Assessment Schedule – 2022

Biology: Demonstrate understanding of gene expression (91159)

Evidence Statement

Q	Expected Coverage	Achievement	Merit	Excellence
ONE	Protein Synthesis: to make / create / form a protein (polypeptide) from the DNA / genetic code / gene. Translation is described: mRNA is used to create a (functional) protein / polypeptide chain Codon: the sequence of three consecutive nucleotides on the mRNA strand. Anti-codon: three consecutive bases on a tRNA molecule that is complementary to mRNA codon. mRNA: is a single-stranded short molecule made up of phosphate, ribose sugar, and nitrogen bases A, U, G, and C / Made during transcription and carries the code / gene / genetic information out of the nucleus. tRNA: carries the amino acid to the ribosome and 'drops' it off for polypeptide chain. Amino Acid: the building blocks of proteins / polypeptides. Polypeptide chain: is a sequence of many amino acids bonded (peptide) together. Translation is explained: mRNA forms a complex with a ribosome. The ribosome is an organelle, which 'reads' mRNA bases in a code of three bases at a time. This is the codon on the mRNA. tRNA brings in amino acids – there is a specific tRNA molecule for each amino acid. Three unpaired bases on the tRNA are known as an anticodon, and have a specific corresponding amino acid that attaches to it. They are complementary to a codon on the mRNA. Codon-anticodon 'matches' using base pairing rule, thus bringing the correct amino acid to the next part of the sequence and attaching to the polypeptide. A start codon initiates the translation. A stop codon ends translation, which causes the ribosome to stop translating and release the mRNA and the polypeptide chain. (Once the polypeptide chain is released from the ribosome, it 'folds' into a three-dimensional structure, becoming a functional protein). Discusses the importance of translation: Translation of the mRNA template converts nucleotide-based genetic information into amino acids chains to create a polypeptide chain / actual protein. Without translation the correct order (sequence) of amino acids would not occur and the polypeptide / protein would not fold into a specific	• Describes translation. • Describes codon. • Describes anti-codon. • Describes mRNA. • Describes tRNA. • Describes amino acids. • Describes a polypeptide chain. • Describe protein synthesis. • Describes why DNA is not directly translated into a polypeptide chain.	• Explains translation including either start or stop codon (idea). • Explains the function of mRNA: to carry the 'message' from the template strand (or of the coding strand) to the ribosome for translation. • Explains the function of tRNA: 'link' between the message of the codon and the specific amino acid. Has complementary anticodon. • Explains how mRNA / tRNA have specific (particular / corresponding) amino acids by mentioning their complementary nature OR the anticodon is part of a specific tRNA that is specific only to ONE amino acid. • Explains why DNA is not directly translated into a polypeptide chain. • Explains the importance of translation.	• Discusses the relationship between codons, anticodons, tRNA, mRNA, and amino acids (transcription and translation) • Discusses importance of translation AND explanation of translation. • Justifies TWO reasons DNA is not directly translated into a polypeptide chain AND explanation of translation.

	3-D shape. Justifies reasons why a polypeptide chain is not directly translated from the DNA strand: • Ribosomes are used to make polypeptide chains, and are not found in the nucleus. • Ribosomes are capable of translating only single-stranded mRNA. • DNA is only one copy of the gene but a cell can produce many mRNA via transcription; therefore many copies of the same gene / protein in response to cell demands. If translation was to occur in the nucleus directly from the DNA template strand, it would be slow, as only one molecule of protein could be produced at a time by each cell, as there is only one copy of the needed DNA. As proteins are large molecules, these may not be able to leave the nucleus, as they would be too large to pass through the pores of the nuclear membrane. • Maintain DNA integrity (keep it safe from damage). Blueprint, working copy of mRNA created with genetic information / DNA cannot leave the nucleus because it will get broken down / damaged / destroyed by enzymes in the cytoplasm.			

NØ	N1	N2	A3	A4	M5	M6	E7	E8
No response; no relevant evidence.	Provides any ONE statement from Achievement column.	Provides any TWO statements from Achievement column.	Provides any THREE statements from Achievement column.	Provides FOUR statements from Achievement column.	Provides any THREE statements from Merit column.	Provides any FOUR statements from Merit column.	Provides the criteria for Excellence for the ONE bullet point.	Provides the criteria for Excellence for TWO bullet points.

Q	Expected Coverage	Achievement	Merit	Excellence
TWO (a)	A mutation is a permanent change in the DNA (sequence) / genetic code / gene.	• Describes a mutation.		
(b)	Substitution mutation – a single nucleotide change / swapped, which may result in a codon that codes for a different amino acid. An insertion is when a base is inserted into the DNA sequence. A deletion is when a base is taken out / removed from the DNA sequence. Substitution mutation – a single nucleotide change / swapped, which may or may not result in a codon that codes for a different amino acid. (Not all substitutions result in a new amino acid, due to redundancy of the code.) On the DNA strand, a single nucleotide is substituted / swapped for another, so the strand still has the correct number of bases / start and stop codons not affected and the protein can be made. Due to degeneracy of the code, a substitution (silent) mutation may code for the same amino acid and the same amino acid is made and the final protein is the correct shape / function. This is called a silent mutation. However, a substitution mutation can cause a different amino acid to be coded for causing the final protein (polypeptide) to fold slightly differently, and therefore not function correctly / differently. Both an insertion and deletion mutation cause a frameshift mutation because they both change the number of bases / length of a gene, either increasing or decreasing the DNA sequence. By adding or removing a single base, every codon / triplet from the point of the mutation is affected (reading frameshift), which would therefore create different codons and different amino acid sequence. The frameshift could also alter start / stop codons, which affects the length of the amino acid sequence and thus the structure / folding of the final protein. Insertion and deletion mutation affect the final protein the most / more than substitution mutations. This is because a substitution may only affect one triplet / codon, and therefore only one amino acid in the polypeptide chain. If only one amino acid is changed, this will change the shape of the protein; however, this change might only be slight. In contrast, insertion and deletion mutations may result in all the amino acids after the mutation to be incorrect. This will result in the final protein folding differently. This drastic change in shape will render the protein completely non-functional. These mutations may also change the position of the stop triplet / codon either by being too early and	• Describes an insertion / Describes a deletion. • Describes a substitution. *(Can use diagrams to describe substation / deletion / ins ertion mutation)* • Describes degeneracy of the code. • Identifies substitution mutation unlikely to change protein. Identifies insertion / deletion as most likely to change protein.	• Explains a substitution mutation has the least effect on the final protein, because: it may code for the same amino acid / does not cause a frameshift • Explains a substitution mutation has the least effect on the final protein, because the length / start stop codons unchanged. • Explains insertion has major effect on the final protein (amino acid sequence / shape / function of protein), because of frame shift. • Explains deletion has major effect on final protein (amino acid sequence / shape / function of protein), because of frame shift. • Amino acid sequence changes / length changes when there is an insertion / deletion but maybe not when substitution. • Explains the mutation causes the polypeptide chain to fold differently, which may affect protein function OR Explains the order of amino acid change which causes a shape change and effecting the function (not mention of mutation)	• Comprehensively discusses that degeneracy of the code is able to buffer the effect of a substitution mutation. A substitution mutation does not change the amino acid; therefore the length and order of bases is exactly the same as the normal order, and the final protein functions correctly. • Discusses how an insertion mutation affects the base sequence causing amino acids order (mostly likely) to change from the insertion mutation onwards causing the protein to fold incorrectly / incorrect shape therefore effecting the final protein structure and function. OR Discusses how a deletion mutation affects the base sequence causing amino acids order (mostly likely) to change from the deletion mutation onwards causing the protein to fold incorrectly / incorrect shape therefore effecting the and the final protein.

	terminating the polypeptide chain early / causing a shorter polypeptide chain or too late extending the polypeptide chain.		• Explains degeneracy of the code: e.g. there are 64 codons / triplets that codes for 20 amino acids therefore more than one codon / triplet codes for the same amino acid.	

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Q	Expected Coverage	Achievement	Merit	Excellence
THREE	An enzyme is a biological catalyst (speeds up) a reaction. A precursor / intermediates are starting molecules or molecules within a pathway that are required for the next step in a metabolic pathway. A final product in a metabolic pathway indicates the end of the pathway. A metabolic pathway is a series of chemical reactions where the product / substrate of one reaction is the substrate for the next. In a metabolic pathway one gene codes for one enzyme. Each enzyme can only catalyse one specific reaction due to its unique shape. In the first step of the Himalayan rabbit metabolic pathway, the gene produces the enzyme (tyrosinase) via protein synthesis. The enzyme (tyrosinase) reacts with the substrate Tyrosine (intermediate) to produce melanin (final product). Each step in the metabolic pathway is indirectly controlled by a gene on the DNA as that gene has the code for the enzyme needed to catalyse that step. (If the gene on the DNA mutates so that the enzyme (tyrosinase) is temperature sensitive, that step in the pathway may not always occur). Darker colour of the Himalayan rabbit extremities: when gene mutates so that the enzyme (tyrosinase) is temperature sensitive, melanin will only be produced at the cooler temperatures of the rabbit's extremities. White colour Himalayan rabbit chest area: when the gene mutates so that the enzyme (tyrosinase) is heat sensitive, it becomes non-functional / denatures / changes shape at the warmer temperatures in the chest area, then melanin is not produced and the chest is white. The mutated temperature sensitive form of the enzyme (tyrosinase) does not work as a catalyst at warm core rabbit body temperatures. This is because the enzyme denatures (loses shape), and as a result, pigment is not produced. The enzyme maintains its shape and its active site / function only at the cooler (temperatures) extremities, so is able to catalyse the breakdown of tyrosine into melanin- these parts of the body are black. The Himalayan rabbit produces the same mutated temperature-sensitive (tyrosinase) enzyme in all parts of its body and throughout its life, so to make a completely white rabbit you would need to keep them in temperatures 30° C and above to deactivate / non-functional enzyme and produce white fur. In contrast to produce a completely black rabbit you would need to keep them at 25° C or lower so the (tyrosinase) enzyme doesn't denature / deactivate and is functional so therefore can react with the tyrosine substrate to produce the final product of melanin. OR technically Himalayan rabbits	• Describes precursor / substrate. • Describe intermediate / final product. • Describes enzyme. • Describes a metabolic pathway (idea of successive reactions). • Describes genes code for enzymes. • Describes interaction between genotype + environment = phenotype (can accept any example at). • Describe enzymes work at low temperatures produces black / melanin.	• Explains the relationship between genes, enzymes and products OR Explains a metabolic pathway in Himalayan rabbits. • Explains how genes (genotype) interact with the environment (temperature) to produce a phenotype (white or black, this context). • Explains the Himalayan rabbits are white on their core body, because the temperature is warmer and deactivates / denatures / ch anges shape the enzyme (tyrosinase). • Explains the Himalayan rabbits are black on their extremities, because the cooler temperature causes the enzyme (tyrosinase) to work correctly / correct shape / functional.	• Explains a metabolic pathway in Himalayan rabbits AND a comprehensive discussion that recognises the rabbit produces the same (tyrosinase) enzymes in all parts of its body (genotype the same), but the environmental temperature affects the enzymes functioning (folding / 3-D shape). • Explains a metabolic pathway in Himalayan • rabbits and a comprehensive discussion that recognises the rabbit produces the same enzyme (genotype) for • its whole life so the environmental temperature would need to warm (white) or low (black) for its whole life to produce white / black fur.

	could never be black because they are warm blooded / body temperature is 37° C and therefore the (tyrosinase) enzyme will always be denatured / non-functional, and cannot produce melanin. The Himalayans rabbit's genotype interacts with the environmental temperature to produce a specific phenotype / genotype + environment = phenotype			

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Cut Scores

Not Achieved	Achievement	Achievement with Merit	Achievement with Excellence
0 – 7	8 - 13	14 - 18	19 – 24