HELICATE · AS AND A-LEVEL BIOLOGY · TOPIC BANK

3.4.2 DNA and protein synthesis

Mark scheme

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TOTAL MARKS	QUESTIONS
60	7

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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Genome, proteome and the structure of RNA 3.4.2

Question	Marking guidance	Mark	Comments
01.1	The full range of proteins that the cell is able to produce;	**1** (1 × AO1)	

Question	Marking guidance	Mark	Comments
01.2	(The) complete set of genes in a cell/organism;	**1** (1 × AO1)	**Accept** all the DNA/all the genetic material/all the genes/all the alleles in a cell/organism **Accept** total number of DNA bases in a cell **Reject** all the DNA/genes within a species/population **Reject** genetic code/genetic information/genotype

Question	Marking guidance	Mark	Comments
01.3	Contains ribose: mRNA and tRNA only Has hydrogen bonds between complementary bases: DNA and tRNA only Is double-stranded: DNA only Has an anticodon: tRNA only 2 marks for all four rows correct;; 1 mark for two or three rows correct	**2** (2 × AO1)	A cross or blank is acceptable for “does not apply” A row with an extra tick is incorrect

Question	Marking guidance	Mark	Comments
01.4	1. Genome: (now) includes the (extra/new) gene (from the plasmid) because the genome is all the genes in the cell; 2. Proteome: (now) includes the enzyme (that breaks down penicillin) because the cell is (now) able to produce/make this (new) protein;	**2** (2 × AO2)	1. **Accept** genome gains/has more DNA/genes 2. **Accept** the range of proteins the cell can make increases/gains one protein 2. **Reject** the proteome gains a new gene **Ignore** references to the cell becoming resistant to penicillin

Transcription and splicing 3.4.2

Question	Marking guidance	Mark	Comments
02	1. Hydrogen bonds between (complementary) DNA bases break OR DNA (double helix) unwinds; 2. Only one (DNA) strand acts as a template; 3. Free RNA nucleotides align/are attracted to (exposed) bases on the template by complementary base pairing; 4. Uracil pairs with adenine (on DNA) OR uracil is used in place of thymine; 5. RNA polymerase joins adjacent RNA nucleotides; 6. By phosphodiester bonds OR by condensation (reactions); 7. (In eukaryotes) this produces pre-mRNA, which is spliced OR introns are removed (from pre-mRNA) (and exons joined); 8. In prokaryotes, mRNA is produced directly (from DNA) OR no pre-mRNA is made OR there is no splicing; 9. Because prokaryotic genes do not have introns;	**6 max** (6 × AO1)	**Max 5** unless point 8 or 9 is given 1. **Accept** H bonds. Reject hydrogen bonds hydrolysed 3. **Accept** nucleotides align by base pairing 4. Full base names are needed; do not credit letters alone 5. **Reject** RNA polymerase forms hydrogen bonds/joins complementary bases/joins bases 6. **Reject** phosphodiester bonds between bases or between DNA and RNA 7. **Accept** non-coding sequences removed for introns removed 7. **Ignore** spliceosome (correct but not needed) 8. **Reject** prokaryotic DNA is single-stranded **Ignore** DNA helicase **Ignore** eukaryotic mRNA is made in the nucleus as the only difference

Question	Marking guidance	Mark	Comments
03.1	Correct answer for 2 marks: 80.3 (%);; Accept for 1 mark: 3660 ÷ 4560 **OR** 19.7 (%) (percentage kept)	**2** (2 × AO2)	**Accept** 80.26 (%) for 2 marks

Question	Marking guidance	Mark	Comments
03.2	1. (RNA of) 4560 (nucleotides) is pre-mRNA/a copy of the whole gene, including introns **and** exons; 2. (RNA of) 900 (nucleotides) is mRNA, made of exons only (312 + 186 + 402 = 900); 3. Pre-mRNA is spliced OR introns are removed (and exons joined) in the nucleus; 4. Only (spliced) mRNA leaves the nucleus/moves to the cytoplasm (through nuclear pores);	**3 max** (1 × AO1) (2 × AO3)	1. **Accept** total of all regions/length of gene for whole gene 2. **Accept** introns have been removed for exons only 3. **Accept** splicing happens before the RNA leaves the nucleus **Ignore** DNA leaves the nucleus. Reject pre-mRNA is translated in the nucleus

Question	Marking guidance	Mark	Comments
03.3	1. 3110: pre-mRNA with intron 1 removed (but intron 2 still present), as 4560 − 1450 = 3110; 2. 2350: pre-mRNA with intron 2 removed (but intron 1 still present), as 4560 − 2210 = 2350; 3. Partly spliced pre-mRNA OR introns are removed one at a time (in either order);	**2 max** (2 × AO3)	Points 1 and 2 need the correct intron for each length **Accept** 3110 = exons 1, 2 and 3 + intron 2 and 2350 = exons 1, 2 and 3 + intron 1 Point 3 alone gains 1 mark only **Reject** mRNA with exons removed

Question	Marking guidance	Mark	Comments
04.1	1. Uracil is (only) found in RNA **and** thymine is (only) found in DNA; 2. So the radioactivity is taken into (new) RNA only OR radioactive thymine would be taken into DNA (during replication) and not RNA;	**2** (2 × AO2)	1. **Accept** RNA contains uracil instead of thymine 1. Full base names are needed 2. **Accept** so only transcription is measured, not DNA replication

Question	Marking guidance	Mark	Comments
04.2	So RNA synthesis and protein synthesis can be compared (although the actual rates/amounts of radioactivity are different) OR to allow for changes in rate that would happen without compound Z (eg over time);	**1** (1 × AO3)	**Accept** so the effect of compound Z alone is shown **Ignore** “to make it a fair test” unqualified

Question	Marking guidance	Mark	Comments
04.3	Correct answer for 2 marks: 53.2 (%);; Accept for 1 mark: 94 − 44 = 50 **OR** (94 − 44) ÷ 94	**2** (2 × AO2)	Plotted values are 94% at 2 hours and 44% at 6 hours **Accept** answers from 51.6 to 54.7 (%) for 2 marks, from readings of 93–95 and 43–45 **Accept** 53 (%) for 2 marks **Reject** 50 (%) for 2 marks (difference only)

Question	Marking guidance	Mark	Comments
04.4	1. Protein synthesis stays high/above 90% for the first 2 hours, although RNA synthesis falls to 10% (by 2 hours); 2. mRNA made before compound Z was added is still (present and) translated (at ribosomes); 3. This mRNA is broken down and is not replaced OR (almost) no new mRNA is made/transcribed; 4. So less mRNA is available for translation, and the rate of protein synthesis falls (steadily) after 2 hours (to 26% at 8 hours); 5. Protein synthesis has not stopped at 8 hours because some mRNA remains OR RNA synthesis is not zero (4%), so a little mRNA is still made;	**4 max** (2 × AO2) (2 × AO3)	**Max 3** if no data from the figure are used 1. **Accept** readings for protein synthesis of 93–100% in the first 2 hours 2. **Accept** existing/old mRNA 3. **Accept** mRNA is used up **Reject** compound Z inhibits translation/ribosomes

Question	Marking guidance	Mark	Comments
04.5	1. (Supports) RNA synthesis falls rapidly (to 24% within 1 hour) while protein synthesis is hardly affected at first, so compound Z affects transcription and not translation (directly); 2. (Against) compound Z may reduce RNA synthesis in another way, eg by stopping uracil entering the cells/stopping RNA nucleotides being made/stopping the DNA strands separating; 3. (Against) RNA synthesis does not fall to zero/stays at about 4%, so RNA polymerase is not completely stopped/may be only partly inhibited; 4. (Against) no direct evidence that compound Z binds to/affects RNA polymerase, eg the enzyme was not tested on its own;	**2 max** (2 × AO3)	**Max 1** if only supporting points or only points against are given **Ignore** “only one experiment” or “no repeats” unless linked to the conclusion **Ignore** DNA helicase

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Translation 3.4.2

Question	Marking guidance	Mark	Comments
05.1	To remove free/unused (radioactive) amino acids, so only amino acids joined into polypeptides are measured;	**1** (1 × AO3)	Both ideas are needed **Accept** so the count is not too high because of amino acids not in polypeptides

Question	Marking guidance	Mark	Comments
05.2	Correct answer for 2 marks: 5.6 (%);; Accept for 1 mark: 270 **and** 4810 **OR** 6.4 (%) (background not subtracted)	**2** (2 × AO2)	**Accept** 5.61 (%) for 2 marks **Reject** 6.4 or 6 (%) for 2 marks

Question	Marking guidance	Mark	Comments
05.3	1. (Hydrolysis of) ATP releases/provides energy; 2. To form peptide bonds (between amino acids); 3. To attach amino acids to tRNA;	**2 max** (2 × AO1)	**Reject** ATP produces/makes energy Points 2 and 3 can be credited as “so (very) few amino acids are joined into polypeptides without ATP”, once only

Question	Marking guidance	Mark	Comments
05.4	1. Ribonuclease hydrolyses/breaks down the mRNA; 2. So there are no codons (for tRNA anticodons to bind to) OR the mRNA cannot be translated (by the ribosomes); 3. (Ribonuclease) also hydrolyses tRNA/ribosomal RNA, so amino acids are not brought to the ribosomes/the ribosomes cannot work;	**2 max** (2 × AO2)	**Accept** breaks phosphodiester bonds in mRNA for point 1 **Reject** ribonuclease breaks down polypeptides/amino acids/peptide bonds

Question	Marking guidance	Mark	Comments
05.5	The extract (still) contained (some) mRNA from the bacterial cells, which was translated;	**1** (1 × AO3)	**Reject** background radiation alone (the count is far above 40 counts per minute) **Reject** DNA was transcribed (DNA was removed)

Question	Marking guidance	Mark	Comments
06.1	1. (Has an) anticodon that binds to a complementary codon (on mRNA); 2. (Has an) amino acid binding site, so it carries a specific amino acid; 3. Folded/clover-leaf shape (held by hydrogen bonds), so the anticodon is exposed/it fits the ribosome;	**2 max** (2 × AO1)	1. **Accept** three (exposed) bases for anticodon. Both anticodon and complementary codon are needed 2. "Specific" or "one type of" is needed. Accept CCA end for amino acid binding site **Reject** tRNA is double-stranded

Question	Marking guidance	Mark	Comments
06.2	1. mRNA: GCU UGU GGA AAG UGU UUC; 2. Amino acids: Alanine, Cysteine, Glycine, Lysine, Cysteine, Phenylalanine;	**2** (2 × AO2)	2. Amino acids must be in the correct order. ECF from an incorrect mRNA sequence if Table 4 is used correctly 2. **Accept** three-letter abbreviations, eg Ala, Cys, Gly, Lys, Cys, Phe. Do not accept single-letter abbreviations **Reject** Arginine, Threonine, Proline, Phenylalanine, Threonine, Lysine for point 2 (template strand read as mRNA)

Question	Marking guidance	Mark	Comments
06.3	CCU;	**1** (1 × AO2)	

Question	Marking guidance	Mark	Comments
06.4	1. Alanine was added at positions 2 and 5/wherever the codon is UGU, instead of cysteine; 2. Because the anticodon (ACA) of the (altered) tRNA bound to the complementary codon (UGU); 3. So the position depends on the tRNA/codon–anticodon binding and not on the amino acid OR the ribosome does not recognise/check the amino acid;	**2 max** (2 × AO3)	3. **Accept** the amino acid is added wherever its tRNA binds **Reject** the mRNA/codon was changed

Question	Marking guidance	Mark	Comments
06.5	1. Normal tRNA (with anticodon ACA) carrying cysteine would also bind to the UGU codons; 2. So cysteine would be added at some of these positions OR the polypeptides would be a mixture; 3. So it would not be clear that every UGU codon is translated using the altered tRNA OR the effect of the altered tRNA could be hidden;	**2 max** (2 × AO3)	**Ignore** "to make it a fair test" or "as a control" unqualified

Question	Marking guidance	Mark	Comments
07.1	1. Anticodon ACC (on tRNA 2) binds to the complementary codon UGG (on mRNA); 2. tRNA 2 carries a specific amino acid (tryptophan) that is coded for by this codon; 3. Peptide bond forms between tryptophan and histidine/the last amino acid of the polypeptide; 4. By a condensation reaction OR water is released; 5. Using energy from (hydrolysis of) ATP; 6. tRNA 1 is released (without its amino acid) (and can collect another amino acid); 7. Ribosome moves along the mRNA by one codon, so a tRNA with the anticodon UUC can bind (to AAG);	**5 max** (3 × AO1) (2 × AO2)	**Max 3** unless at least one codon, anticodon or amino acid from the figure is used correctly 1. **Accept** bases on tRNA 2 pair with bases on mRNA by hydrogen bonds for binds 2. "Specific" or the named amino acid is needed 3. **Reject** peptide bond between tRNA molecules/between amino acid and tRNA 5. **Accept** ATP used to attach the amino acid to tRNA. Reject ATP produces energy 7. **Accept** ribosome moves to the next codon **Ignore** start codon/stop codon (correct but not needed)

Question	Marking guidance	Mark	Comments
07.2	1. tRNA cannot bind (to the ribosome) OR the anticodon cannot bind to the codon (on mRNA); 2. So amino acids are not brought to the ribosome OR no peptide bonds form OR the polypeptide is not extended; 3. So translation stops OR no proteins/enzymes are made; 4. Proteins/enzymes are needed for growth/cell division/named process, eg DNA replication or respiration;	**3 max** (3 × AO2)	**Reject** antibiotic Q kills bacteria by bursting them/breaking the cell wall **Reject** antibiotic Q stops transcription

Question	Marking guidance	Mark	Comments
07.3	Correct answer for 2 marks: 85 (%);; Accept for 1 mark: 1530 OR 1.53 × 10^3 (difference) **OR** 15 (%) (percentage remaining)	**2** (2 × AO2)	**Accept** 85.0 (%)

Question	Marking guidance	Mark	Comments
07.4	1. Antibiotic Q greatly reduces protein synthesis in bacteria (by 85%) but hardly affects it in human cells (decrease of about 2.1%); 2. Bacteria/prokaryotic cells have smaller ribosomes than human/eukaryotic cells (in the cytoplasm); 3. So antibiotic Q does not bind to human ribosomes, so human cells can still make proteins/are not harmed;	**3** (1 × AO1) (1 × AO2) (1 × AO3)	1. **ECF** from 07.3. Accept 9.6 × 10^2 compared with 9.4 × 10^2 for human cells 2. **Accept** 70S (bacteria) compared with 80S (human). Accept ribosomes are a different shape/structure 3. **Accept** the site on human ribosomes is a different shape/not complementary to antibiotic Q

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