Rosetta & PyRosetta Resources

* **See “how to prepare structures for use in rosetta” AND “how to prepare ligands for use in rosetta” + overview of params files**
  + Put in POSE (in FAQ)

1. **Prepare** structures by “relaxing into Rosetta’s energy function”?
   * **See Relax Application**
2. For protein-ligand docking (note that Rosetta does NOT recognize ligands by default):
   * Generate a params file for gold w/ info on name of metal, id code, type ligand, unk amino acid type, charge, bond, other metal-binding atoms, etc.
     + See: /path/to/rosetta/main/database/chemical/residue\_type\_sets
       - Can generate from input mol file
   * Are we modelling ligand flexibility? If so, need library of ligand conformers in PDB format (MOE, openeye Omega… RCSB(?))
     + PDB will likely need cleaning

Ligand: gold ions (gold (III)), then gold(I), then copper (I and II) (so we can assess binding, distance, energy for competition with gold) then IF POSSIBLE, after everything else, lanthanum

* **I want to do “X” page**
  + **Docking**
  + **Symmetric Interfaces**
* Symmetry User’s Guide
* SymDock for predicting symmetric homooligomeric protein assemblies from single subunit’s structure
  + Start with single monomeric structure & use make\_symmdef\_file
    - Use make\_symmdef\_file\_denovo if we don’t know rigid body config
      * Will perturb/refine starting configuration?
      * If required symmetry isn’t encoded in this file, either do by hand or analyze other protein with same symmetry in PDB database, generate symm\_def, and edit to randomize initial orientation
  + Keep seeing “prepacked protein monomer”: **what is pre-packing?**
  + docking:dock\_ppk produces a homomeric output PDB

**If possible, (last thing on list) can we monitor the homodimer linking to the DNA(?)**

* Tam can help with DoF
* Fold and Dock for predicting symmetric homooligomeric protein assemblies starting with the **FASTA sequence (+ location of fragment libraries + de novo symmdef file)** of a subunit:

<https://www.rosettacommons.org/docs/latest/application_documentation/structure_prediction/fold-and-dock>

\*Ab initio options all valid

* PyRosetta docking tutorial: <http://www.pyrosetta.org/tutorials#TOC-Workshop-7:-Docking>
  + If you are using ligands in PyRosetta, please consult the sample script D120\_Ligand\_interface.py and the tool scripts mutants.py, molfile2params.py, and load\_ligand.py (residue params)
  + <http://www.pyrosetta.org/obtaining-and-preparing-ligand-pdb-files>
    - Obtain PDB (RCSB, etc)
    - Get chemical data files & convert to .mdl via openbabel
    - Convert .mdl to params file
    - Obtain ligand PDB (if not present; set ResidueType appropriately & rename chain “X”)
      * May need to insert PDB manually with Python, PyMOL, grep, awk, or Biopython, etc.
    - Load ligand PDB into PyRosetta
    - Alter fullatom chemical database permanently
    - Prep for docking 🡪
  + Make sure both chains (for docking) are part of same Pose
    - Create PDB including both partners
    - Download & clean

<https://www.rosettacommons.org/docs/latest/application_documentation/design/beta-strand-homodimer-design>

This is for creating a homodimer that will form via a surface beta-strand; useful to look at changes made at very least

* Sample degrees of freedom & interpret results

<https://www.rosettacommons.org/docs/latest/getting_started/Analyzing-Results>

PDB file doesn’t exist in database, but we generated a predicted one from one **I-TASSER**

* Can access I-TASSER structures from Tam’s and other’s accounts on website with ID & password

**Can we run homooligomeric symmetry in parallel with generating structure in PyRosetta based on structure?**