Mark scheme

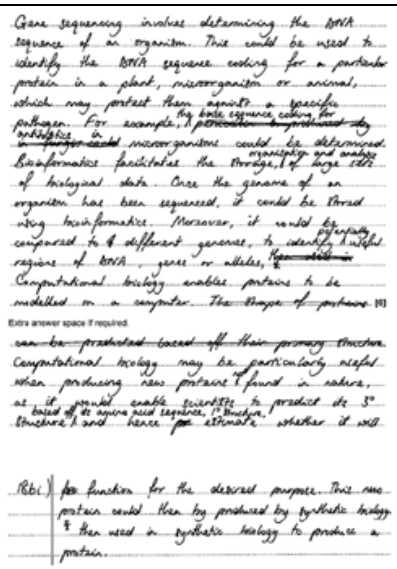
Question			Answer/Indicative content	Marks	Guidance
1	a		identifying / AW , genetic diseases / disease risk / evolutionary relationships / disaster victims ✓ classifying organisms / evidence for evolution ✓ (as part of) breeding programmes ✓	1 max (AO 1.1)	*Mark the first answer* **ALLOW** identifying , siblings / ancestry **IGNORE** to see if people are related (as could be paternity) **IGNORE** medical , diagnosis / screening (for non-genetic diseases) **IGNORE** investigating , genetics / research / mutations **IGNORE** organ transplants / personalised medicine **Examiner's Comments** There were a range of acceptable answers to this question and most candidates gained this mark.
	b	i	polymerase chain reaction ✓	1 (AO 1.1)	**Examiner's Comments** Over half of candidate know what PCR stood for. Some attempted to construct something plausible from the letters and others offered a range of incorrect suggestions, including 'DNA profiling'. Some candidates left the space blank.
		ii	**X** (represents) denaturation / strand separation / breaking of H-bonds ✓ **Y** (represents) annealing / primers added (to DNA) ✓ **Z** (represents) synthesis of a new strand / addition of nucleotides (to new DNA strand) ✓	3 (AO 1.2 x 2) (AO 2.6 x 1)	**X** IGNORE H^+-bonds **Z** ALLOW synthesis / extension / elongation (of DNA strand) **Z** ALLOW description of forming a complementary strand **Z** IGNORE bases / replication **Examiner's Comments** This question differentiated well between candidates of differing abilities. Most candidates achieved 2 marks, usually for X and Y. Many candidates stated that Z was the optimum temperature for DNA polymerase without a sufficient description of what stage Z is trying to achieve, i.e., synthesis of a new strand of DNA.

		iii	<u>optimum</u> (temperature for enzyme) ✓ Taq polymerase allows high(er) <u>rate</u> , of DNA replication / AW ✓ (enzyme) obtained from , thermophilic / AW , organisms ✓ enzyme is able to withstand high(er) temperatures (than normal DNA polymerase) ✓	3 max (AO 2.5 x 2) (AO 2.6 x 2)	**ALLOW** Taq polymerase allows fast(er) <u>rate</u> of reaction **ALLOW** e.g., from bacteria that live in hot springs **ALLOW** doesn't denature at such high temperatures / thermostable **ALLOW** optimum is higher than other forms of DNA polymerase **<u>Examiner's Comments</u>** This also differentiated well. Not very successful answers often achieved the optimum temperature mark and followed this with general discussions of enzyme action. Stronger responses knew that the enzyme used was Taq polymerase and explained why 72-75°C is an appropriate temperature range for that enzyme.
		iv	(initial) sample is small / AW ✓	1 (AO 2.6)	**ALLOW** not much DNA to begin with **IGNORE** to amplify the sample / to get a big enough sample **<u>Examiner's Comments</u>** Around half of responses got this mark.
	c	i	double peaks / they , are heterozygous / have different alleles ✓ single peaks , are homozygous / have the same allele ✓	2 (AO 2.2)	**IGNORE** genes / coding **ALLOW** VNTR length as AW for allele *If no other mark awarded* **ALLOW** 1 mark for using the terms 'homozygous' and 'heterozygous' (not linked to peaks) **<u>Examiner's Comments</u>** This was a challenging question in which only around 1 in 10 responses scored any marks. Candidates were required to understand the context provided and use key terms correctly to express their ideas. Some responses had the right idea, but they confused key terms such as gene with allele, homologous with homozygous (and their hetero-

					equivalents), and polygenic with polymorphic. Autosomal linkage was often seen as an incorrect answer.
		ii	*claim is supported because…* 1 (DNA profiles) are identical / match / AW ✓ 2 probability / chance , of 2 people having identical profiles is <u>very</u> low / AW ✓ however… 3 (6 is) a low number of , loci / peaks ✓ 4 … so they could have been , <u>closely</u> related / AW ✓ 5 could be identical twins ✓	3 max	*Assume correct context unless answer contradicts it* **1 ALLOW** are the same **1 IGNORE** similar / same number of base pairs **2 ALLOW** <u>very</u> low <u>likelihood</u> / near impossibility , that 2 people would have matching profiles **2 IGNORE** so they probably come from the same person **3 ALLOW** only 6 genes were tested **3 ALLOW** 17 loci are needed in court **3 IGNORE** small sample **4 ALLOW** only if mp 3 has been **AWARDED** **<u>Examiner's Comments</u>** Most candidates gained the first marking point but then filled the rest of their answer space with examples to illustrate this point. An explanation of *how strong* support is requires some consideration of what might make the support weak, and few responses attempted to do this. A minority of candidates suggested that S might have belonged to the suspects twin, but many omitted the important detail about twin being identical (or monozygotic). Other marking points were seen, but rarely. Some answers went beyond the claim in the question and discussed whether the suspect was guilty.
			Total	**14**	
2		i	**Level 3 (5–6 marks)** Explains in detail how gene sequencing **AND** bioinformatics **AND** computational biology are used in the production of synthetic proteins. *There is a well-developed line of reasoning which is clear and logically*	6 (AO 2.5)	**Indicative points may include** *Principle* • computational biology can use bioinformatics to make predictions about the structure and function of a synthetic protein using DNA sequences

			structured. The information presented is relevant and substantiated.
			
			Level 2 (3–4 marks)
			
			Explains how gene sequencing **AND** bioinformatics are used in the production of synthetic proteins.
			
			OR
			
			Explains how gene sequencing **AND** computational biology are used in the production of synthetic proteins.
			
			OR
			
			Explains how bioinformatics **AND** computational biology are used in the production of synthetic proteins.
			
			There is a line of reasoning presented with some structure. The information presented is relevant and supported by some evidence.
			
			Level 1 (1–2 marks)
			
			Mentions how gene sequencing **OR** bioinformatics **OR** computational biology are used in the production of synthetic proteins.
			
			There is an attempt at a logical structure with a line of reasoning. The information is in the most part relevant.
			
			0 mark
			
			No response or no response worthy of credit.
					• involves genetic modification of organisms
					
					Gene sequencing
					
					• determines order of bases
					• order of bases linked to order of amino acids
					• order of amino acids is protein primary structure
					• DNA sequence can be inferred from, and implies, protein primary structure
					
					Bioinformatics
					
					• stores and organises large amounts of data
					• databases of
					  ○ DNA and amino acid sequences
					  ○ protein structures
					  ○ metabolic pathways
					• facilitates fast retrieval and sharing of information
					• algorithms and statistical tests
					
					Computational biology
					
					• needed for analysis of large amounts of data
					• rapid processing of data
					• prediction of amino acid sequences
					• modelling of protein structure or function
					• algorithms and statistical tests
					
					QWC
					Award the communication mark if the candidate is able to communicate relevant ideas clearly without confusing terms such as bases and amino acids.
					
					Examiner's Comments

					Candidates who understood the basic idea of the three processes and who could discuss a DNA/protein topic without mixing up bases and amino acids were able to achieve Level 3 fairly easily. However, this question exposed an area that appears to have been poorly addressed in some centres. Many answers discussed genetic modification, electrophoresis and PCR at length to no credit and often at the expense of a quality of written communication mark. Some responses merely paraphrased the information given in the question. Although lengthy discussions of the mechanism of gene sequencing did not gain much credit, they were at least relevant, and did not affect the quality of written communication. For a question such as this one, with three distinct parts, it is very helpful to candidates if they arrange their answer into three sections with a general introduction. **Assessment for learning** In Level of Response questions that cover two or more areas, such as gene sequencing, bioinformatics and computational biology, each of the sections needs to be addressed in order to achieve full marks. Subheadings are a very useful approach to organising answers and can often help with the quality of written communication. **OCR support** The Guide to Level of Response (LoR) questions supports students by providing guidance on how to answer the LoR questions with confidence. Exemplar 1

					 This answer easily achieves L3 and there are no issues that detract from the communication. There are valid points about gene sequencing, computational biology and bioinformatics and the last two lines show that the candidate understands the principle involved.
		ii	*idea* of unknown consequences ✓ (named) ethical issues ✓	1 (AO 2.5)	**IGNORE** tampering with nature / not natural / designer babies / animal welfare **ALLOW** creating bioweapons **Examiner's Comments** A small majority of candidates achieved this mark, usually for citing ethical issues. Fewer suggested that the novelty of these proteins might be associated with unknown consequences, which is a much more scientific answer. It is worth noting that tabloid-headline answers like, 'playing God', or 'designer babies', rarely get much credit in A Level Biology.
			Total	**7**	
3		i	culture heating / heat shock / electroporation ✓	1	**ALLOW** electric shock / electric pulse / virus (as a vector) / transfection / add calcium ions and heat **IGNORE** *Agrobacterium tumefaciens (as used to infect plant cells) / electrofusion (used to fuse 2 cells together) /* vector unqualified**Examiner's Comments**

					A variety of methods were accepted for this question. The most common answer was electroporation or heat shock. However, some candidates were unable to be credited the mark for mentioning electrofusion or just a vector on its own with no reference to a virus being used.
		ii	marker / reporter, genes (added to plasmid) ✓ gene for, antibiotic resistance / fluorescence / nutrient deficiency (added to plasmid) ✓	1max	**ALLOW** use of PCR / DNA sequencing / pyrosequencing / use of electrophoresis **DO NOT ALLOW** 'add fluorescent, tag / dye' **Examiner's Comments** Some candidates answered this question correctly by stating the use of marker genes or the use of antibiotic resistance genes added to the plasmid. However, there were a few candidates who mentioned the process of replica plating but with no reference to antibiotic resistance genes and so gained no marks. Many candidates gained no marks for mentioning using fluorescent tags or dyes rather than adding a gene for fluorescence.
			Total	**2**	
4	a	i	rate of NPQ ✓ rate of CO_2 fixation ✓	1 max (AO3.4)	**Examiner's Comments** This question was answered correctly by most candidates who demonstrated a good knowledge of variables. The most common mistake was to give light intensity as the answer. Some lost the mark for stating the amount of CO_2 taken in rather than rate of CO_2 fixation.
		ii	greater rate (of carbon fixation in GM plants) because , less light energy is converted to heat energy / lower NPQ rate / more energy remains as light ✓ (so) more electrons enter electron	2 max (AO2.1) (AO3.1)	**ora** for unmodified plants **ALLOW** ref to figures for comparison of rates

			transport chain / AW ✓ more, ATP / NADPH / reduced NADP , generated for / supplied to , Calvin cycle (from light-dependent stage) ✓		**ALLOW** 'light-independent stage' for Calvin cycle or a description of the Calvin cycle **Examiner's Comments** Some candidates misinterpreted the data and stated that genetic modification 'decreased the rate of carbon fixation'. These answers compared the rate at 0 and 150 seconds for the GM plant rather than making the correct comparison; GM and non-GM plants at 150 seconds. Some explained why the rate of fixation fell with reduced light rather than why fixation was higher in the GM plants or described the higher rate of fixation in the GM plants (including quoting data from the table) but did not explain why. Nonetheless, many answers did state that the rate was increased by genetic modification because of a reduced NPQ rate. Far fewer were able to make the link between reduced NPQ and increased ATP and NADPH for the Calvin cycle.
		iii	*idea that* company could charge high prices (to farmers / countries) ✓ *idea that* GM crop not available to everyone ✓	1 max (AO1.1)	e.g. 'poorer farmers cannot afford GM seed' **Examiner's Comments** Candidates generally had the right idea and gained the mark for this question. Marks were mostly awarded for the idea of the plant being expensive. A few described what a 'patent' is rather than the possible consequences. Some candidates gave other possible concerns around GM plants which were not related to patenting/access.
	b		sequence genomes (of different varieties) ✓ (*use bioinformatics and computational biology to*) develop / use, (appropriate) software ✓	3 max (AO1.2) (AO2.5) (AO2.7)	**ALLOW** 'develop theoretical models' **ALLOW** 'use a database' / 'storing genomes (on a database)'

			use , algorithms / statistical tests / (mathematical) models ✓ store , data / information (from different DNA sequences) ✓ analyse / identify, differences / similarities, in DNA (sequences) / alleles ✓		**ALLOW** 'comparison of, differences / similarities, in their genes' **Examiner's Comments** This question was proven challenging for the candidates. Only a few candidates were confident with these processes and knew what a genome is. These candidates mentioned storing information on databases or using software or models to compare and identify similarities or differences between the DNA sequences of different varieties of maize. Lots of candidates included irrelevant descriptions of lab methods such as PCR, Southern Blotting, or referenced sequencing amino acids, rather than sequencing genomes. Some candidates went into detail about how sequencing is carried out, or just repeated the stem of the question and talked about 'comparing genomes'.
			Total	**7**	
5			*Similarities* (both) use enzyme that cuts DNA ✓ (both) change base, sequence / order, in the organism ✓ *idea that* they both result in the production of a new polypeptide ✓ *differences* no , gene / DNA , insertion in (this method of) CRISPR ✓ no, marker genes / ligase / bacterial cells / vector, used in CRISPR ✓ *idea that* traditional genetic engineering is illegal in humans ✓	4 max(AO2.5)	**DO NOT ALLOW** 'both use restriction enzymes' **DO NOT ALLOW** 'both change bases' alone (as this implies base substitution) **Ora for genetic engineering** **ALLOW** no donor organism in CRISPR **ALLOW** no deletion in genetic engineering / DNA insertion only in genetic engineering / DNA deletion only in CRISPR **ALLOW** needs an RNA guide sequence in CRISPR **IGNORE** 'plasmids / restriction enzymes, only in genetic engineering' **IGNORE** 'Cas9 only in CRISPR' (because they are mentioned in the question stem)

					Examiner's Comments This was probably the most challenging question on the paper because of the amount of novel information that needed to be processed. Very few candidates achieved more than half marks. The candidates who scored highly organised their answer clearly with a list of similarities separated from a list of differences. Responses were aften confused and appeared more like attempts to describe the processes rather than compare and contrast them. The most common statement given was that CRISPR deletes bases, but then the comparative statement regarding genetic engineering was not correct. Many candidates wrote about the formation of sticky ends and many also rewrote information that was already given to them regarding reference to plasmids, restriction enzymes and Cas9. Specificity of language was not strong – many candidates referred to both techniques requiring enzymes – but didn't describe what for in terms of the similarity, i.e. to cut DNA.
			Total	**4**	
6		i	more adenylyl cyclase ✓ on, cell surface / plasma, membranes ✓ more, cAMP / second messenger, produced ✓ *idea of* adrenaline has greater effect on heart cells ✓ *idea of* improved contraction of, cardiac muscle / heart ✓	2 max(AO2.5)	**ALLOW** more, adenyl / adenylate, cyclase / enzyme e.g. increases responsiveness to, adrenaline / noradrenaline e.g. greater heart rate / increased contraction **IGNORE** 'improved heart function' alone as in question stem **IGNORE** ' heart pumps blood more efficiently' **Examiner's Comments** There were a range of responses for this question; and many candidates did not score any marks as they only described what adenylyl cyclase and cAMP do, rather than what happens to their levels when the genes are expressed. The most commonly

					scored marks were for **increased** adenylyl cyclase and **increased** cAMP, followed by improved heart contraction. Almost no examples of greater effect of adrenaline or the idea of adenylyl cyclase being found on cell surface membranes were seen. Some achieved a mark for increased heart contraction, but many just repeated 'improved heart function' or stated that it could increase or decrease contractions, which gained no marks. Very few answers mentioned adrenaline, and those that did described it as the fight or flight hormone.
		ii	virus / viral vector ✓ liposome ✓	1 max(AO1.2)	**ALLOW** plasmid / yeast artificial chromosome / YAC **IGNORE** 'injection' unqualified **Examiner's Comments** Generally, this question was poorly answered. Few candidates were able to identify a method of inserting the gene during gene therapy. Those that did access the mark here said that you should use a virus or plasmid, with a few mentioning liposomes. Common incorrect answers included: somatic cell nuclear transfer, somatic cell gene therapy, injection (unqualified), vector (unqualified) and genetic engineering/restriction enzymes.
		iii	*idea of* to share knowledge (with other scientists) ✓ *idea of* to allow validation of new knowledge ✓	1 max(AO2.1)	e.g. allow others to repeat the procedure / others can compare results with their own **IGNORE** 'peer review with other scientists' / 'to prevent bias' unqualified e.g. to ensure the integrity of scientific results / check if results are reproducible / to evaluate the results **Examiner's Comments** A large majority of candidates obtained the mark here. While a wide variety of responses were given, most candidates were able to get

					across the idea that publishing data was to allow other scientists to see the information, compare the results, or check the validity/reproducibility. Those candidates whose responses were given no marks suffered from lack of detail, mentioning just peer review, or describing what is included in a journal. Some wrote about the idea of sharing results with the public, not understanding that these are specialist journals.
			Total	**4**	
7			B ✓	1(AO2.7)	**Examiner's Comments** Most answers were correct.
			Total	**1**	