HELICATE · AS AND A-LEVEL BIOLOGY · TOPIC BANK

3.1.1 Monomers and polymers

Mark scheme

Version 1 · 2 October 2026

TOTAL MARKS	QUESTIONS
47	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.

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Monomers and polymers 3.1.1

Question	Marking guidance	Mark	Comments
01.1	A polymer is a molecule made from a large number of monomers joined together;	**1** (1 × AO1)	Proteins are made from many types of amino acid; monomers are joined by condensation; nucleotides are monomers.

Question	Marking guidance	Mark	Comments
01.2	**P**, **Q** and **T** only;	**1** (1 × AO2)	P, Q and T are each made from a large number of monomers (monosaccharides, amino acids and nucleotides). R is a lipid and S is a disaccharide; neither is a polymer.

Question	Marking guidance	Mark	Comments
01.3	1. **S** is made from only two monomers/monosaccharides OR **S** is a disaccharide; 2. A polymer is made from a large number of/many monomers (joined together); 3. Condensation reactions also join molecules that do not form polymers, eg **R**/triglyceride/disaccharides;	**2 max** (1 × AO1) (1 × AO2)	1. **Accept S** is sucrose 2. **Accept** polymers are made of many repeating units **Reject S** is a polysaccharide **Reject S** is not made of monomers

Question	Marking guidance	Mark	Comments
01.4	1. 2999; 2. One water molecule is used for each (glycosidic) bond hydrolysed/broken; 3. Every glucose except one is joined to the rest of the molecule by one bond OR branching does not change the number of bonds (so the number of bonds is one less than the number of monomers);	**2 max** (2 × AO2)	**Max 1** if the number given is not 2999 1. **Reject** 3149 (branch points added) and 3000

Question	Marking guidance	Mark	Comments
02.1	Correct answer for 2 marks: 1.0×10^4;; Accept for 1 mark: 180 − 18 = 162 used as the mass of each glucose monomer in the chain **OR** 10 000 (not in standard form)	**2** (2 × AO2)	**Accept** 1×10^4 or 1.00×10^4 **Accept** $(1.62 \times 10^6 - 18) \div 162 = 9999.9$, rounded to 1.0×10^4 9.0×10^3 (dividing by 180) gains no credit: it ignores the water removed in each condensation reaction

Question	Marking guidance	Mark	Comments
02.2	1. Hydrolysis uses water OR a water molecule is added for each (glycosidic) bond broken; 2. The atoms from the water become part of the glucose (molecules) produced; 3. Each glucose in starch has a mass of 162 but each free glucose has a mass of 180 OR water was removed when the starch was made by condensation;	**2 max** (1 × AO1) (1 × AO2)	**Reject** water is released in hydrolysis 1. **Accept** addition of water to break bonds between monomers **Ignore** 'broken down' unless hydrolysis or water is given

Question	Marking guidance	Mark	Comments
02.3	Correct answer for 2 marks: 9.00 (g);; Accept for 1 mark: 8.10 ÷ 162 (= 0.05) OR ratio 180 ÷ 162 (= 1.11)	**2** (2 × AO2)	**Accept** 9 / 9.0 (g) **ECF** for 1 mark: an incorrect mass per glucose unit used correctly The water at the ends of each starch chain can be ignored: it makes no difference at this precision

Question	Marking guidance	Mark	Comments
02.4	95.0 (%);	**1** (1 × AO2)	**Accept** 95 (%) **ECF** using the student's answer to 02.3

Question	Marking guidance	Mark	Comments
02.5	1. Not all the starch was hydrolysed OR some bonds were not hydrolysed OR some maltose/short chains remained; 2. Some glucose was lost/left behind during separation/transfer (eg stuck to apparatus); 3. The starch was not pure OR contained other substances; 4. Some glucose was used/changed by other reactions, eg by microorganisms or on heating during drying;	**2 max** (2 × AO3)	**Reject** the glucose was not completely dried (this would increase the mass) **Ignore** 'human error' or 'inaccurate measurement' unqualified

Condensation and hydrolysis reactions 3.1.1

Question	Marking guidance	Mark	Comments
03.1	1. Effect on bond: condensation forms a (chemical) bond/joins two molecules **and** hydrolysis breaks a (chemical) bond/separates two molecules; 2. Water: condensation eliminates/releases (a molecule of) water **and** hydrolysis uses (a molecule of) water; 3. Correct example of condensation that names the molecules, eg amino acids joined to form a polypeptide / glucose joined to form glycogen or starch or maltose / nucleotides joined to form DNA or RNA / ADP and phosphate joined to form ATP; 4. Correct example of hydrolysis that names the molecules, eg starch to maltose / protein or polypeptide to amino acids / glycogen to glucose / ATP to ADP and phosphate / triglyceride to glycerol and fatty acids;	**4** (4 × AO1)	1 and 2. Both cells in the row must be correct for the mark 2. **Accept** removes/produces water for eliminates; accept adds/needs water for uses 3. **Accept** glycerol and fatty acids joined to form a triglyceride 3 and 4. **Reject** any example of forming or breaking hydrogen bonds, eg separating DNA strands 4. **Reject** 'digestion' or 'breakdown' unless the molecules are named

Question	Marking guidance	Mark	Comments
03.2	500;	**1** (1 × AO2)	Each glucose added forms one new (glycosidic) bond by condensation, releasing one water molecule, so 500 bonds form.

Question	Marking guidance	Mark	Comments
03.3	1. The (glycosidic) bonds between glucose monomers are hydrolysed, not the glucose (molecules); 2. Water is used/added (for each bond broken), not released;	**2** (2 × AO2)	1. **Accept** glycogen is hydrolysed 2. **Accept** one water molecule is used for each glucose released Each mark needs the correct version, not only the error identified

Question	Marking guidance	Mark	Comments
04.1	1. Hydrolysis (of the bonds between monomers) uses/needs water; 2. (No water, so) bonds between monomers are not broken OR polymer L is not broken into shorter molecules/monomers; 3. No water for (soluble) monomers/products to dissolve in;	**2 max** (1 × AO1) (1 × AO2)	1. **Accept** a water molecule is needed to break each bond **Reject** water is needed for condensation **Ignore** enzymes

Question	Marking guidance	Mark	Comments
04.2	1. Mean number of monomers (in each molecule) falls throughout/from the start (from 1800 to 20); 2. Because bonds between monomers are hydrolysed (using water), so polymer L molecules become shorter; 3. Mass hardly changes up to day 28 (only 6% lost) even though the number of monomers falls from 1800 to 430; 4. Because the shorter polymer molecules are still (too) long/large to be soluble, so they stay in the stitch; 5. Mass falls quickly after day 28 (from 94% to 11%) OR mass falls quickly only once the mean number of monomers is below (about) 430; 6. Because (very) short molecules/monomers/lactic acid/glycolic acid are released, which are soluble so dissolve/diffuse out of the stitch;	**5 max** (2 × AO2) (3 × AO3)	**Max 3** for description (points 1, 3 and 5) without explanation 2. **Reject** hydrolysis of the monomers/lactic acid for hydrolysis of bonds 2. **Reject** 'broken down' unless hydrolysis or water is given 4. **Ignore** the water added by hydrolysis increasing the mass (the effect is negligible) **Accept** values from the table as description, eg 94% at day 28

Question	Marking guidance	Mark	Comments
04.3	These are the conditions in the (human) body/tissues, so the results apply to stitches in a patient;	**1** (1 × AO3)	**Accept** body temperature and the pH of blood/tissue fluid **Ignore** 'fair test' or 'to control variables' unqualified

Question	Marking guidance	Mark	Comments
05	1. Bean protein is a polymer of amino acids (monomers) joined by peptide bonds; 2. (In digestion, the) peptide bonds are hydrolysed (by proteases/enzymes); 3. Using a molecule of water for each (peptide) bond broken; 4. Amino acids are absorbed (into the blood) and carried to the salivary gland cells; 5. Plants and humans/all organisms use the same (types of) amino acids OR amino acids have the same (general) structure in all organisms, so human cells can use amino acids from beans; 6. (In salivary gland cells/at ribosomes,) amino acids are joined by condensation reactions forming peptide bonds; 7. Releasing a molecule of water for each (peptide) bond formed; 8. Amino acids are joined in the sequence for amylase/a different sequence from the bean protein, determined by the person's DNA/gene/mRNA;	**6 max** (5 × AO1) (1 × AO2)	**Max 4** unless the answer names both hydrolysis (point 2) and condensation (point 6) 2. **Reject** 'broken down'/'digested' for hydrolysed 2. **Reject** hydrolysis of amino acids 2. **Accept** named proteases, eg endopeptidases/exopeptidases/dipeptidases 3 and 7. **Reject** any answer where hydrolysis releases water or condensation uses water 5. **Accept** the same 20 amino acids are found in all organisms 6. **Reject** amino acids joined by hydrogen bonds **Ignore** references to evolution

Investigating hydrolysis 3.1.1

Question	Marking guidance	Mark	Comments
06.1	1. (Protease) hydrolyses peptide bonds (between amino acids); 2. Using a water molecule for each bond broken; 3. Protein broken into shorter chains/dipeptides/amino acids, so fewer peptide bonds react with biuret reagent OR so less purple (so less light absorbed); 4. Rate of decrease slows as less protein/fewer peptide bonds (substrate) remain;	**3 max** (2 × AO1) (1 × AO2)	**Max 2** unless point 3 is given 1. **Reject** hydrolysis of amino acids 1. **Reject** 'breaks down' unless hydrolysis or water is given 3. **Accept** fewer molecules with two or more peptide bonds

Question	Marking guidance	Mark	Comments
06.2	(The alkali) denatures the protease/stops hydrolysis, so the absorbance shows the peptide bonds present at that time;	**1** (1 × AO3)	**Accept** stops the reaction so that the reading is for the exact time the sample was taken **Ignore** 'so the results are accurate' unqualified

Question	Marking guidance	Mark	Comments
06.3	Correct answer for 2 marks: 2.8×10^{-2};; Accept for 1 mark: 0.28 ÷ 10 OR 0.028 (not in standard form)	**2** (2 × AO2)	Plotted values: 0.84 at 0 minutes and 0.56 at 10 minutes **Accept** readings of 0.83–0.85 and 0.55–0.57, giving answers from 2.6×10^{-2} to 3.0×10^{-2}, for 2 marks **Ignore** a negative sign

Question	Marking guidance	Mark	Comments
06.4	1. The protease is a protein/contains peptide bonds, which react with biuret reagent; 2. Some peptide bonds were not hydrolysed/cannot be hydrolysed by this protease OR some polypeptides (with three or more amino acids) remained; 3. The protease had become inactive/denatured before all the bonds were hydrolysed; 4. Biuret reagent (is blue so) absorbs some light OR colorimeter not set to zero using a blank of biuret reagent; 5. Other substances in the mixture absorb light/are coloured/make it cloudy;	**3 max** (3 × AO3)	2. **Accept** 'not all the protein was hydrolysed' only if linked to remaining peptide bonds/polypeptides **Reject** amino acids react with biuret reagent

Question	Marking guidance	Mark	Comments
06.5	1. Repeat with boiled/denatured protease OR with water/buffer in place of the protease (same volume); 2. To show that the decrease in absorbance is caused by (hydrolysis by) the (active) protease/enzyme;	**2** (2 × AO3)	1. **Accept** protease solution mixed with water instead of protein, to show the absorbance caused by the protease itself; award 2 for this with its reason 2. **Ignore** 'to compare' unqualified

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