A Level OCR Biology

23 Manipulating genomes – answers

<table>
<tr><th>Question</th><th>Answers</th><th>Extra information</th><th>Mark</th><th>AO
Spec reference</th></tr>
<tr><td>1(a)</td><td>Any two from:
classification ✓
disease (risk) analysis ✓
forensics / criminal investigations / paternity testing ✓</td><td></td><td>2 max</td><td>AO1
6.1.3(c)</td></tr>
<tr><td>1(b)(i)</td><td><table><tr><th>Stage of DNA profiling</th><th>How is this achieved?</th></tr><tr><td>amplification of DNA</td><td>PCR</td></tr><tr><td>digestion / fragments produced / AW</td><td>the use of restriction endonucleases</td></tr><tr><td>separation (of fragments)</td><td>electrophoresis</td></tr><tr><td>visualisation of banding patterns</td><td>hybridisation / radioactive probes / fluorescent probes</td></tr></table></td><td>One mark per correct row</td><td>4</td><td>AO1
6.1.3(c)
6.1.3(d)
6.1.3(e)</td></tr>
<tr><td>1(b)(ii)</td><td>fragments should not be placed at the anode / be placed at the cathode ✓
(because) DNA is negatively charged / moves towards the positive electrode ✓
idea that electrophoresis should not (necessarily) be run for 2 hours ✓
idea that electrophoresis needs to be stopped before fragments reach the anode ✓</td><td>Accept progress of electrophoresis should be monitored</td><td>4</td><td>AO3
2.1.3(g)
6.1.1(b)</td></tr>
<tr><td>1(b)(iii)</td><td>more variation (in VNTRs) ✓
idea of profiles more likely to be unique / differentiate ✓</td><td>Accept reverse argument</td><td>2</td><td>AO2
2.1.3(g)
6.1.1(b)
6.1.3(c)</td></tr>
<tr><td>1(c)</td><td>idea that profiling produces a fingerprint / unique pattern (from a specific section of DNA) ✓
idea that sequencing determines the order of DNA bases ✓</td><td></td><td>2</td><td>AO1
6.1.3(a)
6.1.3(c)</td></tr>
<tr><td>2(a)</td><td>hydrogen ✓
55 °C ✓

(free) nucleotides ✓</td><td>Accept any temperature value in the range 50–56 °C</td><td>3</td><td>AO1
6.1.3(d)</td></tr>
</table>

A Level OCR Biology

23 Manipulating genomes – answers

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<tr><th>Question</th><th>Answers</th><th>Extra information</th><th>Mark</th><th>AO
Spec reference</th></tr>
<tr><td>2(b)(i)</td><td>
<table>
<tr><th>Number of cycles</th><th>Number of fragments</th></tr>
<tr><td>4</td><td>16</td></tr>
<tr><td>6</td><td>2^6</td></tr>
<tr><td>8</td><td>256</td></tr>
<tr><td>11</td><td>$10^{3.3113}$</td></tr>
</table>
</td><td>Award one mark per correct box
Accept correct 2^n and log10 values (i.e., 2^4 and $10^{1.2}$) for row 1.</td><td>4</td><td>AO2
6.1.3(d)</td></tr>
<tr><td>2(b)(ii)</td><td>Any two from:
not enough primers ✓
not enough (free) nucleotide ✓
primers do not join ✓
temperature damage to fragment / template / strand ✓
strands fail to separate ✓</td><td>Accept alternative wording for ‘not enough’</td><td>2 max</td><td>AO2
6.1.3(d)</td></tr>
<tr><td>3(a)(i)</td><td>DNA polymerase ✓</td><td></td><td>1</td><td>AO2
6.1.3(a)</td></tr>
<tr><td>3(a)(ii)</td><td>idea of add solutions of each nucleotide (A, T, G, C) separately / one at a time ✓</td><td>Accept ensure each nucleotide produces a different wavelength / type of light</td><td>1</td><td>AO3
6.1.3(a)</td></tr>
<tr><td>3(a)(iii)</td><td>Any four from:
luciferin is the substrate ✓
(which is) complementary (in shape) to the active site of luciferase ✓
luciferin binds to active site ✓
induced fit ✓
enzyme–substrate / luciferase–luciferin complex ✓</td><td></td><td>4 max</td><td>AO2
2.1.4(c)</td></tr>
</table>

A Level OCR Biology

23 Manipulating genomes – answers

<table>
<tr><th>Question</th><th>Answers</th><th>Extra information</th><th>Mark</th><th>AO
Spec reference</th></tr>
<tr><td>3(b)</td><td>bioinformatics is the creation of databases / algorithms / software / tests (that can be used to solve biological questions) ✓
idea that computational biology is the application of bioinformatics, i.e., how the data are analysed to interpret the data ✓</td><td></td><td>2</td><td>AO1
6.1.3(b)</td></tr>
<tr><td>4(a)(i)</td><td>(using) DNA ligase ✓</td><td></td><td>1</td><td>AO2
6.1.3(f)(ii)</td></tr>
<tr><td>4(a)(ii)</td><td>idea of to distinguish GM mosquitoes from normal / wild mosquitoes ✓</td><td></td><td>1</td><td>AO2
6.1.3(f)</td></tr>
<tr><td>4(a)(iii)</td><td>Any two from:
stops transcription ✓
prevents DNA polymerase from binding (to DNA promoter) ✓
idea of causes post-transcriptional (mRNA) editing ✓</td><td></td><td>2 max</td><td>AO2
2.1.3(g)
6.1.1(b)</td></tr>
<tr><td>4(a)(iv)</td><td>males do not bite humans / females could bite humans ✓</td><td></td><td>1</td><td>AO2
6.1.3(f)</td></tr>
<tr><td>4(a)(v)</td><td>idea of to allow GM males to develop and be released ✓</td><td></td><td>1</td><td>AO2
6.1.3(f)</td></tr>
<tr><td>4(b)</td><td><table><tr><th>Method of vector transfer</th><th>Organisms for which this method can be used</th></tr><tr><td>viral (transfer) / lipsomes</td><td>animals</td></tr><tr><td>viral (transfer) / bacteriophage / plasmid and electroporation / plasmid and culture heating</td><td>bacteria</td></tr><tr><td>A. tumefaciens infection</td><td>plant(s) / named plant taxon</td></tr></table></td><td>Award one mark per correct box</td><td>3</td><td>AO1
6.1.3(f)(ii)</td></tr>
</table>

A Level OCR Biology

23 Manipulating genomes – answers

<table>
<tr><th>Question</th><th>Answers</th><th>Extra information</th><th>Mark</th><th>AO
Spec reference</th></tr>
<tr><td>5(a)(i)</td><td>Any two from:
stem cells are undifferentiated / a source of new red blood cells ✓
all (new) red blood cells (derived / differentiated from these stem cells) would be healthy ✓
no rejection by the immune system ✓</td><td>Accept alternative wording</td><td>2 max</td><td>AO2
2.1.6(j)
2.1.6(m)
6.1.3(h)</td></tr>
<tr><td>5(a)(ii)</td><td>(gene therapy) avoids immune response / rejection ✓</td><td>Accept reverse argument</td><td>1</td><td>AO1
6.1.3(h)</td></tr>
<tr><td>5(a)(iii)</td><td>idea of effects of germline / embryonic gene therapy are uncertain ✓
idea of lack of consent may breach human rights ✓
idea of technology could be used for unethical applications ✓</td><td></td><td>2 max</td><td>AO2
6.1.3(h)</td></tr>
<tr><td>5(b)</td><td><table><tr><th>Therapy type</th><th>somatic cell therapy</th><th>germline therapy</th></tr><tr><td>May require repeat treatments</td><td>✓</td><td></td></tr><tr><td>May target stem cells</td><td>✓</td><td>✓</td></tr><tr><td>Is currently being applied to develop treatments for diseases</td><td>✓</td><td></td></tr></table></td><td>Award one mark per correct row</td><td>3</td><td>AO1
6.1.3(h)</td></tr>
<tr><td>6</td><td>Any five from:
idea that the best method will depend on the application/aim/research being conducted ✓

points supporting the student
(RS II) is quickest / has the shortest sequencing time ✓
(RS II) can read the longest sequences ✓

points not supporting the student
(RS II) is the most expensive ✓
(RS II) cannot read many bases per run compared to the Illumina methods ✓
(RS II) has the highest error rate ✓</td><td></td><td>5 max</td><td>AO3
6.1.3(a)</td></tr>
</table>

A Level OCR Biology

23 Manipulating genomes – answers

Question	Answers	Extra information	Mark	AO Spec reference
7	**Level 3 (5–6 marks)** Outlines most of the differences between semi-conservative replication and PCR, with no or few omissions or errors. *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.* **Level 2 (3–4 marks)** Outlines some differences between semi-conservative replication and PCR. *There is a line of reasoning presented with some structure and use of appropriate scientific language. The information presented is mostly relevant.* **Level 1 (1–2 marks)** Outlines some relevant aspects of semi–conservative replication and PCR. *The information is communicated with only a little structure. Communication is hampered by the inappropriate use of technical terms.* **0 marks** No response or no response worthy of credit.	**Indicative content**: • Semi-conservative replication occurs in cells / PCR occurs *in vitro* • Chromosomes are replicated in semi-conservative replication, (shorter) DNA fragments are replicated in PCR • Strands are separated using helicase in semi-conservative replication / high temperatures break strands in PCR • PCR can be used to replicate and double DNA quantities many times / each semi-conservative replication doubles DNA quantities once • DNA polymerase is resistant to high temperatures in PCR (i.e. Taq DNA polymerase) / in most cases, DNA polymerase is not resistant to high temperatures in semi-conservative replication Primers added in PCR	6	AO1 2.1.3(e) 6.1.3(d)

A Level OCR Biology

23 Manipulating genomes – answers

Question	Answers	Extra information	Mark	AO Spec reference
8	**Level 3 (5–6 marks)** Describes the use of PCR in both applications, with no or few errors and omissions. *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.* **Level 2 (3–4 marks)** Describes the use of PCR in both applications, with some errors and omissions. *There is a line of reasoning presented with some structure and use of appropriate scientific language. The information presented is mostly relevant.* **Level 1 (1–2 marks)** Describes some correct aspects of the use of PCR, with significant errors and omissions. *The information is communicated with only a little structure. Communication is hampered by the inappropriate use of technical terms.* **0 marks** No response or no response worthy of credit.	**Indicative content:** *DNA sequencing* • Amplifies DNA quantities to provide sufficient material for the sequencing process • Interrupted / chain termination PCR • Some nucleotide bases are modified to terminate the growing chain and stop PCR • Different chain lengths are produced • The final bases can be read through different colours of fluorescence • Credit references to other sequencing techniques that use PCR *Forensic analysis* • Often small amounts of DNA are present at crime scenes • PCR amplifies the quantity of DNA available • For use in electrophoresis / DNA profiling • Credit references to relevant DNA sequences (e.g., VNTRs) Credit details of the PCR process	6	AO1 6.1.3(a) 6.1.3(b) 6.1.3(d)

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Skills box answers

Question	Answer
1	5
2	**UGACAGAGUCUCCUC**
3	**ACU**, **GUC**, **UCA**, **GAG**, **GAG**
4	Introns are removed from strands of pre-RNA
5	51 × 3 = 153 2 × 3 = 6 = 159 bases