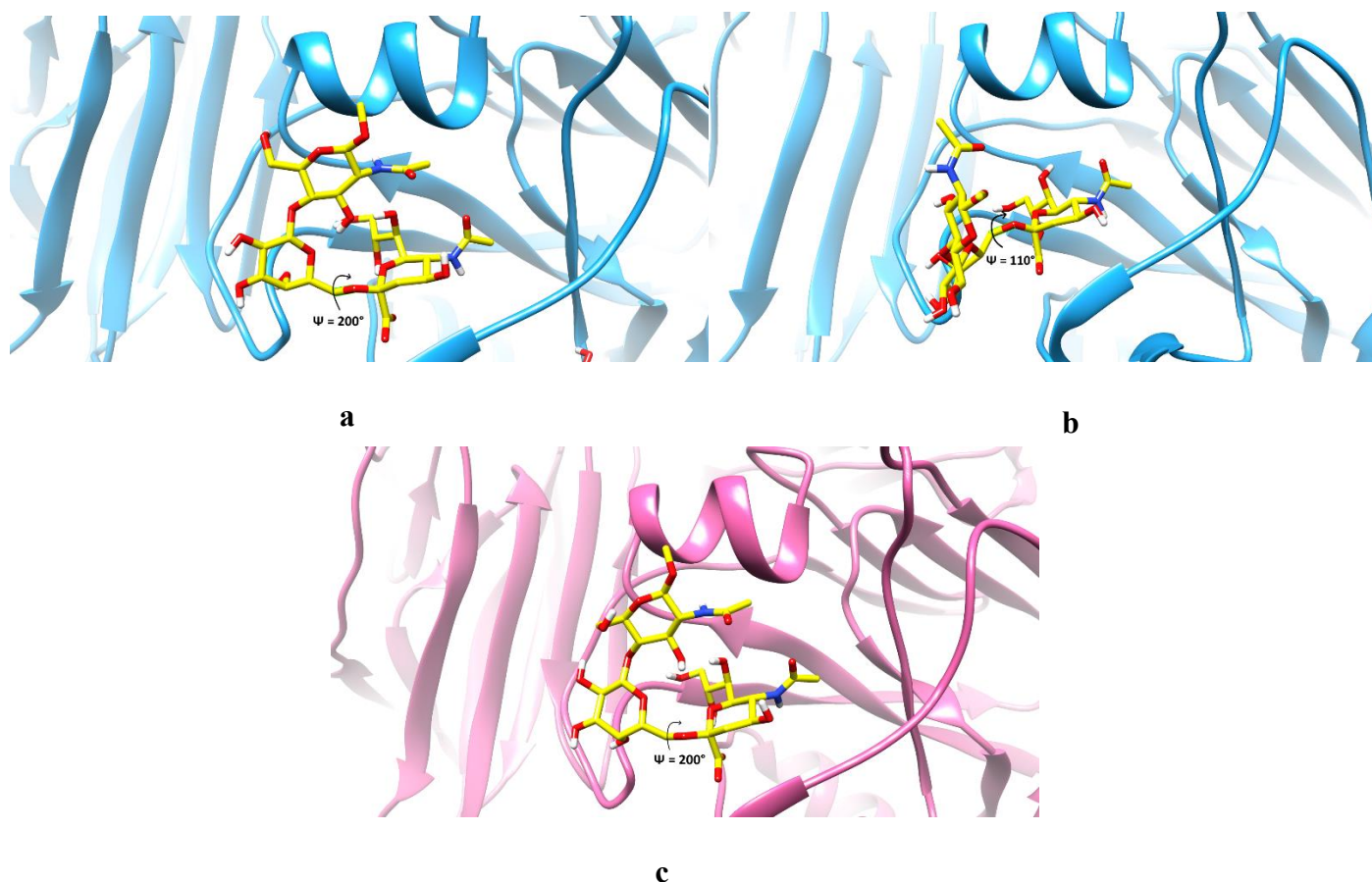


Figure S2: Several conformers of the receptor analog from the MD trajectories



(a) Conformer close to the crystallographic pose (b) conformer associated with the change of the glycosidic torsion angle ψ by 90 degrees related to the complex with the HA of A/Cambodia/e0826360/2020; (c) conformer related to the complex with the HA of A/YANAO/08-01V/2021.

Receptor analog conformation kept close to the crystallographic pose during the full simulation time after the equilibration (Figure S1) for the complex with HA of A/YANAO/08-01V/2021.