2.6 Transcription & Translation

Mark Schemes

Course	DP IB Biology
Section	2. Molecular Biology
Topic	2.6 Transcription & Translation
Difficulty	Medium

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To be used by all students preparing for DP IB Biology SL
Students of other boards may also find this useful

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The correct answer is **C** because:

Base pairing rules can be used to fill in the gaps in the table, eg. number of C on Strand 1 = number of G on Strand 2 = 38

On one strand of DNA the number of nucleotides on strand 1 of the DNA is:

30 A + 30 T + 22 G + 38 C = **120 total**

The **mRNA** that is transcribed from this DNA will also have 120 nucleotides.

3 nucleotide bases form a **codon** which codes for one **amino acid**, therefore the number of amino acids coded for by 120 nucleotide is:

120 ÷ 3 = **40 amino acids**

Completed table:

	Number of nucleotide bases				Total
	A	T	G	C	
Strand 1	30	30	22	38	120
Strand 2	30	30	38	22	120

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The correct answer is **B** because protein synthesis occurs in the following steps:

1. **Transcription**: the reading of the DNA sequence to produce mRNA
2. **Translation**: mRNA leaves the nucleus and binds to a ribosome, which moves along the mRNA. Amino acids are brought into the growing polypeptide chain according to the codon sequence on the mRNA.
3. **Peptide bonding:** peptide bonds form between successive amino acids of the growing polypeptide chain.
4. **Hydrogen bonding:** hydrogen bonds form between the main chain amino acids in the polypeptide which forms the polypeptide's final 3D shape.

Ionic bonding is not a feature of polypeptide structure.

3

The correct answer is **B**.

Statement I is correct. The much smaller molecule of RNA is produced so that the genetic code can be carried out into the cytoplasm.

Statement II is incorrect because transcription makes a copy of the antisense strand, in order to produce an equivalent mRNA base sequence to the base sequence of the DNA sense strand.

Statement III is incorrect because transcription converts a sequence of DNA nucleotides into a sequence of RNA nucleotides.

Statement IV is correct because covalent bonds are how successive nucleotides in a strand of RNA (and DNA) are held together.

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The correct answer is **C** because **mRNA** contains a **start** and **stop codon** to signal to the ribosome the beginning and end of the **coding sequence**.

A is incorrect because the mRNA molecule has a stop codon near its end, followed by a small section of non-coding nucleotides before and after the coding sequence to protect the coding sequence from degradation.

B is incorrect as tRNA are in large supply in the cytoplasm, where translation takes place, and the cell is synthesising many different proteins on different ribosomes at the same time. Therefore, it is unlikely that there would be a lack of tRNA supply that would stop translation.

D is incorrect as RNA polymerase is only found in the nucleus, and ribosomes are only found in the cytoplasm.

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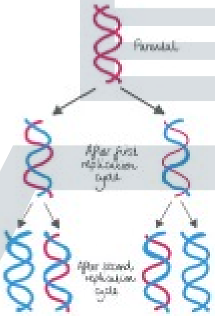
The correct answer is **D** because bacteria is grown in **^{15}N medium** for many generations. This is to ensure that all bacteria in the experiment start with DNA that has **only** ^{15}N nitrogen in its bases

This eliminates Option **A** and Option **C**.

The next stage is that all the DNA must contain only ^{15}N nitrogen in its bases.

This eliminates Option **B**.

As a further check, the remaining sequence in Option **D** makes sense as a logical series of steps and findings. The following diagram shows the main steps of semi-conservative replication. Pink represents a strand with ^{15}N bases, blue with ^{14}N bases.



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The correct answer is **C**.

A is incorrect because one of the sugars is depicted with a hexagon, which implies a hexose sugar. All sugars in DNA (and RNA) are pentose so should be drawn with a pentagon.

B is incorrect because the covalent bonds are shown from each sugar's 2-carbon atom to the phosphate groups; this should be from the 3-carbon atoms.

D is incorrect because the bases are shown bonded to the 2-carbon atoms of the pentose sugars; this should be bonded to the 1-carbon atoms.

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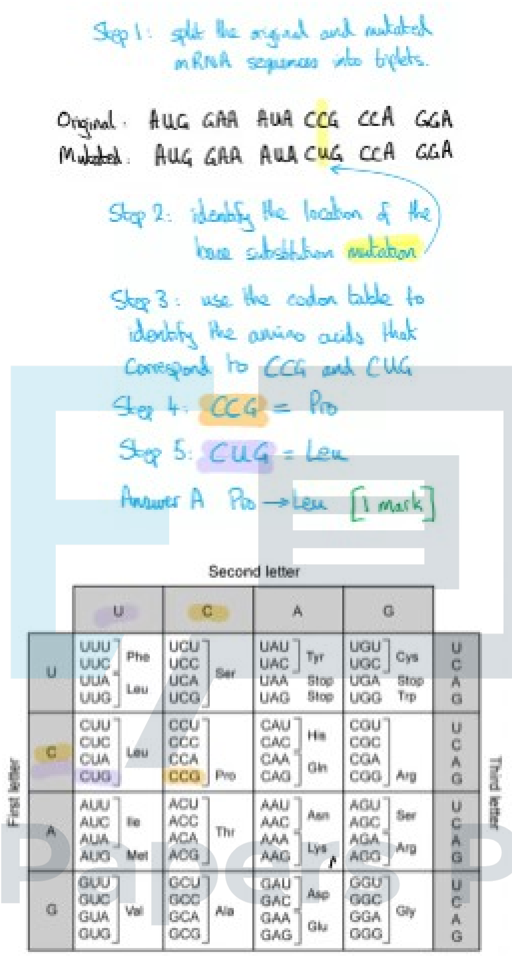
The correct answer is **A** because the mutation falls in the 4th triplet of the sequence, CCG. This mutates to CUG. The amino acid proline (Pro) is substituted by leucine (Leu)



Step 1: split the original and mutated mRNA sequences into triplets.

Original: AUG GAA AUA CCG CCA GGA
Mutated: AUG GAA AUA CUG CCA GGA

Step 2: identify the location of the base substitution mutation

Step 3: use the codon table to identify the amino acids that correspond to CCG and CUG

Step 4: CCG = Pro

Step 5: CUG = Leu

Answer A Pro → Leu [1 mark]

Second letter

First letter	U	C	A	G	Third letter
U	UUU UUC UUA UUG Phe Leu	UCU UCC UCA UCG Ser	UAU UAC UAA UAG Tyr Stop Stop	UGU UGC UGA UGG Cys Stop Trp	U C A G
C	CUU CUC CUA CUG Leu	CCU CCC CCA CCG Pro	CAU CAC CAA CAG His Gln	CGU CGC CGA CGG Arg	U C A G
A	AUU AUC AUA AUG Ile Met	ACU ACC ACA ACG Thr	AAU AAC AAA AAG Asn Lys	AGU AGC AGA AGG Ser Arg	U C A G
G	GUU GUC GUA GUG Val	GCU GCC GCA GCG Ala	GAU GAC GAA GAG Asp Glu	GGU GGC GGA GGG Gly	U C A G

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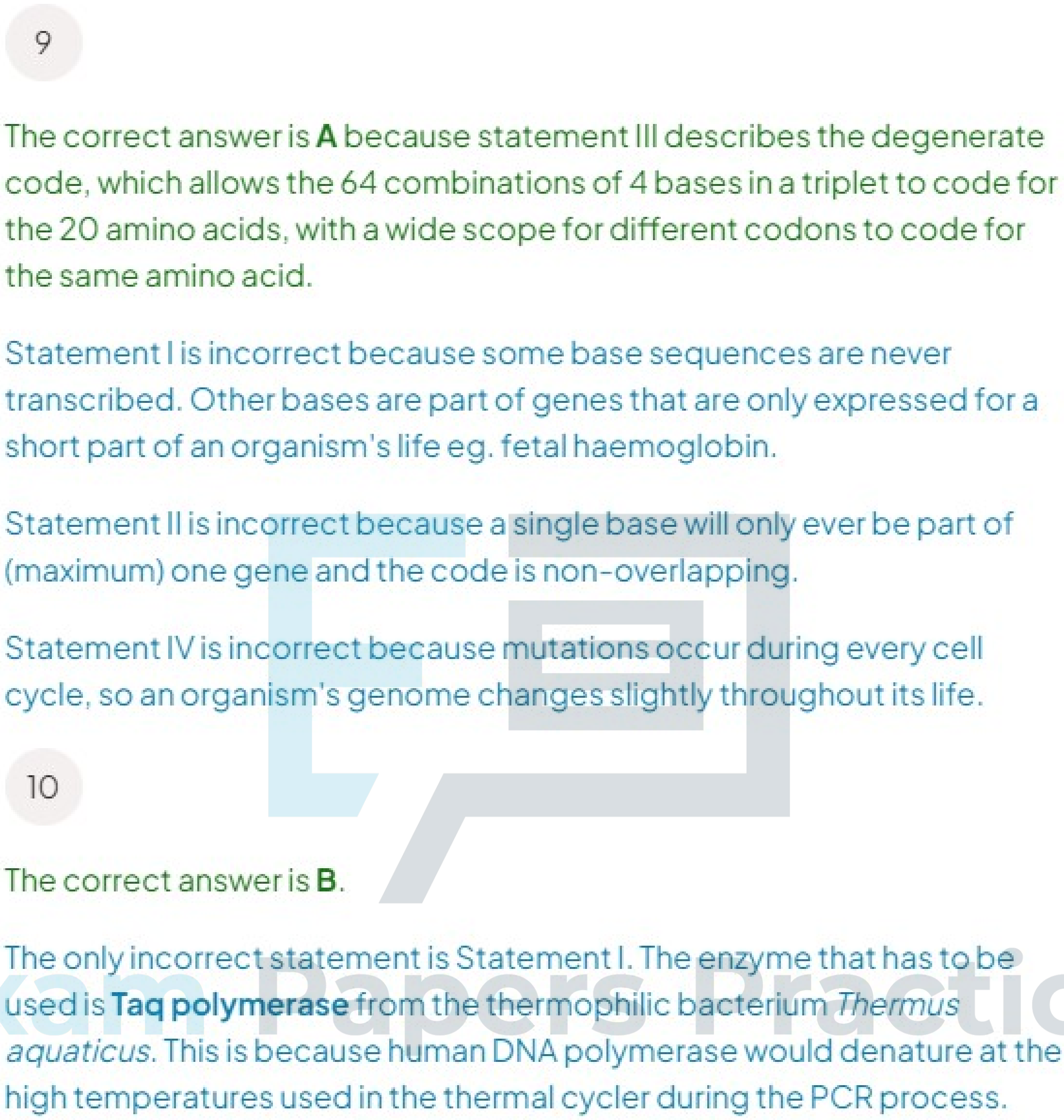
The correct answer is **C.**

A is incorrect because transcription occurs in the nucleus, not the cytoplasm.

B is incorrect because translation produces a polypeptide, not mRNA. mRNA is produced in transcription.

D is incorrect because RNA polymerase is only used in the transcription stage of protein synthesis, not translation.



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The correct answer is **A** because statement III describes the degenerate code, which allows the 64 combinations of 4 bases in a triplet to code for the 20 amino acids, with a wide scope for different codons to code for the same amino acid.

Statement I is incorrect because some base sequences are never transcribed. Other bases are part of genes that are only expressed for a short part of an organism's life eg. fetal haemoglobin.

Statement II is incorrect because a single base will only ever be part of (maximum) one gene and the code is non-overlapping.

Statement IV is incorrect because mutations occur during every cell cycle, so an organism's genome changes slightly throughout its life.

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The correct answer is **B**.

The only incorrect statement is Statement I. The enzyme that has to be used is **Taq polymerase** from the thermophilic bacterium *Thermus aquaticus*. This is because human DNA polymerase would denature at the high temperatures used in the thermal cycler during the PCR process.

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