HELICATE · AS AND A-LEVEL BIOLOGY · TOPIC BANK

3.1.5 Nucleic acids

Mark scheme

Version 1 · 1 October 2026

TOTAL MARKS	QUESTIONS
46	6

How to use this mark scheme

;	Separates marking points. Each semicolon marks the end of one creditable point, and each point is worth one mark.
;;	Two marks for this answer (used for calculations).
/	Alternative words or phrases that are credited for the same point.
OR	An alternative answer for the same mark.
( )	Words in brackets are not needed to gain the mark.
max	More marking points are listed than marks available. Award up to the number of marks shown.
Accept	An alternative answer that gains credit.
Reject	A wrong answer. It does not gain credit and cancels a correct point it contradicts.
Ignore	Neither credited nor penalised. Mark the rest of the answer.
ECF	Error carried forward: credit correct working that uses an earlier wrong answer.
AO	Assessment objective: AO1 knowledge and understanding; AO2 applying knowledge; AO3 analysing, interpreting and evaluating.

Where an answer is correct but not listed, credit it if it is biologically accurate and answers the question at the depth the marks require. Right + wrong = wrong: a contradiction cancels a correct point.

Structure of DNA and RNA 3.1.5.1

Question	Marking guidance	Mark	Comments
01.1	1. Polymer of nucleotides OR polynucleotide; 2. Each nucleotide is made of deoxyribose, a phosphate (group) and a (nitrogen-containing/organic) base; 3. Phosphodiester bonds between (adjacent) nucleotides OR between the phosphate of one nucleotide and the deoxyribose of the next; 4. Two strands held together by hydrogen bonds (between bases); 5. (Specific/complementary) base pairing: adenine with thymine **and** cytosine with guanine; 6. Double helix OR the two strands are twisted (around each other);	**5 max** (5 × AO1)	1. **Accept** chain for polymer 2. **Accept** phosphoric acid for phosphate; all three components are needed 2. **Reject** ribose 3. **Accept** ester or covalent bond only when placed between adjacent nucleotides 3. **Reject** phosphodiester bonds between bases or between the two strands 4. **Accept** H bonds 5. Full names are needed. Ignore letters (A, T, C, G) used alone 5. **Reject** adenosine, thiamine or cysteine as base names 6. **Reject** helix unless double/two strands is also given **Ignore** number of hydrogen bonds, purines/pyrimidines and strand direction (correct but not needed) **Credit** correctly annotated diagrams for equivalent points

Question	Marking guidance	Mark	Comments
01.2	1. Snap connectors for hydrogen bonds (between complementary bases) because the two strands separate/these bonds are broken (by (DNA) helicase) during replication OR because hydrogen bonds are weak; 2. Fixed connectors for phosphodiester bonds (between adjacent nucleotides) because they are (strong) covalent bonds OR so each strand/the sequence of bases stays intact (to act as a template);	**2** (2 × AO2)	Each point needs the connector, the bond **and** a reason 1. **Reject** hydrogen bonds are hydrolysed 2. **Accept** covalent bonds between (adjacent) nucleotides for phosphodiester bonds 2. **Reject** phosphodiester bonds between bases **Ignore** covalent bonds within a nucleotide (the question asks about bonds between nucleotides and between strands)

Question	Marking guidance	Mark	Comments
01.3	Use one colour of rectangle to represent uracil instead of thymine, make the pentagons represent ribose, and build only one strand;	**1** (1 × AO2)	

Question	Marking guidance	Mark	Comments
02.1	1. Only four types of nucleotide/base in DNA compared with 20 (types of) amino acids in proteins, so proteins (seemed to) allow far more variety/possible sequences; 2. (Roughly) equal amounts of each base in every species suggested DNA was the same/a simple repeating sequence in all species, so it could not carry different (genetic) information;	**2** (2 × AO3)	1. **Accept** DNA seemed too simple/to have too little variety to code for (so many) different proteins 2. **Accept** DNA did not seem to differ between species **Ignore** DNA is a small molecule

Question	Marking guidance	Mark	Comments
02.2	0.75;	**1** (1 × AO2)	**Accept** 0.748 **Reject** 1.34 (inverted ratio)

Question	Marking guidance	Mark	Comments
02.3	1. Bases are not present in equal amounts/(about) 25% each, eg in species P adenine is 30.2% but guanine is 19.8%; 2. Proportions of bases/ratio differ between species (1.52 in P, 0.75 in Q), so the base sequence (of DNA) differs between species, so DNA could carry different (genetic) information;	**2** (2 × AO3)	1. **Accept** any correct comparison of an unequal pair of bases within P or within Q, using figures from the table 2. **Accept** correct comparison of one base between P and Q, eg adenine 30.2% compared with 21.4%, for the difference between species 2. **Accept** 'DNA is not the same repeating sequence in every species' for the base sequence differs 2. The link to carrying (different) information is needed for the mark

Question	Marking guidance	Mark	Comments
02.4	Correct answer for 2 marks: 22.7 (%);; Accept for 1 mark, thymine = 27.3 (%) **OR** adenine + thymine = 54.6 (%) **OR** guanine + cytosine = 45.4 (%)	**2** (2 × AO2)	**Reject** 72.7 or 24.2 (complementary pairing not used)

Question	Marking guidance	Mark	Comments
02.5	1. In P and Q, (percentage of) adenine = thymine **and** guanine = cytosine, but in V they are not equal, eg thymine 32.8% but adenine 24.6%; 2. DNA of V is single-stranded/one polynucleotide (chain), so its bases are not in complementary pairs;	**2** (2 × AO3)	1. **Accept** adenine is not equal to thymine in V, with figures, for the pattern 2. **Accept** no complementary strand/not a double helix 2. **Reject** V contains RNA (the table shows thymine) **Ignore** reference to mutation or experimental error

Question	Marking guidance	Mark	Comments
03.1	Nucleotides containing ribose and one of adenine, cytosine, guanine or uracil;	**1** (1 × AO1)	Ribosomes are formed from RNA and protein; the ribonuclease hydrolyses only the RNA

Question	Marking guidance	Mark	Comments
03.2	1. DNA has deoxyribose **and** RNA has ribose; 2. DNA has thymine **and** RNA has uracil; 3. DNA is double-stranded/a double helix **and** RNA is single-stranded; 4. DNA is longer/has more nucleotides **and** RNA is (relatively) short/has fewer nucleotides;	**3 max** (3 × AO1)	Must be comparisons 2. Full names needed. Ignore T and U 3. **Accept** two polynucleotide chains held by hydrogen bonds compared with one chain 3. **Accept** single helix for single-stranded 4. **Ignore** large and small **Ignore** 'RNA has no hydrogen bonds' (RNA in ribosomes contains base pairs)

Question	Marking guidance	Mark	Comments
03.3	1. Active site (of the ribonuclease) is complementary to/specific to (the shape of) RNA; 2. DNA has a different shape (eg contains deoxyribose/is a double helix), so it does not bind to/fit the active site OR no enzyme–substrate complexes form;	**2** (2 × AO2)	2. **Accept** DNA is not complementary to the active site **Reject** active site has the same shape as RNA

DNA replication 3.1.5.2

Question	Marking guidance	Mark	Comments
04.1	It joins adjacent DNA nucleotides in condensation reactions;	**1** (1 × AO1)	

Question	Marking guidance	Mark	Comments
04.2	1. Hydrogen bonds between (complementary) bases are not broken OR double helix is not unwound; 2. Strands do not separate, so no bases are exposed/no template is available for (free DNA) nucleotides to pair with;	**2** (2 × AO2)	1. **Reject** hydrogen bonds not hydrolysed 2. **Accept** no complementary base pairing with free nucleotides

Question	Marking guidance	Mark	Comments
04.3	Correct answer for 2 marks: 40 (minutes);; Accept for 1 mark, 2400 (s) **OR** 80 (minutes) (both directions not taken into account)	**2** (2 × AO2)	**Accept** 2.4×10^3 s for 2400 s

Question	Marking guidance	Mark	Comments
04.4	Correct answer for 2 marks: 2688;; Accept for 1 mark, 896 (thymine in one copy of the section/used in the first round)	**2** (2 × AO2)	896 are used in the first round and 1792 in the second 3584 (original strands counted as new) gains 1 mark only, for 896

Question	Marking guidance	Mark	Comments
05	1. (DNA) helicase unwinds the double helix; 2. (DNA helicase) breaks hydrogen bonds between complementary bases/between the two strands; 3. Both strands act as templates; 4. Free DNA nucleotides are attracted to exposed bases and pair by complementary base pairing, adenine with thymine **and** cytosine with guanine; 5. DNA polymerase joins adjacent nucleotides (of the new strand); 6. In condensation reactions, forming phosphodiester bonds; 7. Each new DNA molecule has one original strand and one new strand; 8. New strand on strand 1 is ATGCCTAG **and** new strand on strand 2 is TACGGATC, so each new strand is identical to the strand that was originally paired with its template;	**6 max** (5 × AO1) (1 × AO2)	**Max 5** from points 1–7 2. **Reject** hydrogen bonds hydrolysed 4. **Accept** A–T and G–C for this point only 5. **Reject** DNA polymerase forms hydrogen bonds/joins complementary bases/joins base pairs 5. **Reject** 'nucleotide bases' for nucleotides 6. **Reject** phosphodiester bonds between bases 7. **Accept** semi-conservative, if described 8. **Accept** base letters for the sequences 8. **Accept** each new molecule has the same base sequence as the original, with both sequences given **Ignore** DNA ligase, primers, strand direction and number of hydrogen bonds (correct but not needed) **Ignore** RNA polymerase and transcription

Evaluating the model of DNA replication 3.1.5.2

Question	Marking guidance	Mark	Comments
06.1	So that (both strands of) all the DNA contained only ^{14}N/was light, so any ^{15}N/heavy DNA must be in strands made after the move;	**1** (1 × AO3)	**Accept** so the starting density of all the DNA is known/the same **Ignore** 'to get enough bacteria'

Question	Marking guidance	Mark	Comments
06.2	1. Generation 1: light 50, intermediate 0, heavy 50; 2. Generation 2: light 25, intermediate 0, heavy 75;	**2** (2 × AO2)	All three values in a row are needed for each mark **Accept** a blank or dash for 0

Question	Marking guidance	Mark	Comments
06.3	1. Generation 1: all DNA is intermediate/no light or heavy DNA, so Model 1 is not supported (it predicts 50% light and 50% heavy); 2. Generation 1 results fit both Model 2 and Model 3 (both predict all DNA is intermediate), so generation 1 alone cannot separate them; 3. Generation 2: DNA is at two densities/some DNA is (fully) heavy, so Model 2 is not supported (it predicts all DNA at a single density between intermediate and heavy); 4. Generations 2 and 3 fit Model 3: about 50% intermediate and 50% heavy, then about 25% intermediate and 75% heavy (observed 52 : 48 and 27 : 73); 5. Model 3/semi-conservative is supported, but only one type of organism/bacterium was tested OR no repeats/variation shown;	**4 max** (4 × AO3)	**Max 3** if Model 1 or Model 2 is not rejected with a reason 4. **Accept** (in Model 3) each molecule keeps one original strand, so the number of molecules with a ^{14}N strand stays the same while the total doubles 4. **Accept** the description or name 'semi-conservative' for Model 3 Do not require the names conservative or dispersive; credit them if used correctly

Question	Marking guidance	Mark	Comments
06.4	Not all bacteria had divided exactly twice OR the bacteria did not all divide at the same time OR (random) error in measuring the amount of DNA at each density;	**1** (1 × AO3)	**Accept** some bacteria divided more or fewer times **Ignore** 'human error' unqualified

Question	Marking guidance	Mark	Comments
06.5	Correct answer for 2 marks: light 12.5, intermediate 87.5, heavy 0;; Accept for 1 mark, heavy 0 **and** light and intermediate both present but with incorrect percentages **OR** 12.5% of strands light **and** 87.5% of strands heavy shown (eg 25 light strands and 175 heavy strands per 100 molecules)	**2** (2 × AO2)	**Accept** 12 or 13 for 12.5 and 87 or 88 for 87.5 if the values total 100

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