame. The triplet arrangement also establishes a clear reading frame and, together with the start codon, enables consecutive, non-overlapping codons to specify amino acids (with some redundancy at the third base, known as wobble).

5. Which statement correctly describes replication origins in eukaryotes?

A. There is only one origin per chromosome.

B. Origins can be hundreds or thousands in a chromosome.

C. Origins are randomly located and do not form bubbles.

D. Origins are the sites where replication begins.

Replication origins are the starting points for DNA duplication. In eukaryotes, there are many origins along each chromosome, not just a single one, and these origins are licensed and activated at different times during S phase. When an origin fires, replication forks move in both directions, creating a replication bubble that expands as replication proceeds. This makes the statement that origins are randomly located and do not form bubbles inaccurate. The correct idea is that origins are the sites where replication begins, with multiple origins per chromosome driving complete and timely duplication.

6. Which statement is true about RNA and genes?

A. Only a single type of RNA is encoded by genes.

B. RNA is not encoded by genes.

C. Three major RNA types (mRNA, tRNA, rRNA) are each encoded by their own genes.

D. RNA is produced by protein-coding genes.

RNA comes from genes in the genome, and several distinct RNA species are built this way. The three major types used in biology—messenger RNA (mRNA), transfer RNA (tRNA), and ribosomal RNA (rRNA)—each have their own sets of genes to be transcribed. mRNA carries the information from DNA to the ribosome and is the transcript that, for protein-coding genes, serves as the template for protein synthesis. tRNA and rRNA are functional RNAs that are not translated into proteins; they are produced from dedicated RNA genes. Because these RNA genes exist independently of protein-coding genes, the statement that each of the three major RNA types is encoded by its own genes is accurate. The other options don’t fit because there are multiple RNA types encoded by genes, RNA is indeed encoded by genes, and not all RNA comes from protein-coding genes (rRNA and tRNA come from RNA genes, while mRNA from protein-coding genes is just one aspect).

7. In DNA, which base pairs with Adenine?

A. Cytosine
B. Guanine
C. Thymine
D. Adenine

In DNA, base pairing follows specific complementary rules: adenine pairs with thymine, and cytosine pairs with guanine. This A–T pairing is favored because adenine is a purine and thymine is a pyrimidine, so they fit together with the same width as a C–G pair, maintaining a uniform double-helix structure. They form two hydrogen bonds, which helps stabilize the DNA molecule. This pairing is essential for accurate replication and transcription. In RNA, thymine is replaced by uracil, which pairs with adenine in the same way. So thymine is the partner for adenine in DNA.

8. What is the process called when RNA is used to synthesize a protein?

A. Splicing
B. Replication
C. Transcription
D. Translation

Translation is the process by which the information in messenger RNA is read by ribosomes to assemble amino acids into a protein. The mRNA provides codons, each specifying a particular amino acid, and transfer RNAs bring the corresponding amino acids to the ribosome. The ribosome links these amino acids together through peptide bonds, forming a polypeptide that later folds into a functional protein. This step relies on a start codon to begin and a stop codon to end. Splicing (RNA processing that removes introns), transcription (DNA to RNA synthesis), and replication (DNA copying) are distinct processes that do not convert RNA into protein in this way.

9. Which sequence correctly describes the flow of genetic information in cells?

A. DNA -> RNA -> Protein
B. RNA -> DNA -> Protein
C. DNA -> Protein -> RNA
D. Protein -> RNA -> DNA

The flow of genetic information in cells follows DNA to RNA to Protein. DNA holds the instructions; during transcription, RNA polymerase reads DNA and synthesizes Messenger RNA that carries that message. Then during translation, the ribosome reads the mRNA sequence and, with transfer RNAs bringing amino acids, builds a polypeptide that folds into a protein. This direction—DNA to RNA to Protein—explains why it's the correct sequence. Moving information from RNA back to DNA, or from Protein back to nucleic acids, is not how cellular information typically propagates (with rare exceptions like reverse transcription in certain viruses, which isn't the standard cell process).

10. Which process involves mismatch repair after DNA replication?

A. Mismatch repair system
B. Nucleotide excision repair
C. Base excision repair
D. Double-strand break repair

The concept here is how cells fix errors that slip past the proofreading done during DNA replication. After the DNA has been copied, the mismatch repair system scans the new strand for mispaired bases and small insertion/deletion loops that polymerase proofreading missed. It differentiates the newly synthesized strand from the template strand using strand-specific signals (in bacteria, differences in methylation; in eukaryotes, nicks in the lagging strand help identify the new strand). Once a mismatch is found, a section of the new strand containing the error is removed, and DNA polymerase fills in the gap followed by ligation, restoring correct base pairing. This targeted repair lowers the mutation rate and maintains genetic stability. Other pathways fix different problems: nucleotide excision repair removes bulky, helix-distorting lesions like thymine dimers; base excision repair fixes small, damaged bases; and double-strand break repair handles breaks in both DNA strands through mechanisms like homologous recombination or non-homologous end joining.

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://molecularbasisofinheritance.examzify.com

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