

**Assessment Schedule – 2007****Science: Describe genetic processes (90729)****Evidence Statement**

Question	Achievement	Achievement with Merit	Achievement with Excellence
1(a)	Piece 1 is DNA. A and T are the same percentages, as are G and C.	Piece 1 is DNA. In DNA the bases pair because of the double strand, A with T, C with G, therefore the number / % of A bases will be equal to the number / % of T bases, and likewise with C and G.	
(b)	ONE idea: <ul style="list-style-type: none"> <li>single-stranded RNA</li> <li>not paired.</li> </ul>	RNA is single-stranded with no base pairing.	
(c)	<ul style="list-style-type: none"> <li>DNA has to stay in the nucleus, mRNA moves out into the cytoplasm</li> <li>mRNA contains a short section of the genetic code, while DNA contains the whole code.</li> <li>DNA is too large to pass through the nuclear pores, while mRNA is small enough to.</li> <li>Intron/exons</li> </ul> <p>ONE of the above.</p>	Any TWO Achievement bullet points linked. Eg: DNA holds the complete code and remains in the nucleus, while mRNA only holds a short portion of the code and moves out of the nucleus.	DNA holds the complete code and is too large to leave the nucleus, while mRNA only holds a small part of the code (gene). The mRNA is small enough to pass through the nuclear pores/out to the ribosome, where the mRNA is used to translate the code into a protein (polypeptide chain).
(d)	rRNA assists in the reading of the base sequence.		
(e)	A = 14%. Evidence of appropriate working.		
2(a)	AUG ACU GAG GUG CCU AAG  (ALL correct.)		
(b)	Met – Thr – Glu – Val – Pro – Lys  All SIX correct.		

(c)	<ul style="list-style-type: none"> <li>TAC codes for the amino acid Met</li> <li>TAC codes for the start of the polypeptide chain/protein.</li> </ul> <p>ONE of the above.</p>	TAC codes for the amino acid Met, which occurs at the start of the polypeptide chain/protein.	
(d)	ACC		
(e)	3rd codon changes to UAG which is a stop codon	3rd codon changes to UAG which is a stop codon which means that the protein/polypeptide is incomplete.	3rd codon changes to UAG, which is a stop codon meaning that the protein/polypeptide is incompletely made and the resulting haemoglobin protein cannot function.
3(a)	Similar pattern between two samples	Suspect and crime scene DNA match.	
(b)	<ul style="list-style-type: none"> <li>polymerase chain reaction</li> <li>replicates/amplifies DNA.</li> </ul> <p>Any ONE of the above.</p>	PCR replicates or amplifies the crime scene DNA so that many scientific tests can be carried out.	
(c)	Contamination.	The wrong DNA may be amplified because the suspect or victim DNA can become contaminated with DNA not belonging to victim or suspect.	
(d)	<ul style="list-style-type: none"> <li>2 examples given other than CSI.</li> <li>Ability to make comparisons between 2 DNA samples.</li> </ul> <p>One given.</p>	<ul style="list-style-type: none"> <li>2 examples given other than CSI.</li> <li>Ability to make comparisons between 2 DNA samples.</li> </ul> <p>TWO of these connected.</p>	<ul style="list-style-type: none"> <li>2 examples given other than CSI.</li> <li>Ability to make comparisons between 2 DNA samples.</li> <li>Clear reason ie: a) no need to sequence b) support or contradiction of other evidence c) accuracy mentioned.</li> </ul> <p>All THREE bullet points connected.</p>

### Judgement Statement

Achievement	Achievement with Merit	Achievement with Excellence
<p>EIGHT opportunities answered at Achievement level or higher.</p> <p>8 × A</p>	<p>NINE opportunities answered with at least FIVE at Merit level or higher.</p> <p>5 × M + 4 × A</p>	<p>TWELVE opportunities answered with at least ONE at Excellence level and SIX at Merit level or higher.</p> <p>1 × E + 6 × M + 5 × A</p>