AB1D Biological Molecules: Depth and Exam Drill

AQA 7402 · Calculator allowed · about 130 minutes

Total Marks

Name: _____ Date: ____ / ____ / _____

Answer ALL questions. Show all your working.

1 This question tests core vocabulary used to describe biological macromolecules.

(a) State what is meant by the term monomer. **(1)**

(b) State what is meant by the term polymer. **(1)**

(c) Explain, in terms of atoms lost and gained, what happens during a condensation reaction between two monomers. **(2)**

(d) State the type of reaction, and the role of water, that breaks a polymer back down into its monomers. **(1)**

(Total for Question 1 is 5 marks)

2 This question tests key facts about carbohydrate, lipid and protein structure. For each part, identify the correct option.

(a) Which bond links two glucose molecules together in maltose? **(1)**

- ☐ A) Peptide bond
- ☐ B) Ester bond
- ☐ C) Glycosidic bond
- ☐ D) Phosphodiester bond

(b) Which statement correctly describes the structure of cellulose that gives it high tensile strength? **(1)**

- ☐ A) Alpha-glucose monomers form coiled, branched chains
- ☐ B) Beta-glucose monomers form straight chains cross-linked by hydrogen bonds into microfibrils
- ☐ C) Glucose monomers are linked by peptide bonds into sheets
- ☐ D) Beta-glucose monomers form a highly branched, compact molecule

(c) Which class of lipid has a phosphate group replacing one fatty acid, making it amphipathic? **(1)**

- ☐ A) Triglyceride
- ☐ B) Steroid
- ☐ C) Phospholipid
- ☐ D) Wax ester

(d) Which level of protein structure is defined as the sequence of amino acids joined by peptide bonds? **(1)**

- ☐ A) Primary structure
- ☐ B) Secondary structure
- ☐ C) Tertiary structure
- ☐ D) Quaternary structure

(Total for Question 2 is 4 marks)

3 This question is about DNA structure and semi-conservative replication, investigated using density-gradient centrifugation. Bacteria were grown for many generations in a medium containing only the heavy nitrogen isotope 15N, so that all their DNA was 'heavy'. They were then transferred to a medium containing only the light isotope 14N and allowed to divide.

(a) State the number of hydrogen bonds that form between an adenine-thymine base pair, and between a cytosine-guanine base pair. **(2)**

(b) Explain what is meant by describing the two strands of the DNA double helix as antiparallel. **(1)**

(c) After one round of replication in the 14N medium, all the DNA formed a single band of intermediate ('hybrid') density on a density gradient. Using semi-conservative replication, explain why every DNA molecule after this first division is hybrid. **(2)**

(d) The bacteria were allowed to divide for a second time in the 14N medium. If semi-conservative replication continues, calculate the fraction of the resulting DNA molecules that are hybrid density and the fraction that are light density. **(2)**

(e) Explain why this second-generation result is inconsistent with a conservative model of replication, in which the original double helix would remain completely intact. **(2)**

(Total for Question 3 is 9 marks)

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4 A student investigated the effect of pH on the rate of reaction of an enzyme by measuring the relative initial rate of reaction (in arbitrary units) at a range of pH values, keeping temperature and substrate concentration constant. The results are shown below.

pH	Relative rate
5	12
6	45
7	100
8	52
9	10

(a) Define the term tertiary structure of a protein. **(1)**

(b) State two types of bond, other than peptide bonds, that hold the tertiary structure of an enzyme in place, and give an example of an interaction that forms each. **(2)**

(c) From the table, state the optimum pH for this enzyme. **(1)**

(d) Calculate the percentage decrease in relative rate between pH 7 and pH 9. **(2)**

(e) Explain, in terms of the enzyme's tertiary structure, why the rate of reaction falls so sharply at pH 9. **(3)**

(Total for Question 4 is 9 marks)

5 Triglycerides are formed by a condensation reaction between one molecule of glycerol and three fatty acid molecules. The degree of unsaturation of a fat sample (the number of carbon-to-carbon double bonds present) can be measured using an iodine value test, in which iodine reacts in a 1:1 ratio with each C=C double bond.

(a) State the type of bond that forms between glycerol and a fatty acid during triglyceride formation, and name this type of reaction. **(2)**

(b) Calculate the number of water molecules released when one molecule of glycerol reacts fully with three fatty acid molecules to form a triglyceride. **(1)**

(c) A 100 g sample of a fat reacts completely with 65.0 g of iodine (molar mass of I_2 = 253.8 g/mol). The molar mass of the fat is 890 g/mol. Calculate the average number of C=C double bonds per triglyceride molecule in the sample. Give your answer to the nearest whole number. **(4)**

(d) Explain what a higher iodine value indicates about a fat sample, and how this generally relates to whether the fat is liquid or solid at room temperature. **(1)**

(Total for Question 5 is 8 marks)

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6 Two potential inhibitors, X and Y, of an enzyme-catalysed reaction were investigated. The initial rate of reaction was measured at a range of substrate concentrations with no inhibitor, with inhibitor X present, and with inhibitor Y present (both inhibitors at the same fixed concentration). Results (relative rate, arbitrary units) are shown below.

[Substrate] mM	No inhibitor	With X	With Y
1	20	8	10
2	40	16	24
4	68	32	55
8	88	55	84
16	96	80	96

(a) Using the data, identify which inhibitor (X or Y) is most likely to be a competitive inhibitor. Justify your answer by reference to the data at high substrate concentration. **(3)**

(b) Explain, in terms of molecular shape, why increasing substrate concentration overcomes the effect of a competitive inhibitor but does not fully overcome the effect of a non-competitive inhibitor. **(3)**

(c) Calculate the percentage decrease in rate caused by inhibitor X compared with no inhibitor, at a substrate concentration of 2 mM. **(3)**

(Total for Question 6 is 9 marks)

7 A student used paper chromatography to identify an unknown amino acid, X, present in a plant extract. The chromatogram was run in a single solvent, and the positions of the solvent front and of each spot were measured from the origin (the pencil line where samples were spotted). The solvent front had travelled 12.0 cm from the origin. Spot X had travelled 8.4 cm. Reference Rf values run under the same conditions were: leucine 0.73, valine 0.61, glycine 0.26.

(a) Calculate the Rf value of spot X. **(2)**

(b) Using the reference Rf values given, identify amino acid X and justify your choice. **(2)**

(c) Explain why the origin must be marked in pencil rather than pen. **(1)**

(d) Suggest one reason the Rf value obtained might differ from the literature value, and explain how the technique could be improved to reduce this source of error. **(2)**

(Total for Question 7 is 7 marks)

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8 Evaluate the evidence provided by the Meselson-Stahl experiment (density-gradient centrifugation of DNA from bacteria transferred from a 15N to a 14N medium) that DNA replication is semi-conservative, rather than conservative or dispersive.

(Total for Question 8 is 6 marks)

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9 ATP (adenosine triphosphate) is described as the immediate energy currency of cells.

(a) Describe the structure of an ATP molecule. **(2)**

(b) Explain why hydrolysis of the terminal phosphate bond of ATP releases usable energy. **(2)**

(c) A cell contains 5.0×10^{-15} mol of ATP. Given that hydrolysis of one mole of ATP releases approximately 30.5 kJ of energy, calculate the total energy, in joules, available from hydrolysing all the ATP in this cell. Give your answer in standard form to 2 significant figures. **(2)**

(d) Explain why ATP, rather than the direct oxidation of glucose, is used to supply energy for most cellular processes. **(2)**

(Total for Question 9 is 8 marks)

10 The circular chromosome of a bacterium contains 4.6×10^6 base pairs. The average molar mass of one base pair (including the sugar-phosphate backbone on both strands) is 650 g/mol. Each base pair contributes a rise of 0.34 nm to the length of the double helix. Avogadro's constant is 6.02×10^{23} per mole.

(a) Calculate the molar mass of this bacterial chromosome, in g/mol, to 3 significant figures. **(2)**

(b) Calculate the mass, in grams, of a single molecule of this chromosome. Give your answer in standard form to 3 significant figures. **(2)**

(c) Calculate the total length of this DNA molecule in micrometres, giving your answer to 3 significant figures, and state how this compares with the length of a typical bacterial cell (about 2 micrometres). **(3)**

(d) Explain briefly why this DNA molecule must be highly supercoiled and packaged within the bacterial cell. **(1)**

(Total for Question 10 is 8 marks)

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11 A particular enzyme has a glutamate residue at position 76 of its primary structure, which forms part of its active site. A gene mutation changes the DNA triplet coding for this residue, altering the mRNA codon from GAA (glutamate) to GUA (valine).

(a) State what is meant by a gene mutation. **(1)**

(b) Explain how the change from glutamate to valine at position 76 could affect the enzyme's tertiary structure and its ability to catalyse its reaction. **(3)**

(c) A different base substitution in the same gene changes a codon from CGA to CGG. Using your knowledge of the genetic code, explain why this substitution is likely to have no effect on the enzyme's structure or function. **(2)**

(d) Under identical conditions, the normal enzyme has a reaction rate of 4.50 arbitrary units. The glutamate-to-valine mutant shows a 92% reduction in rate compared with the normal enzyme. Calculate the reaction rate of the mutant enzyme. **(2)**

(Total for Question 11 is 8 marks)

Mark scheme · AB1D Biological Molecules: Depth and Exam Drill

Question 1

- (a) **B1** a small, basic molecular unit that can join with others of a similar kind to form a larger molecule oe
- **(a) Answer: A small molecule that is a basic monomeric unit of a larger molecule (polymer).**
- (b) **B1** a large molecule made from many repeating monomer units joined together oe
- **(b) Answer: A large molecule made of many monomers joined together.**
- (c) **B1** a chemical bond forms between two monomers oe
- (c) **B1** a molecule of water is released/eliminated in the process oe
- **(c) Answer: A bond forms between the two monomers and a molecule of water is released.**
- (d) **B1** hydrolysis; a molecule of water is added, breaking the bond between monomers oe
- **(d) Answer: Hydrolysis; a water molecule is added to break the bond.**

Question 2

- (a) **B1** C
- **(a) Answer: C**
- (b) **B1** B
- **(b) Answer: B**
- (c) **B1** C
- **(c) Answer: C**
- (d) **B1** A
- **(d) Answer: A**

Question 3

- (a) **B1** adenine-thymine: 2 hydrogen bonds
- (a) **B1** cytosine-guanine: 3 hydrogen bonds
- **(a) Answer: A-T: 2 hydrogen bonds. C-G: 3 hydrogen bonds.**
- (b) **B1** the two strands run in opposite directions, one 5 prime to 3 prime and the other 3 prime to 5 prime oe
- **(b) Answer: The two strands run in opposite directions (one 5 prime to 3 prime, the other 3 prime to 5 prime).**
- (c) **B1** each original heavy strand acts as a template and stays intact, pairing with a newly synthesised light (14N) strand oe
- (c) **B1** so every daughter molecule contains one original heavy strand and one new light strand, giving intermediate density oe
- **(c) Answer: Each daughter DNA molecule keeps one original heavy (15N) strand paired with one newly made light (14N) strand, so every molecule has the same intermediate density.**
- (d) **M1** recognise that of the two strands in each hybrid molecule, only the original heavy strand is again conserved intact, so half of the 4 resulting duplexes are hybrid and half are light
- (d) **A1** 1/2 (50%) hybrid and 1/2 (50%) light, cao
- **(d) Answer: 1/2 (50%) of the molecules are hybrid density and 1/2 (50%) are light density.**
- (e) **B1** a conservative model predicts only fully heavy and fully light bands would ever appear, with no hybrid band at any generation oe
- (e) **B1** since a hybrid band is observed (at generation 1, and persisting at generation 2), the conservative model is disproved oe
- **(e) Answer: Conservative replication predicts only fully heavy and fully light DNA, never hybrid; because hybrid DNA is observed, the conservative model must be wrong.**

Question 4

- (a) **B1** the overall 3D shape of a single polypeptide, formed by further folding of the secondary structure, held by bonds between R groups oe
- **(a) Answer: The overall three-dimensional shape of a polypeptide, formed by folding and held together by bonds between R groups.**
- (b) **B1** ionic bonds, e.g. between oppositely charged R groups oe
- (b) **B1** disulfide bonds (or hydrogen bonds), e.g. between two cysteine R groups (or between polar R groups), oe
- **(b) Answer: Ionic bonds (e.g. between oppositely charged R groups) and disulfide bonds (e.g. between two cysteine residues).**
- (c) **B1** pH 7
- **(c) Answer: pH 7**
- (d) **M1** correct substitution: (100 - 10)/100 x 100
- (d) **A1** 90% cao
- **(d) Answer: 90%**
- (e) **M1** at high pH, H+ ion concentration changes so ionisable R groups (e.g. of acidic/basic amino acids) gain or lose H+, changing their charge oe
- (e) **M1** this disrupts the ionic and hydrogen bonds holding the tertiary structure in place, changing the shape of the enzyme (including the active site) oe
- (e) **A1** the active site no longer complements the shape of the substrate, so fewer/no enzyme-substrate complexes form and the rate of reaction falls oe
- **(e) Answer: At pH 9 the change in H+ concentration alters the charges on ionisable R groups, breaking ionic/hydrogen bonds and changing the tertiary structure so the active site no longer fits the substrate, reducing the rate of enzyme-substrate complex formation.**

Question 5

- (a) **B1** ester bond
- (a) **B1** condensation reaction
- **(a) Answer: An ester bond forms, in a condensation reaction.**
- (b) **B1** 3, cao
- **(b) Answer: 3**
- (c) **M1** moles of I2 = 65.0 / 253.8 = 0.256 mol
- (c) **M1** moles of fat = 100 / 890 = 0.112 mol
- (c) **M1** double bonds per molecule = moles I2 / moles fat = 0.256 / 0.112 = 2.28
- (c) **A1** 2 double bonds per molecule (to the nearest whole number), cao
- **(c) Answer: Approximately 2 C=C double bonds per triglyceride molecule.**
- (d) **B1** a higher iodine value indicates more C=C double bonds (more unsaturation), which generally lowers the melting point, so the fat is more likely to be liquid (an oil) at room temperature oe
- **(d) Answer: A higher iodine value means more unsaturation (more C=C double bonds), which lowers the melting point, making the fat more likely to be liquid at room temperature.**

Question 6

- (a) **B1** inhibitor Y
- (a) **B1** at the highest substrate concentration (16 mM) the rate with Y (96) reaches the same rate as with no inhibitor (96), whereas the rate with X (80) does not oe
- (a) **B1** this shows the effect of Y can be overcome by excess substrate, which is characteristic of competitive inhibition oe
- **(a) Answer: Inhibitor Y is competitive: at 16 mM substrate its rate (96) reaches the same maximum as with no inhibitor, showing excess substrate overcomes its effect.**
- (b) **B1** a competitive inhibitor has a similar shape to the substrate and binds (reversibly) at the active site, competing directly with substrate molecules for that site oe
- (b) **B1** at high substrate concentration, substrate molecules greatly outnumber inhibitor molecules, so substrate is far more likely to bind the active site, restoring the maximum rate oe
- (b) **B1** a non-competitive inhibitor binds at a site other than the active site, changing the enzyme's tertiary structure/active site shape; this is not affected by substrate concentration, so raising substrate concentration cannot fully restore the rate oe
- **(b) Answer: Competitive inhibitors bind reversibly at the active site itself, so excess substrate outcompetes them; non-competitive inhibitors bind elsewhere and distort the active site regardless of substrate concentration, so increasing substrate cannot fully restore the rate.**
- (c) **M1** correct substitution: (40 - 16)/40 x 100
- (c) **M1** = 24/40 x 100
- (c) **A1** 60% cao
- **(c) Answer: 60%**

Question 7

- (a) **M1** Rf = distance moved by spot / distance moved by solvent front = 8.4 / 12.0
- (a) **A1** Rf = 0.70, cao
- **(a) Answer: 0.70**
- (b) **B1** leucine
- (b) **B1** because its Rf value (0.70, ecf from (a)) is closest to the reference Rf for leucine (0.73), compared with valine (0.61) or glycine (0.26) oe
- **(b) Answer: Leucine, because its measured Rf (0.70) is closest to the reference value for leucine (0.73).**
- (c) **B1** pencil marks are insoluble in the solvent so they do not run/dissolve into the chromatogram and interfere with the results, unlike ink oe
- **(c) Answer: Pencil is insoluble in the solvent, so it will not dissolve and run up the paper, unlike ink.**
- (d) **B1** a valid reason, e.g. the solvent front was not marked immediately (it evaporates, so the measured distance is too small), or temperature differed from the reference run, oe
- (d) **B1** a valid improvement matched to the reason given, e.g. mark the solvent front as soon as the chromatogram is removed from the tank, or run the chromatogram in a sealed tank at constant temperature, oe
- **(d) Answer: For example, the solvent front may have partly evaporated before being marked, giving a smaller measured distance; marking the front immediately on removal from the tank (or using a sealed tank at constant temperature) would reduce this error.**

Question 8

- **Level 3** (5-6): A detailed, well-structured evaluation that correctly describes the results at generation 1 and generation 2, explains what each of the three hypotheses (conservative, semi-conservative, dispersive) predicts, and clearly links the observed banding pattern at both generations to ruling out conservative and dispersive replication, reaching a supported conclusion that only the semi-conservative model fits all the evidence.
- **Level 2** (3-4): A reasonably clear evaluation that describes the key results (single hybrid band at generation 1, hybrid plus light bands at generation 2) and makes some links to at least two of the three hypotheses, but the reasoning is incomplete or one hypothesis is not properly addressed.
- **Level 1** (1-2): Limited description of the experiment or results, with little or no explanation of how the results distinguish between the hypotheses; may only restate that replication is semi-conservative without justification.
- **Indicative content:**
  - Conservative model predicts: original double helix stays fully intact (fully heavy) and an entirely new fully light molecule is made, so generation 1 should show two bands (heavy and light) with no hybrid band.
  - Semi-conservative model predicts: each daughter molecule has one original (heavy) strand and one new (light) strand, so generation 1 should show a single hybrid band.
  - Dispersive model predicts: both strands of each daughter molecule are a mixture of old and new DNA, so generation 1 should also show a single band, but of a different (more variable/lower) density pattern than semi-conservative once followed further.
  - Observed result at generation 1: a single band of intermediate (hybrid) density is seen, immediately ruling out the conservative model, which requires two distinct bands.
  - Observed result at generation 2: two bands are seen, in a 1:1 ratio of hybrid to fully light DNA, with no further change in the density of the hybrid band.
  - This generation-2 result rules out the dispersive model, which predicts that all molecules should show a single, gradually lightening band (because every strand is a patchwork of old and new material) rather than two discrete, unchanging density bands.
  - Only the semi-conservative model correctly predicts both the generation-1 hybrid band and the generation-2 mixture of discrete hybrid and light bands.
  - A strong evaluation weighs all three hypotheses against both generations of data, not just generation 1, since generation 1 alone cannot distinguish semi-conservative from dispersive replication.

Question 9

- (a) **B1** adenine (a nitrogen-containing base) attached to a ribose sugar oe
- (a) **B1** a chain of three phosphate groups attached to the ribose oe
- **(a) Answer: ATP is made of adenine bonded to a ribose sugar, which is bonded to a chain of three phosphate groups.**
- (b) **B1** hydrolysis of the bond between the terminal (third) phosphate group and the rest of the molecule, catalysed by ATP hydrolase, forms ADP and inorganic phosphate (Pi) oe
- (b) **B1** the products (ADP + Pi) have a lower energy content than ATP, so energy is released that can be transferred to do cellular work oe
- **(b) Answer: Hydrolysing the terminal phosphate bond of ATP produces ADP and inorganic phosphate; because these products have lower energy content than ATP, energy is released for cellular work.**
- (c) **M1** correct substitution: $5.0 \times 10^{-15} \times 30.5 \times 10^{3}$ J
- (c) **A1** 1.5×10^{-10} J, cao
- **(c) Answer: 1.5×10^{-10} J**
- (d) **B1** ATP releases energy in small, manageable packets suited to individual reactions, whereas oxidising glucose directly releases a much larger amount of energy at once, most of which would be wasted (e.g. as heat) oe
- (d) **B1** ATP hydrolysis is a single-step, rapidly reversible reaction that can be coupled directly to energy-requiring reactions in the cell, providing energy immediately when and where it is needed oe
- **(d) Answer: ATP releases energy in small, immediately usable amounts through a single, rapidly reversible reaction that can be coupled directly to cellular processes, unlike the large, less controllable release of energy from directly oxidising glucose.**

Question 10

- (a) **M1** correct substitution: $4.6 \times 10^6 \times 650$
- (a) **A1** 2.99×10^9 g/mol, cao
- **(a) Answer: 2.99×10^9 g/mol**
- (b) **M1** mass of one molecule = molar mass / Avogadro's constant = $2.99 \times 10^9 / 6.02 \times 10^{23}$, ft from (a)
- (b) **A1** 4.97×10^{-15} g, cao
- **(b) Answer: 4.97×10^{-15} g**
- (c) **M1** length = $4.6 \times 10^6 \times 0.34$ nm = 1.564×10^6 nm
- (c) **A1** convert to micrometres: 1.56×10^3 micrometres (1560 micrometres), cao
- (c) **B1** valid comparison, e.g. this is roughly 800 times longer than a 2 micrometre bacterial cell oe
- **(c) Answer: Approximately 1.56×10^3 micrometres (1560 micrometres), roughly 800 times the length of the bacterial cell itself.**
- (d) **B1** the DNA molecule is far longer than the cell itself, so it must be tightly coiled/supercoiled and looped (e.g. around associated proteins) to fit inside the small volume of the cell oe
- **(d) Answer: Because the DNA is hundreds of times longer than the cell, it must be tightly supercoiled and looped to fit within the cell's small volume.**

Question 11

- (a) **B1** a change in the base sequence of DNA (e.g. a base substitution, insertion or deletion) oe
- **(a) Answer: A change in the base sequence of a gene's DNA.**
- (b) **B1** glutamate has an acidic (negatively charged, polar) R group, whereas valine has a non-polar (hydrophobic) R group, so the chemical properties of the R group at position 76 change oe
- (b) **B1** this can disrupt ionic or hydrogen bonds that this R group previously formed, altering the folding/tertiary structure around the active site oe
- (b) **B1** if the active site shape is changed, it may no longer be complementary to the substrate, so fewer or no enzyme-substrate complexes can form, reducing or abolishing catalytic activity oe
- **(b) Answer: Glutamate's charged R group is replaced by valine's non-polar R group, which can disrupt the ionic/hydrogen bonds that shaped the active site region; if the active site is no longer complementary to the substrate, fewer enzyme-substrate complexes form and catalytic activity falls.**
- (c) **B1** the genetic code is degenerate, so more than one codon can code for the same amino acid; CGA and CGG both code for arginine oe
- (c) **B1** because the same amino acid is still incorporated, the primary structure (and therefore tertiary structure and function) of the enzyme is unchanged - this is a silent mutation oe
- **(c) Answer: CGA and CGG both code for arginine because the genetic code is degenerate, so the amino acid sequence (and hence the enzyme's structure and function) is unchanged - this is a silent mutation.**
- (d) **M1** correct method: 4.50 x (1 - 0.92), oe
- (d) **A1** 0.36 arbitrary units, cao
- **(d) Answer: 0.36 arbitrary units**