Supplementary Data

Identification of Critical Residues for the Tight Binding of Both Correct and Incorrect Nucleotides to Human DNA Polymerase λ

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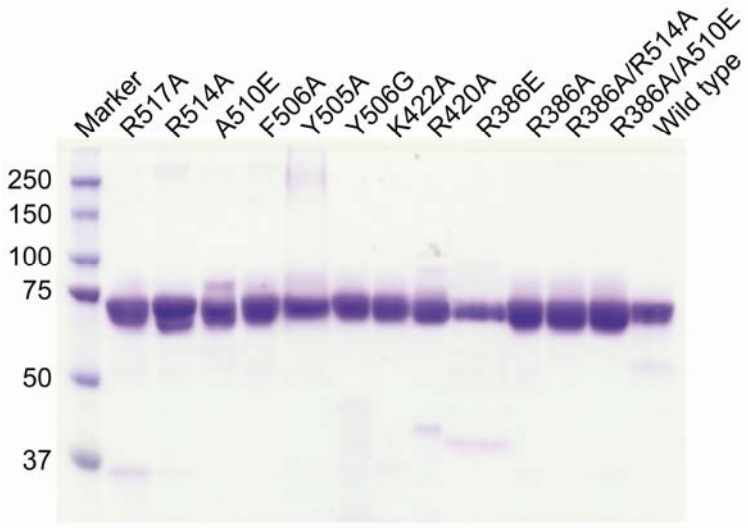
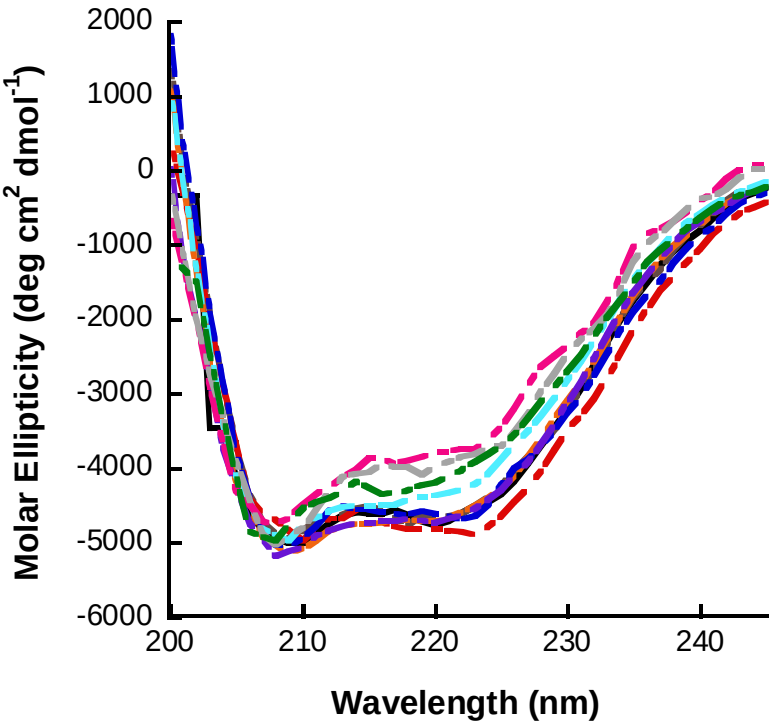
Supplementary Figure 1

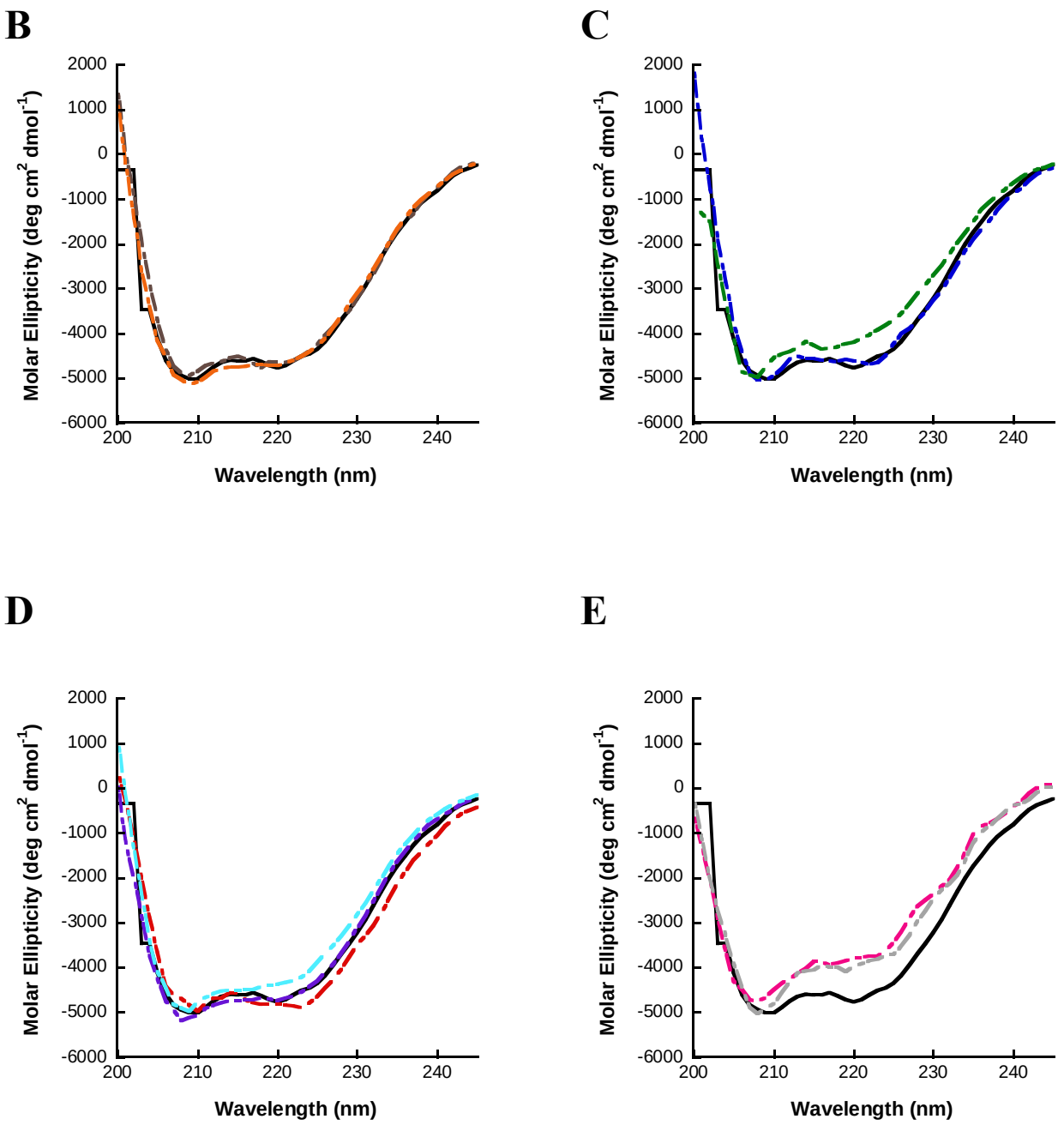


Supplementary Figure 1. Coomassie blue-stained SDS-PAGE of wild-type and mutant Pol λ. The purity of each enzyme was estimated by resolving 5 μg of each protein on an 8% SDS-PAGE gel that was stained with Coomassie blue. The molecular weights (kDa) of the marker are listed along the left side.

Supplementary Figure 2

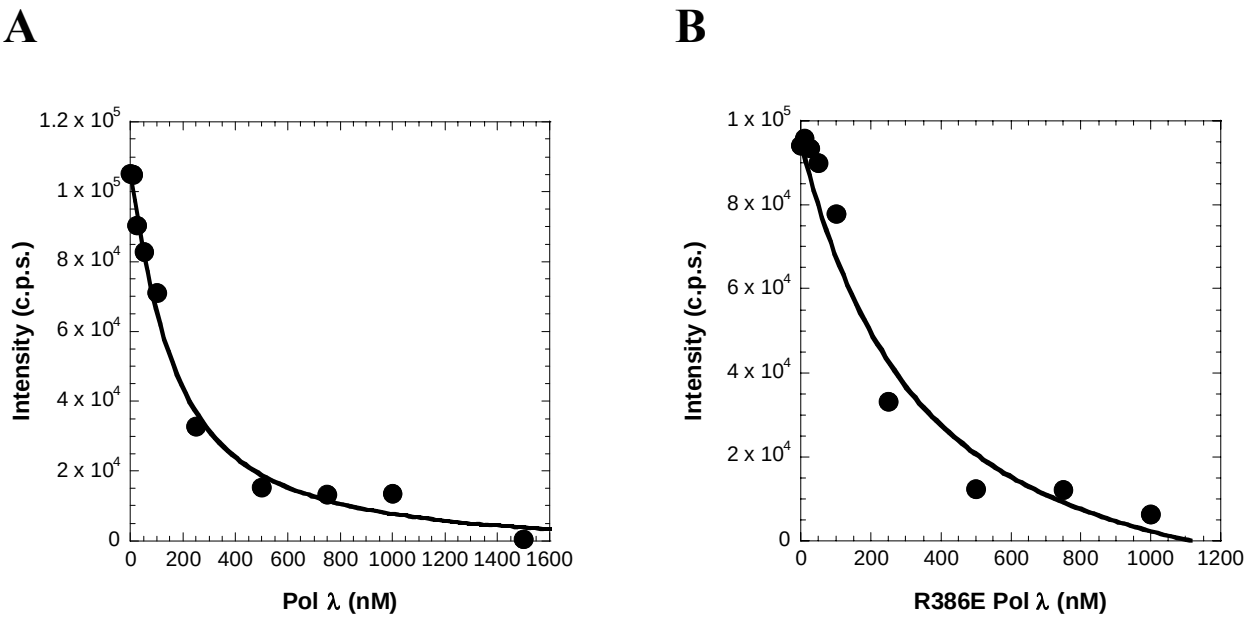
A





Supplementary Figure 2. Circular dichroism spectra for WT and mutant Pol λ. The CD spectra were collected and overlaid for WT (black), R386A (brown), K422A (orange), Y505A (green), F506A (blue), A510E (cyan), R514A (purple), R517A (red), R386A/A510E (pink), and R386A/R514A (gray). The CD spectra indicated that all the proteins were folded. Individual spectra overlaid with wild-type Pol λ are shown for (B) R386A and K422A; (C) Y505A and F506A; (D) A510E, R514A, and R517A; and (E) R386A/A510E and R386A/R514A. The CD spectra for WT, Y505A, and F506A Pol λ are from the work of Brown *et al.*[1]

Supplementary Figure 3



Supplementary Figure 3. Equilibrium dissociation constant for the dissociation of the binary complex Pol λ•DNA. A plot of 2-aminopurine intensity versus the concentration of (A) WT Pol λ or (B) R386E Pol λ was fit to equation 1 which resolved a K_d^{DNA} = 110 ± 20 nM and K_d^{DNA} = 300 ± 100 nM for WT and the R386E mutant, respectively.

REFERENCE

1. Brown, J. A., Fiala, K. A., Fowler, J. D., Sherrer, S. M., Newmister, S. A., Duym, W. W. & Suo, Z. (2010). A Novel Mechanism of Sugar Selection Utilized by a Human X-Family DNA Polymerase. *J Mol Biol* **395**, 282-290.