Electronic Supplementary Material (ESI) for Molecular BioSystems.

Supporting Information

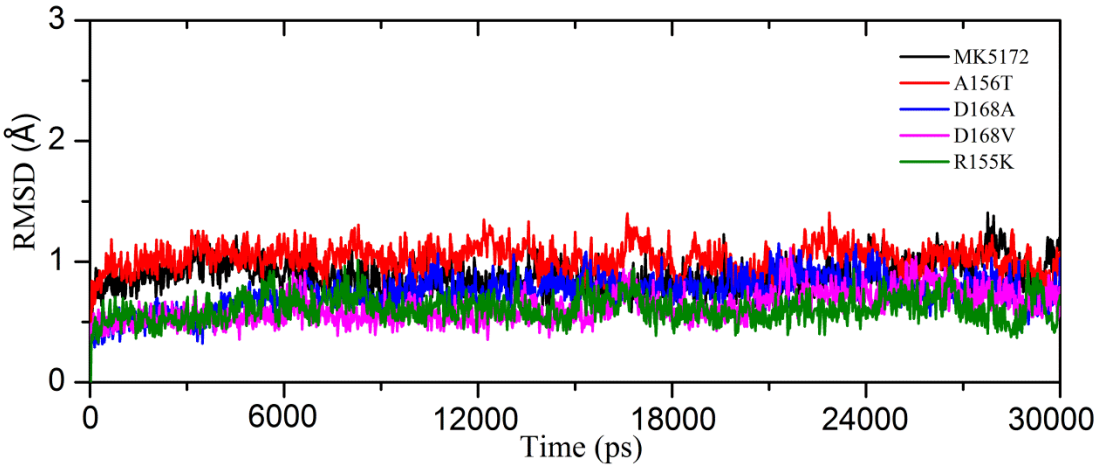

Figure S1. The root mean square deviation (RMSD) of the NS3/4A protease active sites along the 30 ns MD simulations.

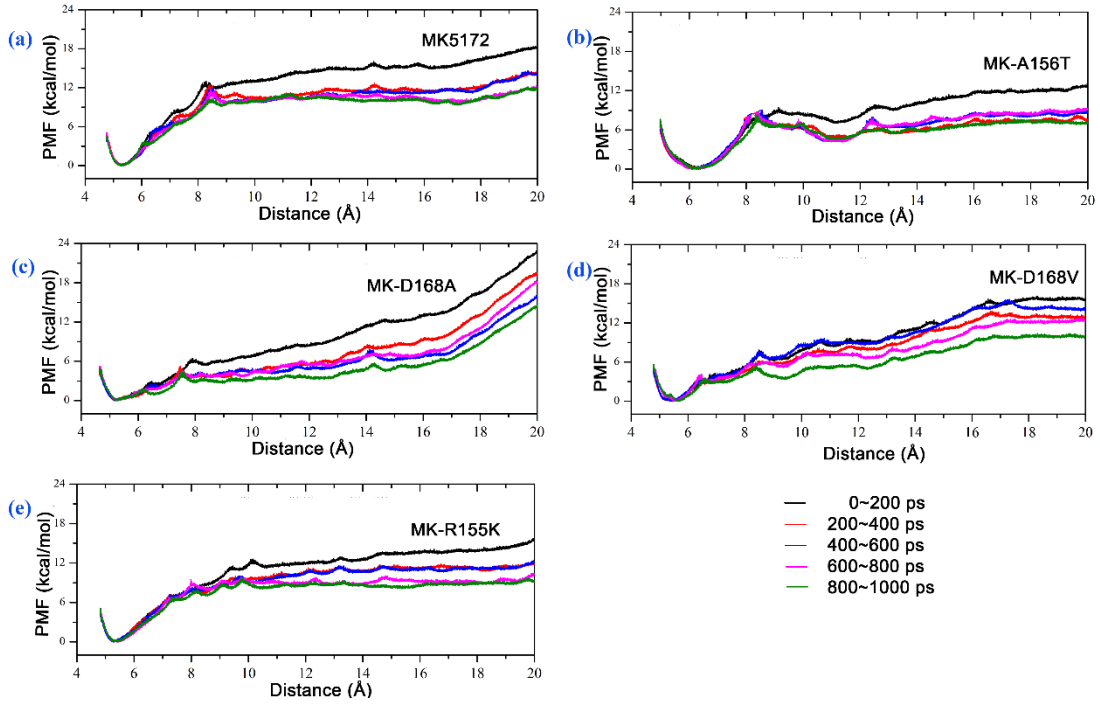

Figure S2. Convergence analysis of PMFs. The PMF values are convergent when the simulation time reaches to 600 ps.

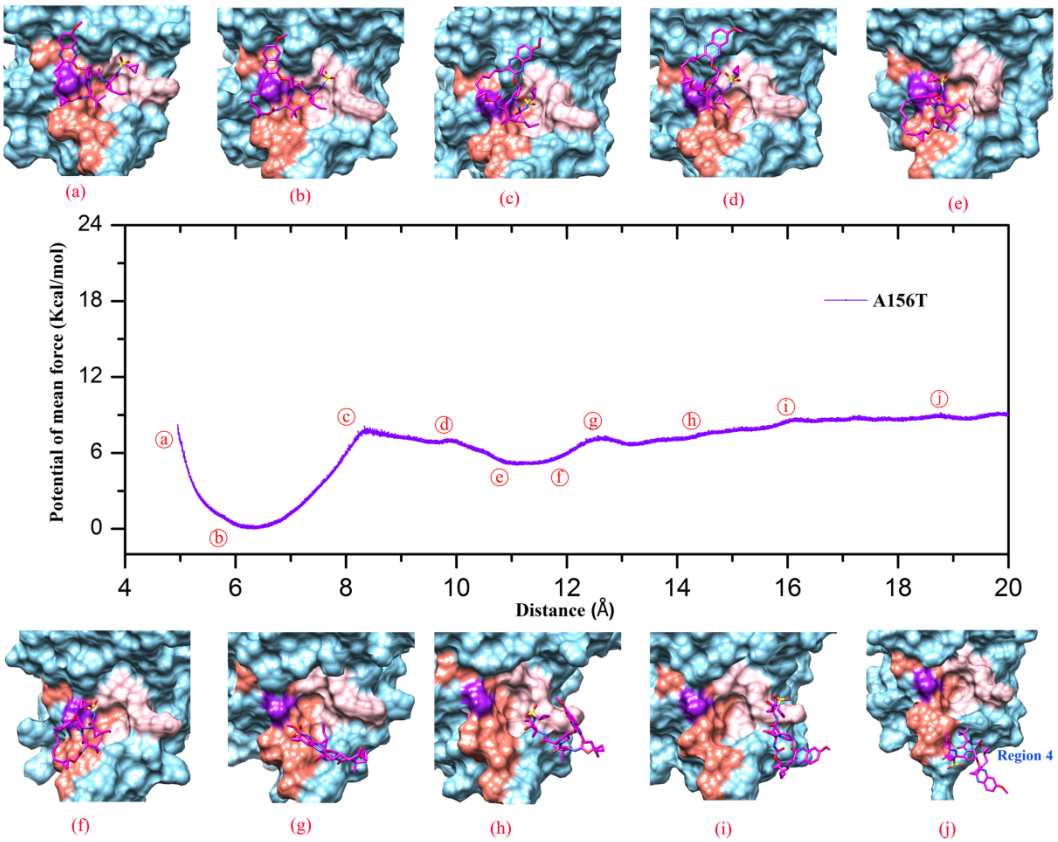

Figure S3. PMF as the function of the drug-target distance along the 1 ns MD simulations in each window (35 windows in total). The NS3/4A protease was enclosed in the solvent accessible surfaces; the strand 135-139 and the strand 154-160 are colored in pink and salmon, respectively. MK5172 is shown in magenta stick model. The mutation A156T is colored in purple. The panels show that MK5172 dissociates from Region 4 of protease.

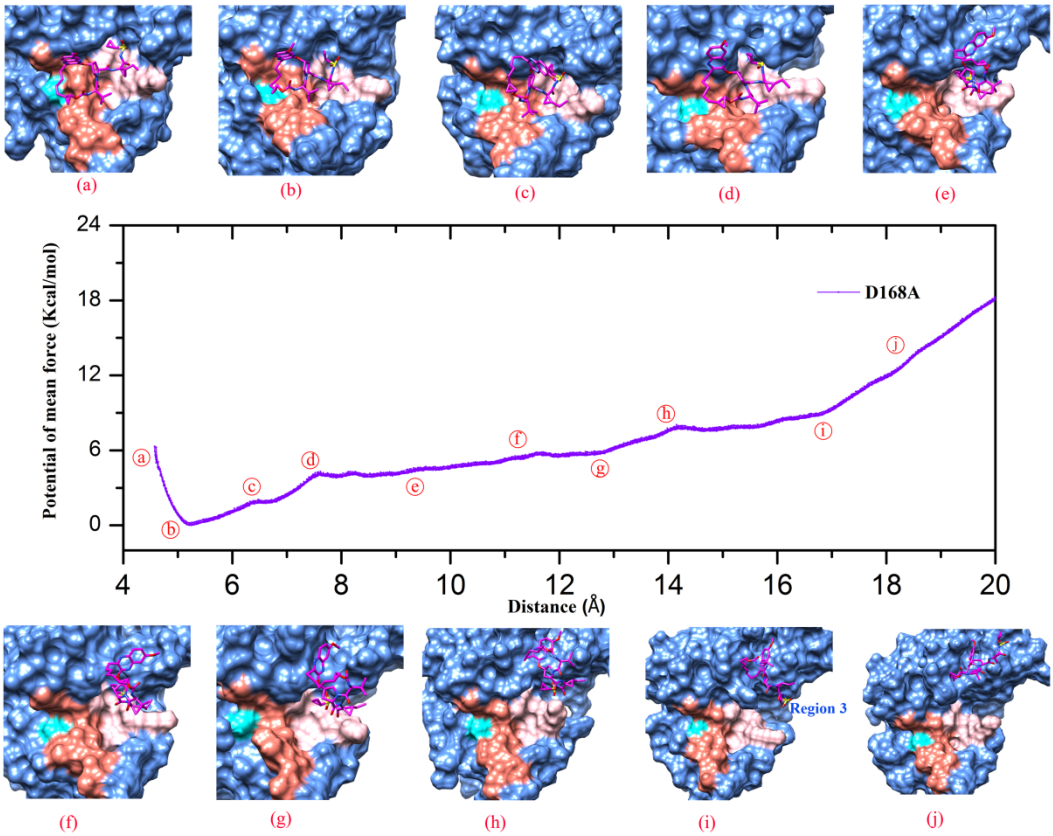

Figure S4. PMF as the function of the drug-target distance along the 1 ns MD simulations in each window (35 windows in totally). The mutation D168A is colored in sky blue. The panels show that MK5172 dissociates from Region 3 of protease.

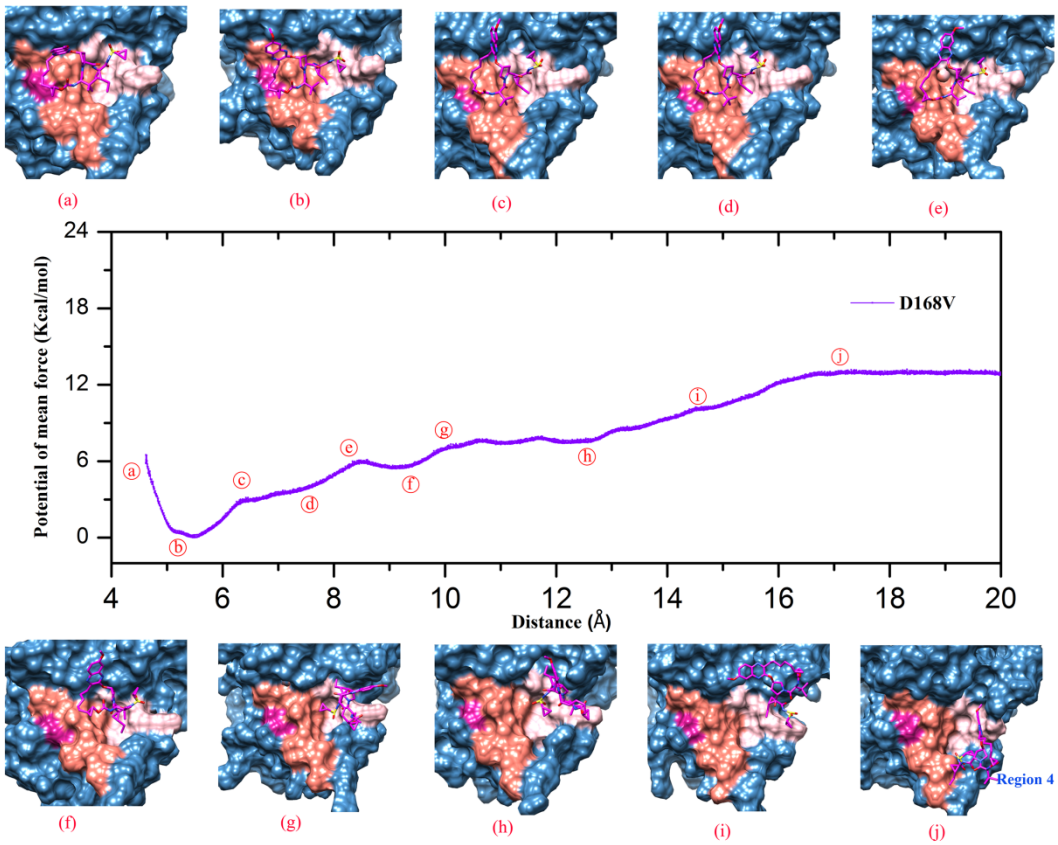

Figure S5. PMF as the function of the drug-target distance along the 1 ns MD simulations in each window (35 windows in totally). The mutation D168V is colored in magenta. The panels show that MK5172 dissociates from Region 4 of protease.

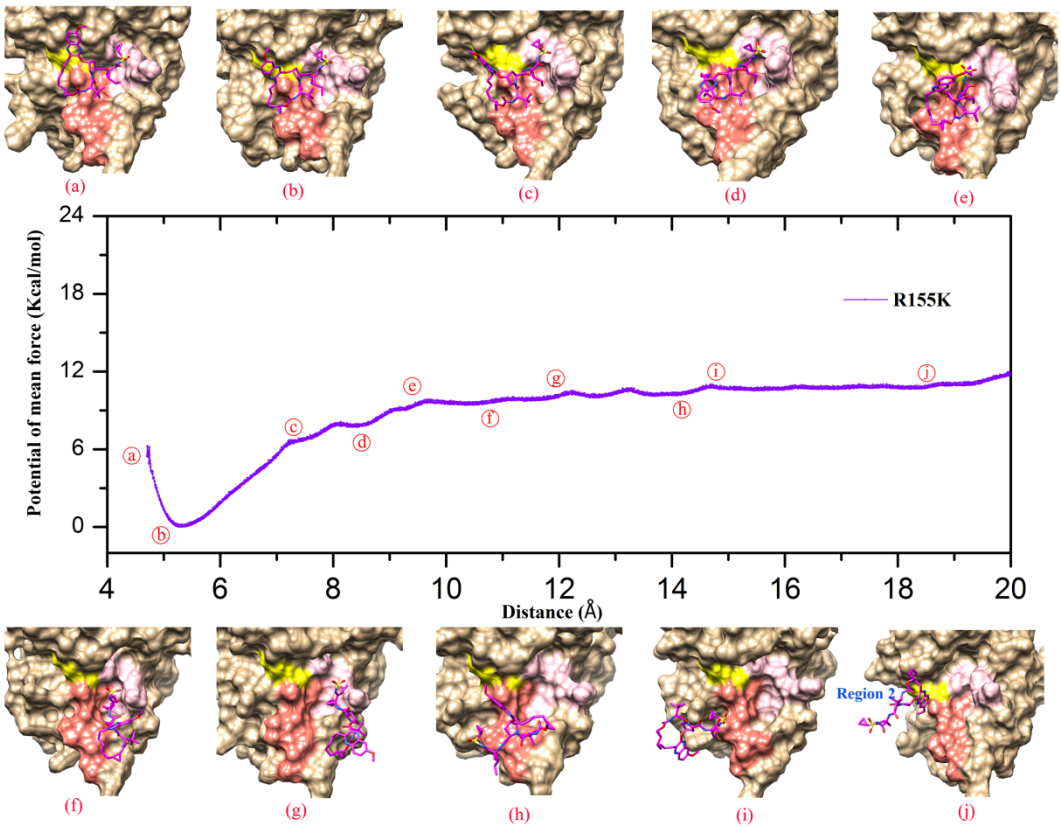

Figure S6. PMF as the function of the drug-target distance along the 1 ns MD simulations in each window (35 windows in totally). The mutation R155K is colored in yellow. The panels show that MK5172 dissociates from Region 2 of protease.

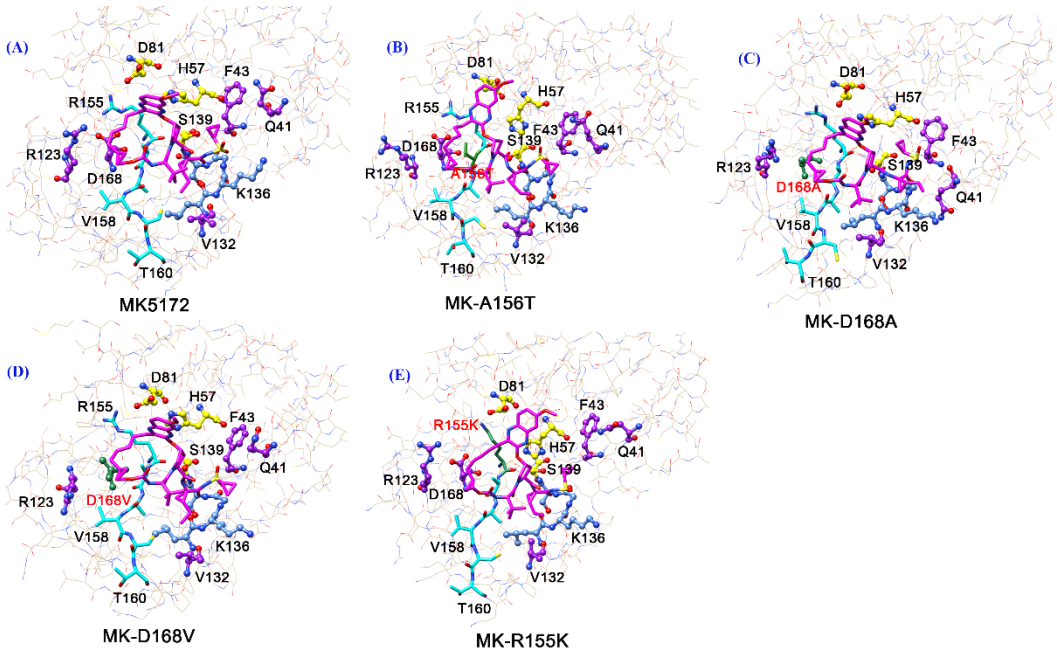

Figure S7. Interaction spectra of MK5172 to the WT and mutated NS3 proteases. The catalytic triad, strand 135-139, and strand 154-160 are colored in yellow, light blue, and sky blue, respectively, and the residues Arg123, Asp168 and Val132 are shown in purple. The mutations are colored in dark green and MK5172 is colored in magenta.