

DNA replication: practice questions

8 questions • 25 marks • mark scheme at the back

For IB Diploma Biology, Standard Level and Higher Level (first assessment 2025). **HL only** is additional higher level content, for HL students only.

Name

Total / 25

1 PAPER 1A STYLE

[1 mark]

What is meant by semi-conservative replication of DNA?

- A. ☐ Half of the DNA in a cell is copied before each division.
- B. ☐ Each new DNA molecule consists of one original strand and one new strand.
- C. ☐ Each new strand is made of sections of old and new nucleotides.
- D. ☐ One new DNA molecule is entirely original and the other is entirely new.

2 PAPER 1A STYLE

[1 mark]

Why do DNA fragments move towards the positive electrode during gel electrophoresis?

- A. ☐ The bases are positively charged.
- B. ☐ The deoxyribose sugars are attracted to the positive electrode.
- C. ☐ The phosphate groups give DNA a negative charge.
- D. ☐ Hydrogen bonds between bases carry a negative charge.

3 PAPER 1A STYLE

[1 mark]

HL only

Which enzyme removes RNA primers and replaces them with DNA during replication in prokaryotes?

- A. ☐ DNA primase
- B. ☐ DNA polymerase I
- C. ☐ DNA polymerase III
- D. ☐ DNA ligase

A student set up a PCR to amplify a 400 base pair region of a plant gene. The thermal cycler was programmed as shown in the table (practice data). (a) State what happens to the DNA during stage 1. [1] (b) Explain why the temperature is lowered in stage 2. [1] (c) Explain why Taq polymerase, rather than a DNA polymerase from a human cell, is used in this reaction. [2] (d) The reaction started with 20 copies of the target region. Calculate the number of copies after the full programme, assuming each cycle doubles the number of copies. [1]

PCR programme used by the student			
Stage	Temperature / °C	Time / s	Number of cycles
1	95	30	25
2	55	30	25
3	72	45	25

Answer =

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5 PAPER 1B STYLE

[5 marks]

DNA profiling was used in a paternity case. Three STR regions (loci) were amplified by PCR and the fragment lengths were found by gel electrophoresis. The table shows the fragment lengths, in base pairs, for a mother, her child and three men (practice data). (a) Identify which man could be the father. [1] (b) Using the data, explain why the other two men are excluded. [2] (c) Explain why several STR loci, rather than one, are used in DNA profiling. [2]

Fragment lengths / base pairs			
Person	Locus A	Locus B	Locus C
Mother	120, 150	210, 230	300, 330
Child	120, 180	230, 250	300, 310
Man 1	150, 200	250, 260	310, 340
Man 2	140, 180	220, 250	310, 320
Man 3	160, 190	240, 270	330, 350

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6 PAPER 2A STYLE

[3 marks]

Outline the roles of helicase and DNA polymerase in DNA replication.

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PAPER 2B STYLE

HL only

[illegible]

PAPER 2A STYLE

HL only

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Mark scheme

One mark for each point unless a maximum is given. Words in brackets are not needed for the mark.

1. [1]

B B;

2. [1]

C C;

3. [1] **HL only**

B B;

4. [5]

- (a) hydrogen bonds (between bases) break / strands separate / DNA denatures;
- (b) allows primers to bind/anneal to (complementary sequences at the ends of) the target region / single strands;
- (c) Taq polymerase is heat stable / not denatured at 95 °C;
- (c) human DNA polymerase would be denatured (in stage 1 of the first cycle) / Taq has optimum temperature of about 72 °C so works in stage 3;
- (c) Taq does not need to be added again each cycle; Accept from *Thermus aquaticus*, a hot-spring bacterium, as context only if linked to heat stability
- (d) $20 \times 2^{25} = 671\,088\,640$ / 6.7×10^8 (copies);
- max 5

5. [5]

- (a) Man 2;
- (b) child's non-maternal fragments are 180 (A), 250 (B) and 310 (C) / fragments not present in the mother must come from the father;
- (b) Man 1 lacks the 180 bp fragment at locus A;
- (b) Man 3 lacks the non-maternal fragments at all three loci / has none of 180, 250, 310;
- (c) one locus may be shared by chance by unrelated people / many people have the same allele at one locus;
- (c) more loci reduce the probability of a false/random match / increase reliability;
- (c) a match at all loci makes the conclusion much more certain; OWTTE
- max 5

6. [3]

- helicase unwinds the double helix;
- helicase breaks hydrogen bonds between (complementary) bases / separates the strands;
- (each) separated strand acts as a template;
- DNA polymerase adds/links free nucleotides to form a new strand;
- DNA polymerase follows complementary base pairing (A-T, C-G) with the template;
- max 3

7. [7] HL only

- the two strands of DNA are antiparallel / run in opposite directions;
- DNA polymerase adds nucleotides only to the 3' end of a strand / synthesis is 5' to 3';
- helicase unwinds DNA at the replication fork;
- DNA primase synthesises RNA primers;
- DNA polymerase III adds nucleotides to the 3' end of the primer;
- leading strand is synthesised continuously (towards the replication fork);
- leading strand needs a primer only once;
- lagging strand is synthesised discontinuously / away from the replication fork;
- lagging strand made as (short) Okazaki fragments;
- each Okazaki fragment needs its own RNA primer / primers needed repeatedly;
- DNA polymerase I removes RNA primers and replaces them with DNA;
- DNA ligase joins Okazaki fragments / seals gaps in the sugar-phosphate backbone;
- max 7

8. [2] HL only

- detects a mismatched base / incorrectly paired nucleotide (at the 3' end of the new strand);
- removes the nucleotide from the 3' end / terminal;
- replaces it with a correctly (complementary) matched nucleotide;
- max 2