

## Solutions

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### 2.1

- Polymerases extend  $5' \rightarrow 3'$  only; on the antiparallel template that means synthesising away from the fork in restarted fragments.

### 2.2

- $4.6 \times 10^6 / (2 \times 1000) = 2300 \text{ s} \approx 38 \text{ min} \checkmark$ .

### 2.3

- Bulky helix-distorting lesions, e.g. UV thymine dimers.

### 3.1

- $\text{Rate} \times 100 \rightarrow 6.4 \times 10^9 \times 10^{-7} \approx 640$  mutations per division  $\checkmark$ .
- Colon epithelium divides constantly, so the elevated rate compounds into driver mutations early.
- Missing: mismatch repair; remaining: polymerase selectivity and proofreading.

### 3.2

- E. coli:  $2300 \text{ s} \approx 38 \text{ min}$  (above).
- Human single origin:  $6.4 \times 10^7 \text{ s} \approx 2.0 \text{ years} \checkmark$ .
- 30 000 origins:  $\sim 35 \text{ min}$  synthesis  $\checkmark$ .
- Many origins because forks stall at damage and chromatin; 8 h because origins fire in timed clusters and chromatin must be opened and reassembled.