

A Level OCR Biology

21 Cellular control – answers

Question	Answers	Extra information	Mark	AO Spec reference										
1(a)	<table border="1"> <thead> <tr> <th>Mutation</th> <th>Number of triplet codes that are changed</th> </tr> </thead> <tbody> <tr> <td>substitution of guanine</td> <td>1</td> </tr> <tr> <td>deletion of the initial cytosine base</td> <td>3</td> </tr> <tr> <td>insertion of cytosine after the first adenine base</td> <td>3</td> </tr> <tr> <td>insertion of three cytosine bases before guanine</td> <td>1</td> </tr> </tbody> </table>	Mutation	Number of triplet codes that are changed	substitution of guanine	1	deletion of the initial cytosine base	3	insertion of cytosine after the first adenine base	3	insertion of three cytosine bases before guanine	1	<p>One mark per correct box The 2nd triplet (CCC) and the 4th triplet (AAA) remain the same The 1st triplet and 2nd triplet (CCC) remain the same</p> <p>Only CTG is changed (to CTC and CCG). Although the sequence of triplets will change, AAA and ATT remain the same.</p>	4	AO2 6.1.1(a)
	Mutation	Number of triplet codes that are changed												
	substitution of guanine	1												
	deletion of the initial cytosine base	3												
	insertion of cytosine after the first adenine base	3												
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1(b)(i)	C to T on (original) 22nd base ✓ A to T on 12th base ✓ A to T on 10th base ✓	3	AO2 6.1.1(a)											
1(b)(ii)	deletion of the eight nucleotides GATTATGG (originally bases 14-21) ✓	1	AO2 6.1.1(a)											
1(c)(i)	change in DNA triplet code / base sequence of DNA / mRNA codon (sequence) ✓ different primary structure of protein / order of amino acids in polypeptide ✓ different tertiary protein structure ✓	3	AO1 2.1.2(m) 2.1.3(g) 6.1.1(a)											
1(c)(ii)	(mutation in) non-coding DNA / intron ✓ point / substitution mutation AND same amino acid produced (by a different triplet) ✓ <i>idea that</i> new primary structure / change in an amino acid has little / no effect on tertiary structure ✓	3	AO1 6.1.1(a)											

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2(a)(i)	U / uracil instead of A / adenine (in mRNA) ✓		1	AO2 2.1.3(a) 2.1.3(g)															
2(a)(ii)	(valine and glutamic acid have) different R groups ✓ (which can) form different hydrogen bonds / hydrophobic interactions / ionic bonds (with other polypeptide chains) ✓		2	AO2 2.1.2(m)															
2(b)	Any two from: epigenetic change / modification / gene silencing ✓ RNA polymerase cannot bind ✓ to promoter ✓		2 max	AO2 2.1.3(g) 6.1.1(b)															
2(c)(i)	more DNA triplets affected / changed ✓ <i>idea of greater change to protein structure</i> ✓	Accept more likely to cause frameshifts	2	AO1 6.1.1(a)															
2(c)(ii)	homozygous recessive AND heterozygous ✓	Accept letters to represent alleles (e.g., cc and Cc)	1	AO2 6.1.2(b)(i)															
3(a)	<table border="1"> <thead> <tr> <th>Level</th> <th>Control mechanism</th> <th>Description</th> </tr> </thead> <tbody> <tr> <td>transcription</td> <td>transcription factors</td> <td><i>idea of</i> molecules bind to DNA to either increase or decrease transcription</td> </tr> <tr> <td rowspan="2">post-transcription</td> <td>mRNA processing to produce mature mRNA</td> <td>introns removed from (immature) mRNA</td> </tr> <tr> <td>(m)RNA editing</td> <td>nucleotides are deleted, added, or substituted</td> </tr> <tr> <td>post-translation</td> <td>protein modification</td> <td>protein folding / addition of (named) non-protein groups / protein shortening / activation by cAMP</td> </tr> </tbody> </table>		Level	Control mechanism	Description	transcription	transcription factors	<i>idea of</i> molecules bind to DNA to either increase or decrease transcription	post-transcription	mRNA processing to produce mature mRNA	introns removed from (immature) mRNA	(m)RNA editing	nucleotides are deleted, added, or substituted	post-translation	protein modification	protein folding / addition of (named) non-protein groups / protein shortening / activation by cAMP	One mark per correct box	4	AO1 6.1.1(b)
	Level	Control mechanism	Description																
	transcription	transcription factors	<i>idea of</i> molecules bind to DNA to either increase or decrease transcription																
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3(b)	Any five from: lac operon ✓ lactose binds to repressor protein ✓ repressor changes shape ✓ stops repressor binding to operator ✓ promoter not covered (by repressor) / available ✓ RNA polymerase binds to the promoter ✓ mRNA transcribed from structural gene(s) (for enzymes) ✓	Accept alternative wording	5 max	AO1 6.1.1(b)
4(a)(i)	Any three from: (control) body plan development ✓ regulate where and when genes are expressed / switched on ✓ (code for) homeodomains / transcription factors ✓ regulate mitosis / apoptosis ✓ idea of ensuring structures develop the correct positions ✓	Accept alternative wording for regulate	3 max	AO1 6.1.1(c)
4(a)(ii)	<i>idea of ensuring</i> (body) structures develop at the correct time / in the correct position ✓		1	AO2 6.1.1(c)
4(a)(iii)	Hox genes are a subset of homeobox genes ✓ (that are) found only in animals ✓	Accept alternative wording for subset	2	AO1 6.1.1(c)
4(b)	Any two from: <i>idea that we need to define what is meant by complexity</i> ✓ <i>(agree)</i> vertebrates have more (homeobox) genes than invertebrates ✓ <i>(disagree)</i> humans have fewer (homeobox) genes than other animals ✓		2 max	AO3 6.1.1(c)
5(a)	mitosis increases cell numbers / allows growth of tissues ✓ apoptosis removes unwanted cells / shapes the structures ✓	Accept alternative wording	2	AO2 6.1.1(d)

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5(b)	Any two from: phagocytes ✓ engulf apoptotic bodies / vesicles / cell fragments ✓ digests / breaks down cell fragments ✓		2 max	AO2 4.1.1(e)(i) 6.1.1(d)
5(c)	Any two from: <i>in apoptosis</i> (hydrolytic) enzymes are not released ✓ (it is a) controlled process ✓ vesicles are formed (to contain cell fragments) ✓		2 max	AO2 6.1.1(d)
6	<p>Level 3 (5–6 marks) Describes the use of mitosis and apoptosis in development in detail, using examples. <i>There is a well-developed line of reasoning, which is clear and logically-structured and uses scientific terminology at an appropriate level. All the information presented is relevant and forms a continuous narrative.</i></p> <p>Level 2 (3–4 marks) Describes some aspects of mitosis and apoptosis in development, using examples. <i>There is a line of reasoning presented with some structure and use of appropriate scientific language. The information presented is mostly relevant.</i></p> <p>Level 1 (1–2 marks) Describes the use of mitosis or apoptosis in development. <i>The information is communicated with only a little structure. Communication is hampered by the inappropriate use of technical terms.</i></p> <p>0 marks No response or no response worthy of credit.</p>	<p>Indicative content:</p> <ul style="list-style-type: none"> Patterns of mitosis and apoptosis are controlled by homeobox genes. <p><i>Mitosis</i></p> <ul style="list-style-type: none"> Cell division Growth of tissues Reference to control by hormones or growth factors <p><i>Apoptosis</i></p> <ul style="list-style-type: none"> Programmed cell death Controlled removal of cells Forms specific shapes of tissues and organs <p><i>Examples</i></p> <ul style="list-style-type: none"> Digits Various organs Neurones 	6	AO1 6.1.1(c) 6.1.1(d)

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7	<p>Level 3 (5–6 marks) Describes the control of gene expression before and after transcription, with few or no errors or omissions.</p> <p><i>There is a well-developed line of reasoning, which is clear and logically structured and uses scientific terminology at an appropriate level. All the information presented is relevant and forms a continuous narrative.</i></p> <p>Level 2 (3–4 marks) Describes the control of gene expression before and after transcription, with some errors or omissions.</p> <p><i>There is a line of reasoning presented with some structure and use of appropriate scientific language. The information presented is mostly relevant.</i></p> <p>Level 1 (1–2 marks) Describes the control of gene expression before or after transcription, with errors and omissions.</p> <p><i>The information is communicated with only a little structure. Communication is hampered by the inappropriate use of technical terms.</i></p> <p>0 marks No response or no response worthy of credit.</p>	<p>Indicative content:</p> <p><i>Before transcription</i></p> <ul style="list-style-type: none"> • Transcription factors • Mechanistic details, roles, and examples of transcription factors <p>Credit the inclusion of information that is not mentioned in the specification (e.g., structural changes in chromatin, epigenetic changes, and eukaryotic operons)</p> <p><i>After transcription</i></p> <ul style="list-style-type: none"> • mRNA processing (e.g., removal of introns) • mRNA editing • control of mRNA binding the activation of proteins by cyclic AMP (post-translational level) 	6	AO1 2.1.3(g) 6.1.1(b)

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Skills box answers

Question	Answer
1	<p>87</p> $q^2 = \frac{1}{2000} = 0.0005, \text{ therefore } q = 0.0224, \text{ and } p = (1 - 0.0224) = 0.9776$ $2pq = 1 - (0.0224)^2 - (0.9776)^2 = 0.0435$ <p>In a population of 2000, $2pq = 0.0435 \times 2000 = 87$. Therefore, if there is one sufferer of cystic fibrosis in a population of 2000, there will be 87 carriers</p>
2	<p>10.9%.</p> $p + q = 1, \text{ therefore } q = 1 - 0.942 = 0.058$ $p^2 + 2pq + q^2 = 1$ <p>Therefore $2pq = 1 - q^2 - p^2 = 1 - (0.058)^2 - (0.942)^2$ $= 0.1094$</p> <p>So the frequency of the heterozygous genotype ($2pq$) = 0.109 To calculate the frequency of $2pq$ as a percentage of the population = $0.109 \times 100 = 10.9\%$</p>