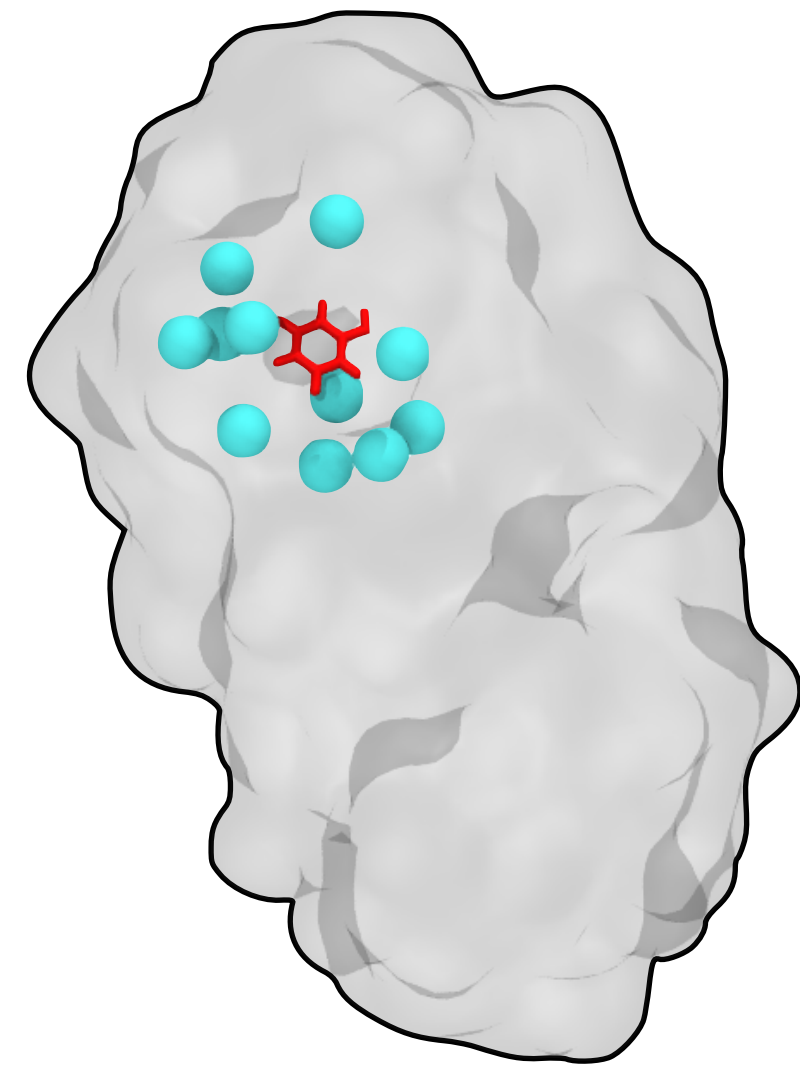
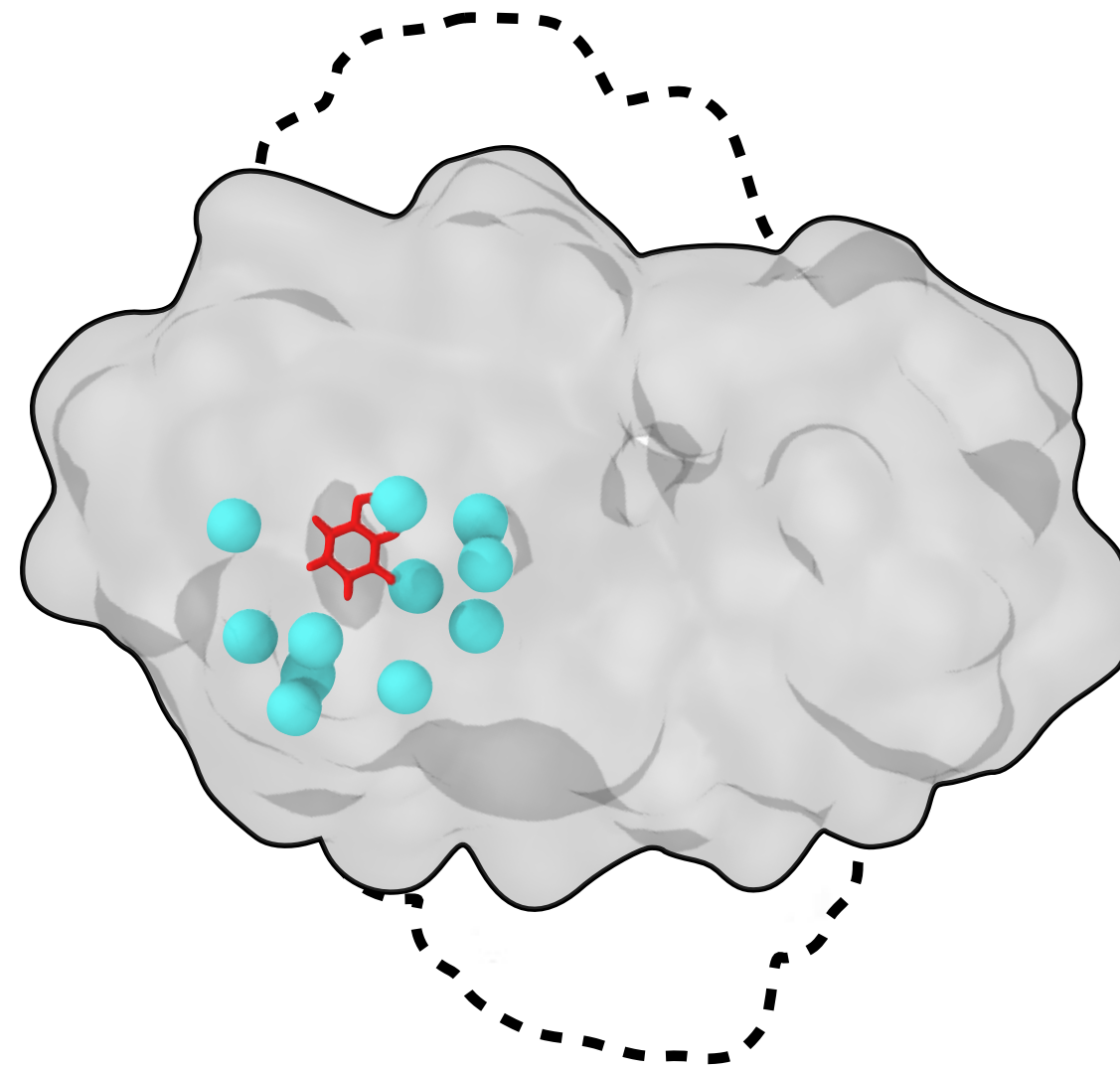
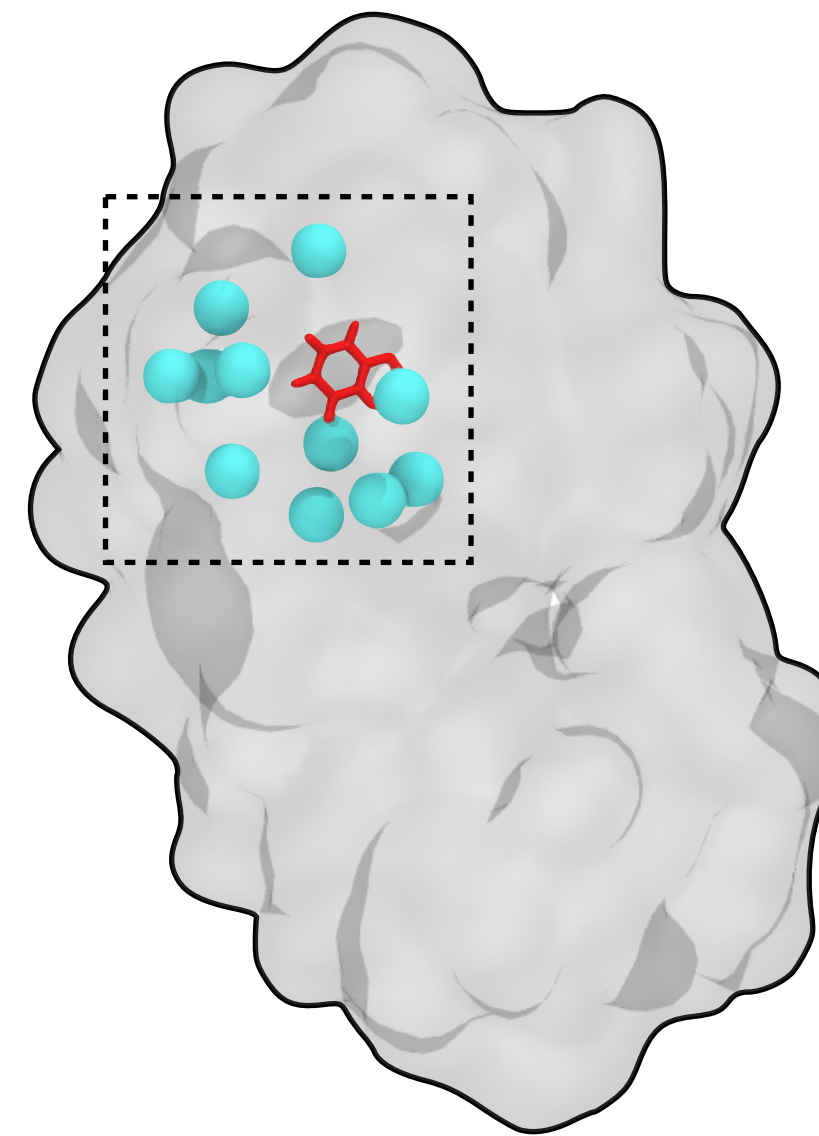
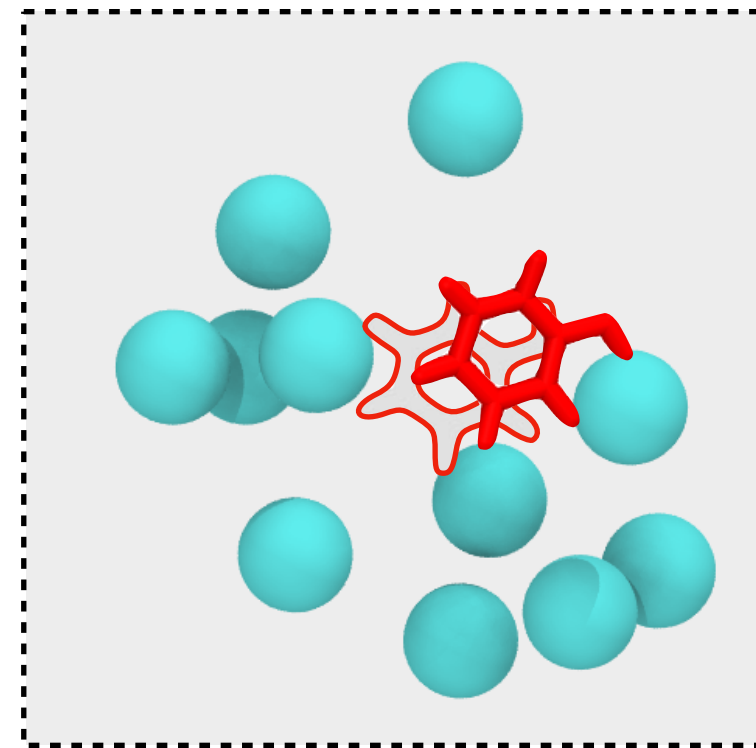


A**B**

Align to reference
using **protein**
fitting group

C

Measure **ligand**
RMSD with respect
to reference

D

Reference Coordinates

Calculation of the Instantaneous DBC