

Supplementary Material

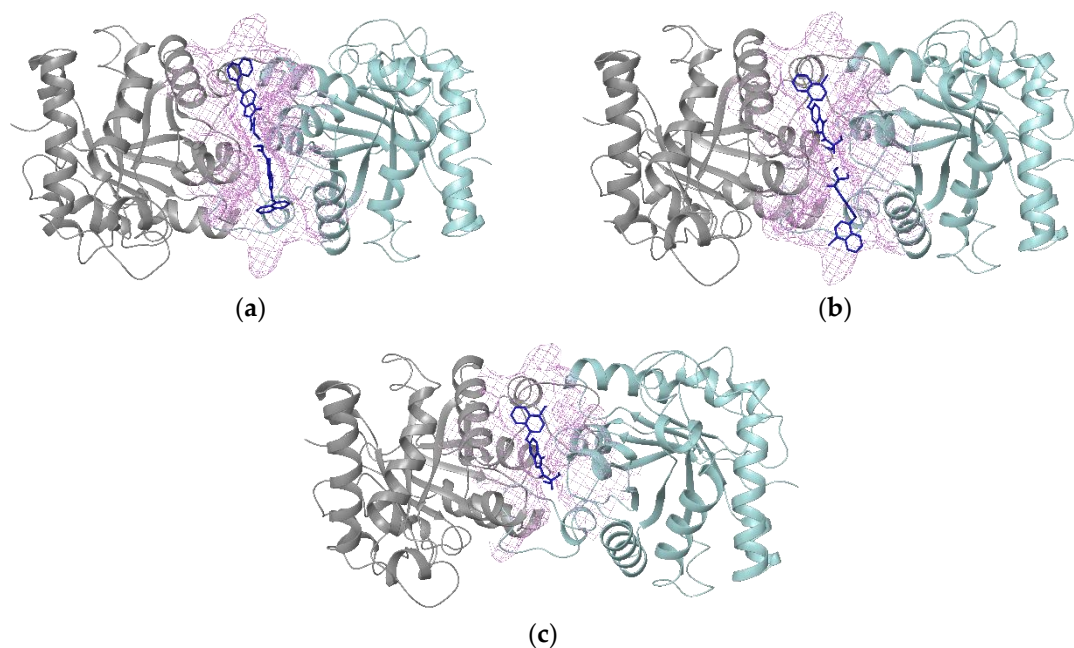


Figure S1. Complete view of the binding mode of compounds (a) 1, (b) 2, and (c) 3, at the dimer interface of TbTIM predicted by docking. For compounds 1 and 2 the two molecules are displayed. Molecular surface is drawn as a purple grid.

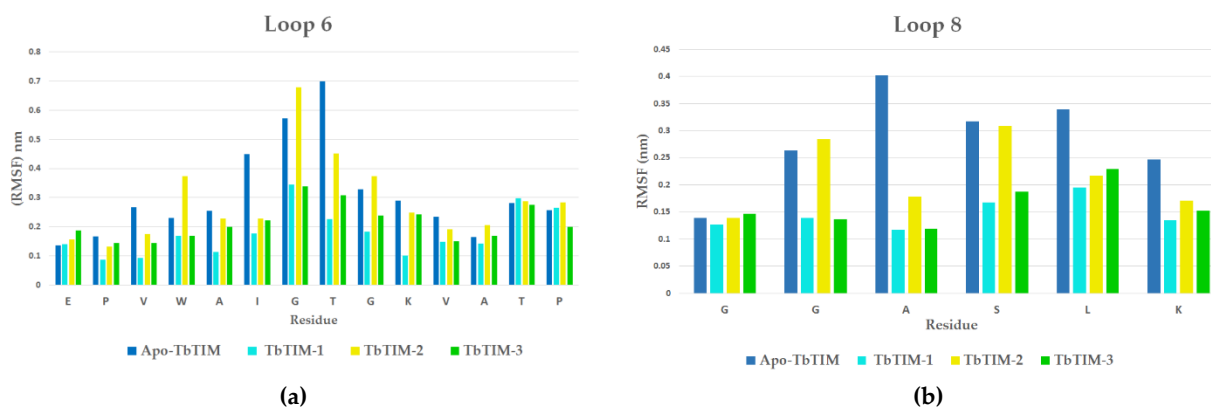


Figure S2. RMSF comparison between Apo-TbTIM and the complexes with compounds 1, 2 and 3. (a) Loop 6 residues. (b) Loop 8 residues.