Unit 7 · Genetic Material

ANSWER KEY · FOR TEACHERS

Full marks 32

Give the marks for the points in the marking scheme; an answer in other words that says the same is right.

1 Key words

1. genetics
2. purines
3. ribose
4. phosphodiester
5. antiparallel
6. uracil
7. Okazaki
8. codon

K · 4

Each carries 0.5 mark.

2 Label the diagram

1. topoisomerase
2. helicase
3. SSB proteins
4. lagging strand: Okazaki fragments
5. leading strand
6. DNA ligase

K · 3

Each carries 0.5 mark.

3 Multiple choice

i. **c.** cytosine and uracil — K · 1

Pyrimidines have one ring: **cytosine, thymine and uracil**. Adenine and guanine, with two rings, are the purines. (A memory trick: "**Pure As Gold**", purines are A and G; and the short word "CUT" for the pyrimidines, whose name is the longer one.)

ii. **b.** it is RNA, because uracil is found only in RNA — U · 1

Uracil is found only in **RNA** (DNA has thymine instead), so this virus is an RNA virus. Since RNA is usually single-stranded, its adenine need not equal its uracil: Chargaff's rule doesn't apply.

iii. **c.** to join Okazaki fragments by forming phosphodiester bonds — U · 1

Ligase (from Latin *ligare*, to tie) seals the nicks between neighboring pieces of the new strand with the missing phosphodiester bond. Helicase unwinds, primase makes primers, DNA polymerase adds nucleotides.

iv. **c.** 300 — A · 1

About **10 base pairs** make one turn of the helix, so 30 turns have about $30 \times 10 = \mathbf{300}$ base pairs (and are $30 \times 3.4 = 102$ nm long, a tempting wrong answer).

v. **c.** nothing: both codons stand for glycine — A · 1

GGU and GGC both code for glycine, so the protein is unchanged. Such "silent" changes are common in the third base because the code is **degenerate**. A change in one base never shifts the codons after it (that needs a base added or lost).

4 Short answers

a. MARKING SCHEME — K · 2

- ✓ One correct difference (e.g. double against single strand).
- ✓ A second (e.g. thymine against uracil, or deoxyribose against ribose).

b. MARKING SCHEME — U · 2

- ✓ Degenerate: one amino acid, several codons, with an example (e.g. glycine's four).
- ✓ Unambiguous: one codon, only one amino acid, with an example.

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c. MARKING SCHEME A · 2

✓ mRNA 5′-AUG GGA CUU-3′.
✓ Met – Gly – Leu.

d. MARKING SCHEME U · 3

✓ E. coli grown on ^{15}N, then moved to ^{14}N; DNA separated by density.
✓ One generation: a single intermediate band rules out conservative.
✓ Two generations: intermediate and light bands rule out dispersive.

5 Numerical problem

ANSWER A · 4

- A pairs with T: **T = 20 %**. G + C = 100 − 40 = 60 %, so **G = C = 30 %**.
- Bases = 2 × 3000 = 6000; guanine = 30 % of 6000 = **1800**.
- Length = 3000 × 0.34 nm = **1020 nm** (1.02 μm).
- Turns = 3000 ÷ 10 = **300**.

MARKING SCHEME

✓ T 20 %, G and C 30 % each.
✓ 1800 guanine bases.
✓ Length 1020 nm.
✓ 300 turns.

6 Long answer

ANSWER U · 4

Proposed by **Watson and Crick** in 1953, from Franklin and Wilkins's X-ray photographs and Chargaff's rule:

- **Two polynucleotide strands** twist round a common axis into a **right-handed double helix**; they are **antiparallel** (5′ → 3′ and 3′ → 5′).
- The **sugar–phosphate backbone** is outside, the **bases inside**, stacked like the steps of a spiral staircase.
- Bases pair by **hydrogen bonds**: **A=T** (two bonds), **G≡C** (three), a purine always with a pyrimidine, so the strands are complementary and A = T, G = C (Chargaff).
- The helix is **2 nm** wide; base pairs are **0.34 nm** apart; one turn is **3.4 nm**, about **10 base pairs**, with a major and a minor groove.

MARKING SCHEME

✓ Two antiparallel strands in a right-handed double helix.
✓ Sugar–phosphate backbone outside, bases inside.
✓ Complementary pairing: A=T by two, G≡C by three hydrogen bonds.
✓ Dimensions: 2 nm wide, 0.34 nm per base pair, 3.4 nm and 10 base pairs a turn.

7 Think

ANSWER HA · 3

At present every new strand grows only **5′ → 3′**, so on one template the new strand must grow **away from the fork**: the **lagging strand**, made as **Okazaki fragments**, each needing its own RNA primer and later joined by **ligase**.
If polymerase could add at either end, **both** new strands could grow **towards the fork** continuously, from one primer each. There would be **no lagging strand**, no Okazaki fragments and far fewer primers to remove and gaps to seal: replication would be **continuous**, not semi-discontinuous (but still semi-conservative).

MARKING SCHEME

✓ Now: growth only 5′ → 3′, so one strand is made in Okazaki fragments.
✓ Then: both strands could be made continuously towards the fork.
✓ No Okazaki fragments, fewer primers and ligation; still semi-conservative.

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8 Activity: A comparison chart of DNA and RNA

(not marked)

WHAT STUDENTS SHOULD FIND

DNA: two strands in a double helix; deoxyribose; A, G, C, T; nucleus (a little in mitochondria and plastids); stores genetic information. RNA: usually one strand; ribose; A, G, C, U; made in the nucleus, works in the cytoplasm and ribosomes; uses the information to make proteins. **Thymine's** color appears only in DNA and **uracil's** only in RNA.

Marks by level	Knowledge	Understanding	Application	Higher ability	Total
Marks	10	11	8	3	**32**

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