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Central Dogma: DNA → RNA → Protein

Study Guide — Protein Synthesis

Pre-med/IB-style questions on transcription and translation fundamentals: DNA strands, RNA synthesis directionality, mRNA processing, ribosome function, tRNA charging/anticodons, reading frames, and start/stop codons (including common conceptual traps).

40 items — Study Guide with Answers

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1 **Which process is an important real-life exception to the simplified “DNA → RNA → protein” pathway, while still NOT implying information flows from protein back to nucleic acids?**

- A Translation
- B Transcription
- C DNA replication
- D **Reverse transcription (RNA → DNA)** ✓
- E Peptide bond hydrolysis

▶ **Explanation:** Reverse transcription (used by retroviruses like HIV) copies RNA into DNA. This is an exception to the simplest pathway DNA→RNA, but it still doesn’t mean protein sequences can be copied back into nucleic acids.

2 **During translation, which molecule provides the direct template that determines the amino acid sequence of a protein?**

- A DNA
- B **mRNA** ✓
- C rRNA
- D tRNA
- E Protein

▶ **Explanation:** The ribosome reads codons on mRNA to build the protein. DNA is the long-term storage, rRNA is structural/catalytic in ribosomes, and tRNA is the adaptor that matches codons to amino acids.

3 **For a particular gene, the DNA strand whose sequence matches the mRNA (except T instead of U) is called the:**

Source: entermedschool.org — Free Medical Education Resources

- A Template (antisense) strand
- B **Coding (sense) strand** ✓
- C Lagging strand
- D Leading strand
- E Non-template intron strand

▶ **Explanation:** mRNA is complementary to the template strand, so it matches the coding strand (with U in place of T). Leading/lagging refer to DNA replication, not transcription identity.

4 RNA polymerase synthesizes RNA in which direction (and therefore reads the DNA template in which direction)?

- A Synthesizes 3 →5 ; reads 3 →5
- B Synthesizes 3 →5 ; reads 5 →3
- C **Synthesizes 5 →3 ; reads 3 →5** ✓
- D Synthesizes 5 →3 ; reads 5 →3
- E Synthesizes 5 →5 ; reads 3 →3

▶ **Explanation:** All known polymerases add nucleotides to the 3 end, so RNA is built 5 →3 while the DNA template is read 3 →5 .

5 Which base pairing rule applies during transcription when RNA is being built from a DNA template?

- A A pairs with T; C pairs with G
- B **A pairs with U; C pairs with G** ✓
- C A pairs with C; U pairs with G

Source: entermedschool.org — Free Medical Education Resources

D A pairs with G; C pairs with U

E A pairs with U; C pairs with T

▶ **Explanation:** In RNA, uracil (U) replaces thymine (T). So A pairs with U, and C pairs with G during transcription.

6 A ribosome translates an mRNA by moving along it in which direction?

A 3 →5

B **5 →3** ✓

C Randomly in both directions

D From the poly-A tail toward the 5 cap

E From introns toward exons

▶ **Explanation:** Ribosomes read codons in the 5 →3 direction. Introns are removed before translation in eukaryotes, so they aren't "read" by ribosomes.

7 A polypeptide is synthesized in which direction?

A C-terminus → N-terminus

B **N-terminus → C-terminus** ✓

C Both ends extend simultaneously

D Side chain → backbone

E Random order determined by tRNA abundance

▶ **Explanation:** Proteins grow by adding each new amino acid to the carboxyl end, so the chain extends from N→C.

8 **In the standard genetic code, the most common start codon is:**

- A UAA
- B UAG
- C UGA
- D **AUG** ✓
- E UUU

▶ **Explanation:** AUG is the typical start codon and codes for methionine (Met). UAA/UAG/UGA are stop codons.

9 **The DNA triplet that corresponds to the mRNA start codon AUG on the coding (sense) strand is:**

- A **ATG** ✓
- B TAC
- C AUC
- D UAG
- E ACG

▶ **Explanation:** The coding DNA strand matches mRNA except T replaces U. So AUG in mRNA corresponds to ATG in DNA (coding strand). TAC would be the complementary template triplet.

10 **Which set lists ONLY stop codons in the standard genetic code?**

A AUG, UGG, UGA

B **UAA, UAG, UGA** ✓

C UAC, UAU, UAA

D AAA, AAG, AGG

E CAA, CAG, CGA

▶ **Explanation:** The three stop codons are UAA, UAG, and UGA. AUG is start (Met), and UGG codes tryptophan.

11 When a ribosome reaches a stop codon, what molecule directly recognizes it in the A site?

A A specific tRNA carrying a “stop amino acid”

B **A release factor protein** ✓

C DNA polymerase

D Aminoacyl-tRNA synthetase

E RNA polymerase

▶ **Explanation:** Stop codons are not matched by tRNAs. Instead, a release factor binds the stop codon and triggers termination by releasing the polypeptide from the tRNA.

12 An mRNA codon is written 5 →3 as 5 -AUG-3 . Which anticodon (written 3 →5) would pair correctly with it?

A **3 -UAC-5** ✓

B 3 -AUG-5

C 5 -UAC-3

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- D 5 -CAU-3
- E 3 -CAU-5

▶ **Explanation:** Codon–anticodon pairing is complementary and antiparallel. AUG pairs with UAC, and the anticodon is conventionally written 3 →5 as 3 -UAC-5 .

13 The "wobble" concept mainly explains why:

- A DNA has a double helix
- B RNA polymerase reads DNA 5 →3
- C **One tRNA can sometimes recognize multiple codons for the same amino acid** ✓
- D Stop codons code for methionine
- E Proteins are made in the nucleus

▶ **Explanation:** Wobble pairing occurs at the third base of the codon (first of the anticodon), allowing a single tRNA to bind more than one codon that specifies the same amino acid.

14 Which enzyme is MOST directly responsible for matching the correct amino acid to its corresponding tRNA?

- A RNA polymerase
- B Ribosomal peptidyl transferase
- C **Aminoacyl-tRNA synthetase** ✓
- D DNA ligase
- E Helicase

▶ **Explanation:** Aminoacyl-tRNA synthetases "charge" tRNAs with the correct amino acids and are a major fidelity checkpoint. The ribosome mainly checks codon–anticodon pairing, not amino acid identity.

15 A tRNA with anticodon 3 -UAC-5 is mistakenly charged with valine instead of methionine. The ribosome encounters AUG. What is MOST likely to be incorporated?

- A Methionine, because AUG always forces methionine to be used
- B **Valine, because the ribosome reads the anticodon–codon match, not the amino acid identity** ✓
- C A stop signal, because the tRNA is incorrect
- D No amino acid; translation stops immediately
- E Glycine, because wobble converts AUG to GGU

▶ **Explanation:** If a tRNA is mischarged, the ribosome can still accept it if the anticodon matches the codon. The wrong amino acid (valine) would be incorporated—highlighting why aminoacyl-tRNA synthetases are crucial for accuracy.

16 In eukaryotic cells, transcription and translation are separated mainly because:

- A Eukaryotes lack ribosomes in the cytosol
- B **DNA is located in the nucleus while ribosomes translate mRNA in the cytosol/rough ER** ✓
- C mRNA cannot leave mitochondria
- D tRNA is made only in the cytosol and cannot enter the nucleus
- E Eukaryotes use protein templates instead of mRNA templates

▶ **Explanation:** Eukaryotes have a nucleus that houses DNA and transcription, while translation happens at ribosomes in the cytoplasm (or on rough ER). This separation enables extensive mRNA processing.

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17 **Which set lists common processing steps for eukaryotic pre-mRNA before it becomes mature mRNA?**

- A **5 cap, poly-A tail, splicing** ✓
- B Shine-Dalgarno addition, removal of stop codons, DNA methylation
- C tRNA charging, peptide bond formation, ribosome assembly
- D Okazaki fragment joining, proofreading, helicase unwinding
- E Translation initiation, elongation, termination

▶ **Explanation:** Eukaryotic pre-mRNA is typically capped at the 5 end, polyadenylated at the 3 end, and spliced to remove introns. Shine-Dalgarno is a prokaryotic translation feature, not mRNA processing.

18 **Splicing primarily removes:**

- A Exons to keep introns
- B **Introns to join exons** ✓
- C Stop codons to keep translation going
- D tRNAs to free ribosomes
- E Amino acids from a polypeptide chain

▶ **Explanation:** Splicing removes introns from pre-mRNA and ligates exons together to form a continuous coding sequence (plus UTRs).

19 **Alternative splicing is important because it allows:**

- A **One gene to produce multiple different protein isoforms** ✓
- B One ribosome to translate DNA directly

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- C Proteins to act as templates for new DNA
- D Stop codons to code for amino acids
- E A single codon to specify multiple amino acids

▶ **Explanation:** By including or skipping certain exons, a single gene can yield different mRNAs and thus different proteins. Codons remain unambiguous (one codon → one amino acid or stop).

⑳ A key difference in prokaryotes is that translation can begin before transcription ends because:

- A **Prokaryotic DNA is in the cytosol and there is no nuclear membrane barrier** ✓
- B Prokaryotes have no mRNA
- C Prokaryotes translate proteins from DNA directly
- D Prokaryotes lack ribosomes
- E Prokaryotes splice introns extensively before translation

▶ **Explanation:** Because prokaryotes lack a nucleus, ribosomes can access newly made mRNA while it's still being transcribed, allowing coupled transcription–translation.

㉑ In many bacteria, the ribosome is positioned correctly at the start codon by pairing with a sequence in the mRNA called the:

- A Kozak sequence
- B **Shine-Dalgarno sequence** ✓
- C TATA box
- D Poly-A signal
- E Splice donor site

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▶ **Explanation:** The Shine-Dalgarno sequence in bacterial mRNA base-pairs with rRNA to align the start codon. Kozak is a eukaryotic start-context, and TATA box is a eukaryotic promoter element.

22 In many eukaryotes, the small ribosomal subunit typically finds the start codon by:

- A Binding a Shine-Dalgarno sequence and jumping to AUG
- B **Scanning from the 5 cap until it encounters an AUG in a good Kozak context ✓**
- C Binding directly to the poly-A tail and moving 3 →5
- D Using DNA polymerase to locate AUG
- E Using spliceosomes to position the start codon

▶ **Explanation:** Eukaryotic initiation often follows the scanning model: the small subunit binds the 5 cap and scans to the first suitable AUG (often aided by the Kozak sequence).

23 Which mutation is most likely to cause a frameshift in the coding region?

- A Substitution of one base that changes one codon
- B Insertion of 3 bases
- C Deletion of 6 bases
- D **Insertion of 1 base ✓**
- E Substitution that creates a synonymous codon

▶ **Explanation:** Insertions or deletions not in multiples of 3 shift the reading frame, changing all downstream codons. A single-base insertion is the classic frameshift.

24 **A “silent” mutation is best described as one that:**

- A Changes the amino acid sequence drastically
- B **Changes a codon but still codes for the same amino acid ✓**
- C Introduces a premature stop codon
- D Deletes an entire exon
- E Prevents transcription completely

▶ **Explanation:** Because the genetic code is degenerate (multiple codons can encode the same amino acid), some base substitutions do not change the amino acid sequence and are called silent (synonymous) mutations.

25 **Which statement about the genetic code is correct?**

- A One codon can specify multiple different amino acids depending on the cell type
- B **The code is degenerate: multiple codons can specify the same amino acid ✓**
- C All amino acids are encoded by exactly one codon
- D Stop codons are read by special tRNAs carrying “stop” amino acids
- E Codons are 2 nucleotides long

▶ **Explanation:** The code is degenerate (many amino acids have several codons) but unambiguous (a given codon specifies only one amino acid or stop). Codons are triplets.

26 **An mRNA coding region (from start codon through stop codon) is 300 nucleotides long. Assuming no introns and no overlapping reading frames, what is the maximum number of amino acids in the translated polypeptide?**

- A 98

B **99** ✓

C 100

D 150

E 300

▶ **Explanation:** 300 nucleotides correspond to 100 codons. One codon is a stop codon and does not add an amino acid, so the polypeptide can have at most 99 amino acids.

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27 **Which statement correctly matches ribosomal sites with their main roles?**

A A site holds the growing peptide; P site is exit; E site is entry

B **A site is entry of aminoacyl-tRNA; P site holds peptidyl-tRNA; E site is exit** ✓

C A site is exit; P site is entry; E site holds the growing peptide

D All tRNAs bind only to the P site during translation

E The ribosome has only one tRNA binding site

▶ **Explanation:** A (aminoacyl) site accepts incoming charged tRNA, P (peptidyl) site holds the tRNA with the growing chain, and E (exit) site releases empty tRNA.

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28 **During translation initiation, the initiator tRNA first binds to which ribosomal site?**

A A site

B **P site** ✓

C E site

D Active site of RNA polymerase

E Spliceosome catalytic site

▶ **Explanation:** Initiation places the initiator tRNA in the P site so that the next aminoacyl-tRNA can enter the A site and elongation can proceed.

29 The ribosome's peptidyl transferase activity (forming peptide bonds) is primarily carried out by:

- A A DNA enzyme embedded in the ribosome
- B Aminoacyl-tRNA synthetase
- C **rRNA in the large ribosomal subunit (a ribozyme)** ✓
- D The mRNA itself acting as a catalyst
- E A membrane receptor

▶ **Explanation:** Peptide bond formation is catalyzed mainly by ribosomal RNA (rRNA), making the ribosome a ribozyme. Synthetases charge tRNAs but do not form peptide bonds in the ribosome.

30 A mutation changes the first AUG start codon of an mRNA to AUA. What is the most likely outcome in a typical eukaryotic scanning model?

- A Translation starts normally at AUA because it is similar to AUG
- B Translation stops immediately at AUA because it becomes a stop codon
- C **Translation may fail to initiate at that site and could start at a downstream AUG, producing a shorter protein** ✓
- D mRNA is converted back into DNA
- E The ribosome reads the mRNA 3 →5 to find AUG

▶ **Explanation:** AUA is not a standard start codon. If the first AUG is lost, initiation can be reduced or shift to a downstream AUG, often producing an N-terminally truncated protein (or no protein if no suitable start exists).

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31 **A mutation changes a stop codon (UAA) into UAU. What is the most likely direct effect on translation?**

- A Translation ends earlier than normal
- B **Translation continues past the original stop site until another stop codon is encountered** ✓
- C Translation cannot begin at all
- D The mRNA will no longer be produced (transcription stops)
- E The ribosome will insert a "stop amino acid" at UAU

▶ **Explanation:** UAU codes for tyrosine, not stop. Losing a stop codon typically results in read-through and a longer protein until a later stop codon appears.

32 **Where is the amino acid attached on a tRNA molecule?**

- A At the 5 end on a poly-A tail
- B At the anticodon loop
- C **At the 3 end (CCA acceptor stem)** ✓
- D On the mRNA cap
- E On the rRNA catalytic center

▶ **Explanation:** Amino acids are covalently linked to the 3 end of tRNA at the conserved CCA sequence. The anticodon loop is for codon recognition, not amino acid attachment.

33 **The immediate energy that drives peptide bond formation during elongation comes most directly from:**

A ATP hydrolysis at the peptide bond site

B **The high-energy ester bond between the amino acid and its tRNA (aminoacyl-tRNA)** ✓

C Breaking hydrogen bonds between mRNA bases

D Oxidation of glucose inside the ribosome

E The energy released when a stop codon is read

▶ **Explanation:** Charging a tRNA (using ATP) creates a high-energy aminoacyl-tRNA bond. That stored energy helps drive peptide bond formation in the ribosome.

34 Which RNA type is a major structural and catalytic component of ribosomes?

A mRNA

B tRNA

C **rRNA** ✓

D snRNA

E miRNA

▶ **Explanation:** rRNA makes up much of the ribosome's mass and forms the catalytic peptidyl transferase center. mRNA is the template and tRNA is the adaptor.

35 Which statement best distinguishes exons from introns in eukaryotic genes (typical case)?

A Exons are removed; introns are kept in mature mRNA

B **Exons are typically retained in mature mRNA; introns are removed during splicing** ✓

C Exons are only found in prokaryotes

D Introns code for amino acids; exons do not

E Introns form ribosomes; exons form tRNAs

▶ **Explanation:** Splicing usually removes introns and joins exons. Exons often include the coding sequence (and can include UTR regions as well).

36 Which statement best compares typical bacterial and typical eukaryotic mRNA organization?

A Bacterial mRNAs are usually monocistronic; eukaryotic mRNAs are usually polycistronic

B **Bacterial mRNAs are often polycistronic; eukaryotic mRNAs are usually monocistronic** ✓

C Both are always polycistronic

D Both are always monocistronic

E Neither bacteria nor eukaryotes use mRNA for translation

▶ **Explanation:** Bacterial operons can produce polycistronic mRNA encoding multiple proteins. Most eukaryotic mRNAs encode one main protein (monocistronic), though there are exceptions.

37 A mutation destroys a gene's promoter but leaves the start codon intact. What is the most direct consequence?

A Translation will start at a different codon

B **Transcription of that gene is greatly reduced or absent** ✓

C The mRNA will be translated faster

D The amino acid sequence changes but mRNA levels stay normal

E Stop codons will become start codons

▶ **Explanation:** The promoter is a DNA regulatory region required for RNA polymerase binding/initiation. If transcription doesn't occur, there is no mRNA for ribosomes to translate, regardless of the start codon sequence.

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38 **The coding DNA strand for a gene segment is 5 -ATG GAA TTT-3 . What is the corresponding mRNA sequence (5 →3) for this segment?**

- A 5 -UAC CUU AAA-3
- B **5 -AUG GAA UUU-3** ✓
- C 5 -TAC CTT AAA-3
- D 3 -AUG GAA UUU-5
- E 5 -AUG CUU AAA-3

▶ **Explanation:** mRNA matches the coding strand except U replaces T. So ATG GAA TTT becomes AUG GAA UUU (all written 5 →3).

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39 **Which statement best explains why identifying the correct start codon is so important for translation?**

- A **The start codon determines the reading frame for all downstream codons** ✓
- B The start codon is the only codon that can be read by the ribosome
- C The start codon changes the DNA sequence during translation
- D The start codon is removed by splicing
- E The start codon is always a stop codon in bacteria

▶ **Explanation:** Reading frame depends on where translation begins. Starting at the wrong position shifts codon grouping, usually producing a very different amino acid sequence and often an early stop codon.

40 Which event most directly causes the newly made polypeptide to be released from the ribosome at termination?

A A tRNA inserts a final amino acid at the stop codon

B A release factor promotes hydrolysis of the bond between the polypeptide and the tRNA in the P site ✓

C RNA polymerase detaches from DNA

D The 5 cap is removed from mRNA

E The ribosome reads the mRNA backward to undo translation

▶ **Explanation:** Termination occurs when a release factor binds the stop codon and triggers hydrolysis of the peptidyl-tRNA linkage, freeing the polypeptide. Then the ribosome and mRNA can dissociate.

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