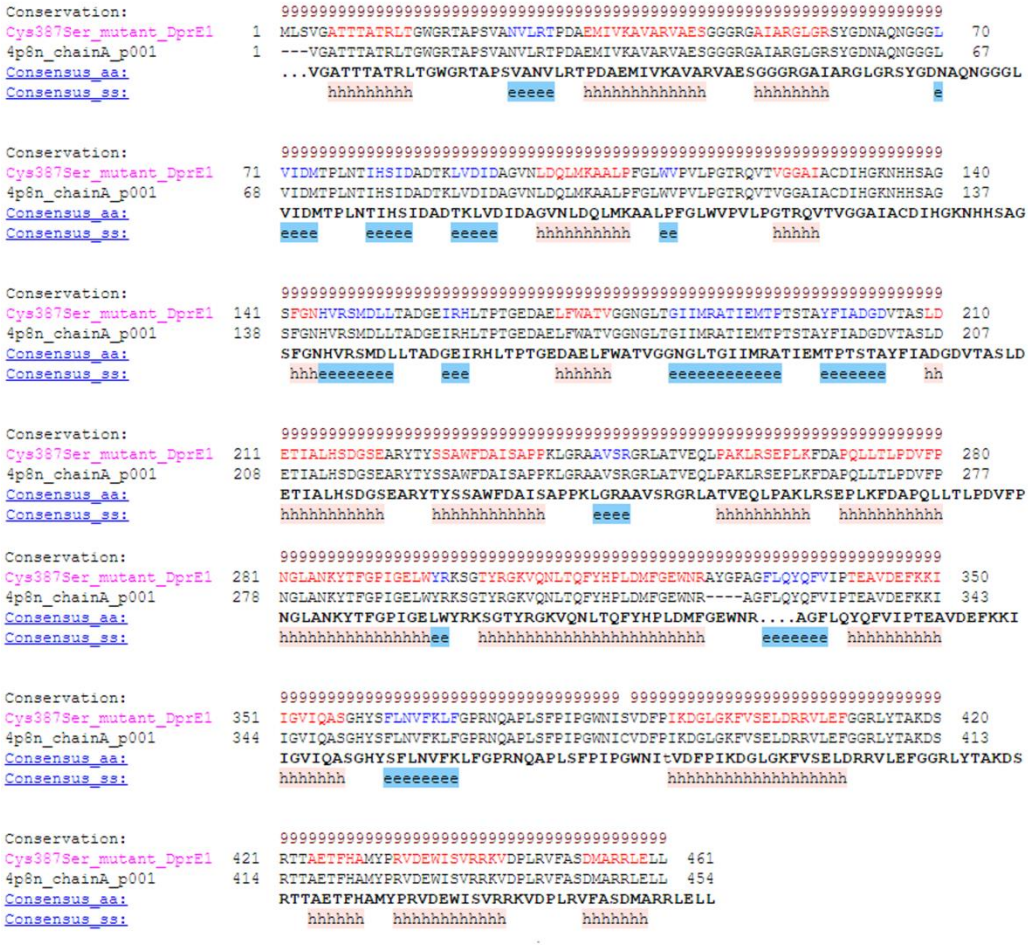

Figure S1 Amino acid sequence alignment of DprE1 (target) over wild DprE1 (template).

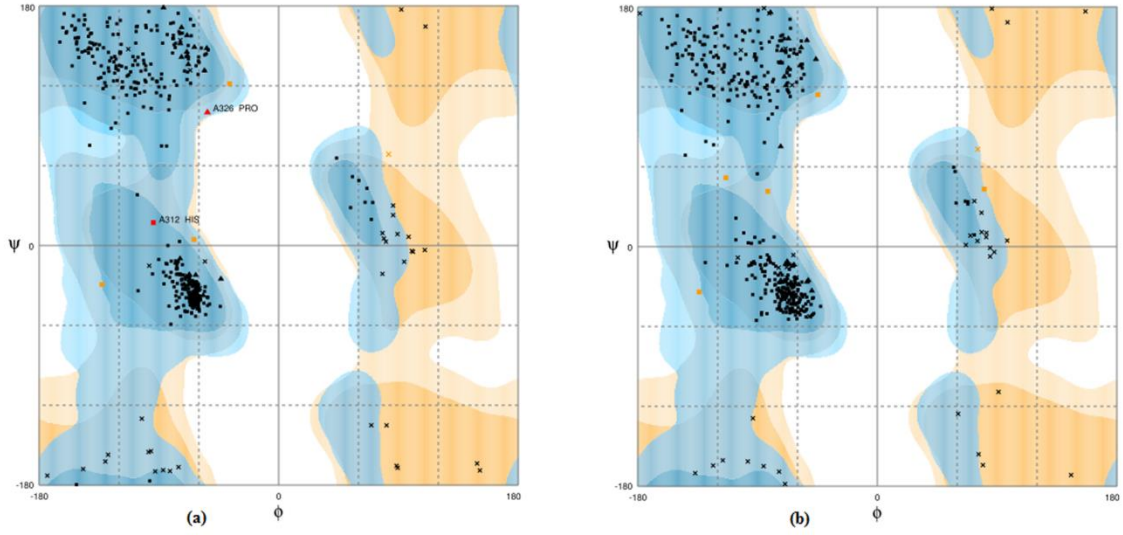

Figure S2 Ramchandran plot of mutant DprE1 structure obtained from RAMPAGE program before (a) and after protein preparation (b).

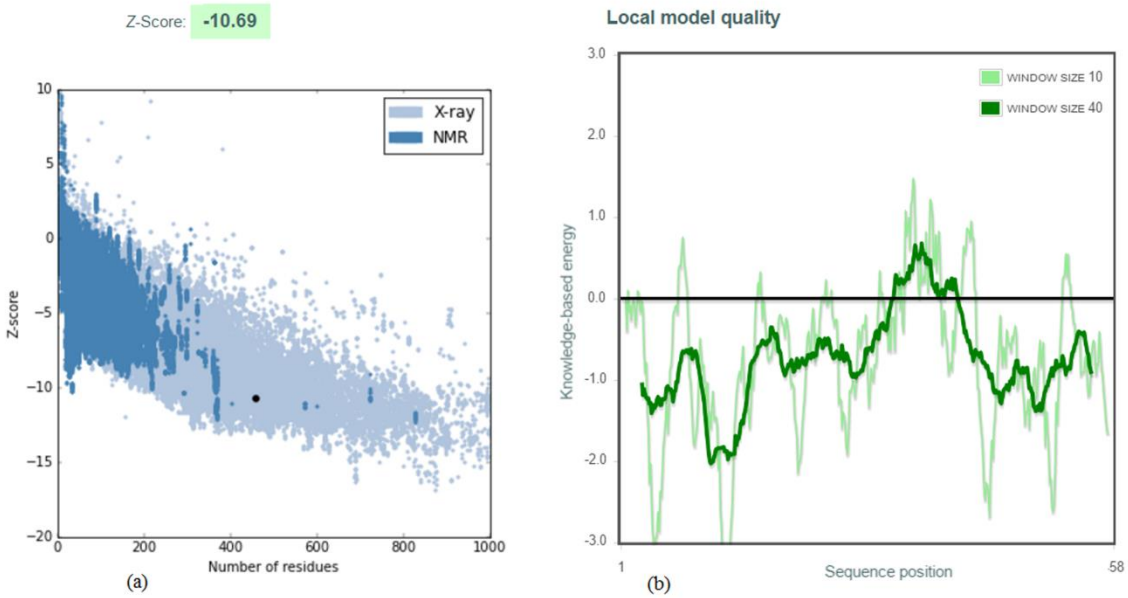

Figure S3 The overall (a) and local quality (b) of homology model of mutant DprE1 model in terms of Z-score obtained from ProSA tool.

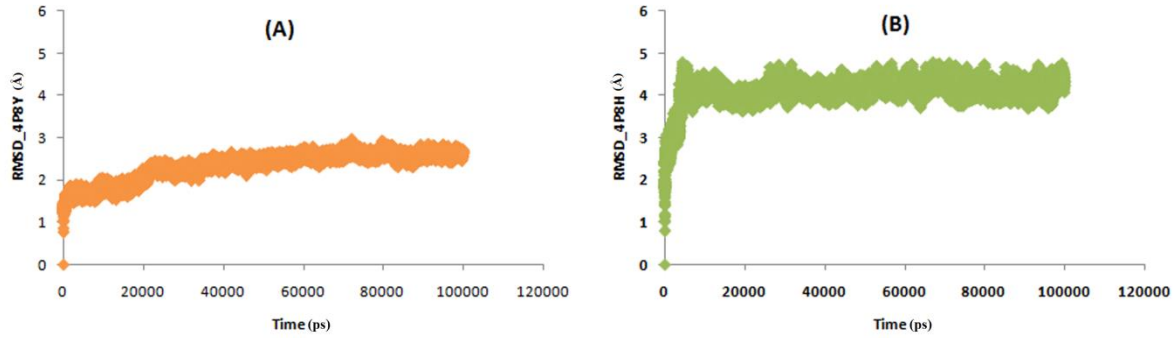

Figure S4 RMSD profile of backbone atoms of two different wild type DprE1, with intermediate (PDB ID = 4P8Y) (a) and poor resolutions (PDB ID = 4P8H) (b).

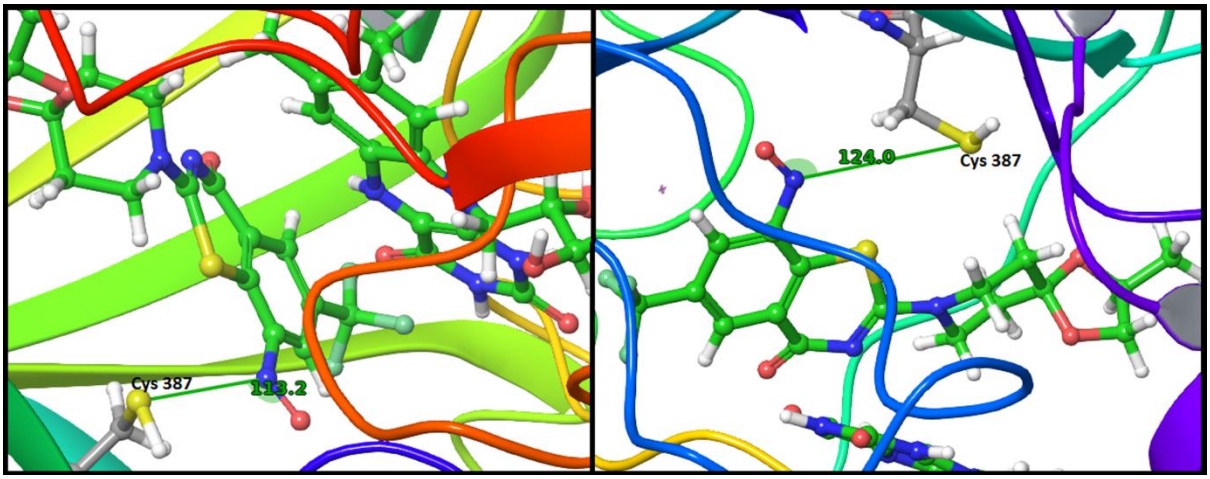

Figure S5 Calculated Burgi-Dunitz angle of wild type DprE1 with intermediate resolution (PDB ID = 4P8Y) (a) and poor resolution (PDB ID = 4P8H) (b).

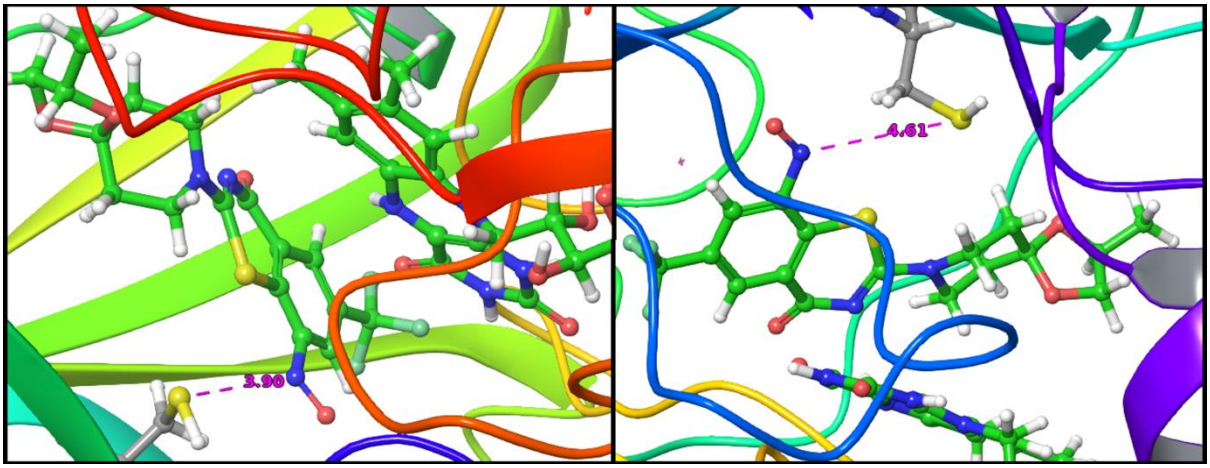

Figure S6 Calculated distances favorable for a nucleophilic attack in case of wild type DprE1 with intermediate (PDB ID = 4P8Y) (a) and poor (PDB ID = 4P8H) resolution (b) using molecular dynamics simulations.

Table S2 DFT based Molecular orbital energies calculations

Ligands	HOMO (eV)	LUMO (eV)	$HOMO_{nucleophile}$ - $LUMO_{electrophile}$ (ΔE)	$HOMO_{Electrophile}$- $LUMO_{nucleophile}$ (ΔE)
Cysteine	-0.238	0.016	$HOMO_{Cysteine} - LUMO_{BTZ043}$ = -0.243eV $HOMO_{Serine} - LUMO_{BTZ043}$ = -0.251eV	$HOMO_{BTZ043}$ - $LUMO_{Cysteine}$ = -0.256eV $HOMO_{BTZ043} - LUMO_{Serine}$ = -0.261eV

Serine	-0.246	0.021	-	-
BTZ043	-0.240	0.005	-	-