**Stage 2 Biology - Formative Test Answers**

**DNA & Proteins (1.1-1.5)**

Multiple Choice

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

Short Answer

1. (a)

A

1. (b)

The processes of DNA replication takes place in the nucleus in eukaryotic cells. The weak hydrogen bonds holding the two strands of the double helix are broken one at a time by helicase. This exposes the two polynucleotide strands so that complimentary nucleotides can be added to each by DNA polymerase. Each half of the original DNA molecule can predict what the newly added strand will be because of the base pairing rules of A with T and G with C. This produces two newly formed double helix molecules that are identical to the parent strand. Each new strand is composed of one of the original parent DNA strands and one newly formed one, meaning the DNA replication is semiconservative.

1. (c)

One of: high heat; toxic chemical, asbestos, radiation

1. (d)

The potential consequences of mutations in germ cells are much more significant than in somatic cells. Somatic cells can experience mutations and this may lead to tumors or malignant cancers, such as carcinoma (skin cancer). When this is the case the mutation may only have local effects and can often be removed from the individual. Other cells around it may not be affected. It is also true that this mutation will not be passed on to any future offspring. When there is a mutation in a germ cell, or gamete, the effects are much greater, as this will mean that the mutation can be passed on to future offspring (through the egg or the sperm). This could result in all offspring being affected and potentially harmed by it. Every cell of the offspring will contain this mutation.

2. (a)

Trypsin has an active site that is complimentary in shape to Chymotrypsinogen substrate. When this substrate enters the active site of the enzyme it triggers a change for the active site to more closely conform to the substrate. The result of this puts pressure on the bonds of the substrate, so that the reaction to break it down requires less energy input from the cell. In this way the breakdown of the substrate is facilitated by the enzyme and can allow it to occur more readily in the cell.

2. (b)

It may be that the peptide byproduct, when in enough concentration, will begin to function as an inhibitor to the enzyme Trypsin. This could occur by it being a competitive inhibitor or a non-competitive inhibitor, binding to an allosteric site on Trypsin which blocks Chymotrypsinogen. This would then alter the rate of the reaction by slowing it down.

2. (c)

As the amount of substrate is increased the rate of reaction increases rapidly, as Trypsin is facilitating the breakdown. However, at a certain point adding more substrate will not increase the rate of reaction, as all of the active sites of the limited amount of enzyme will be occupied at any given moment. Thus adding substrate will not increase the rate of reaction further – it will proceed at a plateaued rate.

Rate of rx

Increasing substrate [ ]

3. (a) i

To amplify the small amount of DNA obtained from the crime scene for further study.

3. (a) ii

Firstly the target DNA is combined with free nucleotides, primers, and Taq polymerase and heated to 96 degrees Celsius in order to denature the DNA (separate the double helix). The temperature is lowered to 55 degrees Celsius for the primers to attach to the target DNA. The temperature is then raised to 72 degrees Celsius in order for polymerase to extend the primers and copy the DNA. This produces two copies of the DNA. The cycle then repeats in order to continue making copies.

3. (b)

The first property is its overall negative charge as a molecule. This will allow it to be attracted toward the positive electrode at the end of the gel.

The second property is its size. Smaller sized fragments will travel further through the gel than larger ones.

3. (c)

A chain terminating version of a nucleotide causes the DNA replication process in PCR to stop at that particular base in the sequence. When the chain terminating A (adenine) nucleotide is used in PCR it will result in many fragments of DNA that all end at one of the A bases in the DNA fragment. When run on a gel the position of each fragment band reveals where there was an A in the sequence. When compared to the same fragment being copied using chain terminating C,T, and G the bands collectively reveal the position of each base in the fragment.

4. (a)

W = thymine; X = Adenine; Y = Guanine

4. (b)

Because there is a pairing complimentary base on one strand for every base on the other.

4. (c)

The template strand determines the primary structure. When the gene is exposed the mRNA is transcribed from the template strand itself. This gives an mRNA strand that has the same sequence of bases (although U instead of T) as the coding strand. This mRNA sequence has the right sequence of base codons to determine the correct order of amino acids arranged in the polypeptide for the protein synthesis during translation. If you were to transcribe the coding strand, the mRNA would have the wrong base sequence and the codons would be incorrect.

4. (d)

1. some of the bases transcribed from the DNA will be removed from the pre-mRNA molecule as they are non-coding introns.

2. some of the bases in the DNA sequence for the gene will be ‘promotor’ regions used simply to indicate to RNA polymerase where to begin transcription.

**Extended Response**

* Each individual has unique sequences of bases in their DNA
* These unique sections are called genetic markers – which are found in introns of genes or non-coding regions
* The introns can have tandem repeating sections of bases that vary in length and sequence between individuals. These are called VNTRs (variable number tandem repeats) or STRs.
* The length of these sections for each individual will influence the length of that particular gene when it is cut out with restriction enzymes. Individuals with few VNTRs within that particular gene will have a shorter fragment of DNA for that gene/region of DNA
* When multiple DNA VNTRs or STRs are compared for length, each person will produce a unique banding pattern for gel electrophoresis – as they will have unique fragment lengths. This means individuals can be identified and compared based on their unique profile that is based on differences in their VNTRs or STRs
* However there are ethical concerns with collecting these profiles
  + This is private and personal information – genetic information should not be shared with others
  + There is concern about who might be able to gain access to this information should it be stored nationally, and what they might use it for
  + If I don’t even know of a genetic condition, why should others?
* There also potential economic implications
  + People might use my genetic information to charge me different insurance premiums
  + This might be expensive for the government to create and curate