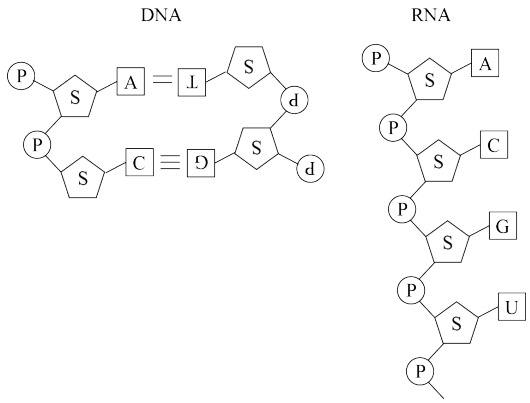
Assessment Schedule – 2017

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. The explanation may involve justifying, relating, evaluating, comparing and contrasting, or analysing.

Evidence

Q	Expected Coverage	Achievement	Merit	Excellence
ONE (a)		DNA • Correctly labels any three of Nucleotide base, Hydrogen Bond, Sugar, Phosphate AND Correctly states that DNA consists of a double stranded molecule while RNA is a single stranded molecule. • Shows correct base pairing of all 4 bases in DNA AND Indicates that RNA has Uracil and not Thymine.	• DNA Draws 4 nucleotides showing base pairing rule (A = T, G ≡ C) AND shows anti-parallel nature of DNA strands.	
(b)	Transcription function is described: mRNA is transcribed code from the DNA. Transcription function is explained: mRNA transcribes the code for a polypeptide from the DNA in the nucleus and carries it to the ribosomes / cytoplasm, so that the original DNA does not get damaged leaving the nucleus. DNA is a double-stranded molecule and is unable to fit through the pores in the nuclear membrane, but mRNA is only a single stranded molecule, so can pass through the nuclear membrane to the cytoplasm. Translation function is described: to use mRNA to make a polypeptide / protein. Translation function is explained: to use mRNA to make a polypeptide / protein. So that the protein can be used for cellular functions (or named example given e.g. to make an enzyme). Transcription process is described: e.g. DNA unwinds and a single mRNA strand is made	• Describes transcription. • Describes translation. • Describes function of mRNA. • Describe function of tRNA. • Describes one reason why the polypeptide chain is not directly translated from the DNA strand.	• Explains transcription. • Explains translation. • Explains why tRNA is shorter than mRNA. • Explains function of tRNA. • Explains function of mRNA. • Explains one reason why the polypeptide chain is not directly	• Comprehensively explains the key stages of protein synthesis and justifies one reason why the polypeptide chain is not translated directly from the DNA strand. • Justifies one additional reason why the polypeptide chain is not

	using U instead of T. The mRNA strand leaves the nucleus through a nuclear pore. Transcription process is explained by giving a substantially correct sequence of steps: an enzyme (RNA polymerase) separates / unzips the DNA strand, exposing the gene / bases / nucleotides. Free nucleotides are matched to the exposed bases on the template strand using the **complementary base pairing rule**, A-U and G-C. Transcription forms a single mRNA strand, with groups of 3 bases (codons) that code for the amino acids. Transcription is complete when mRNA detaches and moves out of the nucleus into the cytoplasm and attaches to a ribosome in preparation for translation. Translation process is described: a codon (3 bases on the mRNA) codes for an amino acid, tRNA carries the amino acid to the ribosome and drops it off. Translation process is explained: by giving a substantially correct sequence of steps: ribosomes move along the mRNA from the start codon until the stop codons is reached. Each sequence of 3 bases (codon) on the mRNA is read by the ribosome and matched to the complementary unpaired three base sequence (anticodon) on the tRNA. The specific amino acid attached to the tRNA is then added (peptide bond forms) to the polypeptide chain being made. Describes why tRNA is a short molecule, as it needs only to deliver an amino acid (small) molecule. Describes why mRNA is longer as it contains the code for producing a polypeptide chain. Explains why tRNA is shorter than mRNA, as it is not required to have the total coding length of the gene but only for one anti-codon to attach one amino acid molecule, while mRNA is a longer molecule because contains the whole code to produce a polypeptide chain (protein) which is made a sequence of amino acids. 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.		translated from the DNA strand.	translated directly from the DNA. strand.

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 any FOUR statements from Achievement column.	Provides any THREE statements from Merit column.	Provides any FOUR statements from Merit column.	Discusses ONE statement for Excellence.	Discusses BOTH statements for Excellence

Q	Expected Coverage	Achievement	Merit	Excellence
TWO (a)	**Normal mRNA** CUG ACU CCU G**A**G UUG **Normal amino acids** Leu Thr Pro Glu Leu **Mutated mRNA** CUG ACU CCU G**U**G UUG **Mutated amino acids** Leu Thr Pro <u>Val</u> Leu	• Correct mRNA sequence. • Correct amino acid sequence. • Correct mutated mRNA sequence. • Correct mutated amino acid sequence.	• All correct normal amino acid sequence AND mutated amino acid sequence produces Val instead of Glu.	
(b)	The sickle cell point mutation is a substitution mutation. The base T has been replaced by A. It affects the amino acids sequence by changing Glu to a Val, but the other amino acids remain the same. Changing the amino acid sequence / order of amino acids may change folding of the peptide chain by changing bonding between amino acids. A substitution point mutation can have little or no effect on the amino acid produced, because amino acids have more than one possible codon sequence for them. This means that if there was a substitution point mutation, then the same amino acid could still be coded for therefore the same protein. However, if a substitution mutation produced a STOP codon, this could have a large effect since translation would stop too soon and produce a shorter / non functional protein.	• Identifies sickle cell mutation as substitution / missense. • Describes a substitution mutation. • Describes amino acid sequence is changed after a mutation. • Describes required protein will not be made correctly due to a mutation. • Describes there is more than one codon for each amino acid / gives an example of this.	• Explains how a substitution mutation affects the sequence of bases. • Explains how any different mutation affects the final protein. • Explains degeneracy of the genetic code. • Explains the effect of a STOP codon being produced/ non existent	• Discusses how the substitution mutation affects the bases sequence and final protein structure. • Discusses that degeneracy of the code is able to buffer the effect of a substitution mutation. A substitution mutation to the 3rd triplet may 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.

NØ	N1	N2	A3	A4	M5	M6	E7	E8
No response; no relevant evidence.	Describes any ONE statement from Achievement.	Describes any TWO statements from Achievement.	Describes any THREE statements from Achievement.	Describes any FOUR statements from Achievement.	Explains any THREE statements from Merit.	Explains any FOUR statements from Merit.	Discusses ONE statement for Excellence.	Discusses TWO statements for Excellence.

Q	Expected Coverage	Achievement	Merit	Excellence
THREE	Enzymes are proteins that control metabolic pathways by speeding up the series of reactions / enzymes build up or break down chemicals, making the substrate for the next reaction in the series. A metabolic pathway is a series of biochemical reactions that are connected by their intermediates: The reactants (or substrates) of one reaction are the products of the previous one. Enzymes join / separate / prepare substrates for the next step in the metabolic pathway. A section of DNA (gene) codes for a specific enzyme. Enzymes are specific to reactions. For example, a specific enzyme (phenylalanine hydroxylase) breaks down phenylalanine into a product which is the substrate for the next enzyme (transaminase). However, a mutation to the gene (1) coding for phenylalanine hydroxylase causes a build-up of phenylalanine and no more products in the pathway are made even if the genes / enzymes in the remaining pathway are normal. A mutation to the gene (3) coding for homogentisic acid oxidase causes a build-up of homogentisic acid and the final product is not produced. A mutation at the start of a metabolic pathway has a more harmful effect on phenotype because precursor substrate is not produced for the remaining reactions therefore there may be a build-up or complete absence of products / The lack of intermediate products will affect more than one pathway and therefore, severely affect phenotype. A mutation at the end of a metabolic pathway has a less harmful effect on the phenotype because the precursor substrates have been present therefore there is less likely to be a build-up or absence or many chemicals, only the final product in the pathway will not be produced / and no other pathways will be affected.	• Describes how enzymes control metabolic pathways. • Describes an enzyme. • Describes a metabolic pathway. • Describes a mutation causes phenylalanine / product to build up. • Describes enzymes are coded for by a specific /gene. • Describes mutations prevent products from being made. • Describes a gene. • Identifies mutations to gene 1 causes severe phenotype.	• Explains the relationship between genes, enzymes and products. • Explains how a gene mutation can affect an enzyme / protein being made. • Explains why any gene mutation will prevent the products after mutation being made / cause a build-up of a product. • Explains one gene codes for one protein. • Explains that the mutation affects the shape / role / function of the protein. • Identifies mutation to gene 1 causes more severe phenotype than mutation to gene 3.	• Discusses how genes and enzymes control the metabolic pathway and how a mutation causes the build-up of products / substrate. • Discusses why a mutation to the gene (1) coding for phenylalanine hydroxylase (enzyme at start of metabolic pathway) causes a more harmful phenotype. • Discusses why a mutation to the gene (3) coding for homogentisic acid oxidase (end of metabolic pathway) causes a less harmful phenotype.

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

Cut Scores

Not Achieved	Achievement	Achievement with Merit	Achievement with Excellence
0 – 6	7 – 13	14 – 18	19 – 24