Table 1: Estimates of Rate and Dissociation Constants Describing Pol δ-Catalyzed Reactions

	Pol δ4	Pol δ3	δ4/δ3[a]
k_{cat}[b]	$0.24 \pm 0.08\ s^{-1}$	$0.18 \pm 0.03\ s^{-1}$	1.3
k_{pol}[c]	$87 \pm 5.7\ s^{-1}$	$19 \pm 2.9\ s^{-1}$	4.6
K_{dNTP}[c]	$3.6 \pm 0.8\ \mu M$	$3.2 \pm 1.6\ \mu M$	1.0
K_{DNA}[d]	34 ± 5.4 nM	35 ± 6.5 nM	1.0
$k_{pol\ (mismatch)}$[e]	$7.6 \pm 2.4\ s^{-1}$	$2.5 \pm 0.6\ s^{-1}$	3.0
k_{exo}[f]	$0.8 \pm 0.2\ s^{-1}$	$1.9 \pm 0.4\ s^{-1}$	0.42
$k_{pol\text{-}exo}$[g]	$0.003 \pm 0.0004\ s^{-1}$	$0.026 \pm 0.003\ s^{-1}$	0.12
$k_{pol\text{-}exo\ (mismatch)}$[h]	$0.062 \pm 0.006\ s^{-1}$	$0.29 \pm 0.03\ s^{-1}$	0.21
$k_{pol\text{-}exo}$:k_{pol}[i]	1:29000	1:730	40
$k_{pol\text{-}exo\ (mismatch)}$:$k_{pol\ (mismatch)}$[i]	1:123	1:8.6	14

[a]Calculated by dividing the value observed with Pol δ4 by the value observed with Pol δ3. [b]Steady-state initial velocities of incorporation performed at various dNTP concentrations were fit to the Michaelis–Menten equation (eq 3) to determine a V_{max} (Figure 3H). The V_{max}/E_t relationship (active sites, Figure 3G) was use to determine a steady-state k_{cat}. Uncertainties are standard errors from three independent reaction sets. [c]Values were obtained by fitting eqs 1 and 2 to time courses obtained at various dNTP concentrations with Pol $\delta 4^{exo-}$ or Pol $\delta 3^{exo-}$ (Figure 3F). Errors are standard errors from nonlinear regression. [d]Values represent the average K_{DNA} obtained when eq 4 is used to fit three independent titrations with DNA (Figure 2B). Errors are standard deviations from three separate fits. [e]Observed first-order rate constant describing the burst phase for extension of a mismatched primer (Figure 1C). Errors are standard errors from nonlinear regression. [f]Observed first-order rate constant describing the degradation of single-stranded DNA (Figure 4A). Errors are standard errors from nonlinear regression. [g]Observed first-order rate constant describing the degradation of matched duplex DNA (Figure 4B). Errors are standard errors from nonlinear regression. [h]Observed first-order rate constants describing the degradation of mismatched duplex DNA (Figure 4C). Errors are standard errors from nonlinear regression. [i]The ratios indicate the probabilities for excision against extension of a primer terminus; alterations in the ratios when a mismatch terminus is present reflect the proofreading efficiency (*37*, *44*, *45*).

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