Assessment Schedule – 2024

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 reasons 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>Achievement with Excellence</th></tr>
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<td>(a)
<table>
<tr><th>DNA</th><th>mRNA</th></tr>
<tr><td>DNA is a double-stranded molecule</td><td>RNA is a single-stranded molecule</td></tr>
<tr><td>Deoxyribose sugar</td><td>ribose sugar</td></tr>
<tr><td>Nitrogen bases are A, T, G, and C (in mRNA the base T is replaced by U)</td><td>Nitrogen bases are A, U, G, and C (in mRNA the base U replaces T)</td></tr>
<tr><td>Long molecule / large size</td><td>Short molecule / small size</td></tr>
<tr><td>Stays within nucleus</td><td>Moves outside of the nucleus</td></tr>
<tr><td>Only one type: DNA</td><td>Three types: mRNA, tRNA, rRNA</td></tr>
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<td>• One Achievement point for TWO correct rows in table.</td>
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<td>(b)
Protein synthesis creates proteins from DNA.
The function of messenger RNA (mRNA) is to carry sections of this genetic information to the ribosome.
Transfer RNA (tRNA) has an anticodon that is three consecutive bases, and codes for a specific amino acid.
Anticodon / codon and amino acids are specific to one another. tRNA function is to carry a specific amino acid to the ribosome, and its anticodon complementary (H-bonding) matches to the codon (three consecutive bases) on the mRNA strand. The amino acid bonds with another amino acid to produce a polypeptide chain and a specific protein.
tRNA has a ‘clover leaf’ shape and the bases are ‘protected’ from enzyme breakdown. The significance of tRNA stability means tRNA can be reused and ‘carry’ many (specific) amino acids to the ribosome / growing polypeptide chain. This ensures accurate,</td>
<td>Describes:
• protein synthesis: to make / create / form a protein (polypeptide) from DNA / genetic code/gene
• the function of mRNA: to carry the genetic information / code / message to the ribosome
• the function of tRNA: to carry an amino acid to the ribosome (mRNA)
• the structure of tRNA: has an anticodon / single stranded folded on itself / L-shaped / cloverleaf-shaped / annotated diagram)
• transcription: the process that makes mRNA</td>
<td>Explains:
• the function of mRNA: to carry a gene / section (indicates beginning and an end) of the DNA from the nucleus to the ribosome (for translation)
• the function of tRNA: is to carry a specific amino acid to the ribosome / polypeptide chain
• the complementary nature of codons and anticodons
• the relationship between mRNA and tRNA with regard to H-bonding / size of bases
• mRNA is unstable because it is single-stranded and ‘unprotected /</td>
<td>Discusses:
• the function of mRNA and tRNA in transferring the genetic code/gene from DNA to the ribosome and its complementarity to the specific tRNA molecule and tRNA (anticodon), forming a specific protein.
• the structure, stability of mRNA and tRNA and their significance in protein synthesis.</td>
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</table>

Expected Coverage	Achievement	Achievement with Merit	Achievement with Excellence
consistent, and reliable translation of genetic material into proteins, maintaining the integrity of the genetic code. mRNA is single-stranded, and the bases are 'unprotected' so are broken down by enzymes (quickly). This unstable structure means mRNA is only used to make protein for a short time. The significance of mRNA instability allows for rapid and precise regulation of protein synthesis.	• translation: mRNA is used to create (turn into) a (functional) protein / polypeptide chain • anticodon: three bases that code for an amino acid OR codon: three conservative bases on mRNA.	open' to enzyme breakdown OR tRNA is stable because it forms a folded structure / the shape enables it to be 'protected' from enzyme breakdown. • the significance of mRNA: mRNA is short-lived, providing valid reason/s, e.g. mRNA is only used to make protein for a short time / don't want to waste materials /regulation of proteins (by breaking down mRNA quickly) / adjusts protein production in response to cell environment • the significance of tRNA: tRNA is long-lived, providing valid reason/s, e.g. its reusability / takes time to 'find/deliver' the amino acid.	

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

N0 = No response; no relevant evidence.

Question Two

<table>
<tr><th>Expected Coverage</th><th>Achievement</th><th>Achievement with Merit</th><th>Achievement with Excellence</th></tr>
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(a) (i)

Normal β-globin polypeptide	**1**	**2**	**3**	**4**
DNA template strand	TGA	GGA	CTC	CTC
mRNA (codon)	ACU	CCU	GAG	GAG
tRNA (anticodon)	UGA	GGA	CUC	CUC
Amino Acid sequence	thr	pro	glu	glu

(a) (ii)

Mutation 1	**1**	**2**	**3**	**4**
DNA template strand	TGA	GGA	C**A**C	CTC
mRNA (codon)	ACU	CCU	GUG	GAG
tRNA (anticodon)	UGA	GGA	CAC	CUC
Amino Acid sequence	thr	pro	val	glu

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- One Achievement point for one (either) fully correct table.

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(b) DNA mutations can be caused by internal (errors in DNA replication) and external / environmental factors (mutagens, UV radiation, X-rays, gamma rays, viruses, chemical mutagen / specific chemical named, breathing in smoke, processed food diet, carcinogen). A mutation is a permanent change in the DNA base sequence. A mutagen is any agent that increases the rate of mutations. The mutation is a base substitution (as only one base / nucleotide has been 'swapped') and has changed the third amino acid from *glu* to *val*. Insertion: one base is inserted into the DNA sequence. Deletion: one base is removed / take out of the DNA sequence. Same-sense / silent: one base is swapped but doesn't change the amino acid. Missense: one base is swapped and changes one amino acid. Nonsense: one base is changed and changes into a stop codon. There is no deletion / insertion, so no reading frameshift has occurred in the mutation (where the bases are moved to the left or right by a base deletion or insertion that is not a multiple of three), i.e. no amino acids downstream will be affected: amount of amino acids / length of the polypeptide chains hasn't been affected. Consequently, the substitution has affected only one amino acid, so a small change to the primary structure and the folding of the protein may only slightly change, so the reduction / increase in oxygen-carrying capacity could be less severe. A frameshift causes many amino acids to change and would be a severe change in order of amino acids and the folding of the protein; thereby, would severely reduce its function to assist with oxygen transport.	Describes or identifies / defines: • TWO causes of mutations • substitution / point mutation / substitution mutation • a (DNA) mutation • that no frameshift has occurred OR frameshift occurs with insertion / deletion mutations • mutagen • a negative consequence of a mutation, linking it to the final protein, e.g. haemoglobin won't 'work' correctly/nonfunctional • another type of mutation: insertion / deletion / silent / missense / nonsense / frameshift.	Explains: • mutagen and gives TWO examples • the mutation as a substitution, and identifies the change in one amino acid • the substitution causes only one amino acid change, i.e. a small change in the polypeptide chain, so there is a small / slight change in overall function / shape of the final protein • no insertion / deletion, so no reading frameshift has occurred that would affect all amino acids downstream; therefore, there is no large change in the polypeptide chain / protein shape / change in the overall function. OR if insertion / deletion, reading frameshift has occurred that would affect all amino acids downstream, resulting in a large change in the polypeptide chain / protein shape / change in the overall function • a silent / same-sense (substitution) mutation: the base is swapped but, due to redundancy (degeneracy) of the code, the same amino acid is added to the polypeptide chain; thereby, the protein folds correctly and is less severe than a substitution mutation (missense) that codes for a different amino acid	Discusses: • the effect of the mutation on the amino acid sequence and the functioning AND shape of the final haemoglobin beta polypeptide • the substitution (missense) mutation compared to another mutation: a insertion / deletion that causes a frame shift OR a frameshift causing a nonsense, resulting in changes to the amino acid sequence / changes in the amino acid sequence downstream from mutation linked to shape and function of haemoglobin, beta polypeptide, and severity of mutation • silent / same-sense mutation, base is swapped but, due to redundancy of the code, the same amino acid is added to the polypeptide chain, resulting in no change to the protein shape, and the protein folds correctly; this is less severe than a substitution mutation (missense) that codes for a different amino acid, as there is no effect on the haemoglobin beta polypeptide.

Expected Coverage	Achievement	Achievement with Merit	Achievement with Excellence
		• Start / stop codon is not affected by this (substitution) mutation, so the length of / number of amino acids is the same OR start/stop codon is affected by this (substitution) mutation: insertion / deletion / nonsense causes a frameshift so the length of / number of amino acids is not the same.	

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Describes ONE evidence point at Achievement.	**Describes** TWO evidence points at Achievement.	**Describes** THREE evidence points at Achievement.	**Describes** FOUR evidence points at Achievement.	**Explains** THREE evidence points at Merit.	**Explains** FOUR evidence points at Merit.	**Discusses** ONE evidence point at Excellence.	**Discusses** TWO evidence points at Excellence.

N0 = No response; no relevant evidence.

Question Three

Expected Coverage	Achievement	Achievement with Merit	Achievement with Excellence
A metabolic pathway is a series of enzyme-controlled reactions where the product of one reaction becomes the substrate for the next (intermediates). An enzyme is a biological catalyst / speeds up biological reactions and is made of protein. In a metabolic pathway, one gene codes for one enzyme. A gene is a section of DNA that codes for a protein / enzyme / trait. A substrate is a substance that an enzyme 'acts' on / binds with (to produce a product). Each enzyme can catalyse only one specific reaction due to its unique shape. In a normal / functioning metabolic pathway, gene 1 codes for enzyme 1, which converts the precursor substrate into the intermediate substrate. The intermediate substrate is then the substrate in the next reaction where gene 2 codes for enzyme 2, which converts the intermediate substrate into haem. If gene 1/ the gene that coded for enzyme 1 **only** is mutated, enzyme 1 will not function as its shape will be incorrect (due to incorrect amino acids being coded for). This will mean enzyme 1 is unable to catalyse the reaction of precursor substrate into intermediate substrate. Ultimately, this will cause the precursor to build up and prevent haem formation. If gene 2 / the gene that coded for enzyme 2 **only** is mutated, enzyme 2 will not function as its shape will be incorrect (due to incorrect amino acids being coded for). This will mean enzyme 2 is unable to catalyse the reaction of the intermediate substrate into haem. This will cause the intermediate to build up and prevent haem formation. If a person with a functioning enzyme 1 and 2 has a <u>low-iron diet</u>, the person would have anaemia because enzyme 1 would catalyse the reaction of the precursor substrate into the intermediate substrate, which would build up; however, the lack of reactant iron would prevent enzyme 2 catalysing the reaction of intermediate substrate into haem formation.	Describes: • a metabolic pathway • an enzyme • the relationship between genes and enzymes / how one gene codes for a specific / one enzyme • a change gene 1 or gene 2 that codes for enzyme 1 or enzyme 2 can cause anaemia / haem not to be produced • for haem to be produced, both genes / enzymes need to be correct / functional. • a mutation to gene 1 will result in no intermediate substrate being formed • a lack of iron prevents enzyme 2 from 'working' (catalysing the reaction) • lead inhibits enzyme 2 from 'working' (catalysing the reaction) • genotype + environment = phenotype • a gene • a substrate or provides an annotated diagram.	Explains: • the relationship between the two genes, two enzymes, and three molecules for this specific metabolic pathway • gene 1 or gene 2 is mutated, meaning enzyme 1 or enzyme 2 is not working, therefore haem is not made / will cause anaemia • how a low-iron diet would prevent enzyme 2 from 'working' / cause the catalysing of the intermediate substrate into haem formation. • how exposure to lead would inhibit enzyme 2 from 'working' / catalysing the reaction of intermediate substrate into haem formation • normal genotype interacts with the environmental factor of low / high iron to express (the phenotype) low / high haem formation / anaemia. • normal genotype interacts with the environmental factor of high lead to express (the phenotype) low haem formation / anaemia • low iron or high lead don't mutate the DNA / gene / genotype.	Discusses: • this specific metabolic pathway, including how anaemia can be caused by mutations in gene 1 or 2 or both • this specific metabolic pathway AND normal genotype (genes) interacting with either the environmental factor of low / high iron to not fully express (the phenotype / non anaemia), changing the rate (amount) of haem formation OR normal genotype interacting with the environmental factor of high lead to not fully express (the phenotype / non anaemia), changing the rate (amount) of haem formation.

Expected Coverage	Achievement	Achievement with Merit	Achievement with Excellence
If a person with a functioning enzyme 1 and 2 was exposed to lead, the person would have anaemia because enzyme 1 would catalyse the reaction of the precursor substrate into the intermediate substrate, which would build up. However, lead would inhibit enzyme 2 from catalysing the reaction of intermediate substrate into haem formation.			

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