

# Transcription and Translation 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

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- 1. UTR stands for**
  - A. Untranslated Region**
  - B. Upstream Transcribed Region**
  - C. Universal Translation Region**
  - D. Unique Transcript Region**
  
- 2. What happens to DNA after the RNA is synthesized during transcription?**
  - A. Renaturation of copied DNA**
  - B. Continued unwinding**
  - C. DNA Degradation**
  - D. No change**
  
- 3. Exons are**
  - A. non-coding regions**
  - B. coding regions expressed**
  - C. introns**
  - D. promoter regions**
  
- 4. The TATA box is composed of which repeating sequence?**
  - A. GC repeats**
  - B. TATA repeats**
  - C. ATG repeats**
  - D. CG repeats**
  
- 5. Why are there only 45 different tRNA for 61 codons?**
  - A. Because of wobble, the specificity for the third nucleotide base in a codon is relaxed**
  - B. Because there are no more tRNA available**
  - C. Because the genetic code has only 45 codons**
  - D. Because ribosome can read codons without tRNA**

- 6. In eukaryotes, termination involves which signal and processing?**
- A. DNA terminator sequence**
  - B. Polyadenylation signal AAUAA with cleavage**
  - C. Rho-dependent termination**
  - D. No termination**
- 7. Which enzyme charges tRNA with its amino acid?**
- A. Aminoacyl-tRNA synthetase**
  - B. DNA ligase**
  - C. RNA polymerase**
  - D. Peptidyl transferase**
- 8. RNA polymerase II primarily transcribes which class of RNA?**
- A. rRNA**
  - B. tRNA**
  - C. mRNA**
  - D. All of the above**
- 9. What moves in translation?**
- A. Ribozyme**
  - B. Protein enzyme**
  - C. DNA polymerase**
  - D. Lipase**
- 10. Which mutation changes a codon to code for a different amino acid?**
- A. Nonsense mutation**
  - B. Silent mutation**
  - C. Missense mutation**
  - D. Frameshift mutation**

## Answers

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

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## **Explanations**

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## 1. UTR stands for

- A. Untranslated Region**
- B. Upstream Transcribed Region**
- C. Universal Translation Region**
- D. Unique Transcript Region**

UTR refers to the Untranslated Region—the parts of an mRNA that are transcribed from DNA but not translated into protein. These regions flank the coding sequence: the 5' untranslated region lies before the start codon, and the 3' untranslated region lies after the stop codon. They don't code for amino acids, yet they orchestrate important regulatory roles, such as controlling translation efficiency, mRNA stability, and localization through sequences and structures that interact with ribosomes and various RNA-binding proteins or microRNAs. The other terms don't match the established meaning. Upstream Transcribed Region isn't a standard term for this concept, and Universal Translation Region or Unique Transcript Region aren't recognized descriptors in molecular biology.

## 2. What happens to DNA after the RNA is synthesized during transcription?

- A. Renaturation of copied DNA**
- B. Continued unwinding**
- C. DNA Degradation**
- D. No change**

Renaturation of the copied DNA is what happens. During transcription, the DNA ahead of the RNA polymerase is temporarily unwound to expose the template strand. Once the RNA transcript is completed and the polymerase moves on or terminates, the unwound region behind it rewinds and the DNA double helix re-forms. This re-annealing restores the original DNA structure. The DNA isn't degraded, and the helix doesn't remain perpetually open, so the other options don't fit.

## 3. Exons are

- A. non-coding regions**
- B. coding regions expressed**
- C. introns**
- D. promoter regions**

Exons are the parts of a gene that carry the information to make a protein and are retained in the mature mRNA. In eukaryotic genes, transcripts often include both exons and introns. After transcription, the introns are removed and the exons are joined together, producing a final mRNA that is translated into a protein. That's why exons are described as coding regions expressed—they contain the sequence information that ends up in the protein. By contrast, introns are noncoding and are spliced out, while promoter regions are DNA sequences that help initiate transcription and are not part of the mature, protein-coding mRNA. Non-coding regions can refer to parts of the gene that do not code for protein, such as introns and regulatory elements.

**4. The TATA box is composed of which repeating sequence?**

- A. GC repeats
- B. TATA repeats**
- C. ATG repeats
- D. CG repeats

AT-rich promoter regions are where transcription often begins in eukaryotes. The TATA box is defined by a sequence pattern rich in thymine and adenine, typically described as repeating "TATA" units. That repeated TATA sequence creates an AT-rich stretch that unwinds more easily, helping RNA polymerase II and transcription factors assemble at the start site. That's why the best description is TATA repeats. GC repeats would make DNA more stable and aren't characteristic of this promoter element; ATG repeats would point to a coding start codon motif, not a promoter sequence; CG repeats are associated with CpG islands and methylation, not the TATA box.

**5. Why are there only 45 different tRNA for 61 codons?**

- A. Because of wobble, the specificity for the third nucleotide base in a codon is relaxed**
- B. Because there are no more tRNA available
- C. Because the genetic code has only 45 codons
- D. Because ribosome can read codons without tRNA

The main idea is that the genetic code is read with flexibility at the third base of the codon. Because the last position can pair in a looser way, a single tRNA molecule can recognize multiple codons that differ there, so you don't need a separate tRNA for every codon. This concept is known as wobble base pairing. For example, a tRNA with inosine at the wobble position of its anticodon can pair with codons ending in U, C, or A. With this wobble flexibility, a smaller set of tRNA molecules can cover all 61 sense codons, which is why you see about 45 different tRNAs suffice. It's not due to a lack of tRNAs or the ribosome skipping codons; it's the relaxed pairing at the third base that expands codon recognition by each tRNA.

**6. In eukaryotes, termination involves which signal and processing?**

- A. DNA terminator sequence
- B. Polyadenylation signal AAUAA with cleavage**
- C. Rho-dependent termination
- D. No termination

In eukaryotes, transcription termination is governed by the processing of the newly transcribed RNA at its 3' end. The key signal is the polyadenylation signal, AAUAAA, which marks the site where the pre-mRNA will be cleaved. After cleavage, poly(A) polymerase adds the poly(A) tail. This 3' end processing is what facilitates termination of transcription and yields a mature mRNA ready for export and translation. This is different from the other options: a DNA terminator sequence works in many bacteria but not in eukaryotic transcription; rho-dependent termination is a bacterial mechanism; and saying there is no termination would be incorrect because transcription ends through this processing-linked mechanism.

## 7. Which enzyme charges tRNA with its amino acid?

**A. Aminoacyl-tRNA synthetase**

**B. DNA ligase**

**C. RNA polymerase**

**D. Peptidyl transferase**

Charging a tRNA with its amino acid is done by aminoacyl-tRNA synthetase. This enzyme is specific for each amino acid and its corresponding tRNA, and it uses ATP to activate the amino acid (forming aminoacyl-AMP) before transferring it to the tRNA's 3' acceptor end. This prepares the tRNA to deliver the correct amino acid during translation, helping ensure fidelity through possible editing steps that remove mischarged charges. The other enzymes have different roles: DNA ligase seals breaks in the DNA backbone, RNA polymerase synthesizes RNA, and peptidyl transferase catalyzes the peptide bond formation on the ribosome but does not attach amino acids to tRNAs.

## 8. RNA polymerase II primarily transcribes which class of RNA?

**A. rRNA**

**B. tRNA**

**C. mRNA**

**D. All of the above**

The main idea is that different RNA polymerases in eukaryotes specialize in different RNA products. RNA polymerase II is the workhorse for making messenger RNA, the transcripts that carry genetic information from DNA to the ribosome to guide protein synthesis. It does produce some noncoding RNAs as well, but its primary product is mRNA. In contrast, ribosomal RNA is mainly transcribed by RNA polymerase I, and transfer RNA by RNA polymerase III. Because of that, the best answer is mRNA. The option that suggests all of the above would be inaccurate since rRNA and tRNA are not primarily transcribed by RNA polymerase II.

## 9. What moves in translation?

**A. Ribozyme**

**B. Protein enzyme**

**C. DNA polymerase**

**D. Lipase**

Translation is driven by the ribosome, and the key chemical step—peptide bond formation between amino acids—is carried out by ribosomal RNA. This RNA component acts as a ribozyme, an RNA molecule that has catalytic activity. So the moving, catalyzing force in translation is the ribosome's RNA-based active site that stitches amino acids together as transfer RNAs bring them to the ribosome. The other options describe enzymes that aren't responsible for this process: a general protein enzyme isn't required for translation's core chemistry, DNA polymerase handles DNA replication, and lipase breaks down lipids.

**10. Which mutation changes a codon to code for a different amino acid?**

**A. Nonsense mutation**

**B. Silent mutation**

**C. Missense mutation**

**D. Frameshift mutation**

When a single nucleotide change causes a codon to specify a different amino acid, the protein's sequence at that position is altered. This is a missense mutation. It directly changes which amino acid is added during translation, which can affect protein structure and function depending on the properties of the new amino acid and its position. In contrast, a nonsense mutation creates a stop codon and truncates the protein; a silent mutation changes the codon to a synonymous one that still codes for the same amino acid; and a frameshift mutation shifts the entire reading frame due to an insertion or deletion, altering many downstream codons. The described scenario matches a missense mutation because only the encoded amino acid changes.

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## 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](mailto:hello@examzify.com).**

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

**<https://transcriptiontranslation.examzify.com>**

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

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