Supporting Information to

Conformational transitions in human AP endonuclease 1 and its active site mutant during abasic site repair

Lyubov Yu. Kanazhevskaya,[‡] Vladimir V. Koval,[‡,§] Dmitry O. Zharkov,[‡,§] Phyllis R. Strauss[‖] and Olga S. Fedorova[*,‡,§]

[‡] *Institute of Chemical Biology & Fundamental Medicine, Siberian Branch of the Russian Academy of Sciences, Novosibirsk 630090, Russia*

[§] *Novosibirsk State University, Novosibirsk 630090, Russia and*

[‖] *Department of Biology, Northeastern University, Boston, Massachusetts 02115, USA*

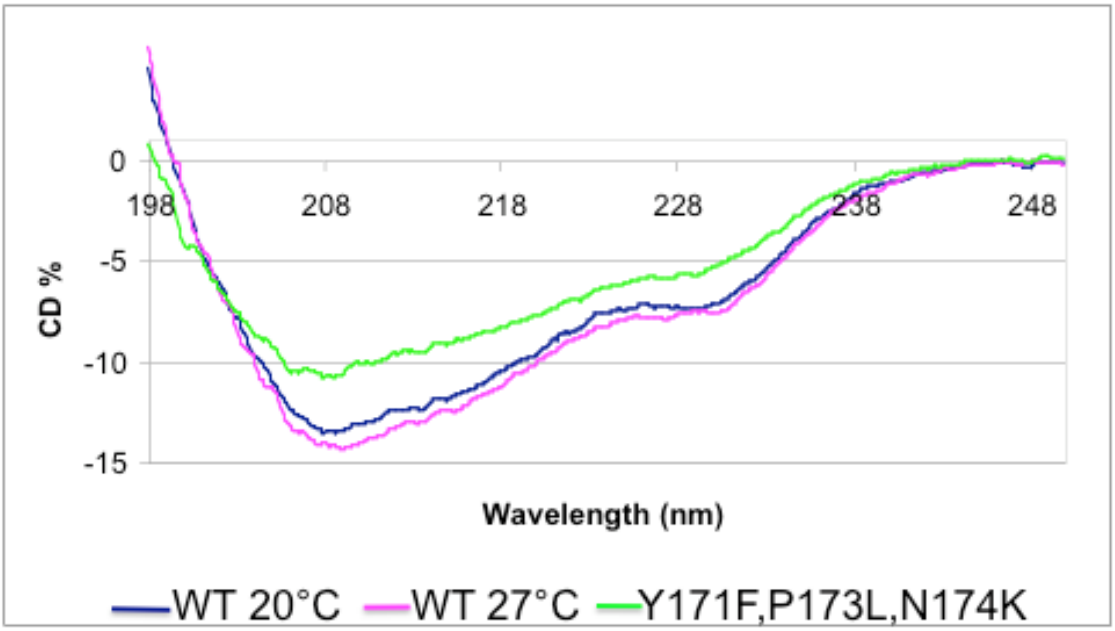

Figure S1: Circular dichroism spectra of wild typeApe1 and mutant (Y171F, P173L, N174K) proteins. Circular dichroism was performed on the wild type protein at both 20 °C and at 27 °C and on the mutant protein at 20 °C using a Jasco J-715 Spectropolarimeter with a 1 cm pathlength cuvette. The contribution of the buffer, which was minimal, was subtracted from each spectrum.

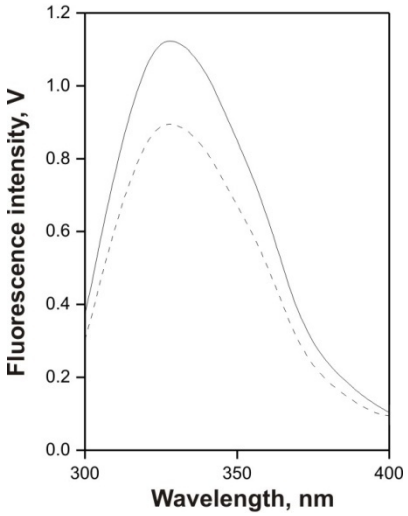

Figure S2: The intrinsic fluorescence spectrum of free APE1 (solid line) and APE1–G-ligand complex (dashed line) with excitation at 280 nm ([APE1] = [G] = 1.5 μM).