**Stage 2 Biology - Formative Test B Answers**

**DNA & Proteins (1.1-1.6)**

Multiple Choice

1. L 2. L 3. L 4. J 5. J 6. J

Short Answer

1a

Since there is only one point mutation here only one codon will be affected in the DNA. Due to the fact that several codons can code for the same amino acid, it may be that the change in this codon will not change the amino acid it codes for. If there is no change to the amino acid sequence then the protein will be expressed the same as with no mutation resulting in the same phenotype.

1b

All four chain terminating nucleotides (ddNTPs A,T,C,G) were used when using PCR to make copies of the target DNA. In the process of many cycles this will produce lengths of DNA that will end at every one of the 39 different nucleotides in this DNA strand. This produces 39 different fragment sizes possible for passing through the capillary gel.

1c

The guide RNA (gRNA) of the CRISPR/Cas9 would need to be designed in the lab so it has the right nucleotide sequence to match and bind to this particular gene.

2a

No this is not conclusive. In order to have a reasonable degree of certainty using STR profiles, there must be many (10-12) STR alleles compared amongst the suspects and crime DNA. Only when all 10-12 match can there be conclusive evidence, as any two people may, by chance, share the same alleles for one particular site.

2b

13 represents 13 repeats of this particular STR sequence at the locus.

19 represents 19 repeats of this particular STR sequence at the locus.

2c

Non coding regions of the DNA are large regions of DNA that do not code for either polypeptides OR RNA molecules. It is here that you find various sites of repeating base sequences like (STRs). \*NOTE: introns are not the same as non-coding DNA.

2d

PCR is a process that makes many copies of DNA in a thermocycler. Firstly, the target DNA is added to a solution containing primers, free nucleotides, and *Taq* polymerase. It is then heated to 96oC to denature the DNA; reduced to 55oC to allow primers to bind; heated to 72oC in order for *Taq* polymerase to add nucleotides to the exposed DNA strands. This process repeats through many cycles and each time doubles the number of DNA copies.

3a

Cytosine

3b

High methylation on a gene will block RNA polymerase from binding to the gene. This will prevent transcription and translation and thus reduce the expression of the gene.

3c

If genes such as tumor suppressor and proto-oncogenes are methylated they may not be expressed or used by the cell. Since they both work to control the rate at which cells divide, preventing them from functioning may lead to uncontrolled cell division and possibly cancer.

3d

You could describe how any of the following work:

* miRNA
* siRNA
* piRNA

The most important ones to know about are the first two above.

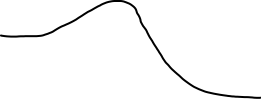
miRNA binds to the mature mRNA for a gene. In doing so it prevents it from being translated properly at the ribosome, thus ‘silencing’ the gene.

siRNA binds to a protein to form a RISC which binds to mature mRNA and breaks the sugar phosphate backbone. This destroys the mRNA and thus ‘silences’ the gene.

3e

tRNA molecules have 3 nucleotide bases that are exposed and can bind to mRNA codons when there is a match. These nucleotides on the tRNA are called anti-codons as they are complimentary to the codons. Each tRNA carries a particular amino acid as well. They are responsible transferring amino acids to the ribosome and binding, when matching, to the mRNA. In this way they bring the amino acids in the correct sequence to be joined together one codon at a time.

4a

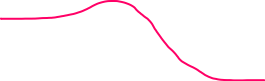


reactants

products

time

energy



4b

The active site conforms closely to the substrate through an induced fit. This puts pressure on the bonds of the substrate and thus lowers the energy required by the cell to break the substrate. Because this is ‘easier’ for the cell the rate of this reaction is increased.

4c

Enzymes have complex and highly specific 3D shapes. This specificity is crucial to their ability to bind to particular substrates. The shape of the enzyme is due to various chemical bonds at the secondary, tertiary and primary levels of its structure. The thermal energy of higher temperatures can affect the stability of these bonds and cause them to break and so change the shape of the enzyme. When it loses its shape (specificity) it will no longer be able to bind to substrate and thus lose function.

4d

They would first need to determine the exact order of amino acids in the protein chain and its 3D shape. Then, using computer software they could predict changes to the folding and final shape when various amino acids in the chain are changed. The newly improved protein could then be synthesized by designing an mRNA strand and modern biotechnology tenchniques.

**Extended Response**

***\* Note:*** *you can choose to do more or less for each of the two parts of the question depending on what you feel more confident with. However, you must address both, and in total you must have enough clear and relevant information to obtain 6 marks total.*

First paragraph(s) – describe transfer techniques

Methods could include:

* recombinant bacterial plasmid vector;
* recombinant viral vector;
* microinjection;
* bacterial transformation
* electroporation

Second paragraph(s) – discuss potential ethical issues

Ethical issues could include:

* Transgenic – ‘playing God’.. we are tampering with life in a way we should not
* Transgenic – we don’t know long term impact of genetic changes to things we eat
* Transgenic – animal rights issues; testing; etc.
* Transgenic – we may create modified species that overtake/wipe out ‘natural’ species
* Editing – the vectors (such as virus’) could cause harm to a person or if released
* Editing – you might edit places that were not intended in DNA
* Editing – editing germ cells leading to designer babies – playing God? Creating superhumans?