Assessment Schedule – 2023

Biology: Demonstrate understanding of gene expression (91159)

Assessment Criteria

Achievement	Achievement with Merit	Achievement with Excellence
Demonstrate ***understanding*** involves: • defining, using annotated diagrams or models to explain, and giving characteristics of, or an account of, gene expression.	*Demonstrate* ***in-depth understanding*** involves: • providing a reason as to how or why biological ideas and processes affect gene expression.	*Demonstrate* ***comprehensive understanding*** involves: • linking biological ideas and processes about gene expression; explanations may involve justifying, relating, evaluating, comparing and contrasting, or analysing.

Cut Scores

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

Evidence

Question One

<table>
<tr><th>Expected Coverage</th><th>Achievement</th><th>Achievement with Merit</th><th>Achieve. with Excellence</th></tr>
<tr>
<td>(a):
<table>
<tr><th>DNA Template</th><th>Normal gene sequence</th><th>Point mutation 1</th><th>Point mutation 2</th></tr>
<tr><td>Middle section of gene</td><td>TAA TAG ATA CCA CAA</td><td>TAA TAG AT<u>G</u> CCA CAA</td><td>TAA TAG AT<u>T</u> CCA CAA</td></tr>
<tr><td>mRNA</td><td>AUU AUC UAU GGU GUU</td><td>AUU AUC <u>UAC</u> GGU GUU</td><td>AUU AUC <u>UAA</u> GGU GUU</td></tr>
<tr><td>Amino acid sequence</td><td>Ile Ile Tyr Gly Val</td><td>Ile Ile <u>Tyr</u> Gly Val</td><td>Ile Ile <u>STOP</u> or
Ile Ile <u>STOP</u> Gly Val</td></tr>
</table>
</td>
<td>• THREE boxes are correct and must include at least ONE mRNA and amino acid sequence / box.</td>
<td>• All mRNA and amino acid sequences are correct.</td>
<td></td>
</tr>
<tr>
<td>(b):
A mutation is a permanent change in the DNA base sequence.
Both mutations are substitution mutations.
Substitution mutation is when one base is swapped in the DNA base sequence.
Point mutation 1 is a silent mutation where the change in the base sequences A to G still codes for the same amino acid, Tyr.
Point mutation 2 changes A to T and codes for a STOP codon.
Point mutation 1 is a silent mutation because of degeneracy of the code; even though ATA changed to ATG, both triplets code for the same amino acid. This is because there are 20 amino acids and 64 triplets / codons. This means that an amino acid will usually have more than one codon / triplet that codes for it. There is no change to the start / stop codons. Consequently, the chain will be the same length and have the same amino acids, meaning it will fold correctly / be the same shape, and so will still be fully functional.
Point mutation 2 will have an effect on the final protein. The change in amino acid to STOP will result in the amino acid sequence being shorter and folding incorrectly / having the wrong shape. This will mean that its shape is very different, and thus its function will be compromised (it will not be able to carry out its function).</td>
<td>Describes:
• a mutation
• point mutation 1 is a silent / same-sense mutation
• point mutation 2 codes for STOP / is a nonsense mutation.
Identifies:
• both mutations as a substitution mutation OR describes a substitution mutation
• that point mutation 1 will not change the final protein OR point mutation 2 will change the final protein
• that more than one codon can code for the same amino acid or mutation 1, due to redundancy / degeneracy.</td>
<td>Explains:
• point mutation 1 does not change the amino acid sequence therefore the protein can still fold into / have the correct shape / not affect function
• point mutation 2 does change the amino acid to a stop codon causing the amino acid sequence to be shorter (than normal) and fold incorrectly / protein does not function correctly
• silent mutations / degeneracy of the code (i.e. more codons than amino acids / redundancy in the code – 64 and 20)
• point mutation 1 will be the same length of gene / same number of amino acids because the start or stop</td>
<td>Discusses, demonstrating comprehensive understanding of:
• why point mutation 1 will not affect the position of the start / stop codons (i.e. does not cause a change in length of amino acid sequence, and it will not change the amino acid, will not change folding / shape, will not impact protein folding / shape AND function; and makes links to silent mutations and degeneracy of the code
• how point mutation 2 causes a premature stop codon, (ATT codes for a stop), therefore changes the length of amino acids (shorter), affects folding / protein shape, and negatively affects function.</td>
</tr>
</table>

Expected Coverage	Achievement	Achievement with Merit	Achieve. with Excellence
		codons remain unchanged / unaffected • in both point mutations 1 and 2, the start codons are not affected; however, in point mutation 2, the stop codon is affected.	

Not Achieved		Achievement		Achievement with Merit		Achievement with Excellence	
N1	N2	A3	A4	M5	M6	E7	E8
ONE evidence point at Achievement.	TWO evidence points at Achievement.	THREE evidence points at Achievement.	FOUR evidence points at Achievement.	THREE evidence points at Merit.	FOUR evidence points at Merit.	ONE evidence point at Excellence.	BOTH evidence points at Excellence.

N0 = No response; no relevant evidence.

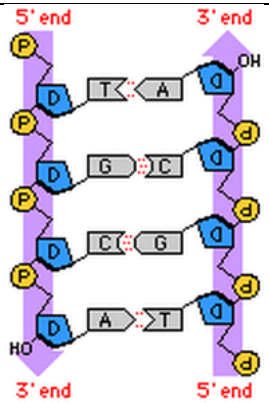
Question Two

Expected Coverage	Achievement	Achievement with Merit	Achievement with Excellence
An environmental factor (non-mutagenic) is a substance / factor that affects gene expression / phenotype but does not change the DNA base sequence / genotype. A mutagen is a substance that changes the DNA base sequence permanently / genotype. An enzyme is a biological catalyst that speeds up a reaction. A metabolic pathway is a series of enzyme-controlled, chemical reactions where the product of one reaction is the substrate for the next. In a metabolic pathway, one gene encodes one enzyme. Each enzyme can only catalyse one specific reaction due to its unique shape. In a normal / functioning metabolic pathway, melanin is produced when gene 1 codes for enzyme 1, which converts phenylalanine into tyrosine. Tyrosine is then the substrate in the next reaction where gene 2 codes for enzyme 2, which converts tyrosine into melanin. Some UV light causes gene 2 to produce more of enzyme 2, which then expresses more melanin in the skin. Therefore, environmental factors (low UV light) + genotype = phenotype. Environmental factors interact with the genes / genotype to express the phenotype type. Melanin is not produced in people with albinism if either or both gene 1 and gene 2 has a mutation. A mutation to either gene would not produce the enzyme which cannot act on the phenylalanine and tyrosine substrates and convert into melanin. People with albinism are more likely to get skin cancer because they do not have melanin pigmentation to protect the DNA in their skin cells. UV light can be both a non-mutagenic environmental factor and a mutagen because some UV light causes gene 2 to code for more of enzyme 2, which in turn converts more tyrosine into melanin, expressing increased pigment / skin colour. This allows the full genetic potential of gene 2 to be expressed without changing DNA / genotype. However, UV light can also cause DNA to permanently change and affect folding / shape / functioning of proteins produced and can cause skin cancer. This changes the genotype of the individual which will also change the phenotype.	**Describes:** • an environmental factor that changes the phenotype but not the genotype • a valid example of an environmental factor, e.g. diet / temperature / rainfall (**not** UV radiation or sunlight) • a mutagen • a metabolic pathway OR that an enzyme is a biological catalyst • that the genes in the metabolic pathway code for the enzymes • mutated DNA in people with albinism means they are not protected from UV light **States** that**:** • albinism is due to no melanin, caused by build of tyrosine / phenylalanine (genes mutated) • phenotype / melanin production **(not** just skin colour) is a product of both the environment and genotype OR G + E → P (equation or in words).	**Explains:** • a metabolic pathway (as for A4 and includes the link to genes coding for enzymes catalysing only one reaction in the pathway) **or** explains this metabolic pathway in full (all genes, enzymes, substrates, and products used in context correctly) to show how melanin is produced • how UV causes increased levels / rates of enzyme 2 production, therefore more melanin is produced • how genes (genotype) + environment factors (UV light) contribute to the phenotype (melanin amount) • that the UV light enables the genotypic potential to be reached because correct / enough melanin is made • how / why melanin is not produced in people with albinism, using the metabolic pathway (gene 2 mutated, enzyme 2 dysfunctional, tyrosine not converted so no melanin made) • why people with albinism are more likely to get skin cancer, i.e. because there is no melanin protecting the underlying skin layers • that excess UV can affect DNA and increase the rate of mutation, e.g. linked to cancer.	**Discusses**, demonstrating comprehensive understanding of how: • UV light causes more enzyme 2 to be made, so more melanin (i.e. change in phenotype); therefore changes the phenotype but the DNA remains unchanged / no change to genotype • UV light causes the genotype to change / mutation in gene 2 dysfunctional / no enzyme 2 made so no melanin is made; therefore the phenotype is changed because of the change in genotype. • UV affects the genotype (mutated gene 2) so no melanin can be made; therefore, greater likelihood of cancer when the underlying skin is not protected by melanin and less likelihood in individuals that can produce melanin.

Not Achieved		Achievement		Achievement with Merit		Achievement with Excellence	
N1	**N2**	**A3**	**A4**	**M5**	**M6**	**E7**	**E8**
ONE evidence point at Achievement.	TWO evidence points at Achievement.	THREE evidence points at Achievement.	FOUR evidence points at Achievement.	THREE evidence points at Merit.	FOUR evidence points at Merit.	ONE evidence point at Excellence.	TWO evidence points at Excellence.

N0 = No response; no relevant evidence.

Question Three

Expected Coverage	Achievement	Achievement with Merit	Achievement with Excellence
(a):  Sourced: https://www.mrgscience.com/topic-26-structure-of-dna-and-rna.html	• Labelled drawing showing correct anti-parallel DNA section, sugars, phosphates, and bases (**one** minor error, e.g. both strands same direction / single bonds between bases).	• Labelled drawing showing correct anti-parallel DNA section, sugars, phosphates, and bases (**no** errors); must have double bonds between AT and triple bonds between GC.	
(b): Transcription: First step of protein synthesis. Translation: Second step of protein synthesis.	**Names:** • transcription AND translation in the correct order.		
(c): Triplet: three consecutive nucleotide bases on the DNA strand. Codon: the sequence of three consecutive nucleotides on the mRNA strand (that is complementary to a triplet). Anticodon: three consecutive bases on a tRNA molecule (that is complementary to mRNA codon). The base-pairing rule states that A can only bind with T (on the DNA) or U (on the RNA), T (DNA) or U (RNA) can only bind with A, and C can only bind with G. The DNA holds the genetic code for the protein. The triplets on the DNA and the codons on the mRNA both code for amino acids. In transcription, the triplets on the DNA need to be made into codons on the mRNA so that the code for the protein / gene can be taken out of the nucleus / into the cytoplasm / ribosome for translation. This must be done accurately so the mRNA carries the correct code / information for the sequence of amino acids for the protein.	**Describes:** • a triplet • a codon • an anticodon • the base-pairing rule (can come from diagram). States that: • protein is made of amino acids • inaccurate transcription / translation leads to incorrect AA sequence / shape protein.	**Explains:** • C binds with G and T / U with A due to the number (2 and the 3) of hydrogen bonds • C binds with G and A binds with T / U because of the size of the bases; double ring purines can only bind with single ring pyrimidines • the triplets / codons determine the specific amino acids in the polypeptide chain • triplets must be transcribed into codons in order for the code to leave the nucleus / go to ribosome • the complementary nature of DNA and mRNA **or** of mRNA and tRNA • accuracy is needed so the protein is folded correctly / has correct shape / functions correctly.	**Discusses**, demonstrating comprehensive understanding that: • links the number of hydrogen bonds that can form between AT and GC nucleotide bases with the reasoning that only certain combinations are possible; therefore, the complementary base-pairing rule ensures accurate transcription / translation of the protein • links the size (either by names or number of loops) of the nucleotide bases with accurate transcription / translation because of complementary base pairing, e.g. given that single ring / small bases can only fit with double ring / larger bases, the base pairing rule ensures accurate transcription / translation • links the accurate transfer of the genetic code to the sequence of

Expected Coverage	Achievement	Achievement with Merit	Achievement with Excellence
In the ribosome, the mRNA is read in order to make the protein. Each codon codes for one amino acid, and the tRNA brings in the amino acids to the ribosome. Each tRNA carries one specific amino acid and has an anti-codon that complements the codon for this amino acid. In the ribosome, the codons are bonded to their complementary anti-codons on the tRNA with the correct amino acid. This ensures that the tRNA will put its specific amino acid into the correct sequence / order in the protein. This accuracy is important in transcription to ensure that each triplet on the DNA is accurately transcribed to the correct codon so that the mRNA carries the correct code for the protein / information to make the protein. In addition, accuracy is important in translation so the tRNA puts the correct amino acid into the correct order in the polypeptide chain. The order of the amino acids determines the shape / folding of the protein / polypeptide, and the shape of the protein needs to be correct for the protein to function. Accurate transcription / translation is ensured by the base-pairing rule. The size of the bases determines which bases can bind together. A large (double ring / purines) base can complement only a small (single ring / pyrimidines) base. For example, A can bind only with T because A is large and T is small. Adenine and guanine are both large so can't fit together in either DNA or RNA. In addition, the placement of hydrogen bonds prevents other bonding combinations. A and T form the same number of hydrogen bonds together, and C and G form the same number of hydrogen bonds together. Adenine can't bind with cytosine because they have different numbers of hydrogen bonds and can't chemically fit together.			amino acids, i.e. correct protein synthesis for protein shape / function.

Not Achieved		Achievement		Achievement with Merit		Achievement with Excellence	
N1	**N2**	**A3**	**A4**	**M5**	**M6**	**E7**	**E8**
ONE evidence point at Achievement.	TWO evidence points at Achievement.	THREE evidence points at Achievement.	FOUR evidence points at Achievement.	THREE evidence points at Merit.	FOUR evidence points at Merit.	ONE evidence point at Excellence.	TWO evidence points at Excellence.

N0 = No response; no relevant evidence.