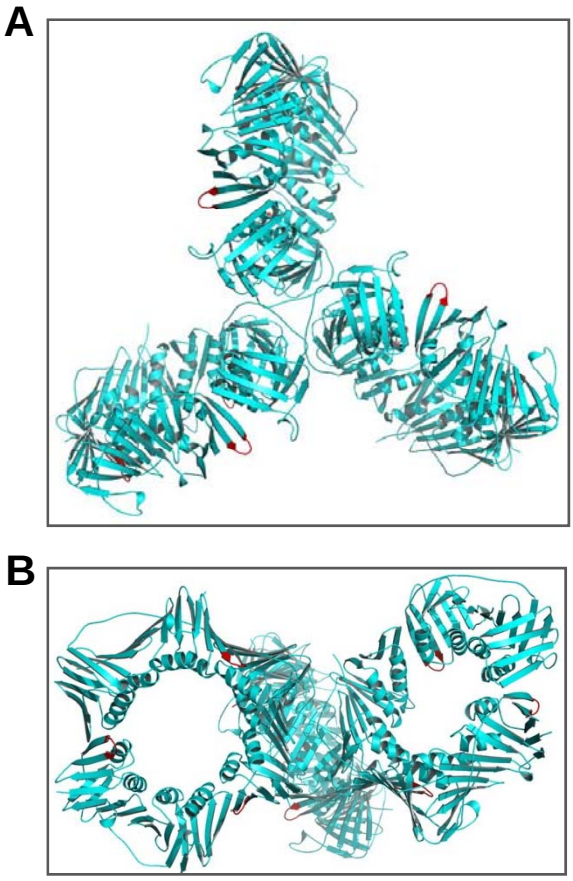
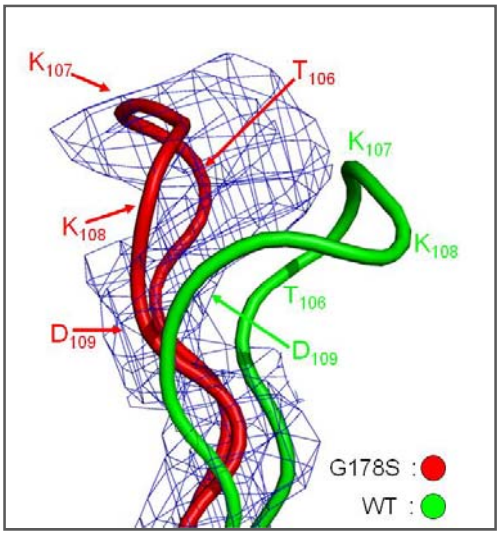
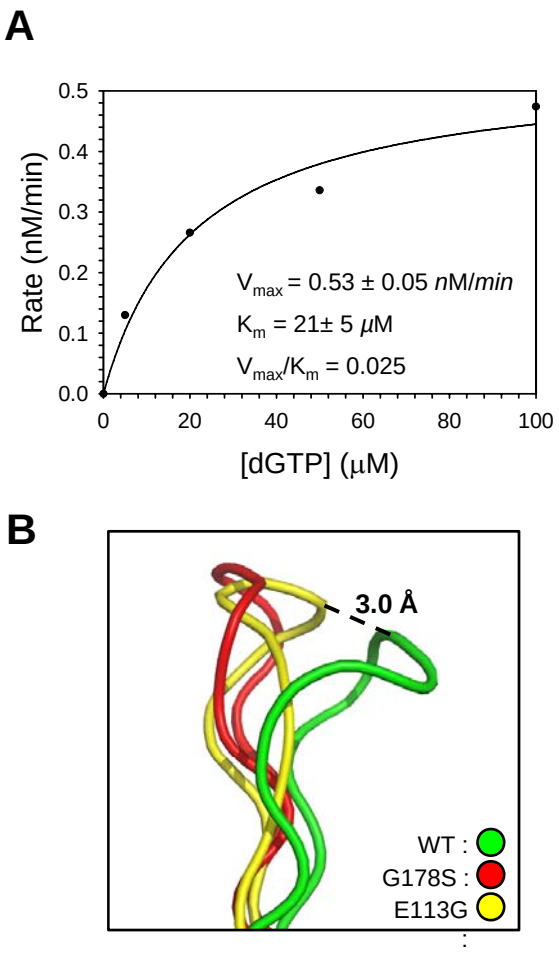


Supplemental Fig. S1. Crystal Packing of the G178S PCNA mutant protein. The crystal packing of three trimeric G178S PCNA mutant proteins is shown from the top (A) and side (B). All monomeric subunits are shown in cyan and loop J is shown in red. Both panels show the PCNA protein packing along the backside of the monomeric subunit near the inter-domain connector loop. This allows loop J to extend freely into the solvent-filled spaces of the crystal lattice.



Supplemental Fig. S2. The position of loop J in the E113G mutant PCNA protein. We have obtained protein crystals of the E113G mutant PCNA protein. These crystals are in the same space group with the same unit cell dimensions as the G178S mutant protein crystals. We have collected data on these crystals to a resolution of 3.6 Å. Shown here is the electron density (level=1.5) for the E113G mutant PCNA protein overlaid with the backbone for the wild type and G178S PCNA mutant protein in ribbon representation. The electron density for loop J of the E113G mutant protein appears much more like that of the G178S mutant protein than the wild-type PCNA protein.



Supplemental Figure S3. Steady state kinetics of pol η on an abasic site in the presence of the E113G PCNA mutant protein (A). The solid line represents the best fit of the data to the Michaelis-Menten equation with a V_{max} equal to 0.53 ± 0.05 nM/min and a K_m equal to 21 ± 5 μM. Shown in (B) are the positions of loop J in the wild-type (green), G178S mutant (red), and E113G mutant (yellow) protein structures. The distance between the αC of residue 107 in the wild-type and E113G protein structures is 3.0 Å. The analogous distance between the wild-type and G178S protein structures is 6.5 Å (see Fig. 2B,C).