Screening docked ligands and viewing trajectories/ensembles

- Demo
  - ViewDock - facilitates screening of ligands output by the program DOCK
  - FindHBond - identifies hydrogen-bonding interactions based on atom types and geometrical relationships
  - MD Movie - tool for visualization/analysis of molecular dynamics trajectories and other structural ensembles
- Hands-on experience
  - ViewDock tutorial (the online version can be accessed from the Chimera Help menu)