

DNA HISTORY, REPLICATION, AND PROTEIN SYNTHESIS PRACTICE TEST (SAMPLE)

STUDY GUIDE



SAMPLE STUDY GUIDE WITH LIMITED QUESTIONS



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THE FULL VERSION STUDY GUIDE**

<https://dnahistoryproteinsynthesis.examzify.com>



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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. What enzyme relieves supercoiling ahead of the replication fork?**
 - A. DNA polymerase
 - B. DNA topoisomerase (DNA gyrase in bacteria)
 - C. Helicase
 - D. Primase
- 2. What role do single-strand binding proteins play during DNA replication?**
 - A. They stabilize exposed single strands and prevent reannealing.
 - B. They unwind the double helix to expose bases.
 - C. They synthesize RNA primers.
 - D. They ligate nicks in the sugar-phosphate backbone.
- 3. Which type of bonds hold complementary base pairs together in DNA?**
 - A. Hydrogen bonds
 - B. Ionic bonds
 - C. Covalent bonds
 - D. Peptide bonds
- 4. Which enzyme synthesizes RNA primers during DNA replication?**
 - A. Primase
 - B. DNA polymerase
 - C. DNA ligase
 - D. Topoisomerase
- 5. Which of the following is NOT one of the four bases found in DNA?**
 - A. Adenine
 - B. Thymine
 - C. Guanine
 - D. Uracil
- 6. Which bases are purines?**
 - A. Adenine and Guanine.
 - B. Adenine and Cytosine.
 - C. Thymine and Cytosine.
 - D. Guanine and Uracil.

- 7. What is the function of single-strand binding proteins during replication?**
- A. They unwind the double helix.
 - B. They stabilize exposed single-stranded DNA to prevent secondary structures and keep it accessible for polymerases.
 - C. They seal nicks in the backbone.
 - D. They synthesize primers.
- 8. What characterizes the synthesis of the lagging strand during DNA replication?**
- A. Continuous synthesis toward the fork.
 - B. Requires RNA primers to begin each fragment but is synthesized in one long piece.
 - C. Synthesized in short segments away from the fork called Okazaki fragments.
 - D. Incorporates RNA nucleotides into DNA.
- 9. Who proposed the double-helix structure of DNA and what evidence supported it?**
- A. Linus Pauling Proposed the Double Helix, Supported by Base-Pairing Rules
 - B. Erwin Chargaff Proposed The Double Helix, Supported by X-Ray Evidence
 - C. Rosalind Franklin Proposed The Double Helix, Based on X-Ray Data
 - D. Watson and Crick Proposed the Double Helix, Supported by Chargaff's Rules and Rosalind Franklin's X-Ray Diffraction Data
- 10. What role do transcriptional and translational regulation play in gene expression?**
- A. Control when and how much gene product is produced
 - B. Determine the sequence of DNA
 - C. Synthesize RNA polymerase
 - D. Repair DNA damage

Answers

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

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Explanations

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1. What enzyme relieves supercoiling ahead of the replication fork?

- A. DNA polymerase
- B. DNA topoisomerase (DNA gyrase in bacteria)**
- C. Helicase
- D. Primase

Relief of supercoiling ahead of the replication fork is handled by topoisomerases. As helicase unwinds the DNA, positive supercoils build up ahead of the fork, which would impede further unwinding. Topoisomerases transiently cut one or both DNA strands, allow the helix to swivel or strands to pass through, and then reseal the breaks, relaxing the torsional stress. In bacteria, this role is carried out by DNA gyrase, a type II topoisomerase that relieves the positive supercoils (and can introduce negative supercoils). This activity is distinct from what DNA polymerase does (synthesis), what helicase does (unwinding without relief of torsion), or what primase does (primer synthesis).

2. What role do single-strand binding proteins play during DNA replication?

- A. They stabilize exposed single strands and prevent reannealing.**
- B. They unwind the double helix to expose bases.
- C. They synthesize RNA primers.
- D. They ligate nicks in the sugar-phosphate backbone.

During DNA replication, the two strands are separated so each serves as a template. After the helicase unwinds the helix, single-strand binding proteins grab onto the exposed single-stranded DNA, keeping it from reannealing and from forming secondary structures. This stabilization is crucial for the DNA polymerases to efficiently copy the template, especially on the lagging strand where many short ssDNA segments appear. SSBs also protect the delicate ssDNA from nucleases. They don't unwind DNA, synthesize RNA primers, or ligate backbone nicks—that role belongs to helicase, primase, and ligase, respectively.

3. Which type of bonds hold complementary base pairs together in DNA?

- A. Hydrogen bonds**
- B. Ionic bonds
- C. Covalent bonds
- D. Peptide bonds

Hydrogen bonds hold complementary base pairs together in DNA. These are the weak, noncovalent attractions that form between specific pairs: adenine pairs with thymine using two hydrogen bonds, and guanine pairs with cytosine using three hydrogen bonds. This bonding type is strong enough to keep the two strands aligned, yet weak enough to allow the strands to separate during replication and transcription. In contrast, covalent bonds connect atoms within each strand's backbone, and peptide bonds link amino acids in proteins; ionic bonds don't mediate base pairing.

4. Which enzyme synthesizes RNA primers during DNA replication?

- A. Primase
- B. DNA polymerase
- C. DNA ligase
- D. Topoisomerase

DNA replication relies on RNA primers to start synthesis because DNA polymerases cannot initiate strands from scratch; they can only extend from a pre-existing 3' end. The enzyme that provides this starting point is primase, a specialized RNA polymerase that makes a short RNA primer complementary to the DNA template. This primer gives DNA polymerase something to extend, allowing continuous synthesis on the leading strand and short fragments on the lagging strand that are later joined. After synthesis, the RNA primer is removed and replaced with DNA, and the gaps are sealed by ligase. Other enzymes have different roles: DNA polymerase builds DNA, not primers; topoisomerase relieves supercoiling; ligase seals nicks in the sugar-phosphate backbone.

5. Which of the following is NOT one of the four bases found in DNA?

- A. Adenine
- B. Thymine
- C. Guanine
- D. Uracil

DNA uses four bases—adenine, thymine, cytosine, and guanine. Uracil is not among them; it is used in RNA in place of thymine. In RNA, adenine pairs with uracil, while in DNA adenine pairs with thymine. So Uracil is the base that is not found in DNA.

6. Which bases are purines?

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

Purines are one of the two families of nitrogenous bases, defined by a two-ring structure. The purines are adenine and guanine. The other bases listed—cytosine, thymine, and uracil—belong to the pyrimidines, which have a single ring. In DNA and RNA, purines pair with pyrimidines (A pairs with T in DNA, or with U in RNA; G pairs with C). Therefore, the bases that are purines are adenine and guanine, making this choice correct. The other options mix purines with pyrimidines, or include only pyrimidines, which is why they aren't correct.

7. What is the function of single-strand binding proteins during replication?

- A. They unwind the double helix.
- B. They stabilize exposed single-stranded DNA to prevent secondary structures and keep it accessible for polymerases.**
- C. They seal nicks in the backbone.
- D. They synthesize primers.

During DNA replication, the DNA strands are unwound to expose single-stranded templates. Single-strand binding proteins quickly bind to these exposed templates to stabilize them, preventing the strands from snapping back together and from forming secondary structures like hairpins. This stabilization keeps the single-stranded DNA accessible for DNA polymerases to copy the sequence accurately. They also help protect the vulnerable ssDNA from nucleases until synthesis is finished. This function is distinct from helicase, which unwinds the helix; primase, which lays down primers to start synthesis; and ligase, which seals nicks in the backbone.

8. What characterizes the synthesis of the lagging strand during DNA replication?

- A. Continuous synthesis toward the fork.
- B. Requires RNA primers to begin each fragment but is synthesized in one long piece.
- C. Synthesized in short segments away from the fork called Okazaki fragments.**
- D. Incorporates RNA nucleotides into DNA.

DNA polymerases can only add nucleotides in the 5' to 3' direction, and the two strands at the replication fork run antiparallel. The leading strand can be made continuously toward the fork, but the lagging strand, which runs in the opposite orientation, must be copied in short, discontinuous pieces. These pieces are produced in the 5' to 3' direction away from the fork and are called Okazaki fragments. Each fragment begins with an RNA primer laid down by primase, and after the fragments are synthesized, the RNA primers are removed and replaced with DNA, and the fragments are sealed together by ligase. That's why this description—short segments away from the fork known as Okazaki fragments—best characterizes lagging-strand synthesis. The other options describe leading-strand synthesis, continuous synthesis, or RNA incorporated into a DNA strand, which is not the standard representation of lagging-strand synthesis.

9. Who proposed the double-helix structure of DNA and what evidence supported it?

- A. Linus Pauling Proposed the Double Helix, Supported by Base-Pairing Rules
- B. Erwin Chargaff Proposed The Double Helix, Supported by X-Ray Evidence
- C. Rosalind Franklin Proposed The Double Helix, Based on X-Ray Data
- D. Watson and Crick Proposed the Double Helix, Supported by Chargaff's Rules and Rosalind Franklin's X-Ray Diffraction Data**

Watson and Crick are the scientists who proposed the double-helix structure. The evidence backing their model came from two crucial lines of data. Chargaff's rules showed that the amounts of adenine and thymine are about equal and the amounts of cytosine and guanine are about equal, implying A pairs with T and C pairs with G—a foundation for complementary base pairing and faithful replication. Rosalind Franklin's X-ray diffraction results revealed a helical shape with a consistent diameter and a regular pattern along the length, providing the geometric constraints (two antiparallel strands with a sugar-phosphate backbone on the outside and base pairs inside) that the model had to fit. The combination of these insights allowed Watson and Crick to construct the accurate double-helix model. The other options point to pieces of the story (Pauling's incorrect triple-helix idea, Chargaff's rules alone, Franklin's data alone) but do not capture the proposed structure and the corroborating evidence together.

10. What role do transcriptional and translational regulation play in gene expression?

- A. Control when and how much gene product is produced**
- B. Determine the sequence of DNA
- C. Synthesize RNA polymerase
- D. Repair DNA damage

Regulation at the transcriptional and translational levels controls when a gene is read and how much protein is made, shaping the amount of gene product available in the cell. Transcriptional control decides whether the gene's DNA is transcribed into messenger RNA and how rapidly that transcription occurs, so the cell determines how much mRNA is available to be used. Translational control comes into play after the mRNA is produced, affecting how efficiently ribosomes translate that mRNA into protein and how long the protein is produced, which can dramatically change final protein levels even with the same mRNA amount. Together, these regulatory steps let cells respond to signals, conserve energy, and fine-tune expression during development or stress without changing the DNA sequence itself. The other ideas describe different roles: changing the DNA sequence, making the RNA polymerase enzyme, or repairing DNA damage are not about adjusting how much gene product is produced in response to conditions.

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://dnahistoryproteinsynthesis.examzify.com>

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

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