ANSWER KEY. Answers and explanations appear after each question, marked by a bar at the left. Answers written in table cells are in italics.

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DNA and Gene Expression Study Guide

Biology | ANSWER KEY

Show your work with units. Use complete sentences when a question asks you to explain.

Key relationships	**Base pairs**: DNA A-T and G-C; RNA A-U. Hydrogen bonds: A-T 2, G-C 3	**Codons** = nucleotides ÷ 3; amino acids = codons − 1 (stop codon)	**Copies of DNA** after n rounds = 2^n	**Double helix**: one turn = 3.4 nm, about 10 base pairs

Part 1. Discovery of DNA's Structure

1. In a Hershey-Chase style experiment, phages were labeled, mixed with bacteria, blended, and spun (illustrative values).

Label	% in supernatant (virus parts)	% in pellet (bacteria)
Protein (S-35)	88	12
DNA (P-32)	35	65

(a) Write a claim, evidence, and reasoning: which molecule entered the bacteria?

(b) 35% of the P-32 stayed in the supernatant. Does that weaken the claim? Explain.

> (a) **Claim: DNA entered the bacteria, so DNA is the genetic material.** Evidence: 65% of the P-32 (DNA) was in the pellet vs 12% of the S-35 (protein); 88% of the protein label stayed outside. Reasoning: the pellet holds the bacteria, so the label found there entered the cells.
>
> (b) **Not much.** The separation was not perfect, but the trend is strong: far more DNA label than protein label went into the cells.

2. The table shows base percentages in DNA from three sources (sample values).

Source	%A	%T	%G	%C
W	29	30	21	20
X	18	18	32	32
Y	24	33	23	20

(a) Which sources fit Chargaff's pattern? One source is a virus with single-stranded DNA. Which one, and how can you tell?

(b) A double-stranded DNA segment is 1,500 base pairs long. Use the Watson and Crick model to find the number of full turns and its length in nm.

> (a) **W and X** (A ≈ T and G ≈ C, even though W and X differ a lot). **Y** is single-stranded: A 24 vs T 33 and G 23 vs C 20 do not match, because there is no partner strand.
>
> (b) 1,500 ÷ 10 = **150 turns**; 150 × 3.4 nm = **510 nm**.

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3. Recall Griffith's result: heat-killed S bacteria mixed with live R bacteria killed the mouse.

(a) Before mixing, the heat-killed S bacteria are treated with an enzyme that destroys DNA. Predict what happens to the mouse, and explain.

(b) What if the enzyme destroys protein instead? What would the two results together show?

> (a) **The mouse lives.** With the DNA destroyed, nothing is left to change the R bacteria into the disease-causing form.
>
> (b) **The mouse dies**, because the DNA is still there to change the R bacteria. Together: **DNA, not protein, is the substance that changes the trait** (as Avery, MacLeod and McCarty found).

Part 2. Nucleotides and Base Pairing

4. (a) A sample of double-stranded DNA is 36% guanine. Find the percent of C, A, and T.

(b) A DNA segment has 60 base pairs, and 22 of them are G-C pairs. How many nucleotides does it have? How many hydrogen bonds hold the strands together? What percent of its nucleotides are guanine?

> (a) **C = 36%**; A + T = 100% − 72% = 28%, so **A = 14% and T = 14%**.
>
> (b) 2 × 60 = **120 nucleotides**. A-T pairs: 60 − 22 = 38; (38 × 2) + (22 × 3) = 76 + 66 = **142 hydrogen bonds**. Guanine: 22 ÷ 120 × 100 ≈ **18.3%**.

5. (a) Write the complementary strand for G A T T C C A G T C A A. How many hydrogen bonds hold this section together?

(b) Explain why C can never pair with T in the double helix.

(c) A cell has 6 linear chromosomes inside a nucleus, wrapped around histone proteins. Is it a prokaryote or a eukaryote? Explain.

> (a) **C T A A G G T C A G T T**. 5 G-C pairs × 3 + 7 A-T pairs × 2 = 15 + 14 = **29 hydrogen bonds**.
>
> (b) **C and T are both small, single-ring pyrimidines; the pair would be too narrow to fit between the backbones.** Each pair has one large and one small base. (c) **Eukaryote**: linear chromosomes in a nucleus and DNA on histones; a prokaryote usually has one circular chromosome and no nucleus.

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Part 3. DNA Replication

6. (a) An 800 base-pair segment of DNA is copied through 5 rounds of replication. How many new nucleotides are needed for the first round? How many molecules are there at the end, and how many contain no original strand?

(b) After proofreading and repair, about 1 base in a billion is copied wrong. About how many errors would there be when 4 billion bases are copied? What do uncorrected errors become?

> (a) $2 \times 800 =$ **1,600 new nucleotides**. $2^5 =$ **32 molecules**; only 2 hold an original strand, so **30** are all new.
> (b) 4,000,000,000 ÷ 1,000,000,000 = **about 4 errors**. **Uncorrected errors become mutations**, a source of genetic variation.

7. Bacteria grown in heavy nitrogen (N-15) are moved to light nitrogen (N-14), as in the Meselson-Stahl experiment.

(a) Using the semiconservative model, what percent of the DNA molecules are hybrid and what percent are light after 3 rounds of copying?

(b) What bands would the conservative model predict after 1 round? Why does the real result rule it out?

> (a) $2^3 = 8$ molecules; 2 hold an old heavy strand: **25% hybrid, 75% light**.
> (b) **A heavy band and a light band** (the old molecule kept whole, the new one all light). **The real result after 1 round was one middle (hybrid) band, so every molecule had one old and one new strand.**

Part 4. Types of RNA

8. The table shows base percentages in three nucleic acid samples (sample values).

Sample	%A	%T	%U	%G	%C
P	21	0	27	30	22
Q	32	32	0	18	18
R	17	30	0	26	27

(a) Identify each sample as DNA or RNA, and as single- or double-stranded if you can. Explain.

(b) An RNA molecule has 150 nucleotides: 40 A, 35 U, and 38 G. How many C does it have?

> (a) **P: RNA** (has U, no T). **Q: double-stranded DNA** (T, no U; A = T and G = C). **R: DNA, probably single-stranded** (T, no U; A 17 vs T 30 do not match).
> (b) $150 - (40 + 35 + 38) =$ **37 C**.

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9. (a) Write the RNA bases made from the DNA template C G T A A G C T.

(b) A drug stops a cell from making rRNA. Predict what happens to protein production, and explain.

(c) Why does a cell use mRNA copies instead of sending its DNA to the ribosomes?

> (a) **G C A U U C G A** (A pairs with U in RNA). (b) **Protein production stops over time: rRNA and proteins form ribosomes, so no new ribosomes can be built.**
>
> (c) **DNA stays protected in the nucleus as the master copy; one gene can be copied into many mRNAs, and short-lived mRNA lets the cell change which proteins it makes.**

Part 5. Transcription

10. (a) A gene's template strand reads TAC GGT CTA ATG TGA ATT. Write the mRNA and the coding strand.

(b) Where does transcription happen in a eukaryotic cell? Which enzyme builds the mRNA?

> (a) mRNA: **AUG CCA GAU UAC ACU UAA**. Coding strand: **ATG CCA GAT TAC ACT TAA** (same as the mRNA with T for U).
>
> (b) **In the nucleus; RNA polymerase.**

11. (a) The coding region of a gene in a bacterium is 1,503 nucleotides long and ends in a stop codon. How many codons and how many amino acids?

(b) A eukaryotic pre-mRNA is 2,400 nucleotides long. Two introns of 600 and 450 nucleotides are removed. How long is the processed mRNA? If all of it codes for protein and it ends in a stop codon, how many amino acids does the protein have?

> (a) 1,503 ÷ 3 = **501 codons**; 501 − 1 = **500 amino acids**.
>
> (b) 2,400 − 600 − 450 = **1,350 nucleotides**; 1,350 ÷ 3 = 450 codons; 450 − 1 = **449 amino acids**.

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Part 6. Translation

12. Use the genetic code chart (third base: top to bottom U, C, A, G in each box) for questions 12 to 14.

First base	Second base U	Second base C	Second base A	Second base G
U	UUU Phe UUC Phe UUA Leu UUG Leu	UCU Ser UCC Ser UCA Ser UCG Ser	UAU Tyr UAC Tyr UAA Stop UAG Stop	UGU Cys UGC Cys UGA Stop UGG Trp
C	CUU Leu CUC Leu CUA Leu CUG Leu	CCU Pro CCC Pro CCA Pro CCG Pro	CAU His CAC His CAA Gln CAG Gln	CGU Arg CGC Arg CGA Arg CGG Arg
A	AUU Ile AUC Ile AUA Ile AUG Met	ACU Thr ACC Thr ACA Thr ACG Thr	AAU Asn AAC Asn AAA Lys AAG Lys	AGU Ser AGC Ser AGA Arg AGG Arg
G	GUU Val GUC Val GUA Val GUG Val	GCU Ala GCC Ala GCA Ala GCG Ala	GAU Asp GAC Asp GAA Glu GAG Glu	GGU Gly GGC Gly GGA Gly GGG Gly

(a) Translate the mRNA from question 10: AUG CCA GAU UAC ACU UAA. How many amino acids are in the protein?

(b) Write the tRNA anticodons for the second and third codons.

> (a) **Met-Pro-Asp-Tyr-Thr**, then stop: **5 amino acids**. (b) CCA: **GGU**; GAU: **CUA**.

13. (a) A protein has 225 amino acids. How many nucleotides are in its coding region, including the stop codon?

(b) A ribosome reads the mRNA G C A U G U U U G G C U A A C. Where does it start? Write the protein. Why does the start codon matter?

> (a) 225 + 1 = 226 codons; 226 × 3 = **678 nucleotides**.
>
> (b) **At the first AUG (bases 3 to 5)**: AUG UUU GGC UAA = **Met-Phe-Gly**, then stop. **The start codon sets the reading frame; starting anywhere else would give different codons.**

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Part 7. Mutations

14. The normal mRNA is AUG CCA GAU UAC ACU UAA (Met-Pro-Asp-Tyr-Thr).

Mutant	mRNA
1	AUG CCG GAU UAC ACU UAA
2	AUG CCA GAA UAC ACU UAA
3	AUG CCA GAU UAA ACU UAA
4 (G inserted after AUG)	AUG G CCA GAU UAC ACU UAA
5 (GAU deleted)	AUG CCA UAC ACU UAA

(a) Classify mutants 1 to 3 as silent, missense, or nonsense, and give each protein.

(b) Translate mutants 4 and 5. Which one is a frameshift? Explain.

> (a) **1: silent** (CCA to CCG, both Pro; Met-Pro-Asp-Tyr-Thr). **2: missense** (GAU to GAA, Asp to Glu; Met-Pro-Glu-Tyr-Thr). **3: nonsense** (UAC to UAA; Met-Pro-Asp).
>
> (b) 4: AUG GCC AGA UUA CAC UUA A = **Met-Ala-Arg-Leu-His-Leu**, no stop. 5: AUG CCA UAC ACU UAA = **Met-Pro-Tyr-Thr**. **Mutant 4 is a frameshift: one added base regroups every later codon. Mutant 5 removes a whole codon (3 bases), so the frame is kept.**

15. Scientists measured the activity of an enzyme made from four versions of its gene (sample values).

Version	DNA change	Activity (% of typical)
P	Silent substitution	100
Q	Deletion of 3 bases	60
R	Insertion of 1 base	0
S	Missense substitution	85

(a) Write a claim, evidence, and reasoning about which kinds of changes harm the enzyme most.

(b) The version R change happens in a lung cell of one person and in an egg cell of another person. Which one can be passed to children? Why?

> (a) **Claim: the frameshift (R) harms the enzyme most.** Evidence: R 0%, Q 60%, S 85%, P 100%. Reasoning: a frameshift changes every later amino acid; losing one amino acid (Q) or swapping one (S) changes the shape less; a silent change keeps the same protein.
>
> (b) **The egg cell.** Only mutations in gametes (egg or sperm) are inherited; a lung cell's mutation stays in that body.

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