

## Supplementary Material

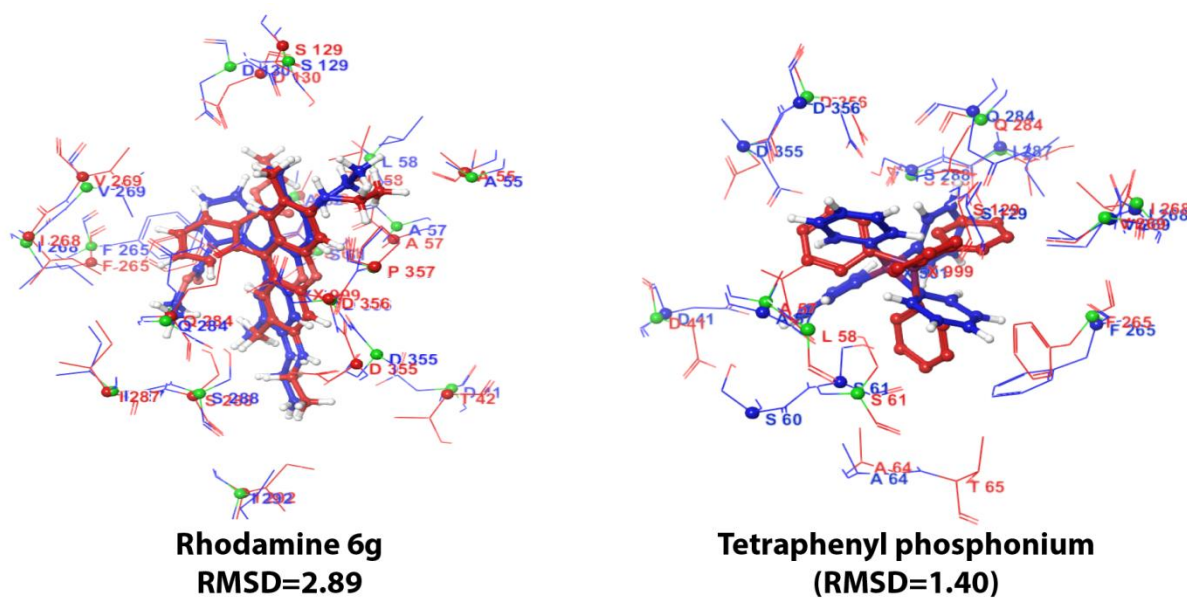


Figure S1. Binding orientation of NorM substrates in central cavity by docking studies,  
Blue=Cocrystal pose, Red=docked pose

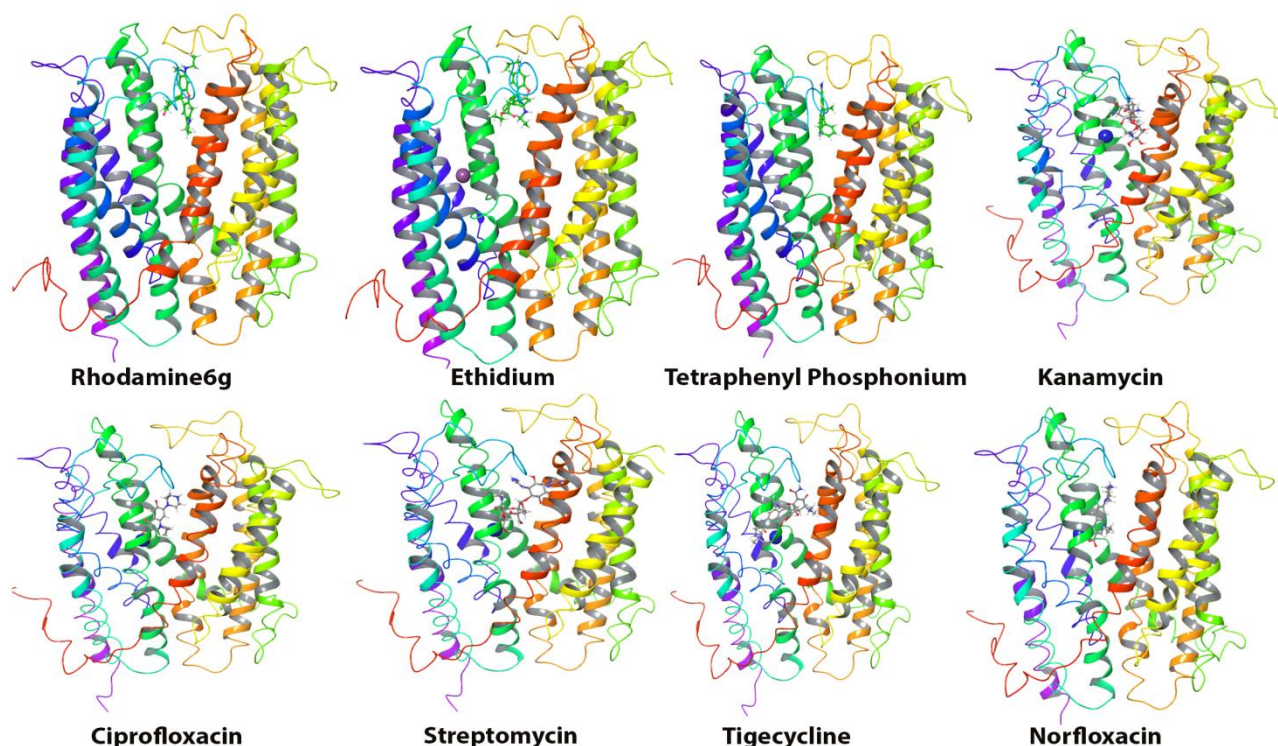


Figure S2a. Spatial binding of NorM substrates in active tunnel

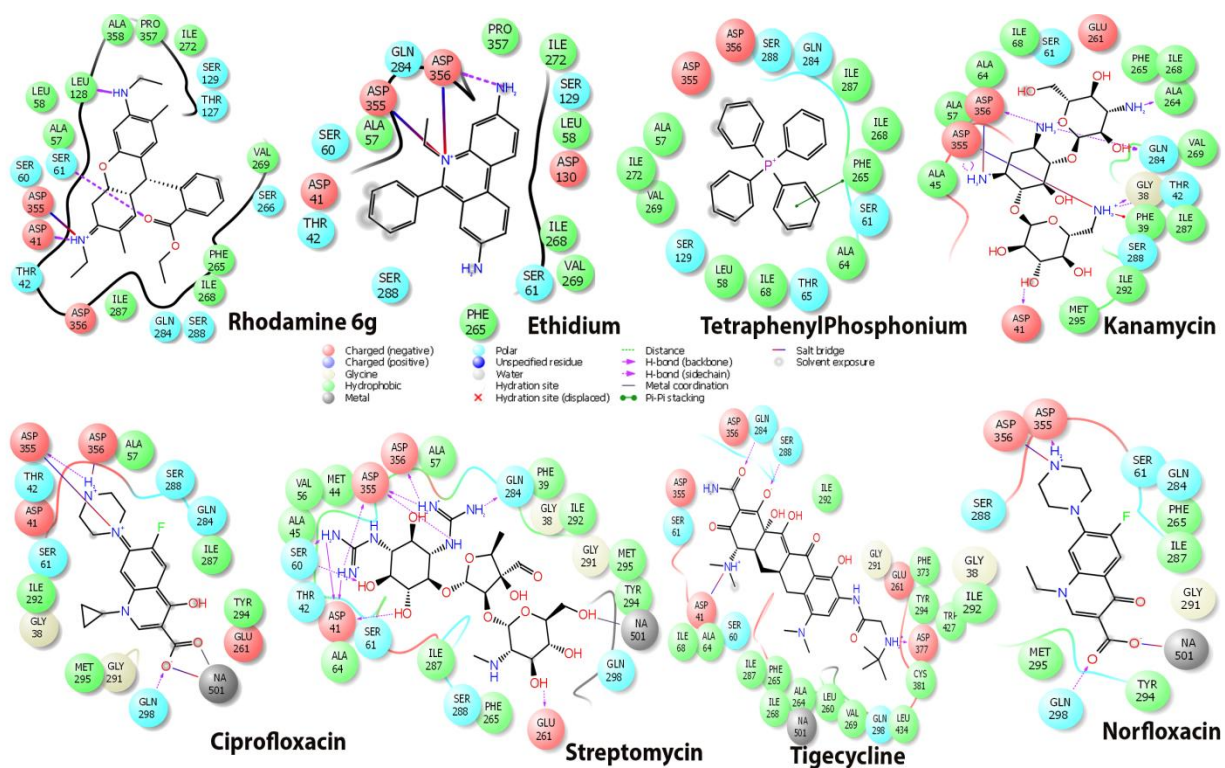


Figure S2b. Hydrogen bonds and Hydrophobic interactions of substrates of NorM transporter



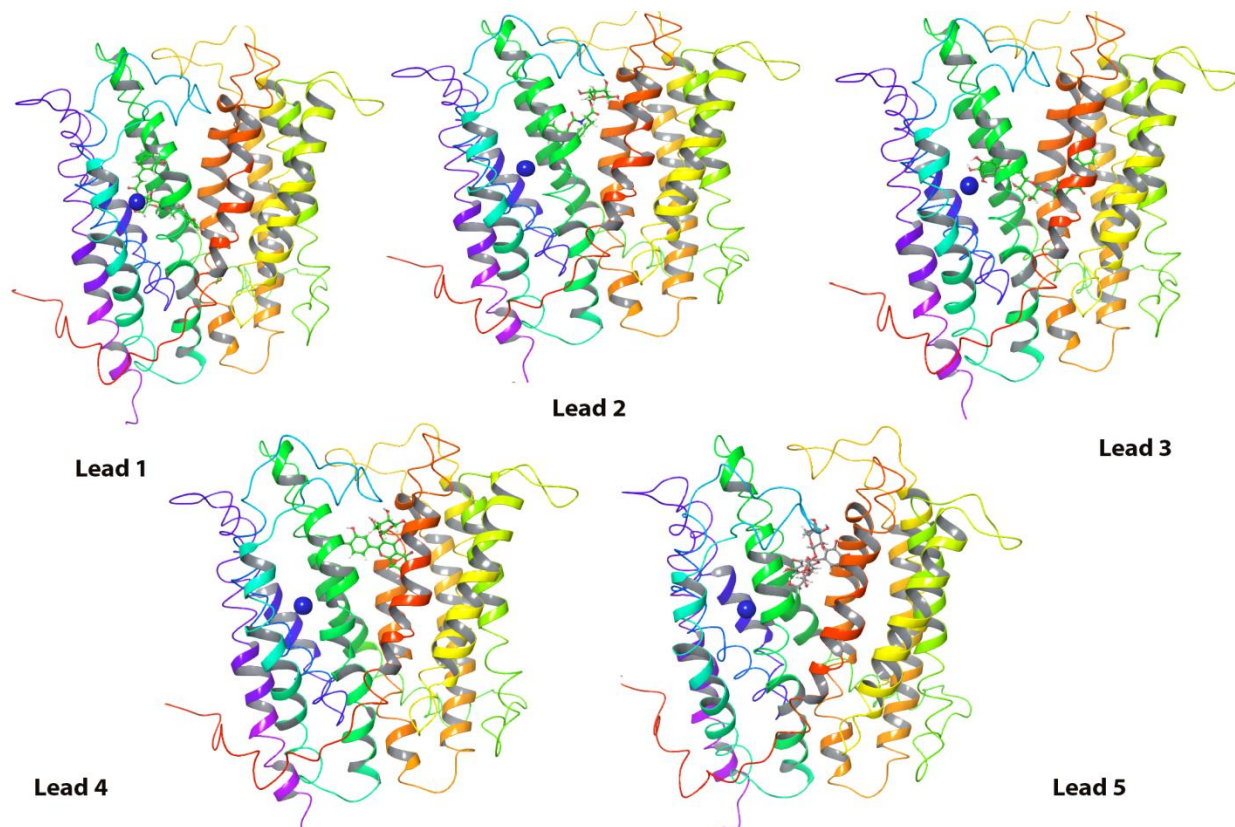


Figure S3a. Spatial binding of identified lead compounds in active tunnel

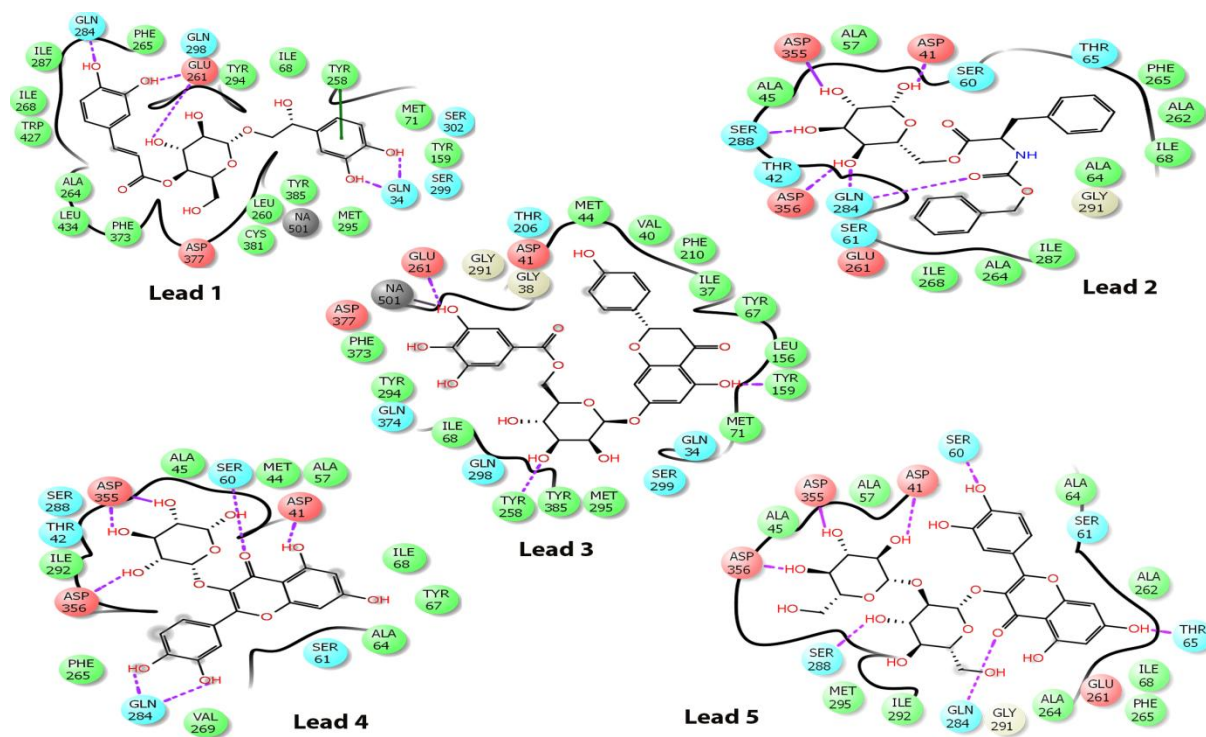


Figure S3b. Hydrogen bonds and Hydrophobic interactions of best lead molecules of NorM transporter

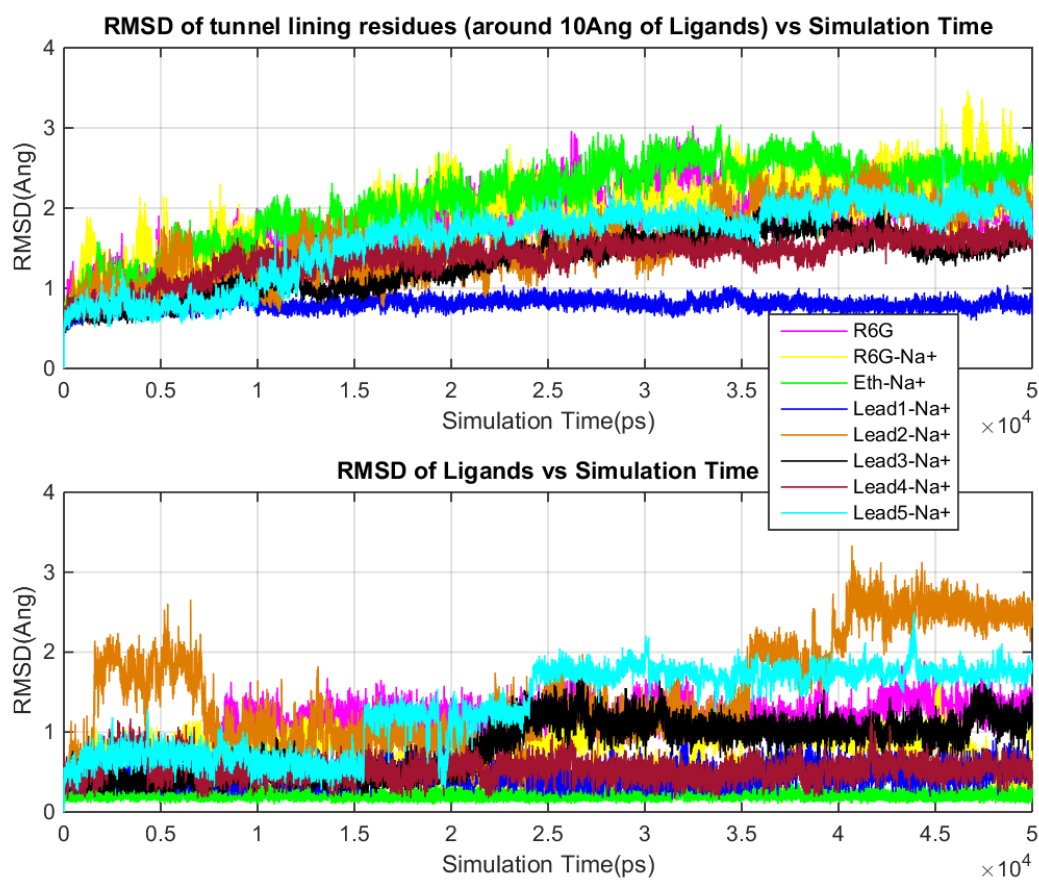


Figure S4. RMSD of active tunnel residues in NorM substrates and best leads molecular complexes and their ligands

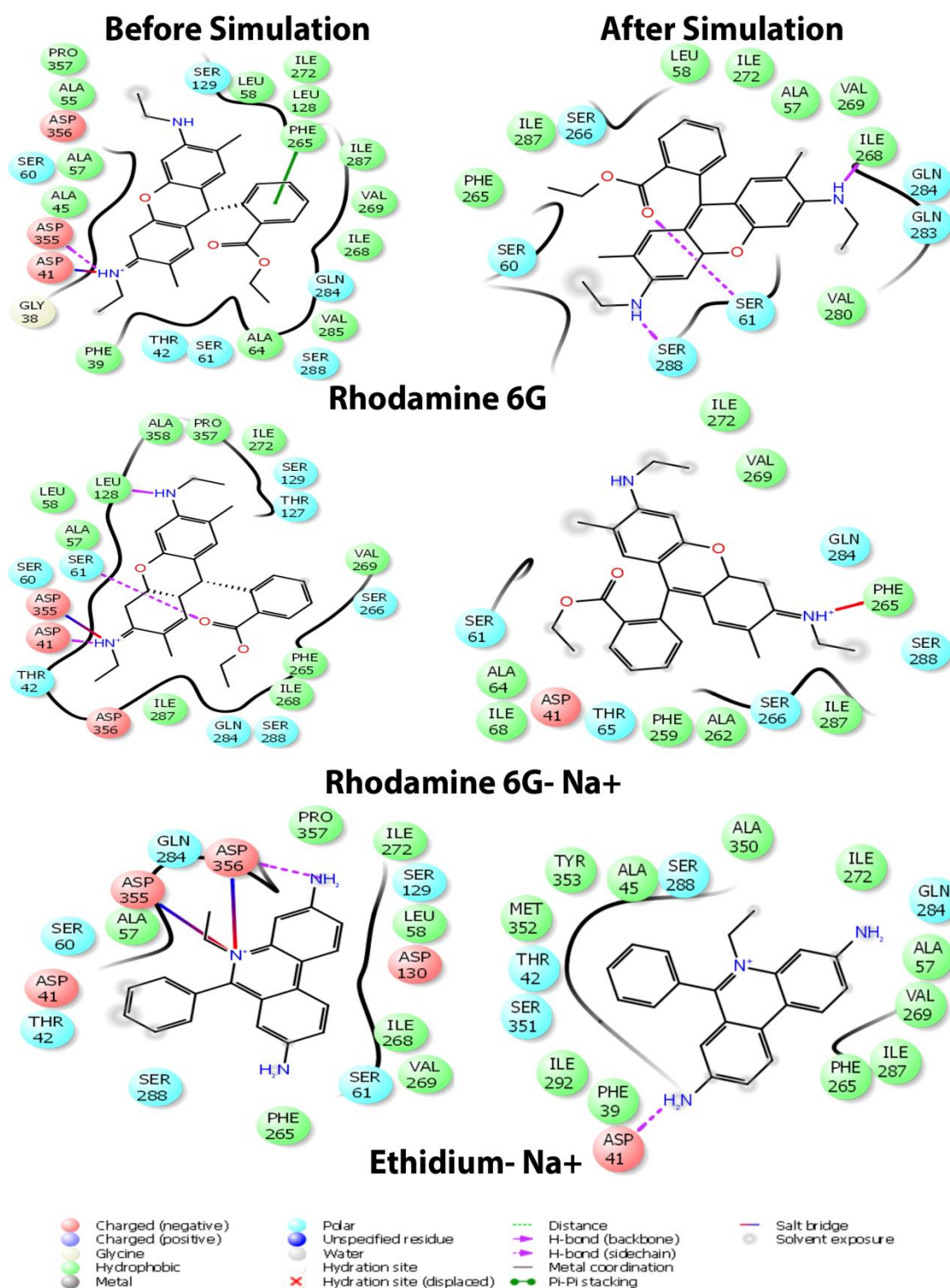


Figure S5(a). Active site interaction of NorM substrates and best leads in initial and averaged conformation from simulation



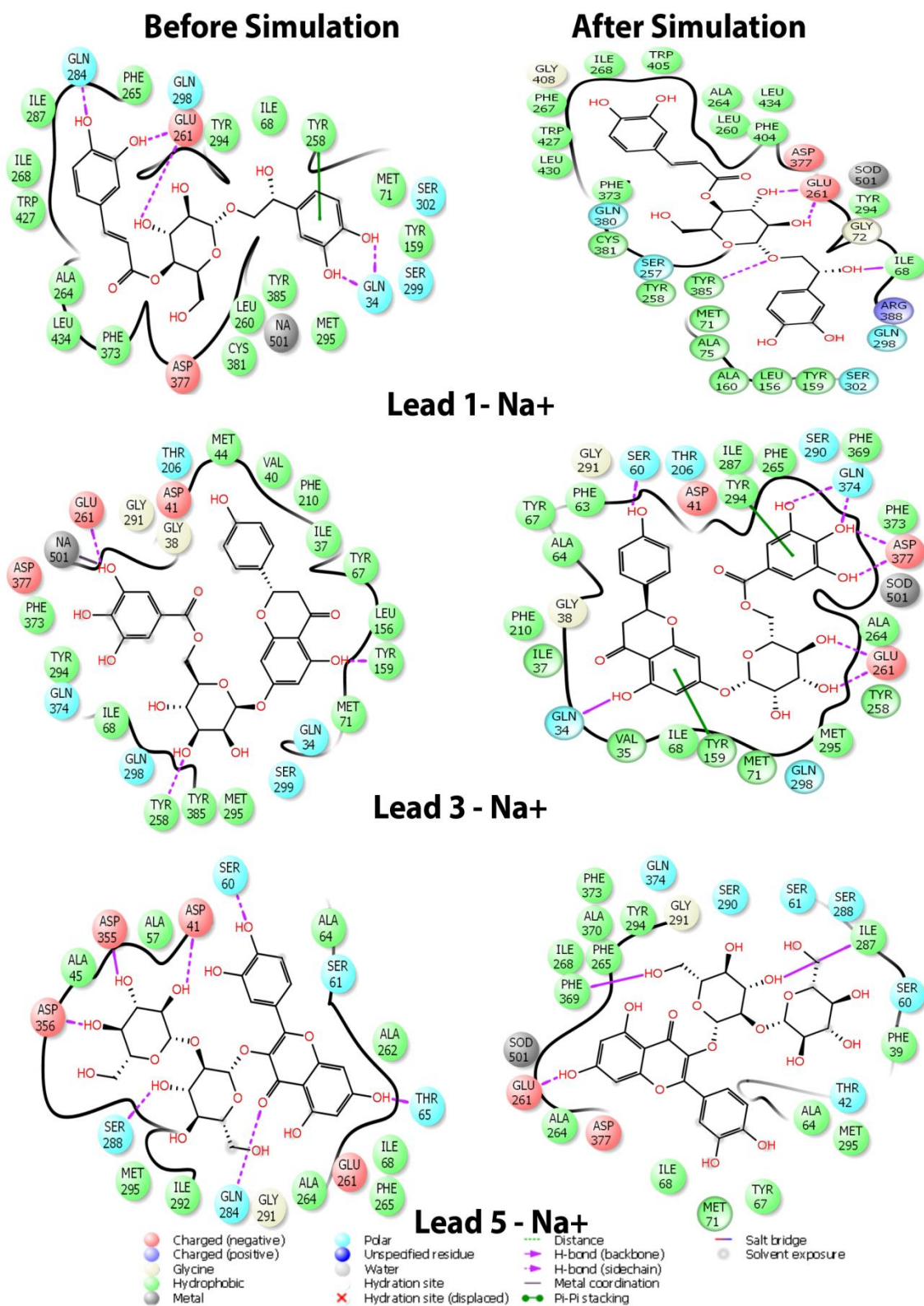


Figure S5(b). Active site interaction of top 3 identified leads in initial and averaged conformation from simulation

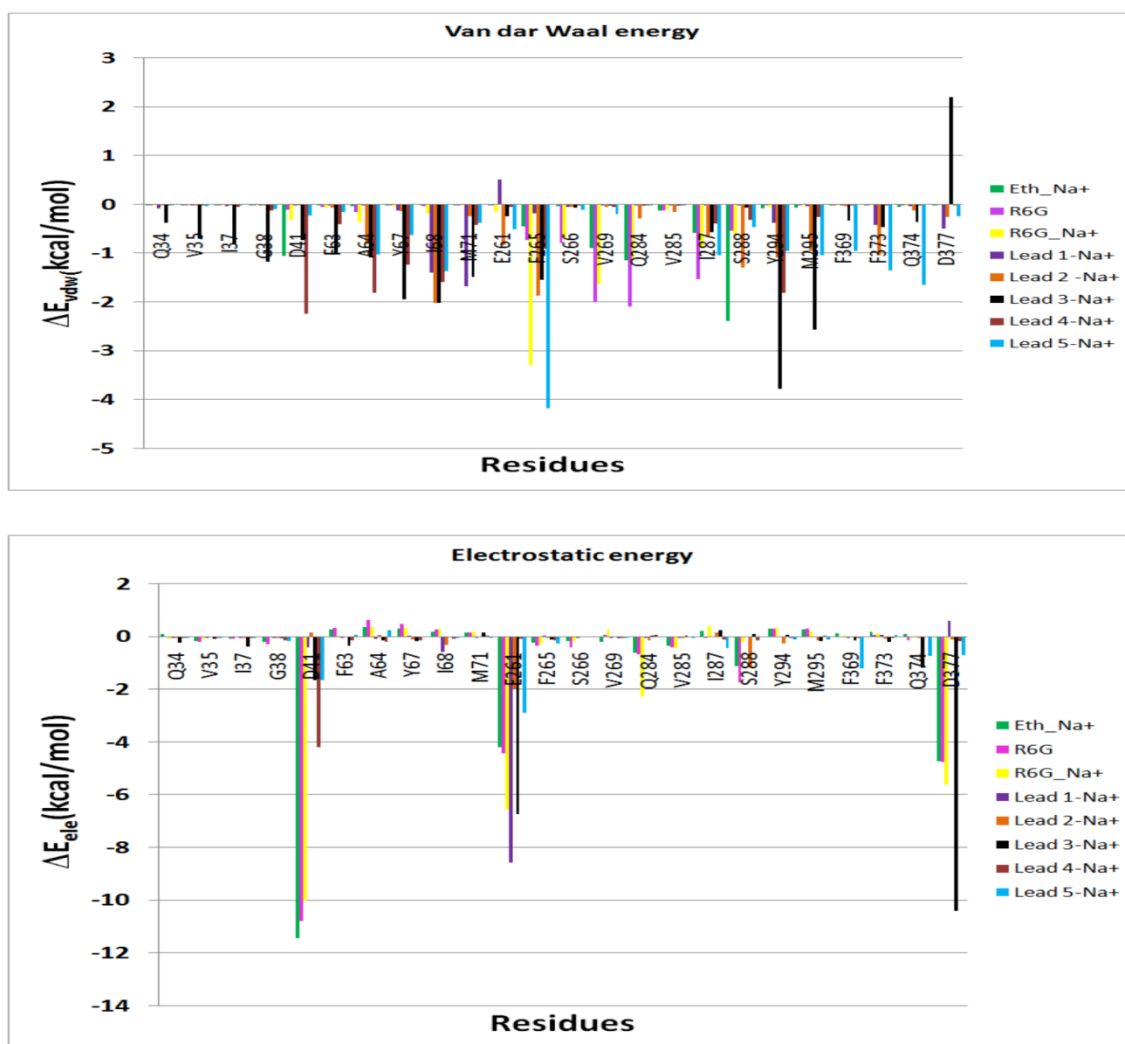


Figure S6. Decomposition of binding free energy into van der Waals, electrostatic for the major active tunnel residues in substrates and best leads with active tunnel residues