

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.