AP Biology Unit 6

Gene Expression & Regulation

One-page sprint review
Free at Sophriva

EXAM WEIGHT	MCQs	FRQ APPEARANCE	SPRINT TIME
12–16%	7–10	Frequent	~2.5 hours

Inside this pack

- **Quick Glance at every Unit topic with priority + format**
- **Topic-by-topic key traps, must-know rules, and exam frames**
- **Worked example questions on the highest-yield topics**

AP BIOLOGY – UNIT 6
Gene Expression & Regulation

12–16% of exam • FRQ favorite • Sprint review

Master the central dogma directions, lac operon

Exam Weight	MCQs	FRQ Appearance	Sprint Time
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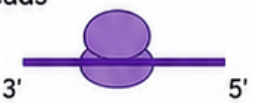
At-a-Glance Priority Map

Topic	Priority	Exam Format	Key Trap / Must-Know
6.1–6.2 DNA Structure & Replication	★★★	MCQ FRQ	Semiconservative; DNA pol only adds 5'→3'; lagging strand = Okazaki fragments + ligase.
6.3 Transcription & RNA Processing	★★★	MCQ FRQ	RNA pol reads **TEMPLATE** strand 3'→5'; mRNA same as **CODING** strand (T→U). Introns **OUT**, Exons **IN**.
6.4 Translation	★★★	MCQ FRQ	AUG = start (Met); UAA/UAG/UGA = stop (no amino acid); anticodon is **ANTIPARALLEL** to codon.
6.5 Gene Regulation	★★★	MCQ FRQ	Lac operon: 4 states. Transcription/translation **COUPLED** in prokaryotes only.
6.6 Cell Specialization	★★	MCQ	All cells have same genome; differential gene expression → cell identity. **HOX** genes = body plan.
6.7 Mutations	★★★	MCQ FRQ	Point mutation = substitution (never frameshift). Frameshift = insertion or deletion **ONLY**.
6.8 Biotechnology	★★★	MCQ Data	Gel: small = travels **FURTHER** (toward +). PCR: 95°C denature → 55°C anneal → 72°C extend

Top 6 Must-Know Rules

1. DNA pol only 5'→3'.


2. RNA pol reads template.


3. mRNA = coding strand with U.


4. Stop codons add no amino acid.


UAA
UAG
UGA

5. Lac operon max ON = lactose present + no glucose.


6. Mutations must be traced DNA → mRNA → AA → protein → phenotype.


6.1–6.2 DNA Structure & Replication

Semiconservative replication, enzyme roles, and leading vs lagging

1 Semiconservative Replication

- Each new DNA molecule contains one parental strand + one new strand.
- Proven by Meselson–Stahl experiment (1958) using ^{15}N / ^{14}N density labeling.
- After 1 round in ^{14}N: all hybrid intermediate-density DNA.
- After 2 rounds: half hybrid + half light.
- Occurs in S phase before mitosis.

Meselson–Stahl Density Gradient Evidence

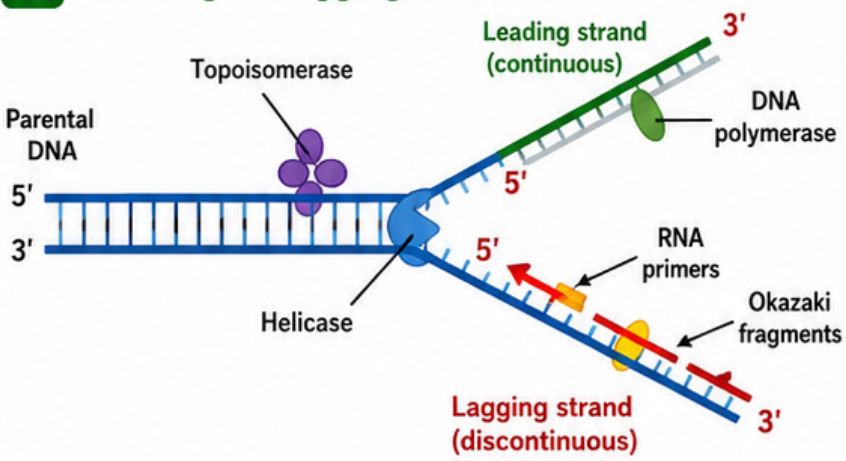
Generation (in ^{14}N)	Conservative Replication (Predicted)	Semiconservative Replication (Observed)
0 (all ^{15}N)	Heavy (^{15}N)	Heavy (^{15}N)
1 (one round)	Light (^{14}N) Heavy (^{15}N)	Hybrid (intermediate)
2 (two rounds)	Light (^{14}N) Heavy (^{15}N)	Light (^{14}N) Hybrid (intermediate)

Heavy (^{15}N) · Hybrid (Intermediate) · Light (^{14}N)

2 Replication Enzymes — Memorize

Enzyme	Function
Helicase	unwinds double helix, breaks H-bonds at replication fork.
Topoisomerase	relieves supercoiling ahead of helicase.
Primase (RNA polymerase)	synthesizes short RNA primer, provides free 3'-OH.
DNA polymerase	adds nucleotides 5'→3', proofreads, cannot start de novo.
Ligase	seals nicks between Okazaki fragments on lagging strand.

3 Leading vs Lagging Strand



- DNA pol only synthesizes 5'→3'.
- **Leading strand**: template 3'→5', polymerase moves **toward** fork, continuous synthesis, **one primer**.
- **Lagging strand**: template 5'→3', polymerase moves **away** from fork, discontinuous, **Okazaki fragments**, **multiple primers**, ligase joins fragments.
- **Okazaki fragments** are short DNA segments each initiated by a separate RNA primer.

Exam Sniper

1. After one replication round in ^{14}N, labeled ^{15}N DNA is intermediate hybrid.
2. RNA primer is required because DNA polymerase can only extend from an existing 3'-OH.
3. If ligase is inhibited, lagging strand is most affected.

Non-negotiable rule

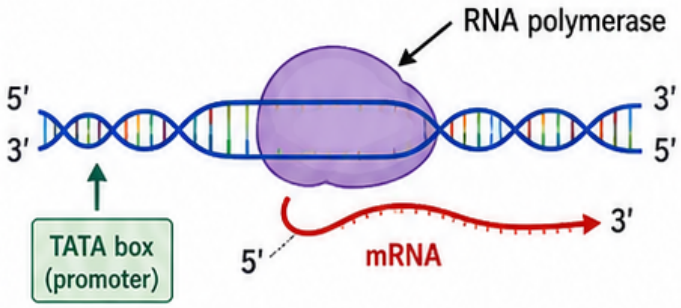
DNA polymerase adds nucleotides ONLY 5'→3'.

6.3 Transcription & RNA Processing

Direction rules, mRNA processing, and prokaryote vs eukaryote differences

1 Transcription Directions

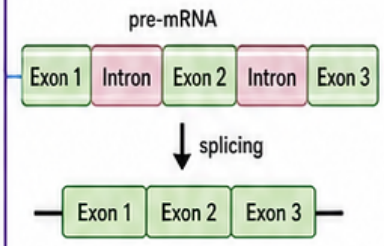
- RNA polymerase reads template strand 3′→5′.
- RNA is synthesized 5′→3′.
- mRNA sequence is the same as the coding strand except T→U.
- RNA pol binds promoter (TATA box) and recruits transcription factors.
- RNA polymerase does not need a primer and starts *de novo*.
- It has **no proofreading**, so it is more error-prone than DNA replication.



2 Eukaryotic mRNA Processing

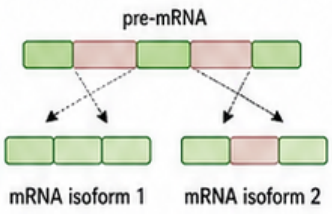
5′ cap — modified guanosine, protects mRNA and helps ribosome attachment.

Poly-A tail — added to 3′ end, protects mRNA and aids export.



RNA splicing — introns removed, exons joined.

Introns OUT, Exons IN
EXons are EXpressed.



Alternative splicing: different exon combinations produce different proteins from one gene, so proteome diversity exceeds genome size.

3 Prokaryotes vs Eukaryotes

	Prokaryotes	Eukaryotes
	No nucleus	Transcription in nucleus
	Transcription and translation are coupled	Translation in cytoplasm, not coupled
	No RNA processing	mRNA processed before export
	Polycistronic mRNA (many genes per mRNA)	Monocistronic mRNA (one gene per mRNA)
	1 RNA polymerase	3 RNA polymerases; Pol II makes mRNA

4 Worked Direction Example

Template strand 3′- T A C G G A -5′

mRNA 5′- A U G C C U -3′

First codon **AUG** = Met

Exam Sniper

- Drug blocking 5′ cap causes faster mRNA degradation and reduced translation.
- Proteins with different functions from the same gene come from alternative splicing.
- *E. coli* can couple transcription and translation because it has no nuclear membrane.

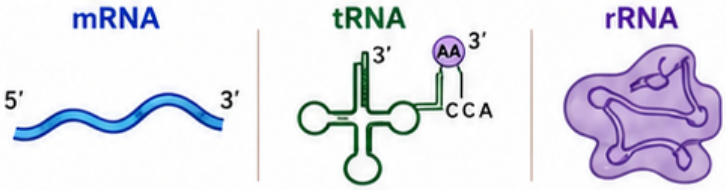
Trap Alert

- RNA polymerase reads the template strand, not the coding strand.
- Introns are spliced ***OUT*** and exons kept.
- Coupled transcription/translation happens in prokaryotes only.

6.4 Translation

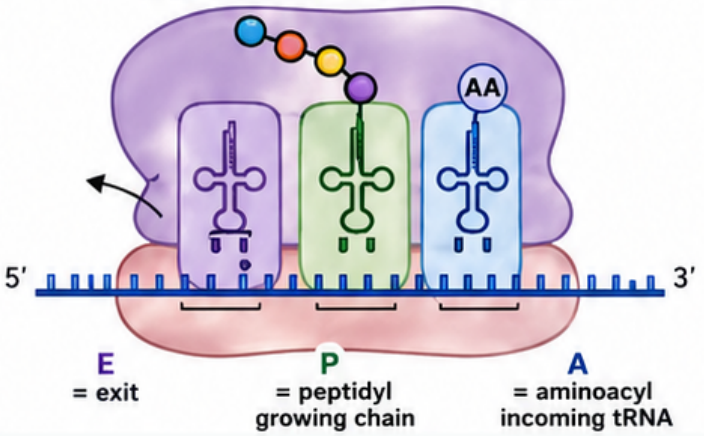
Three RNAs, key codons, and the A-P-E ribosome cycle

1 Three RNAs, One Goal



- **mRNA** carries the genetic message and is read **5′→3′** in codons.
- **tRNA** is the adaptor; anticodon pairs with the codon and carries a specific amino acid at the 3′ CCA end.
- **rRNA** is structural and catalytic; it forms the ribosome and catalyzes peptide bond formation, so it is a **ribozyme**.

Ribosome with A, P, and E sites



2 Key Codons

AUG = **start codon,** Methionine, translation begins here.

UAA, UAG, UGA = **stop codons,** no amino acid added, release factors recognize them.

- The genetic code is **redundant** (most amino acids have multiple codons) but **unambiguous** (each codon specifies only one amino acid).
- The genetic code is **universal** across life, which is strong evidence of common ancestry.

Codon–Anticodon Pairing

mRNA

5′-**AUG**-3′

A U G

‖ ‖ ‖

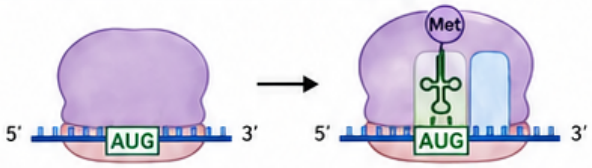
U A C

3′-**UAC**-5′

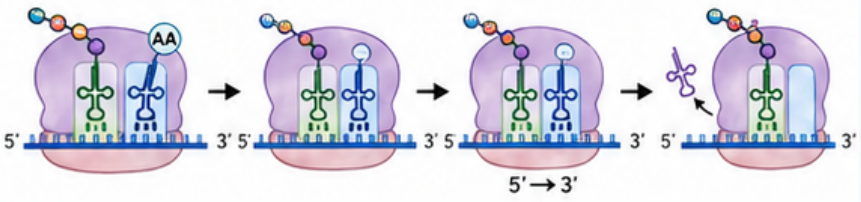
tRNA anticodon

3 Initiation → Elongation → Termination

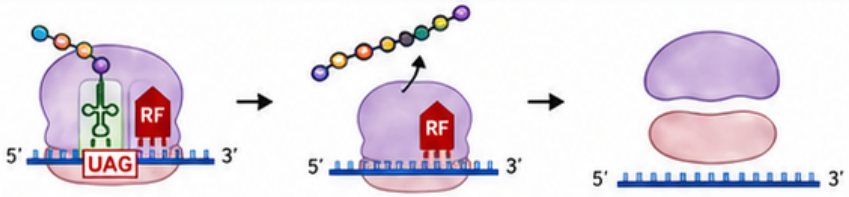
Initiation — ribosome assembles at **AUG** and initiator tRNA enters P site.



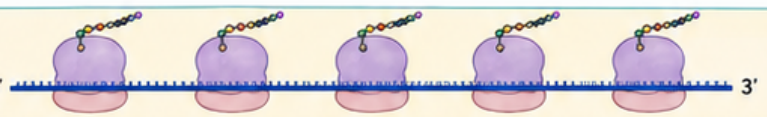
Elongation — aminoacyl tRNA enters A site, peptide bond forms, ribosome translocates 5′→3′, tRNA exits at E site.



Termination — stop codon reaches A site, release factor binds, polypeptide released, ribosome disassembles.



Multiple ribosomes can translate one mRNA simultaneously: **polysome.**



EXAM SNIPER

- Always read mRNA **5′→3′** from **AUG**.
- Anticodon **3′-UAC-5′** carries **Met**.
- At **UAG** a release factor binds, **not a tRNA**.
- **Universal code** suggests common ancestry.

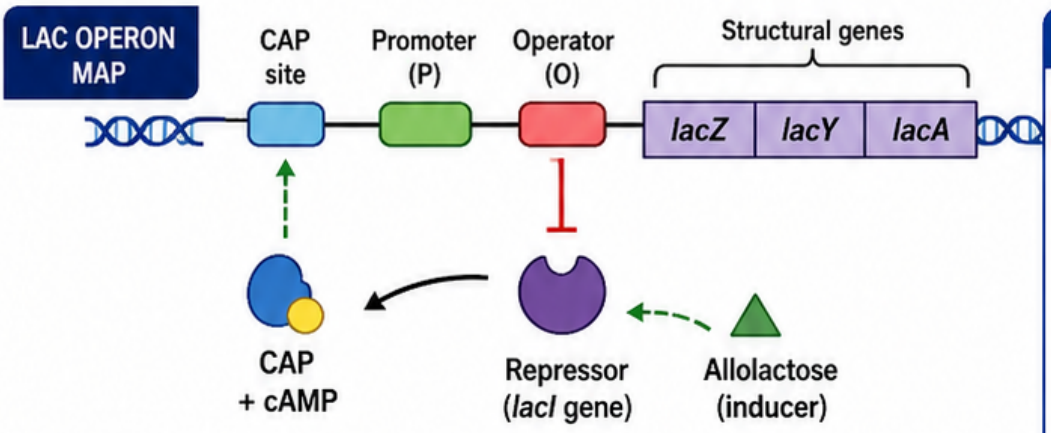
STOP Stop codons do NOT code for amino acids

6.5 Regulation of Gene Expression

Lac operon 4 states + eukaryotic control levels

Prokaryotic Regulation — Lac Operon (All 4 States)

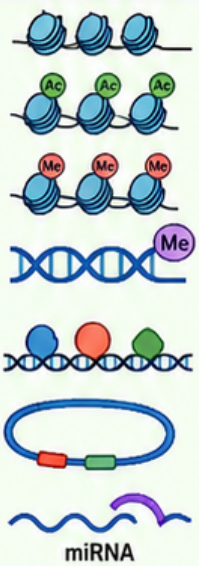
Conditions	Repressor	CAP-cAMP	Transcription Level	Why
1) No lactose + glucose present	repressor bound to operator	CAP inactive	**OFF**	no allolactose and low cAMP
2) Lactose present + glucose present	allolactose removes repressor	CAP inactive	**LOW transcription**	operator is open but no positive activation
3) Lactose present + no glucose	repressor removed	CAP-cAMP active	**MAXIMAL transcription**	allolactose opens operator and high cAMP activates CAP
4) No lactose + no glucose	repressor bound to operator	CAP active	**OFF**	repressor blocks RNA polymerase even though CAP is active



Know the Parts

- **promoter** = RNA pol binding site
- **operator** = repressor binding site
- **structural genes** encode beta-galactosidase and permease
- **allolactose** is the actual inducer
- **CAP-cAMP** is a positive regulator active when glucose is absent

Eukaryotic Gene Regulation — Multiple Levels



- chromatin remodeling
- histone acetylation **loosens** chromatin and increases transcription
- histone deacetylation tightens chromatin and lowers transcription
- DNA methylation silences genes and is epigenetic
- transcription factors bind promoters/enhancers
- enhancers/silencers **loop to promoter**
- **miRNA/siRNA** block translation or degrade mRNA

Exam Sniper

- lactose + no glucose = *lac* operon maximally ON
- inactive *lac* repressor mutation causes constitutive expression
- DNA methylation silences genes by compacting chromatin
- miRNA acts post-transcriptionally

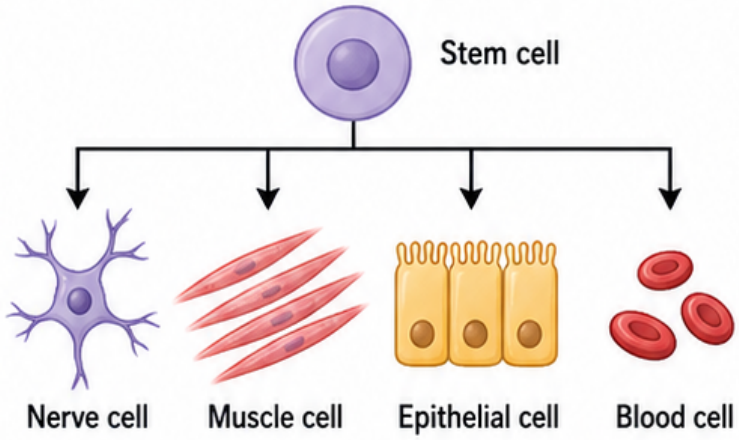
6.6 Gene Expression & Cell Specialization

Differential gene expression creates cell identity

Differential Gene Expression

- All cells in an organism have the same genome.
- Different cell types express different subsets of genes, producing different proteins and functions.
- Cell identity is determined by the combination of transcription factors active in that cell.
- **Differentiation** is the process by which a stem cell becomes a specialized cell through progressive gene activation and silencing.

From Stem Cell to Specialized Cells



HOX Genes & miRNA

- **HOX genes** are master regulatory genes that encode transcription factors and determine body segment identity along the body axis.
- HOX genes are highly conserved across animals, which supports common ancestry.
- Mutation in a HOX gene can cause homeotic transformation, such as a leg growing where an antenna should be in *Drosophila*.
- **miRNA and siRNA** are post-transcriptional silencers that bind target mRNA and either degrade it or block translation; they are essential for normal development.

Stem Cell Potency

Totipotent	can become any cell type, early embryo cells and zygote.
Pluripotent	can become most cell types, embryonic stem cells.
Multipotent	can become limited cell types, adult stem cells.

Exam Sniper

1 **Q:** Why do liver cells and muscle cells have the same DNA but different proteins?

A: Because of differential gene expression—different genes are turned ON in each cell type.

2 **Q:** Why do similar HOX genes in flies and humans indicate common evolutionary ancestry?

A: Because important developmental genes were conserved from a common ancestor.

Same genome, different genes ON.

6.7 Mutations

Master the mutation types and the mutation-to-protein logic

Mutation Types — Master This Table

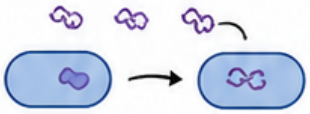
Type	What Changes	Effect on Protein	AP Example
Silent	Nucleotide substitution gives a different codon but same amino acid due to code redundancy.	No protein change; amino acid sequence is unchanged.	**GAA → GAG** both Glu
Missense	Nucleotide substitution changes codon and amino acid.	May alter protein shape or function; effect can be mild to severe.	**Sickle cell:** **GAG → GTG** **Glu → Val** in hemoglobin
Nonsense	Nucleotide substitution creates a premature stop codon.	Truncated protein; usually nonfunctional.	**CAA → UAA** (stop codon)
Frameshift (insertion)	1–2 nucleotides inserted causing downstream reading frame shift.	Usually nonfunctional protein due to altered amino acids and premature stop.	**Example:** Insertion of 1 nucleotide at codon 5
Frameshift (deletion)	1–2 nucleotides deleted causing downstream reading frame shift.	Usually nonfunctional protein.	**Note:** Cystic fibrosis ΔF508 is actually a 3-nt in-frame deletion, not a frameshift, but removes one amino acid.

Which Mutations Are Usually More Disruptive?

- **Frameshifts** and **nonsense** mutations are often the most disruptive.
- **Missense** mutations in active or binding sites can be very damaging.
- **Silent** mutations usually have no effect.
- **Severity** depends on context, location in the protein, and the type of amino acid change (especially charge and polarity).
- **Nonsense** mutations near the **N-terminus** (beginning) are worse than those near the **C-terminus** (end).

Horizontal Gene Transfer in Prokaryotes

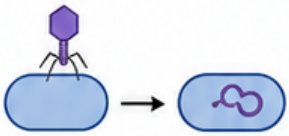
Transformation



Uptake of free DNA from the environment by a bacterium.

Example: Some *Streptococcus pneumoniae* strains take up naked DNA.

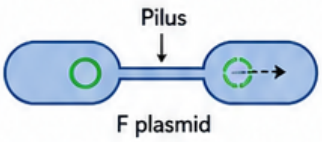
Transduction



Bacteriophage (virus) transfers bacterial DNA from one cell to another.

Example: Phage infects one bacterium and accidentally packages host DNA.

Conjugation



Direct transfer of DNA (plasmid) through a pilus. F plasmid enables transfer and spreads antibiotic resistance.

Example: *E. coli* conjugation spreads resistance genes.

Exam Sniper

1. GAG → GUG at codon 6 is a **missense** mutation (sickle-cell mutation).
2. The mutation type that affects all downstream amino acids is a **frameshift.**
3. If AUG at position 1 changes to GUG, the start codon is lost and **no protein is made.**

Worked Mini MCQ

Q: Consider the following change in the coding strand DNA that affects the mRNA codons.

	1	2	3	4	5
Codons:	CGA	UUU	GGC	CGA	AUA
				↓	
Change:	CGA → UGA (at codon 4)				

Which mutation type and effect best describe this change?

A. Silent; no change in protein
B. Missense; one amino acid is changed
C. Nonsense; translation stops at codon 4
D. Frameshift; all downstream amino acids change

Answer: C

This is a **nonsense** mutation. UGA is a stop codon, so translation stops at codon 4. The result is a short, truncated polypeptide.

6.8 Biotechnology

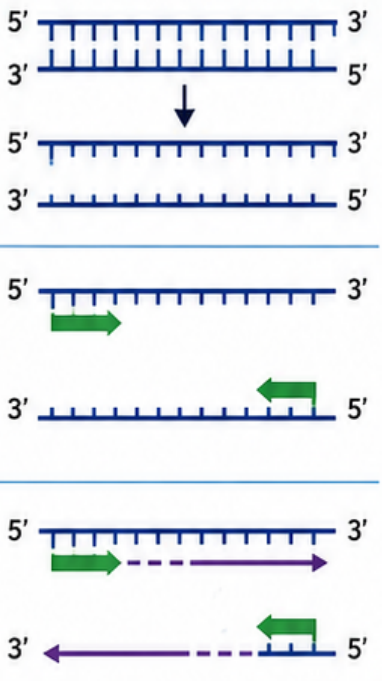
PCR, gel electrophoresis, restriction enzymes, and modern tools

PCR — Polymerase Chain Reaction

1 95°C Denature — heat breaks hydrogen bonds and separates DNA strands.

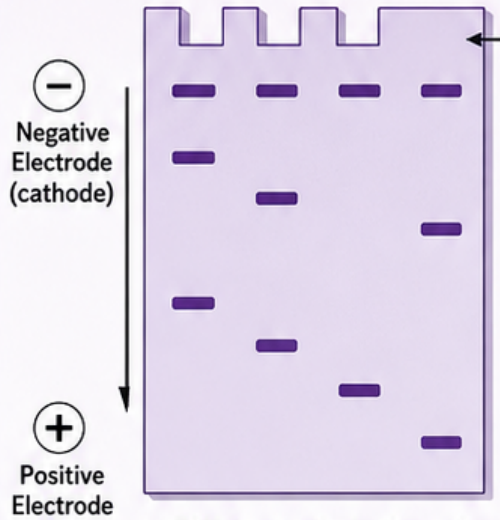
2 55°C Anneal — primers bind complementary sequences flanking the target region.

3 72°C Extend — *Taq* polymerase extends from primers and synthesizes DNA 5′→3′.



- Each cycle doubles DNA, so after *n* cycles there are 2^n copies; about 1 billion copies after ~30 cycles.
- *Taq* polymerase is heat-stable and comes from *Thermus aquaticus*.

Gel Electrophoresis — Read This Right



- DNA is negatively charged and moves toward the positive electrode.
- Smaller fragments travel faster and farther.
- Larger fragments migrate less and remain near the wells.

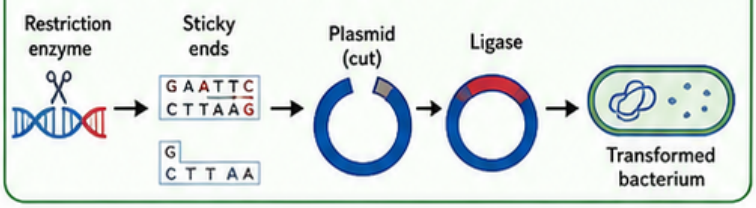
EXAMPLE

← 4000 bp — larger fragment (closer to wells)

← 2000 bp — smaller fragment (farther down the gel)

Restriction Enzymes & Cloning

- Restriction enzymes cut DNA at specific palindromic sequences to create sticky ends.
- Recombinant DNA forms when a foreign gene is inserted into a plasmid cut with the same restriction enzyme.
- Sticky ends anneal and ligase seals.
- Recombinant plasmid transformed into bacteria, which can produce human insulin.
- Selectable markers identify transformed bacteria.



Other Key Biotechnologies

- **DNA sequencing** determines exact nucleotide order; Sanger sequencing uses dideoxy nucleotides.
- **CRISPR-Cas9** uses guide RNA and Cas9 nuclease for targeted gene editing.
- **Bioinformatics** compares gene/protein sequences to find conserved regions and evolutionary relationships.
- **Gene therapy** delivers functional genes to correct disorders.

EXAM SNIPER

- ★ Band closer to wells is larger; band farther down the gel is smaller.
- ★ PCR needs *Taq* polymerase because ordinary DNA polymerases would denature at 95°C.
- ★ First step in making recombinant bacteria: isolate the target gene, cut it and the plasmid with the same restriction enzyme, ligate to form recombinant plasmid, then transform bacteria.

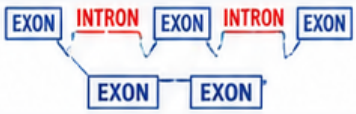
Unit 6 High-Frequency Exam Traps + Checklist

Use this page the night before and the morning of the exam

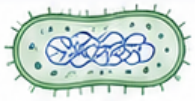
1 High-Frequency Exam Traps

1. 

RNA polymerase reads the **TEMPLATE** strand; mRNA equals the coding strand with **U** instead of **T**.

2. 

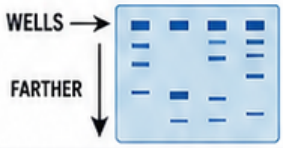
Introns **OUT**, Exons **IN**; alternative splicing uses different exons.

3. 
Coupled transcription and translation happens in **prokaryotes** only.

4. 

Stop codons **UAA/UAG/UGA** do **NOT** encode amino acids; release factors recognize them.

5. 
Point mutations are substitutions and **NEVER** cause frameshifts; frameshifts only come from insertions/deletions.

6. 

In gel electrophoresis, **smaller** fragments travel farther from the wells; **larger** fragments stay near the wells.

7. 
Not all mutations are harmful; mutations generate genetic **variation** for evolution.

2 Pre-Exam 10-Minute Checklist

A. DNA Replication (6.1–6.2)

- ☐ Semiconservative replication
- ☐ DNA pol only 5'→3'
- ☐ Primer required
- ☐ Leading strand continuous
- ☐ Lagging strand has Okazaki fragments and ligase

B. Transcription & Translation (6.3–6.4)

- ☐ RNA pol reads template 3'→5'
- ☐ mRNA = coding strand **T→U**
- ☐ Eukaryotic mRNA processing = 5' cap + poly-A tail + splicing
- ☐ Coupled transcription/translation in **prokaryotes** only
- ☐ **AUG** start, **UAA/UAG/UGA** stop
- ☐ Anticodon antiparallel
- ☐ Ribosome sites **A→P→E**
- ☐ Universal code supports common ancestry

C. Gene Regulation (6.5–6.6)

- ☐ Lactose/allolactose removes repressor
- ☐ No glucose raises cAMP and activates CAP
- ☐ Eukaryotic regulation includes chromatin remodeling, DNA methylation, transcription factors, enhancers/silencers, miRNA
- ☐ All cells have same DNA
- ☐ Differential expression causes specialization
- ☐ HOX genes pattern body plan

D. Mutations & Biotechnology (6.7–6.8)

- ☐ Silent/missense/nonsense/frameshift definitions
- ☐ Substitutions never frameshift
- ☐ PCR cycle **95–55–72** (denature–anneal–extend)
- ☐ Gel small farther
- ☐ Horizontal gene transfer = **transformation**, **transduction**, **conjugation**

Say the process out loud: DNA → RNA → protein → function → phenotype.

Unit 6 Final Cheat Sheet

Central dogma directions, FRQ chain, and AP-style mini problems

RAPID-FIRE MUST-KNOW

DNA replication is semiconservative.

DNA pol only works 5'→3' and needs a primer.

RNA pol reads template 3'→5'; mRNA is coding strand with U instead of T.

AUG = start

A U G

UAA / UAG / UGA = stop

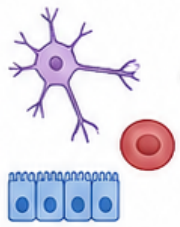
UAA UAG UGA

tRNA anticodon is antiparallel to codon.

ON

Lactose + no glucose = lac operon **MAX ON.**

Lactose (Present) Glucose (Absent)

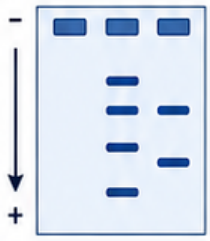


Same DNA, different gene expression = different cell types.

Original: A G C T A

Mutant: A G T T A

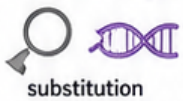
Point mutation substitution never causes frameshift.



Small DNA fragments go farther on a gel.

THE MOLECULAR CHAIN OF EFFECTS — AP'S FAVORITE FRQ

1 Identify mutation type



substitution silent/missense/ nonsense or insertion/deletion frameshift/ in-frame.

2 mRNA change

state the changed codon(s) in the mRNA.

3 Amino acid change

use the codon table to identify the new amino acid or stop.

4 Protein structure

explain how the amino acid change alters shape, charge, polarity, active site, or bonding.

5 Function change

enzyme cannot bind substrate, protein cannot fold, signal peptide lost, etc.

6 Phenotype

explain the organism-level effect.

★ **Note:** AP FRQs award points for each identifiable step, even if an earlier step is wrong.

WORKED MINI MCQ

A Transcription Direction

The template DNA strand is:

3'-TACGGACTTAGG-5'

What is the mRNA sequence produced?

A. 3'-ATGCCUGAAUCC-5'
B. 5'-AUGCCUGAAUCC-3'
C. 5'-UACGGACTTAGG-3'
D. 3'-UACGGACTTAGG-5'

Answer: B. 5'-AUGCCUGAAUCC-3'

Explanation: RNA pol reads the template 3'→5' and synthesizes mRNA 5'→3'. T → A, A → U, C → G, G → C. First codon AUG → first amino acid is Met.

B Lac Operon

A bacterial culture shifts from glucose only to lactose only. Why is there a dramatic increase in lac operon transcription?

A. Lactose hydrolyzes DNA.
B. Allolactose removes the repressor and no glucose raises cAMP so CAP activates transcription.
C. Glucose directly turns on RNA polymerase.
D. Lactose increases the number of ribosomes.

Answer: B

Explanation: Lactose → allolactose binds the repressor (removes it from operator). No glucose → high cAMP → CAP–cAMP binds promoter → strong transcription.

C Gel Electrophoresis

A 6000 bp circular plasmid is cut with EcoRI resulting in two fragments of 4000 bp and 2000 bp. What is true?

A. The 2000 bp band will be closer to the wells than the 4000 bp band.
B. The 4000 bp band will be closer to the wells than the 2000 bp band.
C. The plasmid has exactly two EcoRI cut sites.
D. The gel cannot determine the number of EcoRI sites.

Answer: C

Explanation: Larger DNA fragments migrate less and stay nearer the wells. A single circular plasmid cut into two fragments implies exactly two EcoRI cut sites.

FINAL SPRINT STRATEGY

Trace mutations: DNA → mRNA → AA → protein → phenotype.

Always identify the template strand first.

For lac operon, ask two questions:

☑ Is lactose present?

☑ Is glucose absent?

Connect Unit 6 to:

- Unit 1: nucleotide structure
- Unit 4: signaling
- Unit 5: heredity
- Unit 7: natural selection

Practice FRQ chains out loud. Name each step. Earn every point!

Done with the sheet? Now get marked.

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1

Score

Marked against the published College Board rubric.

2

See

The exact rubric point you gained or dropped, line by line.

3

Practice

Turn around your weak rubric points before exam day.

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