DNA Biology 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 function of enhancers in transcription regulation?**
   - **A. They act as promoters for RNA polymerase**
   - **B. They bind repressors to silence transcription**
   - **C. They are DNA sequences that bind transcription activators to increase transcription**
   - **D. They code for transcription factors**

2. **How does mismatch repair function after DNA replication?**
   - **A. Mismatch repair identifies mispaired bases after replication, removes a DNA segment containing the error, and fills and ligates the gap.**
   - **B. Mismatch repair duplicates the erroneous segment.**
   - **C. Mismatch repair occurs only before replication.**
   - **D. Mismatch repair uses RNA as a template.**

3. **True or False: During RNA splicing, small nuclear ribonucleoproteins called SNRNPs help to remove introns.**
   - **A. True**
   - **B. False**
   - **C. They catalyze the ligation of exons**
   - **D. They recruit ribosomes to the mRNA**

4. **How many bases are encompassed in one complete 360-degree turn of the DNA helix?**
   - **A. 8**
   - **B. 12**
   - **C. 10**
   - **D. 9**

5. **Which chromosomal aberration results in the loss of a chromosome segment?**
   - **A. Deletion**
   - **B. Duplication**
   - **C. Inversion**
   - **D. Translocation**

6. In meiosis, how does independent assortment contribute to genetic variation?

- **A. Homologous chromosomes orient randomly during metaphase I, producing diverse combinations of maternal and paternal chromosomes in gametes.**
- **B. Crossing over alone generates variation.**
- **C. Independent assortment occurs only in mitosis.**
- **D. Variation arises only from mutation, not from meiosis.**

7. The structure that causes the synthesis of RNA to cease is the _________.

- **A. Transcription terminator**
- **B. Promoter region**
- **C. Stop codon**
- **D. Anticodon**

8. New _____________ position themselves along the parent strands through _____________ base pairing.

- **A. Nucleotides; complementary**
- **B. Nucleotides; identical**
- **C. Nucleotides; random**
- **D. Nucleotides; noncomplementary**

9. What is a key consequence of nondisjunction during meiosis?

- **A. Normal segregation with no aneuploidy.**
- **B. DNA replication occurs.**
- **C. RNA processing increases.**
- **D. Failure of homologous chromosomes or sister chromatids to separate during meiosis, leading to aneuploidies such as trisomies or monosomies.**

10. Almost all organisms use this _______, suggesting an early evolutionary origin.

- **A. metabolic pathway**
- **B. transcription**
- **C. genetic code**
- **D. replication**

Answers

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

Explanations

1. What is the function of enhancers in transcription regulation?

A. They act as promoters for RNA polymerase

B. They bind repressors to silence transcription

C. They are DNA sequences that bind transcription activators to increase transcription

D. They code for transcription factors

Enhancers are DNA sequences that bind transcription activators to increase transcription. By bringing these activators near the promoter—often through DNA looping—the transcriptional machinery and coactivators are more effectively recruited to initiate and boost RNA polymerase II activity. This boost can happen even when the enhancer is located far away from the promoter or in a different orientation, and it often depends on the cell type or signaling context because different activators are present in different conditions. This helps distinguish enhancers from promoters, which are the sites where RNA polymerase II assembles to start transcription, and from silencers, which recruit repressors to decrease transcription. Enhancers also don't code for transcription factors themselves; they are regulatory DNA sequences that control when and how much a gene is transcribed.

2. How does mismatch repair function after DNA replication?

A. Mismatch repair identifies mispaired bases after replication, removes a DNA segment containing the error, and fills and ligates the gap.

B. Mismatch repair duplicates the erroneous segment.

C. Mismatch repair occurs only before replication.

D. Mismatch repair uses RNA as a template.

Mismatch repair after replication fixes errors that escaped proofreading by recognizing mispaired bases, identifying the newly made strand, removing a short patch around the mismatch, and filling in the correct nucleotides before sealing the backbone. In bacteria, this starts when a mismatch is found by MutS, MutL helps coordinate, and MutH nicks the new strand at a nearby GATC site. An exonuclease then removes the patch containing the error, DNA polymerase fills in the correct bases, and DNA ligase seals the nick. In eukaryotes, similar players (like MSH2–MSH6 or MSH2–MSH3 for recognition and MLH1–PMS2 for coordination) carry out the same idea, using signals such as nicks or PCNA to distinguish the newly synthesized strand. The essential idea is removing the erroneous segment on the new strand and resynthesizing it using the old strand as a template, which is exactly what this option describes. The other statements don't fit because they describe wrong timings or mechanisms: duplicating the erroneous segment would propagate the error, mismatch repair does not occur before replication, and the repair process does not use RNA as a template for fixing DNA.

3. True or False: During RNA splicing, small nuclear ribonucleoproteins called SNRNPs help to remove introns.

- **A. True**
- **B. False**
- **C. They catalyze the ligation of exons**
- **D. They recruit ribosomes to the mRNA**

RNA splicing relies on the spliceosome, a complex in the nucleus built in part from small nuclear RNPs. These snRNPs contain snRNAs and proteins that pair with pre-mRNA at the splice sites and branch point, helping to assemble and position the catalytic core of the spliceosome. As the spliceosome forms, it carries out two transesterification reactions that remove the intron and join the exons, so snRNPs are directly involved in intron removal. They're not responsible for recruiting ribosomes to mRNA—that's a step in translation in the cytoplasm, not splicing. So the statement is true: snRNPs help remove introns during RNA splicing.

4. How many bases are encompassed in one complete 360-degree turn of the DNA helix?

- **A. 8**
- **B. 12**
- **C. 10**
- **D. 9**

In B-form DNA, one full turn of the helix corresponds to about 3.4 nanometers of length, and each base pair stacks 0.34 nanometers apart. Divide the turn length by the rise per base pair: 3.4 nm / 0.34 nm per base pair = 10 base pairs per turn. So there are 10 base pairs, which means 20 individual bases total when counting both strands, per full 360-degree turn. The standard measure used in questions like this is base pairs per turn, so 10 is the correct value.

5. Which chromosomal aberration results in the loss of a chromosome segment?

- **A. Deletion**
- **B. Duplication**
- **C. Inversion**
- **D. Translocation**

This question tests how chromosomal abnormalities affect the amount of genetic material. A deletion is when a part of the chromosome is removed, so genes in that region are lost. That's exactly what is meant by the loss of a chromosome segment. In contrast, a duplication adds an extra copy of a segment, increasing material rather than removing it. An inversion rearranges the order of a segment without losing any genes, so the total amount of material stays the same. A translocation moves a segment to another chromosome, which rearranges where the genes are but doesn't inherently remove them. So the deletion is the mechanism that causes the loss of a chromosome segment.

6. In meiosis, how does independent assortment contribute to genetic variation?

A. Homologous chromosomes orient randomly during metaphase I, producing diverse combinations of maternal and paternal chromosomes in gametes.

B. Crossing over alone generates variation.

C. Independent assortment occurs only in mitosis.

D. Variation arises only from mutation, not from meiosis.

The main concept is that random orientation of homologous chromosome pairs during meiosis I creates different combinations of maternal and paternal chromosomes in gametes. As pairs line up on the metaphase plate, which member of each pair goes to each daughter cell is independent and unpredictable. This means the assortment of paternal or maternal chromosomes received by a gamete varies, producing many possible genetic combinations. If there are n chromosome pairs, there are 2^n possible gamete chromosome sets from independent assortment alone (humans have 2^23, over 8 million combinations), and this variety is further expanded when crossing over during prophase I shuffles alleles between homologs. The other options miss that this source of variation comes from how entire chromosomes are separated, that meiosis—not mitosis—handles this process, and that mutation is another, separate contributor to variation rather than the sole source.

7. The structure that causes the synthesis of RNA to cease is the _________.

A. Transcription terminator

B. Promoter region

C. Stop codon

D. Anticodon

Transcription termination signals stop RNA synthesis. A transcription terminator is the DNA sequence that tells RNA polymerase to stop and release the RNA transcript. In bacteria, termination can occur intrinsically when the newly made RNA forms a GC-rich hairpin followed by a string of uracils, which destabilizes the transcription complex, or with the help of the Rho protein that catches up to the polymerase and prompts release. The promoter region is what starts transcription, not ends it; a stop codon terminates translation, not transcription; and an anticodon is part of tRNA involved in decoding mRNA during translation.

8. New _____________ position themselves along the parent strands through _____________ base pairing.

A. Nucleotides; complementary

B. Nucleotides; identical

C. Nucleotides; random

D. Nucleotides; noncomplementary

The main idea here is how DNA is copied with fidelity. During replication, new nucleotides align along each exposed parental strand by complementary base pairing. That means each base on the template strand binds its partner: A with T and C with G. So the new strand that is formed is complementary to its template and, together with the template, creates a correct, identical copy of the double helix information. If the added nucleotides were identical to the template, random, or noncomplementary, the hydrogen bonding wouldn't hold properly and the genetic information wouldn't be copied accurately. This complementary pairing is what makes DNA replication reliable and is central to the semi-conservative model, where each daughter molecule contains one old strand and one newly synthesized complementary strand.

9. What is a key consequence of nondisjunction during meiosis?

A. Normal segregation with no aneuploidy.

B. DNA replication occurs.

C. RNA processing increases.

D. Failure of homologous chromosomes or sister chromatids to separate during meiosis, leading to aneuploidies such as trisomies or monosomies.

Nondisjunction during meiosis is the failure of separation of homologous chromosomes or sister chromatids, resulting in gametes with an abnormal chromosome number. When such a gamete fertilizes a normal one, the zygote often becomes aneuploid, carrying an extra chromosome (trisomy) or missing one (monosomy). This direct outcome explains why conditions like trisomy 21 or monosomy X arise. The other ideas—DNA replication happening or RNA processing increasing—aren't consequences of mis-segregation in meiosis, and normal segregation would avoid producing aneuploid gametes.

10. Almost all organisms use this _______, suggesting an early evolutionary origin.

A. metabolic pathway

B. transcription

C. genetic code

D. replication

The genetic code is the set of rules that translates the instructions in mRNA into the amino acids that build proteins. This code is used by almost all organisms, with only a few tiny, well-documented exceptions in some mitochondria and certain single-celled life. That near-universal usage points to a very ancient origin, inherited from a common ancestor before life diversified. Because changing the genetic code would disrupt the vast majority of proteins, it has remained highly conserved for billions of years, making it the strongest indicator of an early evolutionary origin.

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://dnabiology.examzify.com

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