# A Level AQA Biology

## 2 Proteins and enzymes – answers

| Question | Answers | Extra information | Mark | AO<br>Spec reference |
|---|---|---|---|---|
| **01.1** | circle drawn around $CH_3$; | Accept a clear annotation that indicates $CH_3$ | 1 | AO1<br>3.1.4.1 |
| **01.2** | ($R_f$ =) 0.38; | *The correct answer of 0.38 should be awarded 2 marks even when no working is shown*<br>Accept any value in the range 0.36 to 0.40.<br>If the final answer is incorrect, 1 mark should be awarded for dividing any value by 5 (cm). | 2 | AO2<br>3.1.4.1<br>AT g |
| **01.3** | $R_f$ = 0.13;<br>glutamine; | | 2 | AO2<br>3.1.4.1<br>AT g |
| **01.4** | similar chemical properties;<br>similar R groups;<br>similar solubility; | Accept all other suitable answers | 2 max | AO2<br>3.1.4.1<br>AT g |
| **01.5** | leave a larger gap between the pencil line and the solvent;<br>add cap to jar (to prevent solvent evaporation);<br>monitor solvent rather than leaving it for a set time; | | 2 max | AO3<br>3.1.4.1<br>AT g |
| **02.1** | sodium hydroxide;<br>volumes;<br>purple / violet; | | 3 | AO1<br>3.1.4.1<br>AT f |
| **02.2** | amine of one amino acid reacts with carboxyl group of another amino acid;<br>condensation reaction **OR**<br>water released / produced; | Accept 'amino' for 'amine' and 'carboxylic acid' for 'carboxyl group'. | 2 | AO1<br>3.1.4.1 |

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| **02.3** | peptide bond shown between the amine group of aspartic acid and the carboxyl group of lysine;<br>peptide bond shown between the amine group of lysine and the carboxyl group of aspartic acid;; | Award one mark for a bond using the NH2 in lysine's R group and/or the COOH in aspartic acid's R group. | 3 | AO2<br>3.1.4.1 |
| **03.1** | C, H, O, N;<br>S; | Accept names or chemical symbols for each element | 2 | AO2<br>3.1.4.1 |
| **03.2** | (34 350 × 3) = 103 050 (RNA nucleotides) | Accept 103 053 (if a stop codon is referenced) or 103 056 (if a stop codon and a start codon are referenced) | 1 | AO2<br>3.4.2 |
| **03.3** | primary structure is a polypeptide containing 348 amino acids;<br>secondary structure has alpha helices;<br>formed by hydrogen bonds;<br>tertiary structure has disulphide bonds;<br>(rhodopsin is) a glycoprotein / conjugated;<br>retinal is a cofactor / prosthetic group;<br>*idea that* (rhodopsin must have) hydrophobic regions (within the membrane) and hydrophilic regions (either side of the membrane); | The descriptions should be linked to the correct level of protein structure for marks 1–4 to be awarded. | 5 max | AO2<br>3.1.4.1 |
| **03.4** | active site **or** specific 3D shape (which can be inferred from the complementary binding of ADP);<br>*idea of* subunits changing shape for induced fit;<br>hydrophilic regions on the exterior (i.e. exposed to water and dissolved ADP, phosphate and $H^+$ ions); | | 2 max | AO2<br>3.1.4.2 |

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| **03.5** | tertiary; | | 1 | AO2<br>3.1.4.1<br>3.1.4.2 |
| **03.6** | hydrogen bonds break;<br>enzyme denatures;<br>tertiary structure changed;<br>active site no longer complementary to substrate / ADP; | | 3 max | AO1<br>3.1.4.2 |
| **04.1** | *idea of* dilute 1 part protein solution to 4 parts water; | | 1 | AO2<br>3.1.4.1<br>AT b and c |
| **04.2** | use a clean pipette each time;<br>remember or write down the order of the solutions (because cuvettes cannot be labelled); | | 1 max | AO3<br>3.1.4.1<br>AT b and c |
| **04.3** | the biuret test produces a purple colour;<br>(which means) green light is absorbed;<br>(using the filter) increases the resolution of the results; | | 2 max | AO3<br>3.1.4.1<br>AT b and c |
| **04.4** | $x$-axis labelled 'percentage (concentration of) protein (solution)' **AND** $y$-axis labelled 'absorbance / AU';<br>straight line from origin showing a positive correlation; | | 2 | AO2<br>3.1.4.1<br>AT b and c |
| **04.5** | protein solution concentration / volume;<br>temperature;<br>volume of protease solution;<br>biuret solution concentration / volume;<br>pH; | | 2 max | AO3<br>3.1.4.1<br>AT b and c |
| **05.1** | $1.58 \times 10^{-7}$ (mol dm$^{-3}$); | Allow one mark for 0.000 000 158 (not in standard form) | 2 | AO2<br>3.1.4.2 |

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| Question | Answers | Extra information | Mark | AO<br>Spec reference |
|---|---|---|---|---|
| **05.2** | **temperature**<br>more kinetic energy;<br>hydrogen bonds break;<br><br>**pH**<br>change in charges;<br>hydrogen and ionic bonds break;<br><br>**general**<br>active site/tertiary structure changes shape; | | 4 max | AO1<br>3.1.4.2 |
| **05.3** | competitive inhibitor binds to active site and non-competitive inhibitor binds to allosteric site;<br>non-competitive inhibitor changes tertiary structure;<br>non-competitive inhibitor lowers $V_{max}$; | Allow 'site other than active site' for 'allosteric site'<br>Or reverse argument<br>Or reverse argument<br><br>Do not allow reversible/ irreversible because these terms can apply to either inhibitor | 3 | AO1<br>3.1.4.2 |
| **06.1** | curved line below the original line;<br>new line labelled as 'lower activation energy with enzyme'; | Allow alternative wording | 2 | AO2<br>3.1.4.2 |
| **06.2** | (original model was) lock and key;<br>active site and substrate(s) have specific and complementary shapes;<br><br>(new model is) induced fit;<br>substrate binds and changes the shape of the active site;<br>providing a better fit; | | 4 max | AO1<br>3.1.4.2 |

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<table>
<tr><th>Question</th><th>Answers</th><th>Extra information</th><th>Mark</th><th>AO<br>Spec reference</th></tr>
<tr><td>07</td><td>The following are suitable topic areas from the specification that could be used to describe the formation of polymers. A polymer can include any chain of monomers. Lipids are therefore not considered to be polymers.<br><br>Please note that to obtain full credit, students must use information to describe the formation of polymers, not just write about topics that include polymers. These topics can include the enzymes and organelles involved in polymer formation, when relevant. In order to fully address the question and reach the highest mark bands students must also include at least five topics in their answer, to demonstrate a synoptic approach to the essay.<br><br>
<table>
<tr><th>Specification reference</th><th>Topic area</th></tr>
<tr><td>3.1.1</td><td>Monomers and polymers</td></tr>
<tr><td>3.1.2</td><td>Carbohydrates</td></tr>
<tr><td>3.1.4.1</td><td>General properties of proteins</td></tr>
<tr><td>3.1.4.2</td><td>Many proteins are enzymes</td></tr>
<tr><td>3.1.5.1</td><td>Structure of DNA and RNA</td></tr>
<tr><td>3.1.5.2</td><td>DNA replication</td></tr>
<tr><td>3.4.2</td><td>DNA and protein synthesis</td></tr>
</table>
<br>Students may be able to show the relevance of other topics from the specification.<br><br>Note: other topics from beyond the specification can be used, providing they relate to the title and contain factually correct material of at least an A-level standard. Credit should not be given for topics beyond the specification which are below A-level standard.</td><td></td><td>25</td><td>AO1<br>3.1.1<br>3.1.2<br>3.1.4.1<br>3.1.4.2<br>3.1.5.1<br>3.1.5.2<br>3.4.2</td></tr>
</table>

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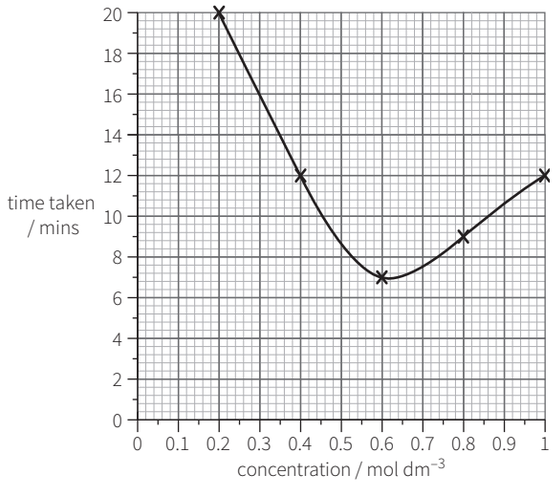
### Skills box answers

| Question | Answer |
|---|---|
| **1** |  <br>• a line graph should be drawn with pH on the $x$-axis and volume of apple juice on the $y$-axis<br>• the scaling and tick marks should be regular<br>• a curve of best fit |
| **2** | 5 |
| **3** | use more pH values between pH 2–6 |