

SUPPLEMENTAL DATA

Structural Basis for Proficient Incorporation of dTTP Opposite *O*⁶-Methylguanine by Human DNA Polymerase ϵ

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J. Biol. Chem. **285**, XXX-XXX (2010)

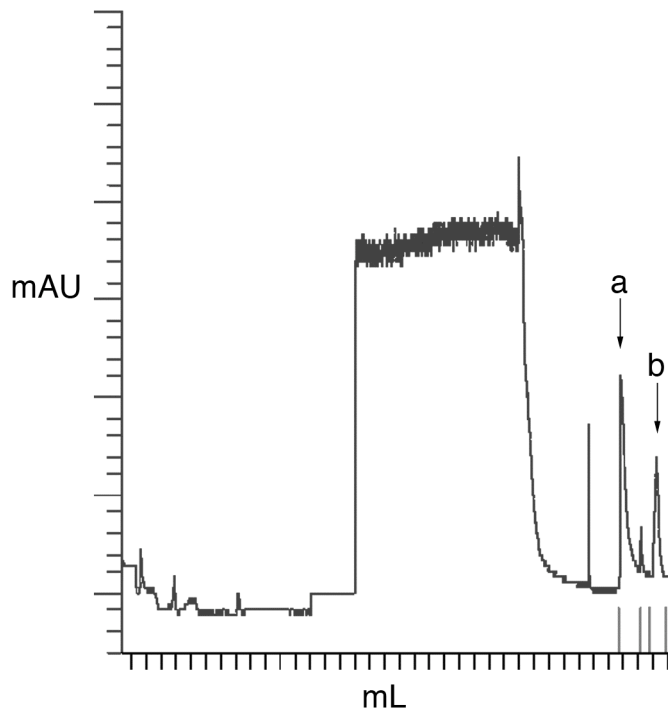
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FIGURE S1. Purification of the human pol ϵ catalytic fragment (amino acids 1-420).

FIGURE S1. Purification of the human pol ι catalytic fragment (amino acids 1-420). *A*, FPLC elution profile showing peaks from PreScission Protease incubation (a) and after washing with 20 mM glutathione (b). *B*, SDS-PAGE of purified human pol ι . Lane 1: Markers (M), lane 2: Pre-induction sample (Pre), lane 3: Pol ι (a, corresponds to peak a from Fig. S1A), lane 4: empty, and lane 5: glutathione wash (b, corresponds to peak b from Fig. S1A).

Figure S1

A



B

