

1.4 Gene expression: transcription and translation

Name: _____ Class: _____ Date: _____

Total: 24 marks

KEY WORDS splicing

Objective

Apply codon arithmetic, timing estimates and splice mechanics to expression problems.

1 Key knowledge and worked examples

■ The code

$4^3 = 64$ codons = 61 sense + 3 stop, for 20 amino acids; degeneracy concentrated at base three. Pol II ~20 nt/s; ribosome ~3 aa/s.

■ Worked example: one molecule, one minute

Preproinsulin (110 aa): translation $110/3 \approx 37$ s; its 0.5 kb mRNA transcribed in ~25 s – so secretion pre-builds and stores ✓.

2 Practice

2.1 Why must codons be triplets, not doublets? [3]

2.2 Translate the timing: a 300 aa protein at 3 aa/s. [3]

2.3 Why are third-base substitutions often silent? [3]

3 Exam-style questions

3.1 A gene whose pre-mRNA is 4.2 kb, with one 1.8 kb intron removed, leaves a 2.4 kb mature mRNA.

Compute the transcription time at 20 nt/s. Compute the translation time of its 220-codon ORF at 3 aa/s. Explain why several ribosomes (polysomes) translate one mRNA simultaneously, and what this does to protein output per transcript. [8]

3.2 A (fictional) sequencing case: anaemia, no coding mutation, a new splice donor inside an intron.

Explain the mechanism from new donor site to disease. State what happens to the reading frame if 47 bases are retained. Predict whether a single-base third-position change in an exon would likely cause disease, with a reason. [7]

Solutions

2.1

- $4^2 = 16 < 20$ amino acids; $4^3 = 64 \geq 20$ with degeneracy spare.

2.2

- $300/3 = 100$ s.

2.3

- Degeneracy sits at base three: many third-base changes encode the same amino acid (tRNA wobble).

3.1

- Pol II transcribes the full 4.2 kb: $4200/20 = 210$ s ✓ (the intron is removed AFTER transcription).
- $220 \text{ codons} / 3 \text{ aa/s} \approx 73$ s ✓.
- Polysomes: each ribosome reads independently, so one mRNA yields many proteins concurrently.
- Output scales roughly with ribosome count per transcript.

3.2

- The spliceosome follows consensus sequences; a new donor diverts it → intron retention or exon skipping.
- 47 retained bases is not a multiple of 3 → frameshift → premature stop.
- Third-position change: likely silent (degeneracy) → unlikely to cause disease.