# Mark scheme

| Question | | | Answer/Indicative content | Marks | Guidance |
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| 1 | | | B✓ | 1 (AO 1.1) | **Examiner's Comments**<br><br>Around 50% of candidates were able to apply the idea of a degenerate genetic code to the idea that a mutation could leave the primary protein structure unchanged. |
| | | | **Total** | **1** | |
| 2 | | | C✓ | 1 (AO 1.2) | **Examiner's Comments**<br><br>Around half of candidates got this right. |
| | | | **Total** | **1** | |
| 3 | | | B ✓ | 1 (AO2.1) | **Examiner's Comments**<br><br>Candidates answered **A** and **C** in equal measure, which possibly suggests that candidates did not realise that the structural gene product is a protein , which doesn't contain nucleic acids. The question was answered correctly (option **B**) by candidates who scored highly on other parts of the paper. |
| | | | **Total** | **1** | |
| 4 | | | C ✓ | 1 (AO1.1) | **Examiner's Comments**<br><br>About half of the candidates selected the correct response, option **C**. A lot of candidates chose option **A**, perhaps this was due reading statement 1 without the 'bind to'. |
| | | | **Total** | **1** | |
| 5 | | | **Level 3 (5–6 marks)**<br>A detailed description of the general roles of homeobox genes **and** valid suggestions for the roles in the development of the brain.<br><br>*There is a well-developed line of reasoning which is clear and logically structured. The information presented* | 6 (AO1.2) (AO2.5) | **Indicative scientific points may include (but are not limited to):**<br><br>*General roles*<br><br>• determine overall body plan<br>• switch different genes on and off in different cells and tissues |

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| | | | *is relevant and substantiated.*<br><br>**Level 2 (3–4 marks)**<br><br>A description of the general role of homeobox genes **and** a valid suggestion for a role in the development of the brain.<br><br>*There is a line of reasoning with some structure. The information presented is relevant and supported by some evidence.*<br><br>**Level 1 (1–2 marks)**<br><br>An outline of the general role of homeobox genes **or** a valid suggestion for a role in the development of the brain.<br><br>*The information is basic and communicated in an unstructured way. The information is supported by limited evidence and the relationship to the evidence may not be clear.*<br><br>**0 mark**<br><br>No response or no response worthy of credit. | | • (and therefore) determine cell identity<br>• expressed in a set order during development<br>• regulate patterning and positioning of (named) structures<br>• determine polarity<br>• regulate levels of apoptosis and mitosis<br><br>*Roles in brain development*<br><br>• determine the head and tail regions / anterior and posterior regions and therefore where the brain and spinal cord will develop<br>• expressed in a set order to determine (named) regions of the brain<br>• and neural organisation in the brain<br>• switch genes on or off in the brain<br>• to form specialised, neurones / nerve cells<br>• regulate mitosis and apoptosis of neurones to adjust neural organisation<br><br>**<u>Examiner's Comments</u>**<br><br>Candidates who achieved Level 3 in this question were able to accurately describe the roles of homeobox genes in general and in the brain in equal measure. The best responses generally included reference to body plan, apoptosis and mitosis and the control of gene expression. Better answers suggested that homeobox genes may determine the placement of particular lobes or regions (e.g. the cerebellum at the back of the brain, the medulla oblongata in the brainstem), that the control of apoptosis and mitosis may shape neuronal pathways and synapses, and that certain genes will be turned on and off the production of neuronal cells in the brain. |

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| | | | | | However, few candidates gained Level 3 overall. Candidates not achieving Level 3 often lost out because their responses were unbalanced, with a much larger proportion relating to the general role of homeobox genes and far less attention given to their role in the brain.<br>Many responses began with a description of homeobox genes as being 'highly conserved' and 'containing 180 base pairs' and the differences between homeobox genes. Some candidates used much of the answer space to write these descriptions without linking their response with the question. Some responses also included lengthy descriptions of the role of homeobox genes as transcription factors, but without relating this to the switching on or off of genes. Some candidates gave very detailed descriptions of the mechanism of the *lac* operon, while others wrote at length about the role of RNA polymerase, which was not relevant to the question. Almost all candidates were able to gain at least Level 1 by demonstrating knowledge of at least one role of homeobox genes but struggled to link their knowledge to the brain.<br><br>**OCR support**<br><br>Our teaching guide on 'Cellular control' offers overview of key concepts and suggested classroom activities.<br><br>**Exemplar 3** |

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| | | | | |  <br>Homeobox genes are a set of 180 base pairs present in all animals, plants and fungi, and their role is body plan development. These genes are highly conserved so every one one same in all plants humans and fungi. A subset of this are Hox genes which are only present in humans. Hox genes contain clusters, and each cluster codes for a different development in the human body these are also highly conserved so that the correct anatomical structures are present. Hox genes code for transcription factors which regulate gene expression in eukaryotic cells and can turn genes on and off, also in the post transitional expression which activates enzyme such as the phosphorylation of kinase cascade. Homeobox genes are very important in the development of the brain as it allows different lobes and structures to be created and have their own individual role to whereas the Cerebrum which controls fine muscle movements and the cerebrum [6]<br>Additional answer space if required.<br>which affects conscious thought and memory. Another role of homeobox genes are the transcription factors which code for introns and exons and are involved in the process of RNA splicing which codes for the primary structure of a protein<br><br>This response was given Level 2 and scored 4 marks. The response mentions a couple of general points about homeobox genes (.... "correct anatomical structures present".... and "turn genes on and off") and one clear potential role in brain development (.... "allows different lobes to be developed"e.g., cerebellum). More than one role in brain development would be needed to gain Level 3. The answer is well organised and so was given the communication mark. |
| | | | **Total** | **6** | |
| 6 | a | | environmental ✓<br><br>stimuli ✓<br><br>apoptosis ✓<br><br>enzymes ✓<br><br>phagocytes / phagocytosis ✓ | 5(AO1.2) | **ALLOW** stress / factors<br><br>**ALLOW** proteases / caspases<br>**IGNORE** lysosomes<br><br>**ALLOW** macrophages / endocytosis<br><br>**Examiner's Comments**<br><br>The majority of responses for the first three blank spaces were correct. Few responses were able to gain full marks. For each blank, the most common incorrect responses were 'hormonal' and 'conditions'.<br><br>Nearly all candidates got this right, although spellings that were not phonetically similar were not given marks. Examples of these are: phagocytes, lysosomes and lysozyme, exocytosis, enzymes and vesicles. |
| | b | | Hox / homeotic / homeobox ✓ | 1(AO1.2) | **IGNORE** regulatory<br><br>**Examiner's Comments** |

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| | | | | | The vast majority answered correctly. Occasional incorrect responses were 'regulatory' or '*lac* operon'. |
| | | | **Total** | **6** | |
| 7 | | i | 1 = threonine ✓<br>2 = proline ✓ | 2(AO2.1) | **Examiner's Comments**<br><br>Almost all candidates got both marks here. |
| | | ii | joins / adds , (RNA) nucleotides ✓<br><br>forms phosphodiester bonds (between nucleotides) ✓ | 2(AO1.2) | **IGNORE** bases<br><br>**ALLOW** forms sugar–phosphate backbone<br>**IGNORE** covalent bonds<br><br>**Examiner's Comments**<br><br>This question differentiated well between candidates of differing abilities but only a minority of candidates gained both marks. Many candidates thought RNA polymerase formed hydrogen bonds between the mRNA and the template strand and a few confused it with DNA polymerase or even helicase. |
| | | iii | CAC ✓ | 1(AO2.1) | **ALLOW** cytosine adenine cytosine<br>**IGNORE** CAU<br><br>**Examiner's Comments**<br><br>Not many candidates gave the correct answer to this stretch and challenge question. Some used Fig. 16.3 to identify an anticodon for valine but did not appreciate that GUG was the only substitution mutation of GAG that would result in valine. Many candidates suggested codons, rather than anticodons. |
| | | iv | **Level 3 (5–6 marks)**<br>Explains in detail why mutations may leave the function of a protein unchanged using Fig 16.3 **and** referring to more than one level of protein structure.<br><br>*There is a well-developed line of reasoning which is clear and logically* | 6(AO2.1) | **Indicative points may include**<br><br>*Mutations*<br><br>• genetic code is degenerate<br>• point mutation might code for the same amino acid |

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| | | | *structured. The information presented is relevant and substantiated*.<br><br>**Level 2 (3–4 marks)**<br>Explains why mutations may leave the function of a protein unchanged using Fig 16.3 **and** referring to protein structure.<br><br>*There is a line of reasoning presented with some structure. The information presented is relevant and supported by some evidence*.<br><br>**Level 1 (1–2 marks)**<br>Suggests why mutations may leave the function of a protein unchanged using Fig 16.3 **or** referring to protein structure.<br><br>*There is an attempt at a logical structure with a line of reasoning. The information is in the most part relevant*.<br><br>**0 marks**<br>*No response or no response worthy of credit*. | | • use of example from Fig 16.3 to support<br><br>*Protein structure and function*<br><br>• haemoglobin function is dependent on tertiary structure<br>• silent mutation would leave primary structure unchanged<br>• unchanged primary structure would leave tertiary structure unchanged<br>• substitution of amino acid with similar properties to the original amino acid might leave tertiary or secondary structure unchanged<br>• mutation might change part of the tertiary structure away from the functional part of the protein, e.g. away from the active site of an enzyme<br><br>**Examiner's Comments**<br><br>The question asked candidates to refer to three things in their answers: Figure 16.3, mutations and levels of protein structure. Responses that did not do all three were limited to Level 1. However, the question provided a good spread of marks and differentiated well between candidates.<br><br>Most candidates appreciated the degenerate nature of the genetic code and most illustrated this with reference to Fig. 16.3. Many could also explain the implications of this degeneracy in terms of silent mutations. Some of these candidates could also clearly explain why a silent mutation would have little impact on protein structure. Some even discussed the effect of substituting an amino acid for another with an R-group with similar properties. Many responses showed poor understanding within both sections, which was often illustrated by inaccurate use of technical terms. Confusion between bases and amino acids was evident, as were frequent references to amino acids, bases or |

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| | | | | | DNA being degenerate. Candidates seemed more confident discussing mutations than they were protein structure, but a few candidates appeared to think that the amino acids were *produced*, as opposed to *selected*, on the basis of the generic code.<br><br>Some responses were not given the communication mark because of confusing use of technical terms. Many other responses were presented as either an explanation of the three types of mutation and their effects or as a description of protein structure which did not answer the question that had been asked.<br><br>**Exemplar 1**<br><br>  <br><br>Level 3 was achieved in the first 13 lines of this response. The rest of the response was irrelevant to the question that was asked and so was a waste of the candidate's time. |
| | | | **Total** | **11** | |