

Table 1 Kinetic parameters (means \pm S.D.) for formation of all possible correct and incorrect base pairs and fidelity in single-nucleotide gap-filling DNA synthesis catalysed by Pol β

The DNA substrates used as base pair templates were 25A-19/45TX, shown in Figure 1(B). Fidelity is defined as $[(k_{\text{pol}}/K_{\text{d}})_{\text{c}} + (k_{\text{pol}}/K_{\text{d}})_{\text{i}}]/(k_{\text{pol}}/K_{\text{d}})_{\text{i}}$, where subscripts c and i represent correct and incorrect nucleotide incorporation, respectively.

| Base pair template:dNTP | k_{pol} (s^{-1}) | K_{d} (μM) | $k_{\text{pol}}/K_{\text{d}}$ ($\text{M}^{-1} \cdot \text{s}^{-1}$) | Fidelity |
|----------------------------|--------------------------------------|----------------------------------|--|----------|
| A:T | 21.9 ± 0.5 | 5.4 ± 0.7 | 4100000 | |
| T:A | 36.3 ± 4.4 | 8.5 ± 2.4 | 4300000 | |
| G:C | 12.5 ± 0.5 | 1.9 ± 0.2 | 6600000 | |
| C:G | 18.4 ± 0.8 | 3.6 ± 0.8 | 5100000 | |
| A:C | 0.23 ± 0.02 | 190 ± 50 | 1200 | 3400 |
| A:G | 0.16 ± 0.05 | 1600 ± 300 | 100 | 41000 |
| A:A | 0.031 ± 0.01 | 310 ± 50 | 100 | 41000 |
| T:G | 0.96 ± 0.01 | 620 ± 150 | 1500 | 2800 |
| T:C | 1.3 ± 0.12 | 510 ± 100 | 2500 | 1700 |
| T:T | 0.15 ± 0.01 | 1300 ± 200 | 120 | 37000 |
| G:T | 0.37 ± 0.09 | 650 ± 300 | 570 | 12000 |
| G:A | 0.019 ± 0.001 | 270 ± 40 | 70 | 93000 |
| G:G | 0.040 ± 0.002 | 360 ± 40 | 110 | 59000 |
| C:A | 0.24 ± 0.01 | 470 ± 70 | 510 | 10000 |
| C:T | 0.22 ± 0.01 | 877 ± 70 | 250 | 20000 |
| C:C | 0.026 ± 0.002 | 370 ± 50 | 70 | 73000 |