

## RosettaLipid Protocol Capture

### **Prediction (TransformMover and HighResMover)**

This protocol capture describes the RosettaLipid protocol. Rosetta can be obtained through [www.rosettacommons.org](http://www.rosettacommons.org). The following protocol has been tested with Rosetta version ad2739a. Here the example structure is the Serotonin 2B receptor crystallized in a complex with cholesterol (PDB: 4IB4). The complex was downloaded from <https://opm.phar.umich.edu>. All files are included in the Rosetta/main/demos/protocol\_capture/rosetta\_lipid\_cholesterol

### **Input/**

The following files are included in the **inputs/** directory to run the Prediction protocol:

4ib4.pdb	Serotonin 2B PDB downloaded from OPM
4ib4_A.pdb	Cleaned protein
4ib4_A_relax.pdb	Relaxed protein
4ib4_A_dock.pdb	Combined protein and cholesterol for docking input
4ib4_A_positions	Lipid accessible regions for global docking ( <a href="https://rosie.graylab.jhu.edu/mp_lipid_acc">https://rosie.graylab.jhu.edu/mp_lipid_acc</a> )
4ib4_A.span <sup>1</sup>	Rosetta spanfile
CLR.params <sup>2</sup>	Rosetta params file for cholesterol
CLR.pdb	Cholesterol pdb file
CLR_conformers.pdb <sup>3</sup>	Cholesterol conformer library
CLR_conformers.sdf	Cholesterol conformer output from MOE
dock.sh	Rosetta run command for docking
dock.xml	RosettaScripts XML file for docking
relax.sh	Rosetta run command for relaxing the protein
relax_wo_clr.xml	RosettaScripts XML file for relaxing the protein

<sup>1</sup>Indicates protein segments that should be embedded in the membrane.

<sup>2</sup>Pre-computed information about the geometry and chemical features of the cholesterol.

<sup>3</sup>Necessary for ligand flexibility.

### **Model Preparation**

Before docking in Rosetta, we must prepare the protein and cholesterol separately.

#### *Protein*

#1 The PDB file is cleaned and renumbered for use in Rosetta.

```
Rosetta/tools/protein_tools/scripts/clean_pdb.py 4ib4.pdb A
```

**Output: 4ib4\_A.pdb**

#2 Generate a spanfile from the cleaned PDB to indicate the transmembrane spanning regions.

```
Rosetta/main/source/bin/span_from_pdb.linuxgccrelease -in:file:s  
4ib4_A.pdb
```

**Output: 4ib4\_A.span**

#3 Refine the protein to correct local errors and optimize the membrane position. The protein is relaxed without cholesterol.

```
## relax_wo_clr.sh command
```

```
Rosetta/main/source/bin/rosetta_scripts.linuxgccrelease
```

```
-in:file:s 4ib4_A.pdb
```

```
-mp:setup:spanfiles 4ib4_A.span
```

```
-parser:protocol relax_wo_clr.xml
```

```
-relax:jump_move true
```

```
-packing:pack_missing_sidechains false
```

```
-mp:scoring:hbond true
```

```
-relax:constrain_relax_to_start_coords
```

```
## relax_wo_clr.xml XML
```

```
<ROSETTASCRIPTS>
```

```
<SCOREFXNS>
```

```
<ScoreFunction name="frank" weights="franklin2019"/>
```

```
</SCOREFXNS>
```

```
<TASKOPERATIONS>
```

```
<InitializeFromCommandline name="commandline_init"/>
```

```
<RestrictToRepacking name="restrict_to_repacking"/>
```

```
</TASKOPERATIONS>
```

```
<MOVERS>
```

```
<AddMembraneMover name="add_memb"/>
```

```
<MembranePositionFromTopologyMover name="init_pos"/>
```

```
<FastRelax name="fastrelax" disable_design="True" scorefxn="frank"
```

```
task_operations="commandline_init,restrict_to_repacking"
```

```
repeats="3"/>
```

```
</MOVERS>
```

```
<PROTOCOLS>
```

```
<Add mover="add_memb"/>
```

```
<Add mover="init_pos"/>
```

```
<Add mover="fastrelax"/>
```

```
</PROTOCOLS>
```

```
</ROSETTASCRIPTS>
```

**Output: 4ib4\_A\_relax.pdb**

#1 The SDF file is downloaded from PubChem and conformers are generated with MOE.

**Output: CLR\_conformers.sdf**

#2 Generate Rosetta-readable params file for ligand.

```
ROSETTA/main/source/scripts/python/public/molfile_to_params.py -n  
CLR -p CLR --conformers-in-one-file CLR_conformers.sdf
```

**Output: CLR.params, CLR.pdb, CLR\_conformers.pdb**

## Docking

- #1 Calculate lipid accessible regions on the protein for global docking using the Rosie server:
- Reduce XYZ coordinates from per atom to center of mass of each residue (centroid) in output PDB
  - Change the resname (example: ASP) to water (HOH) in output PDB
  - Change the atoms (example: CA) to oxygen (O) in output PDB
  - Change ATOM to HETATM in output PDB

**Output: 4ib4\_A\_positions.pdb**

#2 Prepare docking input file

- Combine **4ib4\_A\_relax.pdb** with **CLR.pdb**

**Output: 4ib4\_A\_dock.pdb**

#3 Dock cholesterol to the protein and generate 10 models

## dock.sh command

Rosetta/main/source/bin/rosetta\_scripts.linuxgccrelease

```
-in:file:s 4ib4_A_dock.pdb
-mp:setup:spanfiles 4ib4_A.span
-in:file:extra_res_fa CLR.params
-packing:pack_missing_sidechains false
-parser:protocol dock.xml
-nstruct 10
```

## dock.xml XML

```
<ROSETTASCRIPTS>
  <SCOREFXNS>
    <ScoreFunction name="frank" weights="franklin2019"/>
  </SCOREFXNS>
  <SCORINGGRIDS ligand_chain="X" width="25" name="lipid">
    <LipidMemGrid grid_name="head" weight="0.8" mem_weight="2"
ligand_atom="O1" kbpot_file="chol_o_mem_z_smooth_energies"/>
    <LipidMemGrid grid_name="tail" weight="1.0" mem_weight="2"
ligand_atom="C25" kbpot_file="chol_c25_mem_z_smooth_energies"/>
    <ClassicGrid grid_name="classic" weight="0.00000001"/>
  </SCORINGGRIDS>
  <MOVERS>
    <StartFrom name="start" chain="X" >
      <PDB filename="4ib4_A_positions" atom_name="O"/>
    </StartFrom>
    <Transform name="transform" chain="X" box_size="6"
move_distance="0.2" angle="20" cycles="500" repeats="5"
temperature="5" grid_set="lipid"/>
  </MOVERS>
</ROSETTASCRIPTS>
```

**Output/**

The following files are included in the **outputs/** directory:

The head and tail atoms of the lipid are optimized independently. The score.sc file contains the individual score terms labeled head\_grid\_X and tail\_grid\_X, respectively.

4ib4_A.000*.pdb	output files
score.sc	scorefile

### **Specificity Filter Calculation**

After running the Prediction protocol protein-cholesterol complexes can be further analyzed with the *spec\_score* script. *spec\_score* is a python script used to predict the likelihood that an integral membrane protein-cholesterol interface is specific.

### **Input/**

The following files are included in the **inputs/** directory to run the SpecificityFilter:

4ib4_A_pdbs/	Prediction protocol output pdbs
buried_area.csv	Names of pockets to investigate with their corresponding buried area ( <a href="http://schuellerlab.org/dr_sasa/">http://schuellerlab.org/dr_sasa/</a> )
4ib4_A_consulf.txt	Consurf rate of evolution predictions ( <a href="http://consurf.tau.ac.il">consurf.tau.ac.il</a> )
4ib4_A_netsurfp.txt	Netsurfp lipid accessibility predictions ( <a href="https://services.healthtech.dtu.dk/service.php?NetSurfP-3.0">https://services.healthtech.dtu.dk/service.php?NetSurfP-3.0</a> )
4ib4_A_lips.pdb	Rosetta lipid accessibility prediction ( <a href="https://rosie.graylab.jhu.edu/mp_lipid_acc">https://rosie.graylab.jhu.edu/mp_lipid_acc</a> )

```
#1 Use spec_score command to generate the specificity.csv file
```

```
## python spec_score.py
-q inputs/buried_area.csv
-p inputs/4ib4_A_pdbs/
-c inputs/4ib4_A_consulf.txt
-l inputs/4ib4_A_lips.pdb
-n inputs/4ib4_A_netsurfp.txt
```

### **Output/**

The following files are included in the **outputs/** directory:

The output is a csv file containing the Escore, Pscore and specificity score.

specificity.csv	output file
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