

Exercise walk-through

1.4

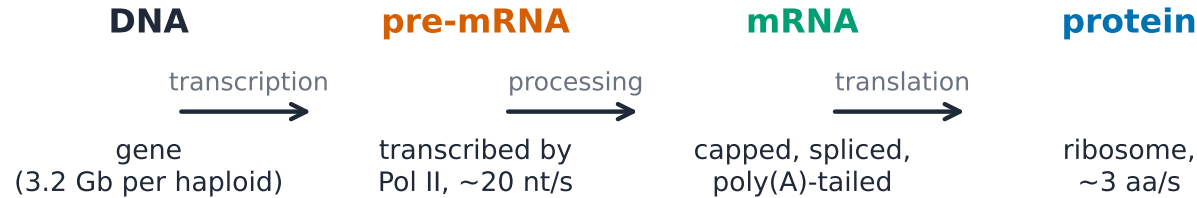
Gene expression – transcription and translation

University Medicine

Expression: recipe to machine

- 1 **Timing** Preproinsulin (110 aa): $110/3 \approx 37$ s to translate, its 0.5 kb mRNA ~ 25 s to transcribe - one molecule $\approx$ one minute.
- 2 **Splice** A new splice site inside a β -globin intron: exon skipped, frame shifted, premature stop - thalassaemia with no amino-acid change.
- 3 **Code** Two bases give $16 < 20$ amino acids - too few; three give 64 with spare for degeneracy.

Central dogma with processing



splicing: one gene → several proteins (alternative exons)

the code: $4^3 = 64$ codons = 61 sense + 3 stop, for 20 amino acids

Transcription, processing, **translation** - three stages, three chances for regulation, 64 codons for 20 amino acids.

Exercises 2.1-2.3

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]

Exercises 2.1-2.3

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

2.1

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

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

2.2

- $300/3 = 100$ s.

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

2.3

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

Exercise 3.1

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]

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3.1

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

Exercise 3.2

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]

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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.