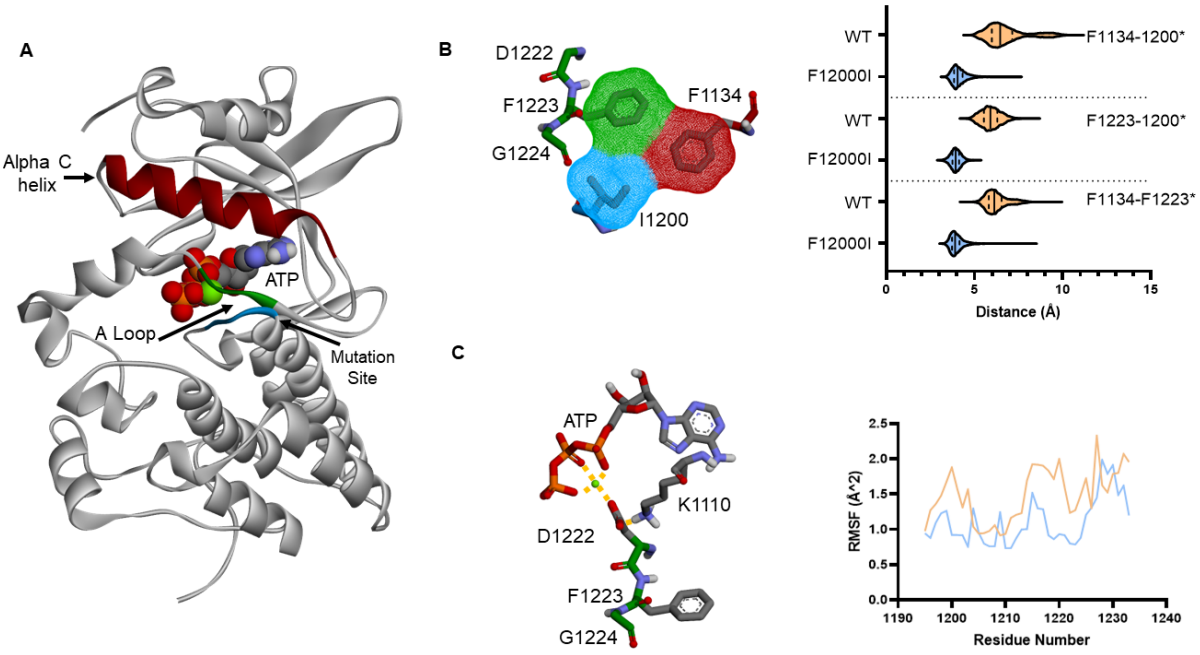
Supplementary Figure 19



Supplementary Figure 19. Equilibration of interactions that drives ATP affinity in the presence *MET* F1200I mutant. (**A**) Representative structure of ATP bound MET F1200I with the regions of interest highlighted [alpha C helix (red), DFG site (green), mutation site (blue)]. (**B**) π - π stacking interactions that bridge the alpha C helix and DFG site are conformationally controlled through residues position 1200. π - π stacking interactions were calculated between ring centers. Distances between F1200I and neighboring residues were measured from the F1200I side chain center of mass to the ring centers of the aromatic rings. (**C**) root-mean-square deviation (RMSD) calculations show a stabilization of the activation loop in the F1200I system. *Indicates that statistical testing with the Mann–Whitney–Wilcoxon test resulted in a P value < 0.01.