## Example pose prediction

- To extract the bound state from YANK results and align the protein to the first frame: <a href="https://github.com/daveminh/Chem456/blob/master/static\_files/tutorials/bromodomains-YANK/getBoundState.ipynb">https://github.com/daveminh/Chem456/blob/master/static\_files/tutorials/bromodomains-YANK/getBoundState.ipynb</a>
- To predict the ligand binding pose: <a href="https://github.com/daveminh/Chem456/blob/master/static\_files/tutorials/bromodomains-YANK/ligandPosePrediction.ipynb">https://github.com/daveminh/Chem456/blob/master/static\_files/tutorials/bromodomains-YANK/ligandPosePrediction.ipynb</a>
- Results are in poses.dcd