



Protein synthesis: practice questions

8 questions • 24 marks • mark scheme at the back

For IB Diploma Biology, Standard Level and Higher Level (first assessment 2025). **HL only** is additional higher level content, for HL students only.

Name

Total / 24

1 PAPER 1A STYLE [1 mark]

During transcription, which base on the RNA strand pairs with adenine on the DNA template strand?

- A. ☐ Thymine
- B. ☐ Uracil
- C. ☐ Guanine
- D. ☐ Cytosine

2 PAPER 1A STYLE [1 mark]

The codons GAA and GAG both code for glutamic acid. Which feature of the genetic code does this show?

- A. ☐ Universality
- B. ☐ It is a triplet code
- C. ☐ Degeneracy
- D. ☐ It is non-overlapping

3 PAPER 1A STYLE [1 mark]

HL only

During elongation, which site of the ribosome holds the tRNA attached to the growing polypeptide?

- A. ☐ A site
- B. ☐ E site
- C. ☐ P site
- D. ☐ The small subunit binding site

4 PAPER 1B STYLE

[5 marks]

The table shows part of the mRNA codon table. A short section of mRNA has the sequence AUG UUU CAU GAG UGG UAA. (a) Deduce the sequence of amino acids coded by this mRNA. [2] (b) Deduce the base sequence of the DNA template strand for the first two codons. [1] (c) A mutation changes the fourth codon from GAG to GUG. Using the table, state the effect on the polypeptide and suggest how this could affect the protein's function. [2]

Part of the mRNA codon table	
Codon	Amino acid
AUG	Met (start)
UUU	Phe
CAU	His
GAG	Glu
GUG	Val
UGG	Trp
UAA	stop

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5 PAPER 2A STYLE

[2 marks]

Explain why the genetic code must be a triplet code.

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PAPER 2B STYLE

Describe how a polypeptide is elongated during translation.

[illegible]

PAPER 2A STYLE

HL only

Outline how pre-mRNA is modified in eukaryotic cells, and how this allows one gene to code for more than one polypeptide.

[illegible]

PAPER 2A STYLE

HL only

(a) Outline the two-stage modification of pre-proinsulin to insulin. [3] (b) State why cells constantly break down proteins in proteasomes. [1]

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Mark scheme

One mark for each point unless a maximum is given. Words in brackets are not needed for the mark.

1. [1]

B B;

2. [1]

C C;

3. [1] **HL only**

C C;

4. [5]

- (a) Met – Phe – His – Glu – Trp;
- (a) translation ends at UAA / stop codon (no amino acid added); Award [1] for four correct amino acids in order
- (b) TAC AAA; Accept 3'-TAC AAA-5' or 5'-AAA CAT-3'
- (c) glutamic acid replaced by valine (at that position) / one amino acid changed;
- (c) different R group / hydrophobic instead of charged, so the polypeptide folds differently / changes shape;
- (c) protein may lose function / function altered, e.g. as in haemoglobin S; OWTTE
- max 5

5. [2]

- there are 20 (types of) amino acids (to be coded for) and 4 bases;
- a doublet code gives only $4^2 = 16$ combinations, which is not enough;
- a triplet code gives $4^3 = 64$ combinations, which is enough (with some to spare for start/stop or degeneracy);
- max 2

6. [6]

- mRNA binds to the small subunit of the ribosome;
- mRNA is read in codons / triplets of bases;
- tRNA carries a specific amino acid;
- tRNA anticodon pairs with the complementary codon on mRNA;
- by hydrogen bonding / complementary base pairing (A-U, C-G);
- two tRNAs bind (to the large subunit) at the same time;
- a peptide bond forms between the amino acid and the growing polypeptide;
- the polypeptide is transferred to the (amino acid on the) second tRNA;
- the ribosome moves along the mRNA by one codon;
- the first tRNA (without an amino acid) is released;
- process repeats, adding one amino acid at a time in the order set by the codons;
- max 6

7. [4] HL only

- introns are removed;
- exons are spliced/joined together (to form mature mRNA);
- 5' cap added;
- 3' polyA tail added;
- cap and tail stabilise the mRNA;
- alternative splicing joins different combinations of exons;
- producing different polypeptides from the same gene;
- max 4

8. [4] HL only

- pre-proinsulin is the polypeptide produced by translation (at the rough ER);
- stage 1: signal sequence/peptide removed to give proinsulin;
- proinsulin folds and disulfide bonds form;
- stage 2: C-peptide removed / cut out;
- leaving A and B chains linked by disulfide bonds (active insulin);
- (a) [max 3]
- (b) sustaining a functional proteome requires constant breakdown (and synthesis) of proteins / removes damaged, misfolded or unneeded proteins / amino acids are recycled for new protein synthesis;
- max 4