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Central Dogma: DNA → RNA → Protein

Exam — 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 — Printable Exam

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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

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

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

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

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

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

D A pairs with G; C pairs with U

E A pairs with U; C pairs with T

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

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

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

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

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

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

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

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

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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

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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

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

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

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

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

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

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

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

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

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

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

Source: entermedschool.org — Free Medical Education Resources

E Substitution that creates a synonymous codon

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

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

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

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

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

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

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

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

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

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

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

- **A** mRNA
- **B** tRNA
- **C** rRNA
- **D** snRNA
- **E** miRNA

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

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

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

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

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

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

Source: entermedschool.org — Free Medical Education Resources

Answer Key

#	Ans	Answer Text
1	**D**	Reverse transcription (RNA → DNA)
2	**B**	mRNA
3	**B**	Coding (sense) strand
4	**C**	Synthesizes 5 →3 ; reads 3 →5
5	**B**	A pairs with U; C pairs with G
6	**B**	5 →3
7	**B**	N-terminus → C-terminus
8	**D**	AUG
9	**A**	ATG
10	**B**	UAA, UAG, UGA
11	**B**	A release factor protein
12	**A**	3 -UAC-5
13	**C**	One tRNA can sometimes recognize multiple codons for the same amino acid
14	**C**	Aminoacyl-tRNA synthetase
15	**B**	Valine, because the ribosome reads the anticodon–codon match, not the am...
16	**B**	DNA is located in the nucleus while ribosomes translate mRNA in the cyto...
17	**A**	5 cap, poly-A tail, splicing
18	**B**	Introns to join exons
19	**A**	One gene to produce multiple different protein isoforms
20	**A**	Prokaryotic DNA is in the cytosol and there is no nuclear membrane barri...
21	**B**	Shine-Dalgarno sequence
22	**B**	Scanning from the 5 cap until it encounters an AUG in a good Kozak cont...
23	**D**	Insertion of 1 base
24	**B**	Changes a codon but still codes for the same amino acid
25	**B**	The code is degenerate: multiple codons can specify the same amino acid
26	**B**	99
27	**B**	A site is entry of aminoacyl-tRNA; P site holds peptidyl-tRNA; E site is...
28	**B**	P site
29	**C**	rRNA in the large ribosomal subunit (a ribozyme)
30	**C**	Translation may fail to initiate at that site and could start at a downs...
31	**B**	Translation continues past the original stop site until another stop cod...
32	**C**	At the 3 end (CCA acceptor stem)
33	**B**	The high-energy ester bond between the amino acid and its tRNA (aminoacy...
34	**C**	rRNA
35	**B**	Exons are typically retained in mature mRNA; introns are removed during ...
36	**B**	Bacterial mRNAs are often polycistronic; eukaryotic mRNAs are usually mo...
37	**B**	Transcription of that gene is greatly reduced or absent
38		5 -AUG GAA UUU-3