HELICATE · AS AND A-LEVEL BIOLOGY · TOPIC BANK

3.4.1 DNA, genes and chromosomes

Mark scheme

Version 1 · 9 October 2026

TOTAL MARKS	QUESTIONS
48	8

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.

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DNA in prokaryotic and eukaryotic cells 3.4.1

Question	Marking guidance	Mark	Comments
01.1	Shape of DNA molecule: Circular Associated with histones: No Length compared with nuclear DNA: Shorter;	**1** (1 × AO1)	

Question	Marking guidance	Mark	Comments
01.2	1. (Bacterial) DNA is double-stranded OR is a double helix; 2. Most of the DNA is (in) a (single, large) circular DNA molecule (free in the cytoplasm) OR plasmids are only small/extra (circular) DNA molecules (not present in all bacteria); 3. (Bacterial) DNA is not associated with histones/proteins;	**3** (3 × AO1)	Points may be given in any order 2. **Ignore** 'loop' alone; circular is needed for the first alternative 2. **Reject** any answer that still states bacteria have DNA only in plasmids 2. **Accept** nucleoid for the (single) circular DNA molecule, but it is not required 3. **Reject** 'bacterial DNA is associated with fewer histones' **Ignore** correct statements about nuclear DNA that do not correct an error

Question	Marking guidance	Mark	Comments
02.1	1. To hydrolyse/remove DNA outside the organelles OR to remove nuclear DNA (from broken nuclei) that contaminated the fractions; 2. Enzyme D cannot cross the (envelope/double) membrane of intact organelles, so DNA inside them is not hydrolysed; 3. So all the DNA extracted (from each fraction) comes from inside the chloroplasts/mitochondria;	**2 max** (2 × AO3)	1. **Accept** 'to remove contamination by other DNA' 2. **Accept** enzyme D is washed out so it cannot hydrolyse the organelle DNA once the organelles are broken open **Ignore** 'to make it a fair test' unqualified

Question	Marking guidance	Mark	Comments
02.2	1. Nuclear DNA is linear, so it has (free) ends, so enzyme E can hydrolyse it/remove nucleotides; 2. Chloroplast and mitochondrial DNA is circular, so it has no free ends, so (most of it) is not hydrolysed by enzyme E; 3. Histones (only) in sample 1 because nuclear DNA is associated with histones/proteins, but chloroplast and mitochondrial DNA is not; 4. The small hydrolysis (3–4%) of chloroplast/mitochondrial DNA is because some circular molecules were broken (during extraction), so they had free ends;	**3 max** (1 × AO1) (2 × AO2)	1. and 2. The shape **and** its link to free ends are both needed 2. **Ignore** 'loop' alone; circular is needed 3. **Accept** nuclear DNA forms chromosomes (with histones) **Reject** chloroplast/mitochondrial DNA is single-stranded

Question	Marking guidance	Mark	Comments
02.3	1. Shows (chloroplast DNA) is hydrolysed by enzyme E once it has (free) ends/once the circle is cut/opened; 2. So the result for sample 2 is due to the DNA being circular/having no free ends, not to another property of chloroplast DNA OR not because something in the sample stops enzyme E working;	**2** (2 × AO3)	**Accept** 'as a control' only if the purpose is explained 2. **Accept** shows that the base sequence/nucleotides of chloroplast DNA can be hydrolysed by enzyme E

Question	Marking guidance	Mark	Comments
02.4	Chromosome;	**1** (1 × AO1)	**Accept** chromatin **Ignore** chromatid **Reject** centromere, nucleosome, nucleolus

Question	Marking guidance	Mark	Comments
02.5	Correct answer for 2 marks: 51 (μm);; Accept for 1 mark, 5.1×10^4 (nm) OR 51 000 (nm)	**2** (2 × AO2)	**Accept** 5.1×10^1 μm for 2 marks **Accept** 0.051 mm for 1 mark only (answer not in μm)

Genes and the genetic code 3.4.1

Question	Marking guidance	Mark	Comments
03.1	Locus;	**1** (1 × AO1)	**Accept** loci **Reject** allele, gene, triplet, chromosome

Question	Marking guidance	Mark	Comments
03.2	Some genes code for a functional RNA, such as tRNA, instead of a polypeptide;	**1** (1 × AO1)	

Question	Marking guidance	Mark	Comments
03.3	In all organisms, the same triplet codes for the same amino acid;	**1** (1 × AO1)	

Question	Marking guidance	Mark	Comments
04.1	1. (Overlapping code:) each base is part of (up to) three triplets, so changing one base changes (up to) three triplets, eg base 5 is in triplets 3, 4, 5; 2. (Non-overlapping code:) each base is part of only one triplet, so only one triplet (and so only one amino acid) can change;	**2** (2 × AO2)	1. A correct example from the figure can be used instead of the general statement 1. and 2. Ignore 'amino acid is produced/formed'; triplets code for amino acids **Ignore** references to the code being degenerate

Question	Marking guidance	Mark	Comments
04.2	1. No strain had more than one amino acid changed OR 61 strains had (only) one amino acid changed; 2. In an overlapping code, (many) substitutions would change two or three (adjacent) amino acids, so the code is (likely to be) non-overlapping; 3. 19 strains had a base substituted (within a triplet) but no change in the amino acid sequence; 4. So the new triplet codes for the same amino acid as the original triplet OR more than one triplet codes for the same amino acid, so the code is degenerate;	**4** (4 × AO3)	2. **Accept** each base is (part of) only one triplet, if linked to the data 4. **Reject** 'the same amino acid is produced/formed'; the triplet must code for the amino acid 4. **Ignore** 'DNA is degenerate'; the idea of more than one triplet for an amino acid is needed **Ignore** references to introns (the gene is in a bacterium and the base substituted was within a triplet)

Question	Marking guidance	Mark	Comments
04.3	32;	**1** (1 × AO2)	1 × 4 × 2 × 4 = 32

Exons, introns and non-coding DNA 3.4.1

Question	Marking guidance	Mark	Comments
05.1	Correct answer for 2 marks: 0.97 (%);; Accept for 1 mark, 3.0×10^7 (base pairs in exons) **OR** 0.968 (%) (not to two significant figures)	**2** (2 × AO2)	**Accept** 9.7×10^{-1} (%) **Reject** 0.0097 for 2 marks (fraction not converted to a percentage); award 1 mark

Question	Marking guidance	Mark	Comments
05.2	1. Bacterial genes have no introns OR human genes contain introns (which are non-coding); 2. Bacterial DNA has little/no non-coding DNA between genes OR human DNA has many non-coding (multiple) repeats (of base sequences) between genes;	**2** (2 × AO2)	2. **Accept** bacterial genes are closer together 2. **Accept** telomeres for non-coding repeats in human DNA, but it is not required **Ignore** 'bacterial DNA is shorter' or 'bacteria have fewer genes' **Reject** bacterial DNA is single-stranded

Question	Marking guidance	Mark	Comments
06.1	Exons code for (a sequence of) amino acids/the amino acid sequence (of the polypeptide) but introns do not OR but introns are non-coding;	**1** (1 × AO1)	Both halves of the contrast are needed for the mark **Ignore** 'exons code for a polypeptide/protein' alone **Accept** exons code for primary structure **Do not credit** 'introns do not code for an amino acid' (singular) **Ignore** 'introns are removed' or 'introns are junk DNA' **Reject** introns are found between genes

Question	Marking guidance	Mark	Comments
06.2	Correct answer for 2 marks: 85.4 (%);; Accept for 1 mark, introns total 6 147 (base pairs) **OR** 14.6 (%) (percentage that is exons) **OR** 85.375 OR 85.38 (%) (not to three significant figures)	**2** (2 × AO2)	

Question	Marking guidance	Mark	Comments
06.3	1. The human gene is about 6.8 times as long (7200 ÷ 1062), so the first part of the statement is correct; 2. Most of the human gene/85% is introns, which are non-coding/do not code for amino acids; 3. Only the exons code for amino acids, and they total 1053 base pairs; 4. A triplet/three bases codes for one amino acid, so the human exons code for (up to) 351 amino acids; 5. The bacterial gene has no introns, so all of it codes for amino acids, (up to) 354 amino acids; 6. So both enzymes contain a similar number of amino acids, and the student's conclusion is wrong;	**5 max** (2 × AO2) (3 × AO3)	**Max 3** if no figures from Figure 2 or the stem are used **Max 4** unless a judgement on the statement (point 6) is given 4. **Accept** 350 or 351 (allowing for a triplet that does not code for an amino acid) 5. **Accept** 353 or 354 (allowing for a triplet that does not code for an amino acid) 4. **Accept** 'codon' for triplet 5. **Accept** bacterial (prokaryotic) DNA has no introns/is all coding 5. **Ignore** 'bacterial DNA is shorter/has fewer genes'; the absence of introns is needed 2. and 5. Ignore 'introns are removed' unless linked to not coding for amino acids

Question	Marking guidance	Mark	Comments
07.1	Correct answer for 2 marks: 32;; Accept for 1 mark, 342 − 150 = 192 **OR** (342 − 150) ÷ 6	**2** (2 × AO2)	**Reject** 57 (150 base pairs not subtracted)

Question	Marking guidance	Mark	Comments
07.2	1. The repeats are between genes/not part of gene K or L OR the repeats are non-coding; 2. So the base sequence of (the exons of) genes K and L is the same, so the same amino acid sequence/primary structure is coded for;	**2** (2 × AO2)	1. **Reject** the repeats are introns 2. **Accept** same triplets for same base sequence 2. **Reject** 'the same amino acids are produced' unless linked to the base sequence coding for them

Question	Marking guidance	Mark	Comments
07.3	1. To find the length of the yeast fragments by comparing the distance they moved with the distance moved by fragments of known length OR to produce a calibration (curve) of distance moved against length; 2. The distance moved depends on the conditions, eg time, voltage/current, type/concentration of gel, so the known fragments must be run in the same conditions/on the same gel;	**2** (2 × AO3)	2. **Accept** so differences in distance moved are only due to length **Ignore** 'to make it a fair test' unqualified **Accept** DNA ladder or marker for fragments of known length

Extended response: DNA in organelles 3.4.1

Question	Marking guidance	Mark	Comments
08	1. Mitochondrial/chloroplast DNA is circular, like prokaryotic DNA; 2. Mitochondrial/chloroplast DNA is short(er) (than nuclear DNA), like prokaryotic DNA; 3. Mitochondrial/chloroplast DNA is not associated with histones/proteins, like prokaryotic DNA; 4. Nuclear DNA is linear; 5. Nuclear DNA is (very) long(er); 6. Nuclear DNA is associated with histones/proteins OR forms chromosomes (with histones); 7. Organelle DNA is (more) similar to prokaryotic DNA than to the nuclear DNA of the same cell, so the organelles are likely to have come from prokaryotes (rather than from the nucleus/the rest of the cell);	**6 max** (5 × AO1) (1 × AO2)	**Max 5** if point 7 is not given **Max 4** if organelle DNA is compared with only prokaryotic DNA or only nuclear DNA **Max 4** if prokaryotic or organelle DNA is described as single-stranded 1. **Ignore** 'loop' alone; circular is needed 4.–6. Accept these as contrasts written alongside points 1–3, eg 'circular, not linear like nuclear DNA' gains points 1 and 4 6. **Accept** chromatin; credit chromatids joined at a centromere as extra detail, but it is not required **Ignore** statements about introns or non-coding DNA, including introns in mitochondrial or chloroplast DNA **Ignore** features other than DNA, eg ribosomes or membranes

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