

UNIT 6: GENE EXPRESSION
AND REGULATION

COGNITOEDU.LINK/AP-BIO-U6

Scan for Unit 6 notes

20 AP-style MCQs across topics 6.1 to 6.8. Practice, review, revisit.

WHAT'S INSIDE

- ✓ 20 MCQs, four options each, in the style of the real AP exam
- ✓ Every question tagged to a Unit 6 topic so you know what to revise
- ✓ Full answer key with a short explanation for every question
- ✓ Mix of standalone and stimulus-style stems, matching real AP question formats

HOW TO USE IT

- 1. Untimed pass.** Work through slowly, aiming for around 90 seconds per question. Read every option before you commit.
- 2. Timed pass.** Redo the pack in 30 minutes. That matches AP exam pace (1.5 minutes per MCQ) and builds stamina.
- 3. Review.** Check the answer key and mark every miss. Revise those topics on Cognito, then retry after a week.

TOPICS COVERED

- **6.1** DNA and RNA Structure
- **6.2** Replication
- **6.3** Transcription and RNA Processing
- **6.4** Translation
- **6.5** Regulation of Gene Expression
- **6.6** Gene Expression and Cell Specialization
- **6.7** Mutations
- **6.8** Biotechnology

STRUGGLING WITH A TOPIC?



Any topic tricky? Scan the QR to jump straight to the Unit 6 notes on Cognito. For the full AP Biology course (all 8 units, lessons, quizzes, flashcards and past-paper FRQs), head to **cognitoedu.link/ap-bio-notes**. Rework the questions you got wrong a week later to lock the concepts in.

AP EXAM CONTEXT

12-16% 60

UNIT WEIGHT (MCQ
SECTION)

MCQS ON THE REAL EXAM

1.5m

AVERAGE TIME PER MCQ

AP BIOLOGY

Unit 6: Gene Expression and Regulation

SECTION I • MULTIPLE CHOICE

Time—30 minutes

20 Questions

Directions: Each of the questions or incomplete statements below is followed by four suggested answers or completions. Select the one that is best in each case and mark it clearly on your answer sheet or circle your choice below.

- Which combination of features best distinguishes RNA from DNA?
 (A) RNA has thymine and deoxyribose; DNA has uracil and ribose.
 (B) RNA has uracil and ribose; DNA has thymine and deoxyribose.
 (C) Both molecules have the same bases and sugars.
 (D) RNA has adenine; DNA has guanine.
- During DNA replication, DNA polymerase adds nucleotides only to the 3' end of the growing strand. Which best explains why replication produces one continuous leading strand and one discontinuous lagging strand at each replication fork?
 (A) Only one strand contains the correct bases for replication of the DNA molecule.
 (B) DNA polymerase runs out of nucleotides on the lagging strand template during replication.
 (C) The two template strands run antiparallel, so only one can be read in the direction of fork movement.
 (D) The lagging strand is copied by RNA polymerase, not DNA polymerase, at each replication fork.
- Which model of DNA replication is best supported by the density bands in Table 1?
 (A) Conservative replication, in which one daughter molecule is fully heavy and the other fully light after a round of replication in the light medium.
 (B) Dispersive replication, in which each daughter DNA is a random patchwork of heavy and light segments throughout.
 (C) Semiconservative replication: each daughter molecule has one heavy strand and one light strand.
 (D) No replication occurs, because the DNA density stays constant.
- Which claim is best supported by the 40-minute results in Table 1?
 (A) Every parental DNA strand has been degraded by 40 min after transfer to the light medium containing ^{14}N .
 (B) Half of the DNA molecules at 40 min contain no ^{14}N nucleotides.
 (C) Some DNA molecules at 40 min still contain one heavy parental strand.
 (D) All DNA molecules at 40 min are fully heavy.
- Which enzyme catalyzes the synthesis of mRNA from a DNA template in eukaryotic cells?
 (A) DNA polymerase
 (B) RNA polymerase
 (C) Reverse transcriptase
 (D) DNA ligase
- Before a eukaryotic mRNA leaves the nucleus, it undergoes three main forms of processing. Which of the following is NOT one of them?
 (A) Addition of a 5' cap that helps ribosomes recognize the mature mRNA.
 (B) Addition of a poly-A tail.
 (C) Splicing to remove introns.
 (D) Removal of the promoter sequence from the transcript before it leaves the nucleus.

Questions 3, 4 refer to the following information.

Meselson and Stahl grew *E. coli* in medium containing heavy ^{15}N so that all of the DNA became heavy. Cells were then transferred to light ^{14}N medium and DNA density was measured after 0, 20, and 40 minutes (each roughly one round of replication).

Table 1. DNA density bands after transfer to ^{14}N medium

Time after transfer (min)	Heavy band	Intermediate band	Light band
0	Present	Absent	Absent
20	Absent	Present	Absent
40	Absent	Present	Present

AP BIOLOGY · Unit 6: Gene Expression and Regulation · Section I (continued)

Questions 7, 8 refer to the following information.

A short internal segment of the nontemplate (coding) DNA strand of a gene reads 5'-TACGGATCA-3'. Students traced its transcription and translation using the standard genetic code and recorded the intermediate molecules in Table 2.

Table 2. From DNA to peptide for a short sequence

Molecule	Sequence (5' to 3')
Nontemplate DNA strand	TACGGATCA
Template DNA strand	TGATCCGTA
mRNA	UACGGAUCA
Peptide (N to C)	Tyr–Gly–Ser

- Based on Table 2, which mRNA codon codes for the amino acid glycine (Gly)?
(A) AGG
(B) GGA
(C) UAC
(D) UCA
- A single base substitution changes the second mRNA codon in Table 2 from GGA to GGU. Predict the effect on the peptide sequence.
(A) The peptide changes to Tyr–Val–Ser.
(B) The peptide changes to Met–Val–Ser.
(C) The peptide changes to Tyr–Stop–Ser, so translation ends early with a truncated protein product.
(D) The peptide stays Tyr–Gly–Ser; GGA and GGU both code for glycine.
- In eukaryotic cells, transcription factors bind specific DNA sequences to help control which genes are transcribed. Which best describes how a transcription factor typically controls gene expression?
(A) By altering the amino acid sequence of the transcription factor itself.
(B) By binding regulatory sequences and recruiting or blocking RNA polymerase at the promoter.
(C) By replacing RNA polymerase to directly build the mRNA.
(D) By hydrolyzing every mature mRNA transcript before it can leave the nucleus and reach the ribosome.

Questions 10, 11 refer to the following information.

The trp operon in *E. coli* codes for enzymes that make the amino acid tryptophan. The expression of the trp operon was measured under different concentrations of tryptophan in the growth medium.

Table 3. trp mRNA level vs. tryptophan supply

Tryptophan in medium	trp mRNA level (% of max)
None	100
Low	70
Medium	20
High	3

- Which claim about the trp operon is best supported by Table 3?
(A) Adding tryptophan to the culture suppresses transcription of the biosynthetic genes.
(B) Adding tryptophan raises expression in a dose-dependent way across the range tested.
(C) Expression is the same under every condition tested.
(D) The operon is only transcribed when tryptophan is abundant.
- Which mechanism best explains the pattern in Table 3?
(A) Tryptophan binds the trp repressor and activates it to bind the operator, blocking transcription.
(B) Tryptophan removes the trp repressor from the operator, so transcription of the operon increases sharply.
(C) Tryptophan speeds RNA polymerase, so more trp mRNA is produced.
(D) Tryptophan blocks translation of trp mRNA but not transcription.

AP BIOLOGY · Unit 6: Gene Expression and Regulation · Section I (continued)

Questions 12, 13, 14 refer to the following information.

The lac operon in *E. coli* codes for enzymes that break down lactose. β -galactosidase activity was measured under four conditions.

Table 4. β -galactosidase activity in the lac operon

Condition	Lactose	Glucose	β -galactosidase activity (%)
1	Absent	Present	1
2	Present	Present	6
3	Absent	Absent	1
4	Present	Absent	100

12. Under which condition in Table 4 is β -galactosidase activity highest?
- (A) Condition 1 (no lactose, glucose present)
 (B) Condition 4 (lactose present, no glucose)
 (C) Condition 2 (both sugars present)
 (D) Condition 3 (neither sugar present)

Questions 15, 16 refer to the following information.

Four adult human tissues were tested for the presence of the mRNAs and proteins of four genes: hemoglobin β -chain (HBB), insulin (INS), myosin (MYH7), and lactase (LCT). Present = detected; Absent = below detection.

Table 5. Tissue-specific gene expression (mRNA / protein)

Gene	Red blood cell precursors	Pancreatic β -cells	Cardiac muscle	Small intestine
HBB	Present / Present	Absent / Absent	Absent / Absent	Absent / Absent
INS	Absent / Absent	Present / Present	Absent / Absent	Absent / Absent
MYH7	Absent / Absent	Absent / Absent	Present / Present	Absent / Absent
LCT	Absent / Absent	Absent / Absent	Absent / Absent	Present / Present

15. Which claim is best supported by the tissue-expression pattern in Table 5?
- (A) Each cell type expresses only a specific subset of the genes in its genome.
 (B) The four tissues each contain a completely different set of genes in their nuclear DNA.
 (C) Every gene in the genome is expressed at some level in every tissue.
 (D) Cardiac muscle cells transcribe INS but do not translate it.
16. A student proposes that HBB, INS, MYH7, and LCT are physically deleted from the DNA of tissues where they are not expressed. Which further experiment would best test this proposal?
- (A) Measure protein levels of HBB in red blood cell precursors using an antibody-based blot.
 (B) PCR-amplify each gene from genomic DNA of every tissue and check for a product.
 (C) Sequence the mRNA of each tissue for splicing errors.
 (D) Grow each cell type in different culture media and re-test mRNA levels.

AP BIOLOGY · Unit 6: Gene Expression and Regulation · Section I (continued)

Questions 17, 18 refer to the following information.

Four types of single-base mutations were introduced into the same protein-coding gene. The predicted effect on the resulting protein was recorded.

Table 6. Predicted effects of four single-base mutations

Mutation	Codon change	Amino acid change	Notes
M1	GAA → GAG	Glu → Glu	Same amino acid
M2	GAA → GUA	Glu → Val	Different R group
M3	CAG → UAG	Gln → STOP	Chain terminates early
M4	Single base inserted	Reading frame shifts	Every codon after change

17. Which mutation in Table 6 is most likely to have the smallest effect on protein function?
- (A) M1
(B) M2
(C) M3
(D) M4
18. Each mutation in Table 6 occurs near the start of the coding sequence. Which mutation is typically expected to change every downstream amino acid in the resulting protein, and why?
- (A) M1, because a silent codon change alters every amino acid downstream.
(B) M2, because a missense change at one codon propagates to all later codons.
(C) M3, because a premature stop codon inserts extra amino acids downstream of the change.
(D) M4, because the reading frame shifts and every downstream codon is read in a new frame.

Questions 19, 20 refer to the following information.

A DNA restriction enzyme, EcoRI, cuts linear DNA at every occurrence of the recognition sequence GAATTC. A 6,000 bp linear DNA sample was digested with EcoRI and the fragment sizes were separated by gel electrophoresis.

Table 7. Fragment sizes from EcoRI digestion (bp)

Fragment	Size (bp)
1	3,200
2	1,800
3	1,000

19. Based on Table 7, how many EcoRI recognition sites (GAATTC) does the 6,000 bp linear DNA contain?
- (A) 0
(B) 1
(C) 2
(D) 3
20. In gel electrophoresis of the digest in Table 7, which fragment would migrate the farthest from the loading well?
- (A) The 3,200 bp fragment, because larger DNA moves faster through the pores of the agarose gel matrix.
(B) The 1,800 bp fragment, because it is intermediate in size.
(C) The 1,000 bp fragment, because smaller DNA moves faster through the gel matrix.
(D) All three fragments would migrate exactly the same distance.

Q1. Answer: B

Topic 6.1 · DNA and RNA Structure

RNA uses ribose as its sugar and uracil in place of thymine. DNA uses deoxyribose and thymine. A swaps the two molecules. C ignores the sugar and base differences. D is wrong because both molecules contain both adenine and guanine.

Q2. Answer: C

Topic 6.2 · Replication

Because the two strands are antiparallel and DNA polymerase can only add nucleotides at the 3' end, only the strand whose 3' end runs toward the moving fork can be copied continuously (leading). The other must be copied in short pieces (Okazaki fragments) that are later joined by DNA ligase. A, B, and D are all factually wrong (both template strands contain valid bases; polymerase does not run out of nucleotides mid-fork; and DNA polymerase, not RNA polymerase, copies the lagging strand).

Q3. Answer: C

Topic 6.2 · Replication

After one round in ^{14}N (20 min), all DNA sat at the intermediate density: every molecule had one heavy strand paired with one new light strand, which is the semiconservative prediction. After a second round (40 min), a light band appeared alongside the intermediate band, matching the semiconservative pattern (some molecules now have two light strands, while others retain a parental heavy strand paired with a light one). A predicts heavy + light bands at 20 min. B is consistent with 20 min but predicts a single band between intermediate and light at 40 min, not two distinct bands. D contradicts the density change.

Q4. Answer: C

Topic 6.2 · Replication

At 40 min, both intermediate (one heavy + one light strand) and light (two light strands) bands are present. The intermediate band shows that the original parental heavy strands are still present, each paired with a new light strand. A contradicts the intermediate band. B is unsupported: Table 1 gives no molecular proportions, only presence/absence of bands. D contradicts the absence of a heavy band at 40 min.

Q5. Answer: B

Topic 6.3 · Transcription and RNA Processing

RNA polymerase (RNA polymerase II for protein-coding genes in eukaryotes) reads the template DNA strand 3' to 5' and builds mRNA 5' to 3'. DNA polymerase replicates DNA (A). Reverse transcriptase makes DNA from RNA (retroviruses and some lab uses) (C). DNA ligase joins DNA fragments (D).

Q6. Answer: D

Topic 6.3 · Transcription and RNA Processing

The three canonical processing steps for eukaryotic pre-mRNA are 5' capping, 3' polyadenylation (poly-A tail), and splicing to remove introns and join exons. The promoter is a DNA sequence upstream of the gene and is never part of the mRNA transcript, so 'removing it from the transcript' is not something cells do. A, B, and C are all real steps.

Q7. Answer: B

Topic 6.4 · Translation

The mRNA (5' to 3') is UAC-GGA-UCA and the peptide is Tyr-Gly-Ser. Reading in-frame codons pairs UAC with Tyr, GGA with Gly, and UCA with Ser. So GGA codes for Gly. A (AGG, arginine) does not appear in this reading frame. C (UAC) codes for Tyr. D (UCA) codes for Ser.

Q8. Answer: D

Topic 6.4 · Translation

The genetic code is redundant: GGA and GGU both code for glycine. This is a silent (synonymous) mutation and leaves the peptide unchanged. A and B invent amino acid substitutions that do not follow from the codon change. C invents a stop codon that GGU is not.

Q9. Answer: B

Topic 6.5 · Regulation of Gene Expression

Transcription factors bind sequences such as enhancers or silencers and either recruit RNA polymerase and the general transcription machinery to the promoter (activators) or block it (repressors). A confuses the factor's own sequence with its regulatory role. C misdescribes RNA synthesis. D describes mRNA degradation, not transcription control.

Q10. Answer: A

Topic 6.5 · Regulation of Gene Expression

Expression falls from 100% with no tryptophan to 3% with high tryptophan. When the amino acid product (tryptophan) is available from the environment, the cell shuts down its own biosynthesis, matching the classic repressible operon pattern. B reverses the direction. C contradicts the range of values. D is contradicted by the pattern (highest expression when tryptophan is absent).

Q11. Answer: A

Topic 6.5 · Regulation of Gene Expression

In the trp operon, tryptophan is a corepressor: it binds an otherwise inactive repressor protein, activating it to bind the operator and block transcription. Without tryptophan, the repressor is inactive and the operon is transcribed. B reverses the effect (removing the repressor would activate expression, not decrease it). C misidentifies the mechanism as speeding polymerase, when the data show falling expression. D confuses transcriptional and translational control; Table 3 measures trp mRNA level, so the fall must occur at transcription.

Q12. Answer: B

Topic 6.5 · Regulation of Gene Expression

Activity peaks (100%) only when lactose is present and glucose is absent. Lactose (via its derivative allolactose) inactivates the repressor, and cAMP-CAP activates the operon strongly when glucose is low. A (glucose only, 1%) and D (neither sugar, 1%) have no inducer so activity is at background. C (both sugars, 6%) has the inducer but glucose suppresses cAMP levels, so activity stays low (catabolite repression).

Q13. Answer: D

Topic 6.5 · Regulation of Gene Expression

Condition 4 (lactose only) gives 100% activity, but condition 2 (lactose and glucose) gives only 6%. Adding glucose sharply reduces expression even though the inducer lactose is still there, matching catabolite repression: high glucose lowers cAMP, so CAP cannot activate the operon. A reverses the effect of glucose. B is contradicted by condition 1 (glucose alone, activity is 1%). C is contradicted by the change from condition 3 (1%) to condition 4 (100%), which shows lactose does affect expression.

Q14. Answer: A

Topic 6.5 · Regulation of Gene Expression

The repressor blocks transcription when lactose is absent. If it cannot bind the operator, that block is gone, and the operon is transcribed even without an inducer. Activity will still be modulated by CAP and cAMP (glucose availability), but the strict lactose requirement is lost. B contradicts the loss of repression. C also does not match the loss. D ignores that a broken binding site changes regulation.

Q15. Answer: A

Topic 6.6 · Gene Expression and Cell Speci...

Every tissue in Table 5 shows a distinct expression pattern despite carrying the same genome; each cell type transcribes and translates only a subset of its genes. This is exactly what differential gene expression means. B misstates cellular biology (all somatic cells share the genome). C contradicts the many 'absent / absent' entries. D is contradicted by the table: INS mRNA is absent in cardiac muscle, so the cell is not transcribing it.

Q16. Answer: B

Topic 6.6 · Gene Expression and Cell Speci...

Physical deletion means the DNA is gone. PCR from genomic DNA would fail in tissues where the gene is truly deleted. Finding intact genomic PCR products in every tissue would falsify the proposal (which is what actually happens: the gene is present but silent). A tests expression, not deletion. C looks at post-transcriptional errors. D tests induction, not deletion.

Q17. Answer: A

Topic 6.7 · Mutations

M1 is a silent (synonymous) mutation: the codon changes from GAA to GAG, but both code for glutamic acid, so the protein sequence is unchanged. M2 (missense) swaps Glu for Val, which changes R group chemistry. M3 (nonsense) truncates the protein at the mutation. M4 (frameshift) scrambles every amino acid downstream and produces the largest effect, not the smallest.

Q18. Answer: D

Topic 6.7 · Mutations

A single-base insertion (or deletion) shifts the reading frame from that point on, so every codon downstream is read in a new frame and the resulting amino acid sequence is entirely different from that point onward. A contradicts the definition of a silent mutation (no amino acid change at all). B overstates a single-residue swap; a missense change alters only the one codon where the substitution happens, not every downstream codon. C misdescribes a premature stop (the chain ends, so downstream codons are not translated rather than being changed).

Q19. Answer: C

Topic 6.8 · Biotechnology

A linear DNA with n cuts is broken into $n + 1$ fragments. Three fragments means two cuts, so the DNA contained two EcoRI recognition sites. The fragment sizes also add up: $3,200 + 1,800 + 1,000 = 6,000$ bp. Zero cuts leaves one fragment; one cut gives two; three cuts would give four.

Q20. Answer: C

Topic 6.8 · Biotechnology

In agarose gel electrophoresis, DNA is negatively charged and migrates toward the positive electrode. Small DNA fragments navigate the pores of the gel matrix more easily and migrate farthest, while larger fragments are held back. Between 3,200, 1,800, and 1,000 bp, the 1,000 bp fragment travels the greatest distance. A reverses the size relationship. B is the middle band. D contradicts how gel electrophoresis works.