



Molecules (Continuity and change) practice questions

24 questions • 72 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 / 72

DNA replication **Spec D1.1**

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 =

.....

.....

.....

.....

.....

.....

.....

.....

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

.....

.....

.....

.....

.....

.....

.....

.....

6 PAPER 2A STYLE**[3 marks]**

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

.....

.....

.....

.....

.....

7

HL only

[7 marks]

[illegible]

8

HL only

[2 marks]

.....

.....

.....

.....

Spec D1.2

9

During

[1 mark]

A. ☐ Thymine
B. ☐ Uracil
C. ☐ Guanine
D. ☐ Cytosine

10

The co

[1 mark]

A. ☐ Universality
B. ☐ It is a triplet code
C. ☐ Degeneracy
D. ☐ It is non-overlapping

11 PAPER 1A STYLE

[1 mark]

HL only

During elongation, which site of the ribosome holds the tRNA attached to the growing polypeptide?

- A. ☐ A site
- B. ☐ E site
- C. ☐ P site
- D. ☐ The small subunit binding site

12 PAPER 1B STYLE

[5 marks]

The table shows part of the mRNA codon table. A short section of mRNA has the sequence AUG UUU CAU GAG UGG UAA. (a) Deduce the sequence of amino acids coded by this mRNA. [2] (b) Deduce the base sequence of the DNA template strand for the first two codons. [1] (c) A mutation changes the fourth codon from GAG to GUG. Using the table, state the effect on the polypeptide and suggest how this could affect the protein's function. [2]

Part of the mRNA codon table	
Codon	Amino acid
AUG	Met (start)
UUU	Phe
CAU	His
GAG	Glu
GUG	Val
UGG	Trp
UAA	stop

13 PAPER 2A STYLE

[2 marks]

Explain why the genetic code must be a triplet code.

14

[6 marks]

Describe how a polypeptide is elongated during translation.

[illegible]

15

[4 marks]

HL only

Outline how pre-mRNA is modified in eukaryotic cells, and how this allows one gene to code for more than one polypeptide.

[illegible]

16

[4 marks]

HL only

(a) Outline the two-stage modification of pre-proinsulin to insulin. [3] (b) State why cells constantly break down proteins in proteasomes. [1]

[illegible]

Mutation and gene editing Spec D1.3

17

PAPER 1A STYLE

[1 mark]

Which mutation is most likely to cause a frameshift?

- A. ☐ Substitution of one base
- B. ☐ Deletion of three adjacent bases
- C. ☐ Insertion of one base
- D. ☐ Insertion of six adjacent bases

18

PAPER 1A STYLE

[1 mark]

A base substitution changes the codon GAA to GAG, but the polypeptide is unchanged. What explains this?

- A. ☐ The genetic code is universal.
- B. ☐ The genetic code is degenerate.
- C. ☐ The mutation occurred in an intron.
- D. ☐ Proofreading removed the change.

19

PAPER 1B STYLE

[6 marks]

Samples of the same bacterial culture were exposed to ultraviolet (UV) light for different times. After exposure, the frequency of mutants unable to make a particular amino acid was measured (practice data). (a) Describe the relationship between exposure time and mutant frequency. [2] (b) Calculate how many times greater the mutant frequency is at 40 s than at 0 s. [1] (c) Suggest why mutants occur in the sample with no UV exposure. [1] (d) Explain how UV light increases the frequency of mutation. [2]

Mutant frequency after UV exposure	
Exposure time / s	Mutants per 10 ⁶ surviving cells
0	2
10	15
20	38
30	61
40	80

[2 marks]

.....

.....

.....

.....

[5 marks]

[illegible]

[4 marks]

[illegible]

[3 marks]

[illegible]

HL only

What is the purpose of producing a knockout mouse?

- A. ☐ To increase the expression of a gene to study its product
- B. ☐ To investigate the function of a gene by making it inoperative
- C. ☐ To produce a clone of a mouse with a useful mutation
- D. ☐ To insert a human gene so the mouse makes a human protein

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

9. [1]

B B;

10. [1]

C C;

11. [1] HL only

C C;

12. [5]

- (a) Met – Phe – His – Glu – Trp;
- (a) translation ends at UAA / stop codon (no amino acid added); Award [1] for four correct amino acids in order
- (b) TAC AAA; Accept 3'-TAC AAA-5' or 5'-AAA CAT-3'
- (c) glutamic acid replaced by valine (at that position) / one amino acid changed;
- (c) different R group / hydrophobic instead of charged, so the polypeptide folds differently / changes shape;
- (c) protein may lose function / function altered, e.g. as in haemoglobin S; OWTTE
- max 5

13. [2]

- there are 20 (types of) amino acids (to be coded for) and 4 bases;
- a doublet code gives only $4^2 = 16$ combinations, which is not enough;
- a triplet code gives $4^3 = 64$ combinations, which is enough (with some to spare for start/stop or degeneracy);
- max 2

14. [6]

- mRNA binds to the small subunit of the ribosome;
- mRNA is read in codons / triplets of bases;
- tRNA carries a specific amino acid;
- tRNA anticodon pairs with the complementary codon on mRNA;
- by hydrogen bonding / complementary base pairing (A-U, C-G);
- two tRNAs bind (to the large subunit) at the same time;
- a peptide bond forms between the amino acid and the growing polypeptide;
- the polypeptide is transferred to the (amino acid on the) second tRNA;
- the ribosome moves along the mRNA by one codon;
- the first tRNA (without an amino acid) is released;
- process repeats, adding one amino acid at a time in the order set by the codons;
- max 6

15. [4] HL only

- introns are removed;
- exons are spliced/joined together (to form mature mRNA);
- 5' cap added;
- 3' polyA tail added;
- cap and tail stabilise the mRNA;
- alternative splicing joins different combinations of exons;
- producing different polypeptides from the same gene;
- max 4

16. [4] HL only

- pre-proinsulin is the polypeptide produced by translation (at the rough ER);
- stage 1: signal sequence/peptide removed to give proinsulin;
- proinsulin folds and disulfide bonds form;
- stage 2: C-peptide removed / cut out;
- leaving A and B chains linked by disulfide bonds (active insulin);
- (a) [max 3]
- (b) sustaining a functional proteome requires constant breakdown (and synthesis) of proteins / removes damaged, misfolded or unneeded proteins / amino acids are recycled for new protein synthesis;
- max 4

17. [1]

C C;

18. [1]

B B;

19. [6]

- (a) mutant frequency increases as exposure time increases / positive correlation;
- (a) increase is roughly linear / steady between 10 and 40 s / rises from 2 to 80 per 10^6 cells; Accept use of data
- (b) $80 \div 2 = 40$ (times);
- (c) spontaneous mutations / errors in DNA replication or repair (not caused by UV);
- (d) UV is a mutagen / mutagenic radiation;
- (d) UV changes the structure of DNA / causes adjacent bases to bond together;
- (d) leading to incorrect base pairing / changed base sequence when DNA is replicated or repaired;
- (d) longer exposure causes more DNA damage, so more mutations;
- max 6

20. [2]

- germ-cell mutation can be inherited / passed to offspring, whereas somatic mutation is not inherited;
- germ-cell mutation will be in every cell of the offspring, whereas a somatic mutation is only in cells descended from the mutated cell;
- somatic mutation can cause cancer (in the individual);
- max 2

21. [5]

- mutation is the original source of all genetic variation;
- mutation creates new alleles;
- meiosis/sexual reproduction only recombines existing alleles;
- mutations occur at random / not in response to need;
- most mutations are harmful or neutral (for an individual);
- some mutations give an advantage in a particular environment;
- individuals with advantageous alleles are more likely to survive and reproduce;
- so these alleles increase in frequency in the population over generations;
- without mutation there would be no (new) variation for selection to act on;
- max 5

22. [4] HL only

- guide RNA made with a base sequence complementary to the target sequence;
- guide RNA combined with Cas9;
- guide RNA binds to the target DNA by complementary base pairing;
- Cas9 cuts (both strands of) DNA at the target site;
- repair of the cut can disable the gene / introduce small insertions or deletions;
- a supplied DNA template can be used in repair to insert/correct a sequence;
- named example, e.g. editing blood stem cells so they make fetal haemoglobin to treat sickle-cell disease;
- max 4

23. [3] HL only

- (a) a sequence that remains identical or similar over long periods of evolution / across distantly related groups;
- (b) the gene product has strict functional requirements, so mutations make it less functional;
- (b) (and) natural selection removes such mutations;
- (b) the sequence has a slower rate of mutation;
- max 3

24. [1] HL only

B B;