**Assessment Schedule – Biology 2.7: Demonstrate understanding of gene expression (AS 91159)**

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| QUESTION ONE - Evidence | Achievement | Merit | Excellence |
| Nucleotides consist of:* Phosphate
* Sugar (ribose or deoxyribose)
* Nitrogenous base (ATGCU)

Base pairs combinations between DNA-RNA during transcription are as follows: A-U, C-G, G-C and T-ATranscription produces a single strand of mRNA which is complementary to the template strand and which carries the same code as the coding strand of DNA with U wherever T was located.The product of translation is a polypeptide chain made up of amino acids joined by peptide bonds.DNA triplets determine the order of amino acids, but are transcribed into codons on mRNA and then translated with the help of anticodons on tRNA. The ribosome is an organelle, which ‘reads’ mRNA bases in a code of three bases at a time. This is known as a codon.tRNA brings in amino acids – there is a different kind of tRNA for each amino acid. Three unpaired bases on the tRNA are known as an anticodon. They are complementary to a codon on the mRNA. Codon-anticodon ‘matches’ combine with base pairing, thus bringing the correct amino acid to the next part of the sequence.A start codon initiates the translation.Peptide bonds form between amino acids building a polypeptide chain.A stop codon ends translation. The polypeptide chain is released from the ribosome and ‘folds’ into a three-dimensional structure, becoming a functional protein. | Describes * Nucleotides as a phosphate, sugar and base with correct RNA and DNA sugars and bases
* All base pair combinations given
* Identifies the mRNA as the product of transcription
* Identifies one polypeptide chain/protein as the product of translation
* Describes two of: triplets, codons and anti-codons with their correct function
 | * Explains relationship of the coding strand of DNA to the mRNA. It is the same sequence of bases, but T has been replaced with U and all nucleotides are RNA instead of DNA in the mRNA.
* Explains the relationship between the non-coding strand and the mRNA. It serves as the template for transcription and is complementary to the mRNA
* Explains the relationship between mRNA codons and tRNA anti-codons with respect to translation
* Explains the relationship between tRNA and amino acids and how this relationship works.
 | * Full discussion of protein synthesis outlining the relationship between triplets, codons, ant-codons and the polypeptide/protein produced.
* Discussion includes role of start and stop codons with respect to amino acid sequence/length of polypeptide chain/protein **AND** the structure of the product.
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| NØ | N1 | N2 | A3 | A4 | M5 | M6 | E7 | E8 |
| No response or no relevant evidence. | Provides any ONE statement from Achievement. | Provides any TWO statements from Achievement. | Provides any THREE statements from Achievement. | Provides any FOUR statements from Achievement. | Provides any TWO statements from Merit. | Provides THREE statements from Merit. | Provides one point for Excellence. | Provides both points for Excellence  |
| **Q** | **Expected Coverage** | **Achievement** | **Merit** | **Excellence** |
| TWO(a) | Understanding of transcription is shown by the base-pairing rules for DNA and RNA.Sequences are completed to be:UAU and CCU | * In (a) correctly completes both strands.
* In (b) identifies both amino acids
* In (c) identifies that the polypeptide will be shortened by the STOP codon
* Defines redundancy, eg each amino acid can have more than one triplet/codon/anticodon code for it.
* Defines degeneracy, eg a change in the nucleotide sequence due to mutation.
 | * In (c) explains frame shift in relation to translation.
* In (c) explains the structural implication of the stop codon as changing the specific shape of the polypeptide due to a change in the sequence of amino acids
* Explains the relationship between structure and function of an enzyme
* Gives reasons how / why more than one codon can code for the same amino acid
* In (d) explains why degeneracy leads to redundancy e.g. more than one codon for an amino acid means that some codons are redundant
 | * In (c) fully discusses links between mutation in the DNA (triplet) to corresponding codon, anticodon and amino acid (the process of translation).
* Fully links change in amino acid sequence (stop codon) to structure and catalytic function in neurons.
* In (d) fully discusses redundancy due to degeneracy in the context of Ser (3rd amino acid)
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| (b) | Understanding of translation is shown by the correct amino acids LEU and PRO |
| (c) | Translation is where the code sequence carried on the mRNA is used to create a functional protein.**Frame shift mutations:** occur when a nucleotide(s) is inserted or deleted, changing the reading frame of each triplet code. This can alter the ‘meaning’ of all the bases that follow the shift. The gene product in turn is changed in length/shape.The Tay Sachs mutation alters several amino acids and terminates translation early resulting in a shorter than normal gene product. |
| (d) | Shape/length of polypeptide determines function.Enzymes with active sites are examples of protein gene products that catalyse (speed up) biochemical reactions.The result of an early stop codon or altered sequence of amino acids causes the protein to fold incorrectly. This can block the active site, or cause part of the active site to not be formed correctly. Degeneracy occurs when a change in genetic code such as a mutation occurs. Although the code changes due to the Tay Sachs mutation, not all the amino acids in the polypeptide change as a result. For instance, the third triplet/codon in the HEXA allele has been affected by the mutation changing the third nucleotide. This however does not result in a change in amino acid, since there are multiple t-RNA molecules that carry the same amino acid Ser. These two triplets/codons/anticodons are thus redundant since they do the same job. Redundancy due to degeneracy in the code refers to the fact that no structural change in the polypeptide need happed when the nucleotide sequence of a gene is altered.  |

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| NØ | N1 | N2 | A3 | A4 | M5 | M6 | E7 | E8 |
| No response or no relevant evidence. | Provides any ONE statement from Achievement. | Provides any TWO statements from Achievement. | Provides any THREE statements from Achievement. | Provides any FOUR statements from Achievement. | Provides any THREE statements from Merit. | Provides FOUR or more statements from Merit. | Provides TWO criteria for Excellence | Provides the criteria for all THREE Excellence criteria. |

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| **QUESTION THREE - Expected Coverage** | **Achievement** | **Merit** | **Excellence** |
| The phenotype of an organism results from the interaction between the genotype and the environment. The expression of the genotype can be affected by the environmental conditions that exist internally or externally for an organism without the genotype itself being altered in any way.The genotype provides the instruction set for a particular structure or function, but this may not be able to be fully expressed if the environmental conditions work against it. Eg. Genes code enzymes whose activity is affected by temperature.Ametabolic pathway is a series of biochemical reactions that are connected by their intermediates: The product(s) of one reaction are the reactants (substrates) for subsequent reaction(s).Because there are a series of biochemical reactions, each one usually controlled by an enzyme, multiple genes are involved in regulating the pathway.In the simple pathway A → B → C, the conversion of compound A to B occurs through the action of enzyme 1, and the conversion of B to C occurs through the action of enzyme 2.If enzyme 1 is unable to catalyse the first step in the process, then the end product can not be made even if enzyme 2 is fully functional.Mutations result in new alleles which alter the functioning of genes product. | * Describes the term metabolic pathway, eg a series of enzyme controlled reactions.
* The product(s) of one reaction are the reactants (substrates) for subsequent reaction(s)
* Identifies that mutations result in new alleles which alter the structure of enzymes
* Identifies that temperature can affect the shape of an enzyme.
* Identifies that the shape of an enzyme influences its ability to function
* Gives an account of how temperature is an environmental factor affects expression of colour.
 | * Explains how the metabolic pathway may be affected when any one enzyme is unable to function. Explains the inability to make eumelanin to the lack of dopaquinone with TYR inactivation.
* Relates difference in black and cinnamon phenotype to changes in the **efficiency** of the TYRP1 enzyme. The difference in phenotype is due to different amounts of the **same** product caused by a mutation in the TYRP1 gene.
* Relates the difference in the catalytic optimal temperature range of normal and mutant TYR to changes in enzyme structure due to mutation.
* Links the changing phenotype of white kittens to changes in body temperature as they mature (outside of mum, extremities cooler than core).
 | * Discusses that since there is no allele for white coat (both parents are pure breeding for black) this phenotype must be due to the breakdown along the metabolic pathway caused by another enzyme. Links the lack of an intermediate substrate to the failure of the black allele to be expressed.
* Despite all cells having the same genotype and all producing the same gene product (Himalayan TYR enzyme), the expression of the gene was only observed in the cells that had the optimal temperature range which allowed the structure of the Himalayan TYR to be active. Links warmth of mother’s body heat at birth/cooler extremities to enzyme function.
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| NØ | N1 | N2 | A3 | A4 | M5 | M6 | E7 | E8 |
| No response or no relevant evidence. | Provides any ONE statement from Achievement. | Provides any ONE statement from Achievement. | Provides any THREE statements from Achievement. | Provides any FOUR statements from Achievement. | Provides any TWO statements from Merit. | Provides THREE statements from Merit. | Provides EITHER statement for Excellence. | Provides BOTH statements for Excellence. |

# Judgement Statement

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|  | Not Achieved | Achievement | Achievement with Merit | Achievement with Excellence |
| Score range | 0 – 6 | 7 – 12 | 13 – 18 | 19 – 24 |