



ANSWER BOOK

The genetic code and transcription

Nucleic acids, genomes and protein synthesis · Unit B05

AQA 3.4.2 · OCR A 2.1.3, 6.1.1 · Edexcel A Topic 2.8 · CAIE 6.2

5 questions · 18 marks

NAVY EDITION

SECTION A · Short, 1 to 2 marks

- A1** **B1** degenerate: most amino acids are specified by more than one triplet. **B1** [2]
non-overlapping: each base belongs to one triplet only, and the triplets are read one after another.
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SECTION B · Standard, 3 to 5 marks

- B1** **B1** RNA polymerase binds to a promoter region at the start of the gene. **B1** the [5]
enzyme unwinds a short section of the double helix, breaking the hydrogen bonds between the paired bases. **B1** only one of the two exposed strands, the template strand, is read. **B1** free RNA nucleotides align against the template by complementary base pairing, with uracil pairing to adenine wherever thymine would have gone. **B1** RNA polymerase joins the aligned nucleotides by condensation into phosphodiester bonds, moving along the gene until it reaches a stop signal and releases the pre-mRNA.
- B2** **B1** the pre-mRNA is a copy of the whole gene, introns included. **B1** [4]
spliceosomes cut the introns out and join the exons together, so the introns are not represented in the mature mRNA. **B1** in alternative splicing, different combinations of exons are retained in the mature mRNA. **B1** so several different mRNA molecules, and therefore several different polypeptides, can come from the same gene.
- B3** **B1** the code is read in threes from a fixed starting point and is [4]
non-overlapping, so each base belongs to one triplet only. **B1** inserting a base pushes every subsequent base one place along, so every triplet after the insertion is read differently, which is a frame shift. **B1** the amino acid sequence after that point is therefore completely altered rather than altered in one place. **B1** a shifted reading frame produces stop codons at positions where there were none, so translation ends early and the polypeptide is short.
- B4** **B1** template strand CTA GGT AAC, each base complementary to the coding [3]
strand. **A1** mRNA GAU CCA UUG. **B1** the mRNA matches the coding strand, with uracil in place of every thymine.
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