

RosettaLigand Docking Tutorial

Rosetta Workshop – November 7, 2018

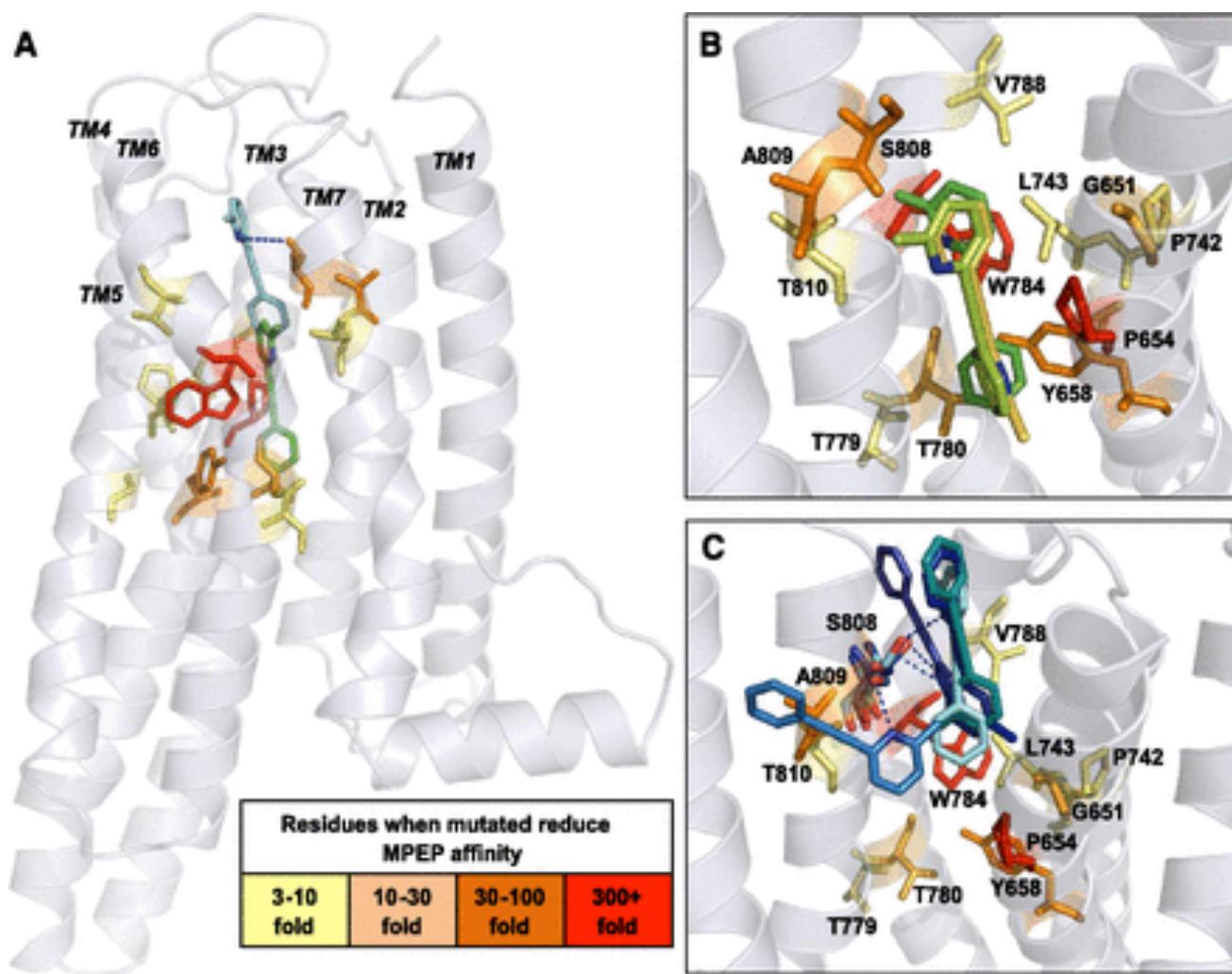
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Ligand Docking and Rosetta



Some Quick and Dirty Terminology

- Ligand: small molecule binder (“drug-like”)
- Chain: identifier for protein/ligand molecule
- Low-resolution/Coarse-grained: fast centroid or grid based sampling steps
- High-resolution/Atomistic: full-atom steps with complete Rosetta energy function
- Integer: 0,1,2,3,4...etc.
- Float: 1.2, 2.3, 0.78...etc.
- Boolean: True/False
- String: alpha/numeric/symbol combination

RosettaLigand History

Meiler and Baker 2006

Protein and ligand ensembles
Side chain flexibility

Davis and Baker 2009

Backbone flexibility near binding site

Lemmon and Meiler 2012

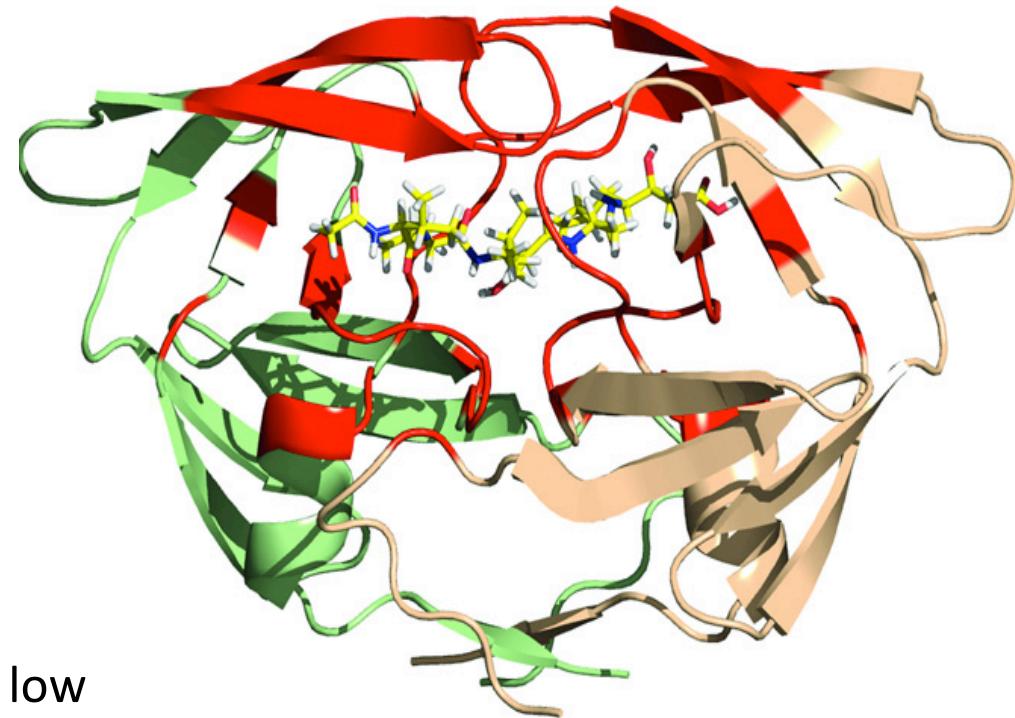
XML Scripts

Deluca and Meiler 2015

High throughput screening and improved low resolution sampling

Fu and Meiler 2018

RosettaLigand Ensemble



HIV-1 PR homodimer (green/wheat) with acetylpepstatin (yellow) in binding site (red)

G. Lemmon et. al. *Chemical biology & drug design* (2012).

When is RosettaLigand likely to work?

Crystal structures (ideally in complex with ligand of similar chemotypes)

Rigid, well-defined binding pocket

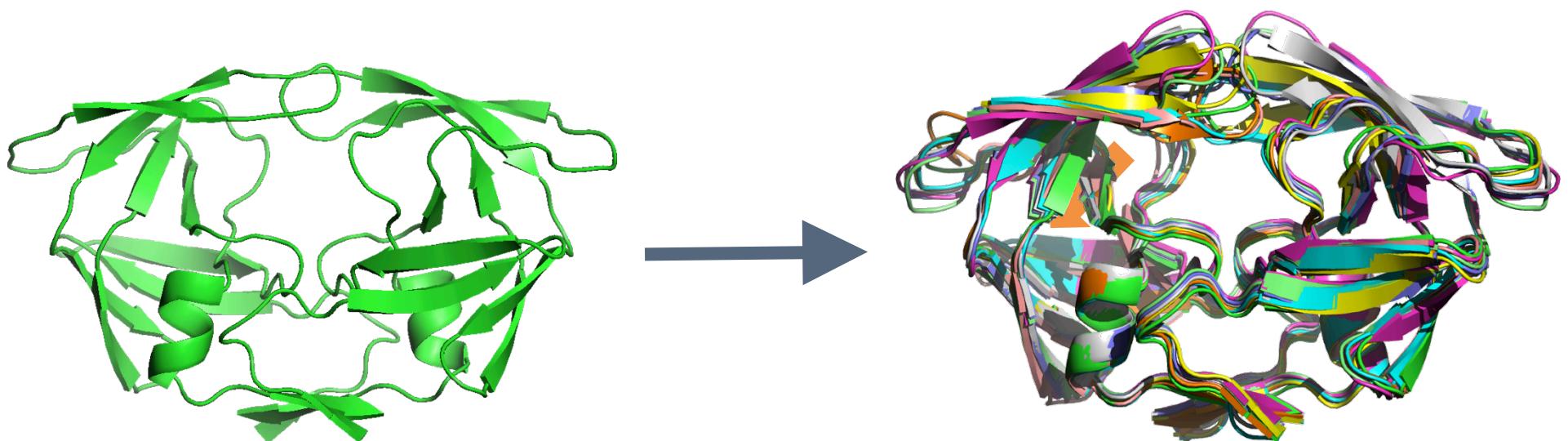
Drug-like small molecules capable of making hydrophilic/H-bond interactions

Experimental restraints

Docking (finding binding mode) is much easier than ranking or predicting activity!

Protein Model Selection

Protein conformation sources:
Crystal structures/NMR
Comparative modeling



Better to run dock into multiple models

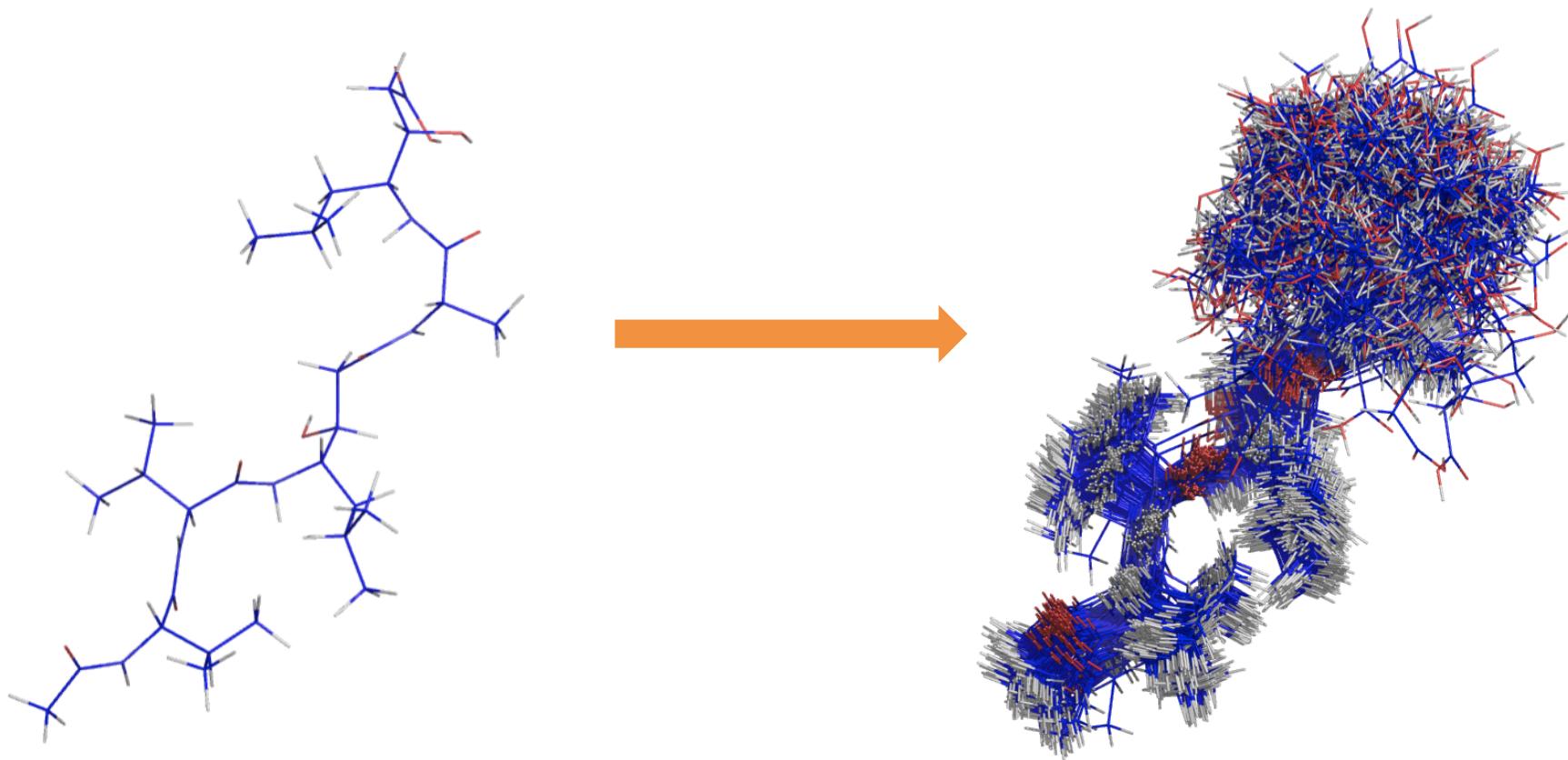
Ligand Conformer Generation

Ligand conformation sources:

BioChemicalLibrary (BCL) <http://www.meilerlab.org/servers/bcl-academic-license>

Commercial software: MOE/OpenEye

FROG2 Server <http://bioserv.rpbs.univ-paris-diderot.fr/services/Frog2/>



The Ligand Params File

Residue Parameter Files define:

- Residue name and type

- Atom names, types, and partial/total charges

- Bonds, chi angles, and rotamers

- Internal coordinates

- Additional properties

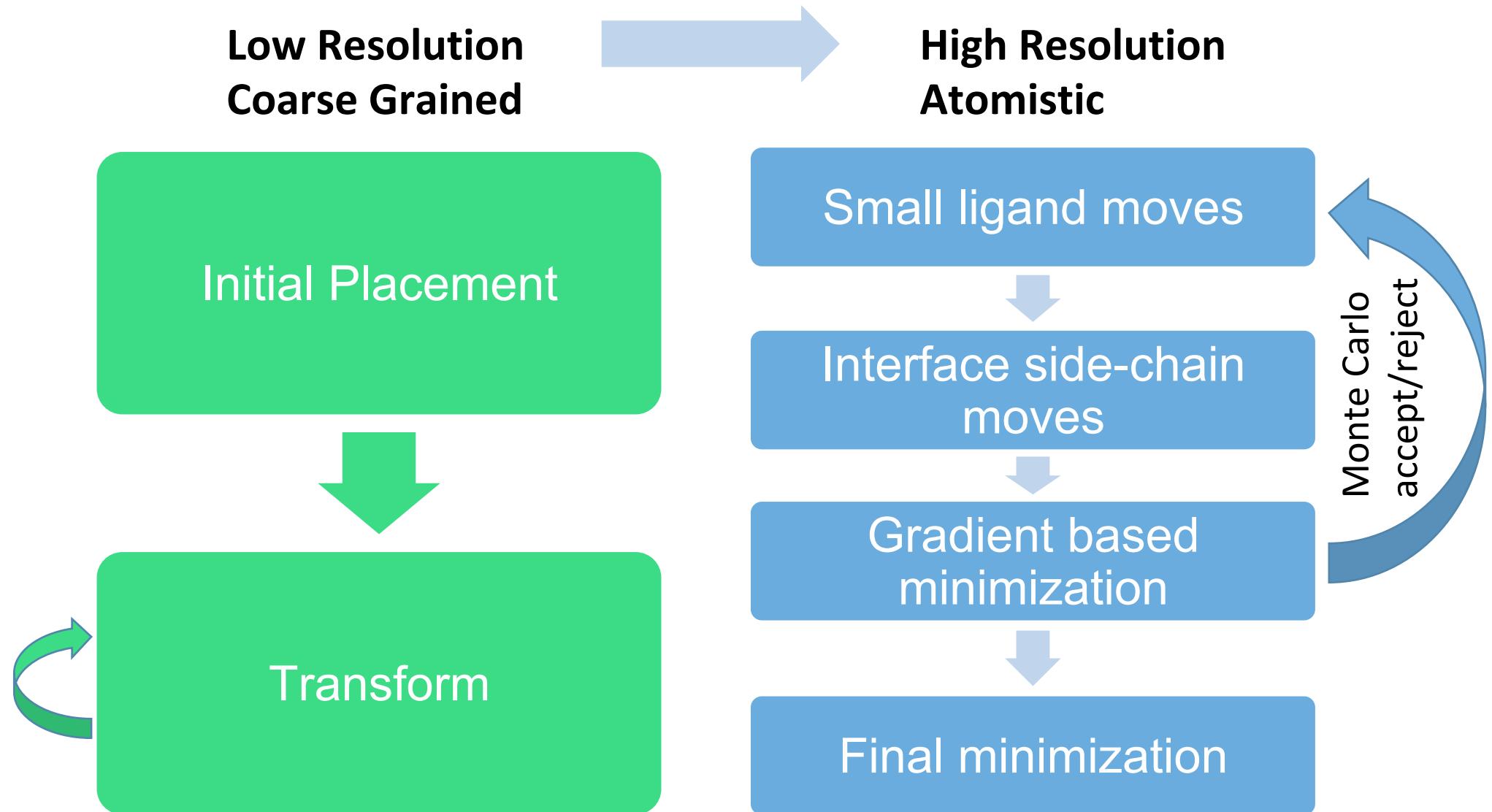
- Points to conformer file

Rosetta Database has existing parameter files for amino acids, but we need to generate custom ones for ligands

Script to generate params file:

`/$ROSETTA/main/source/scripts/python/public/molfile_to_params.py`

RosettaLigand Algorithm Overview



Overview of XML Script

SCOREFXNS

Soft-rep

Hard-rep

SCORINGGRIDS

LIGAND_AREAS

INTERFACE_BUILDERS

Side-chain and backbone

MOVEMAP_BUILDERS

Docking and Minimization

MOVERS

StartFrom

Transform

HighResDocker

FinalMinimizer

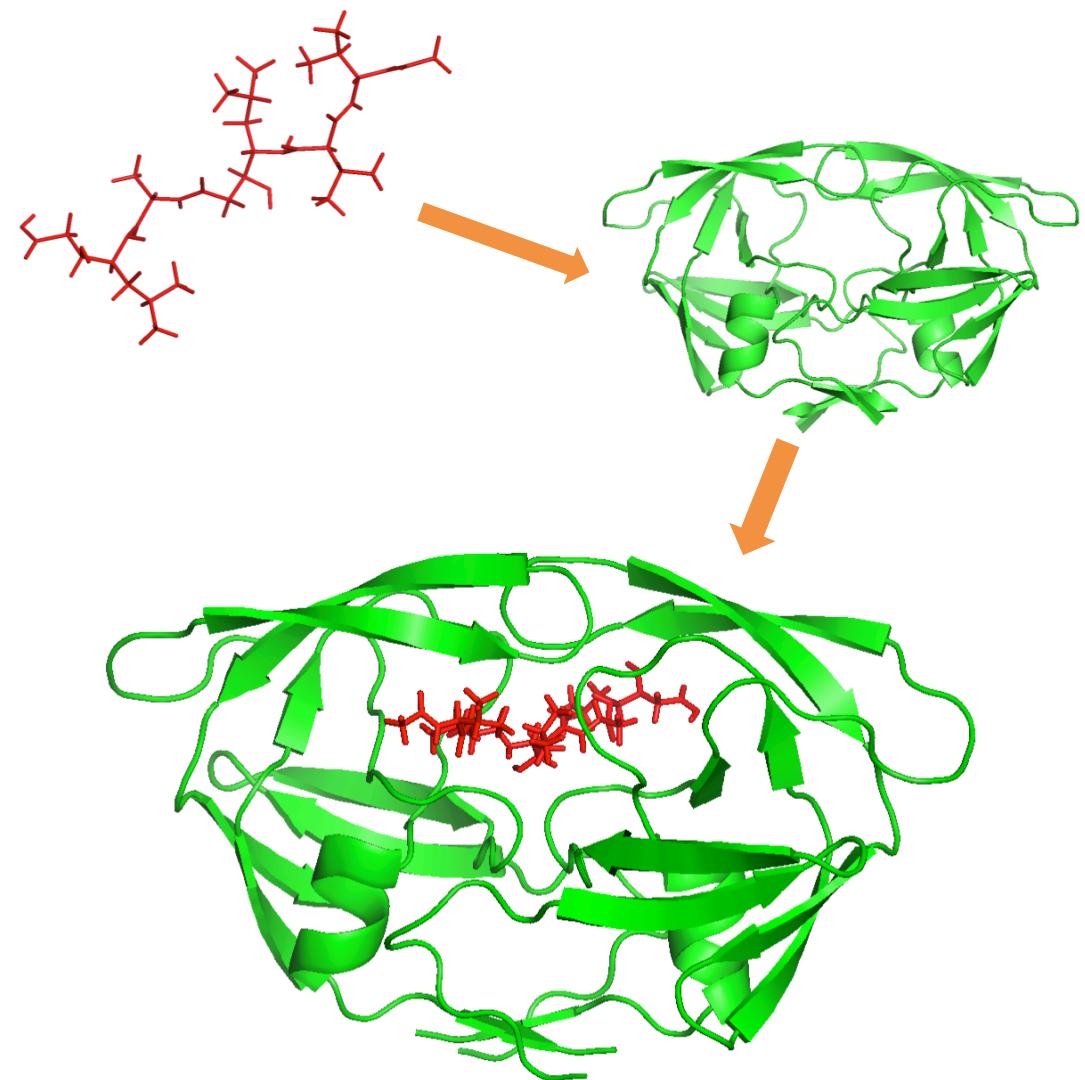
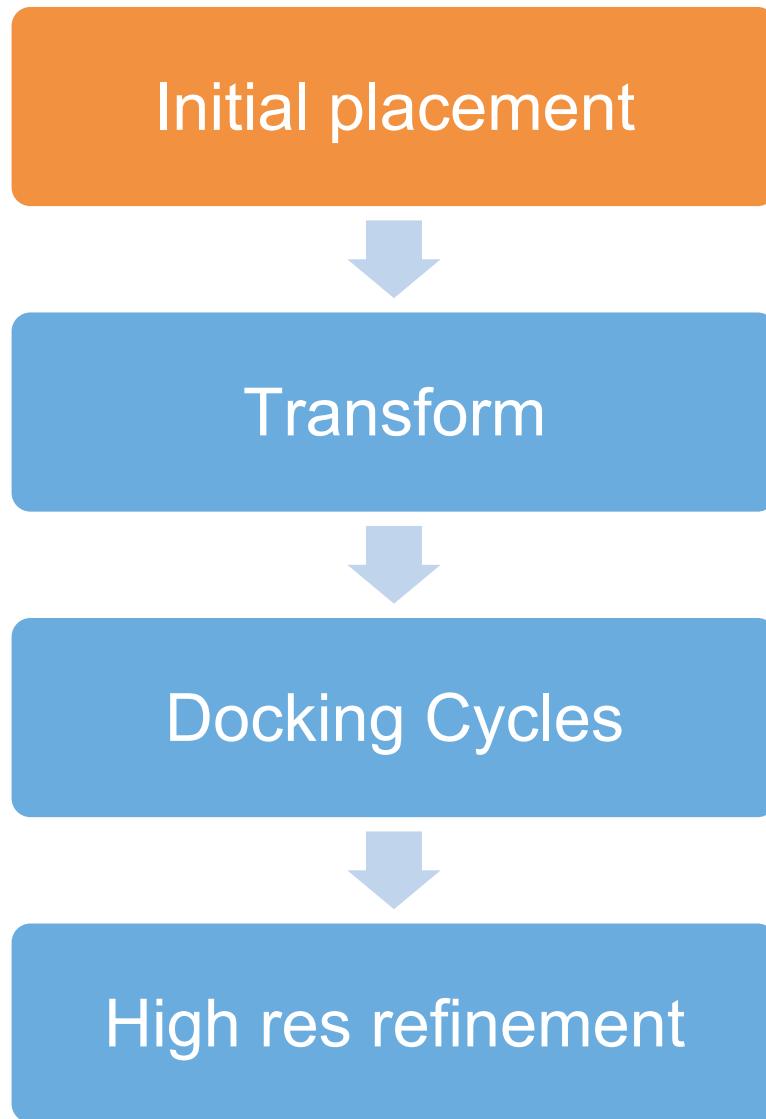
InterfaceScoreCalculator

Low Resolution Steps

High Resolution Steps

Evaluation Steps

RosettaLigand Algorithm



StartFrom

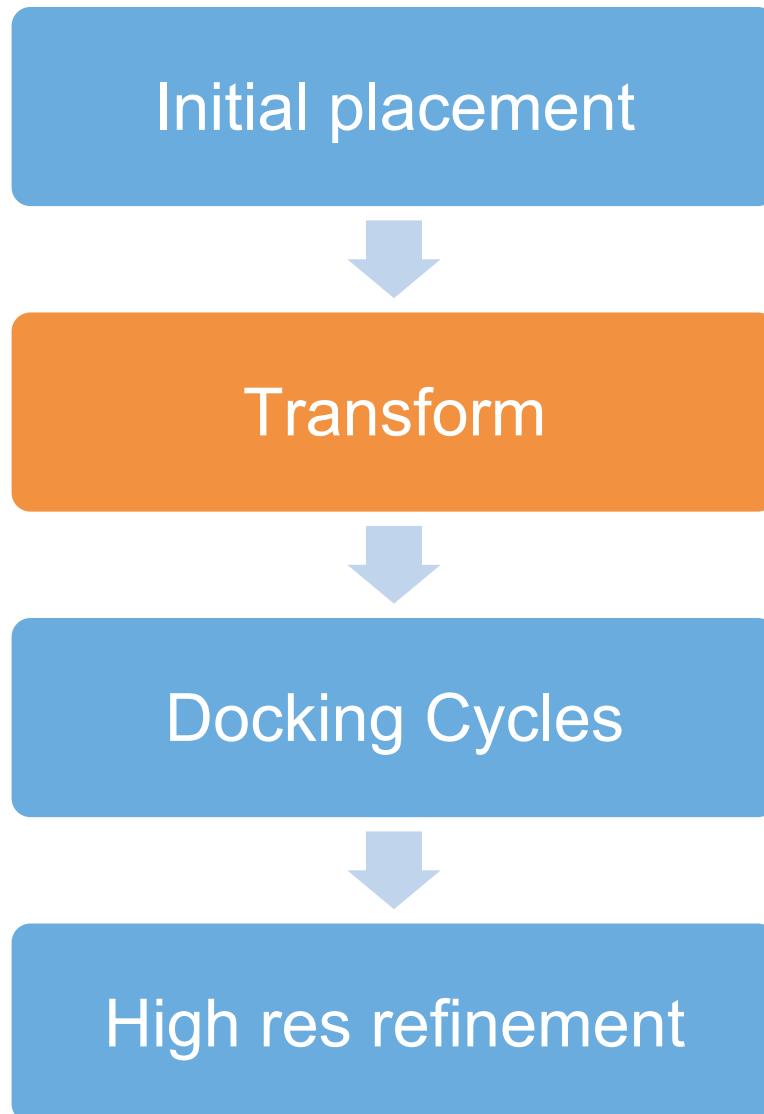
Can also manually move ligand to the starting position

```
<StartFrom name=(string) chain=(string)/>  
  <Coordinates x=(float) y=(float) z=(float)/>  
</StartFrom>
```

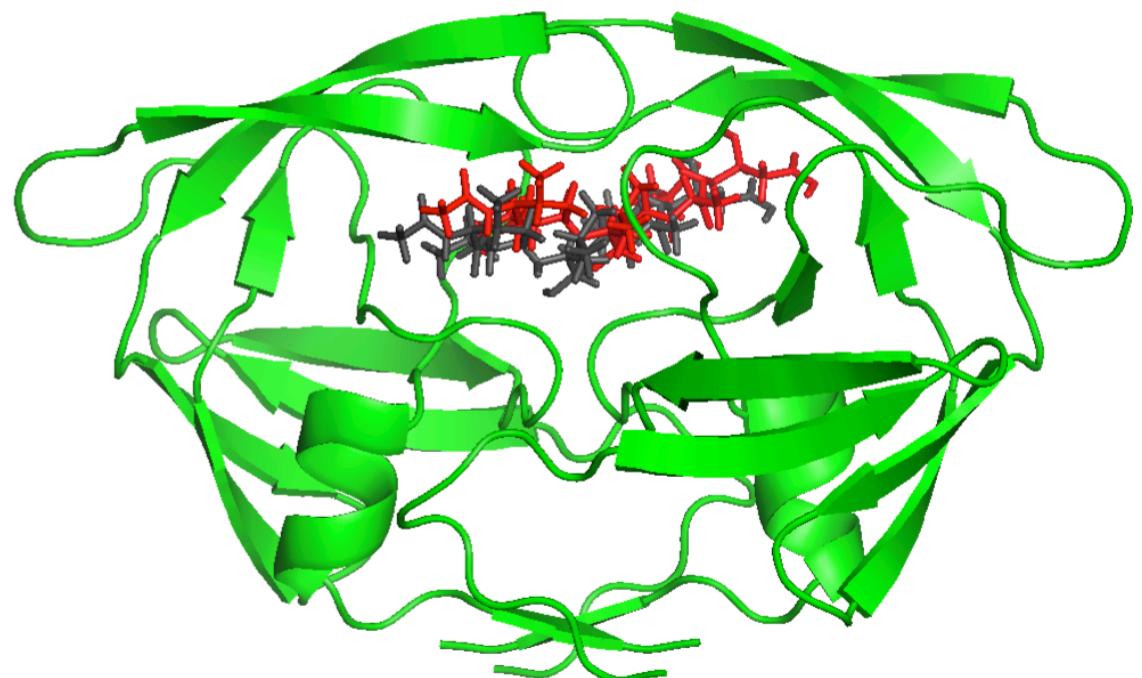
Places the centroid of the ligand into the starting spot

Optional. Provide a list of possible XYZ starting coordinates.
One of these will be chosen at random for initial ligand placement.

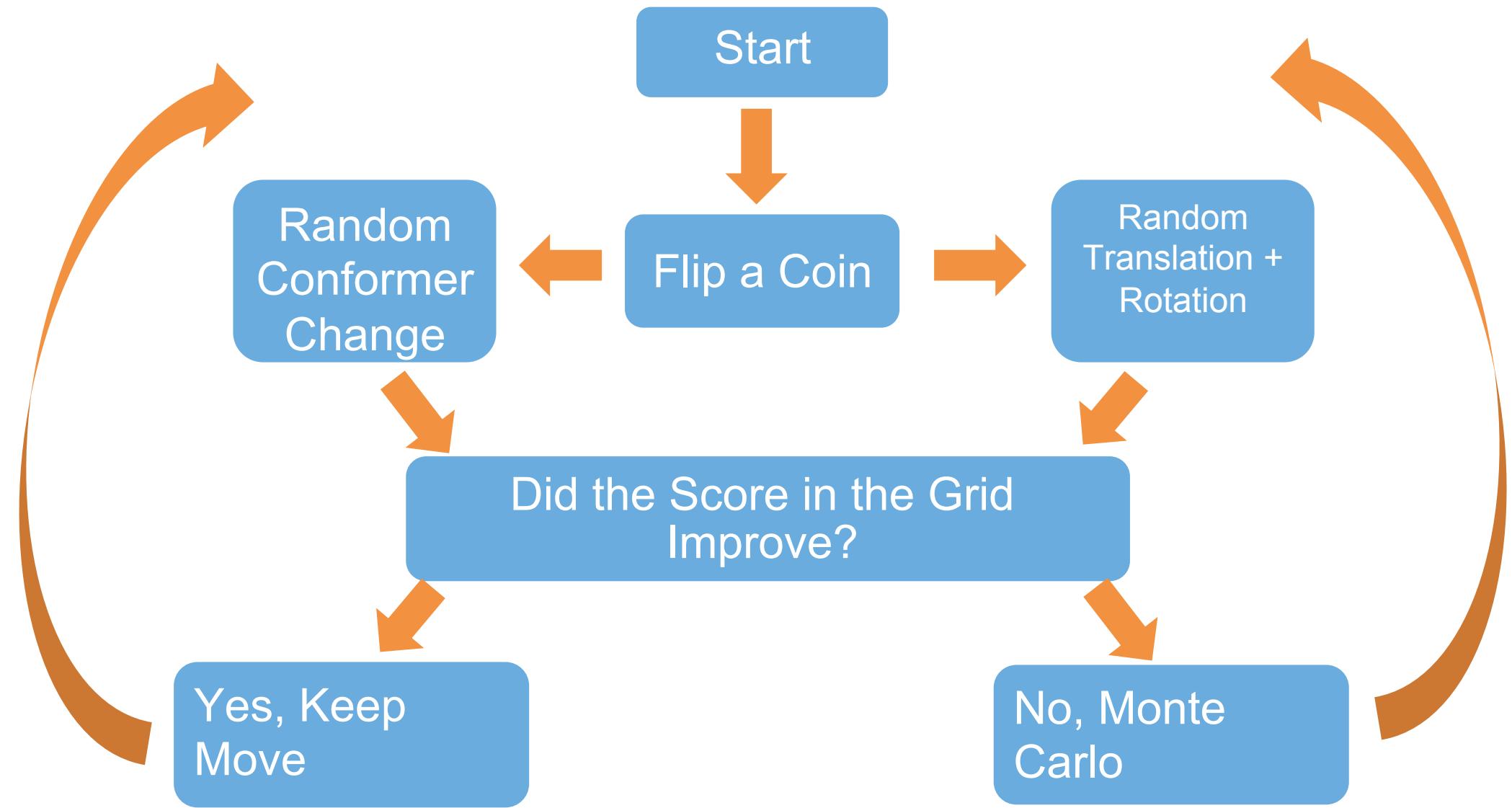
RosettaLigand Algorithm



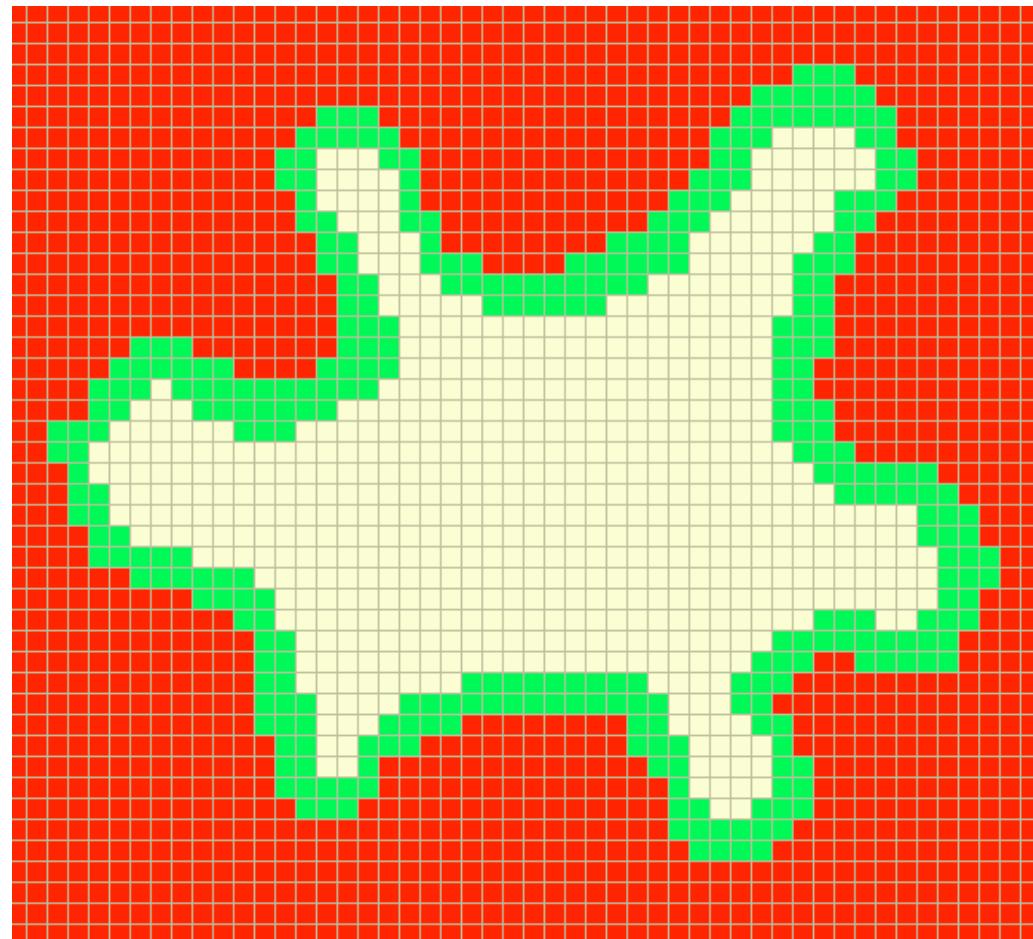
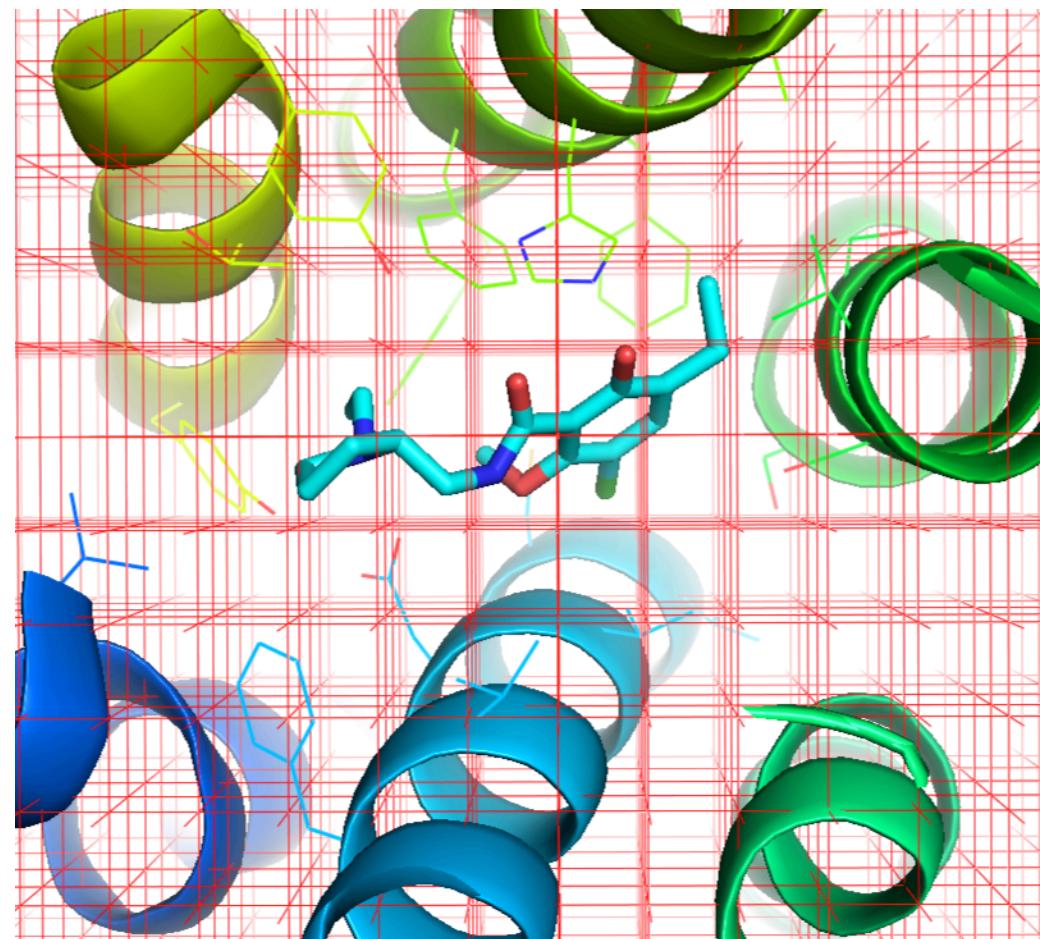
Grid based Monte-Carlo
Translation, Rotation, and
Conformation Sampling



Transform Algorithm



Setting Up The Grid for Transform Step



- Calculates score at each point in grid
- Determines where the ligand can move
 - This only based on sterics

Grid Manager

```
<SCORINGGRIDS ligand_chain=(string) width=(float)>
  <classic grid_type="ClassicGrid" weight=(float)/>
  <Another Grid>
</SCORINGGRIDS>
```

Sets up scoring the grid(s) around the ligand

Ligand_chain: Identifies the ligand to build around (Typically X)

Width: Grid width to keep all atoms in

GridType: Type of grid to use, classic grid is shape complementarity

Weight: Scoring weight to use if we have multiple grids

Transform Step

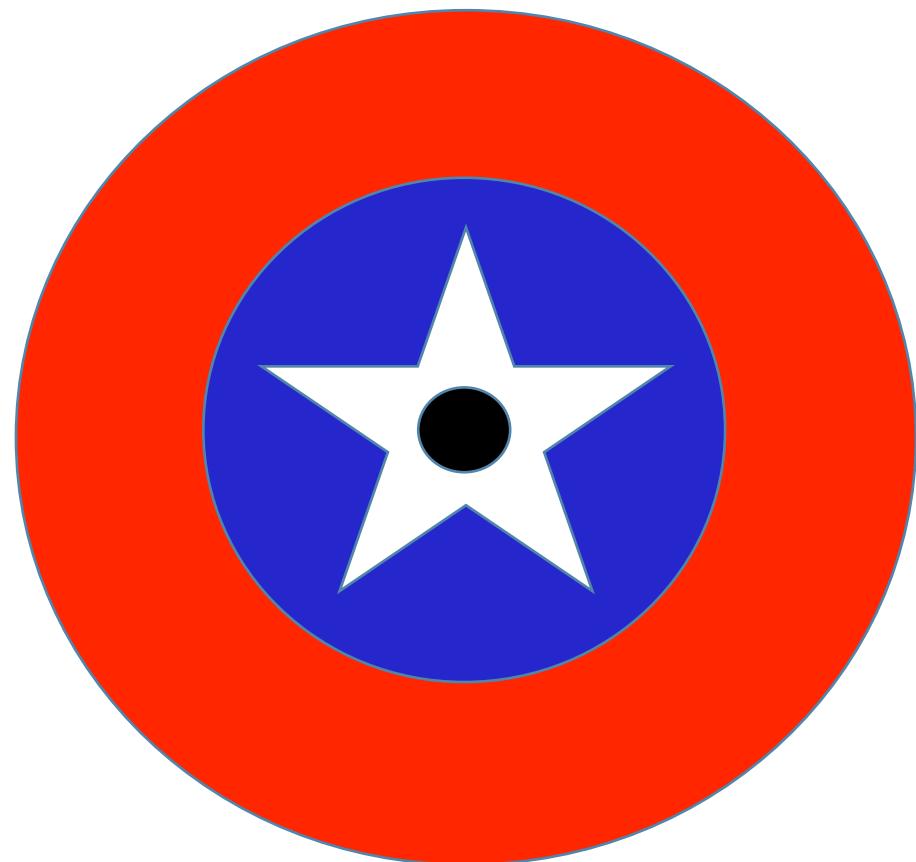
Center: Initial center of ligand
that acts as center of grids

Box size: The center of ligand
cannot move outside this box

Grid Width: No ligand atoms are
allowed outside this box

Translation: Random 3D
translation between 0 and move
distance (Gaussian distribution)

Rotation: Random 3D rotation
between 0 and angle
(Gaussian distribution)



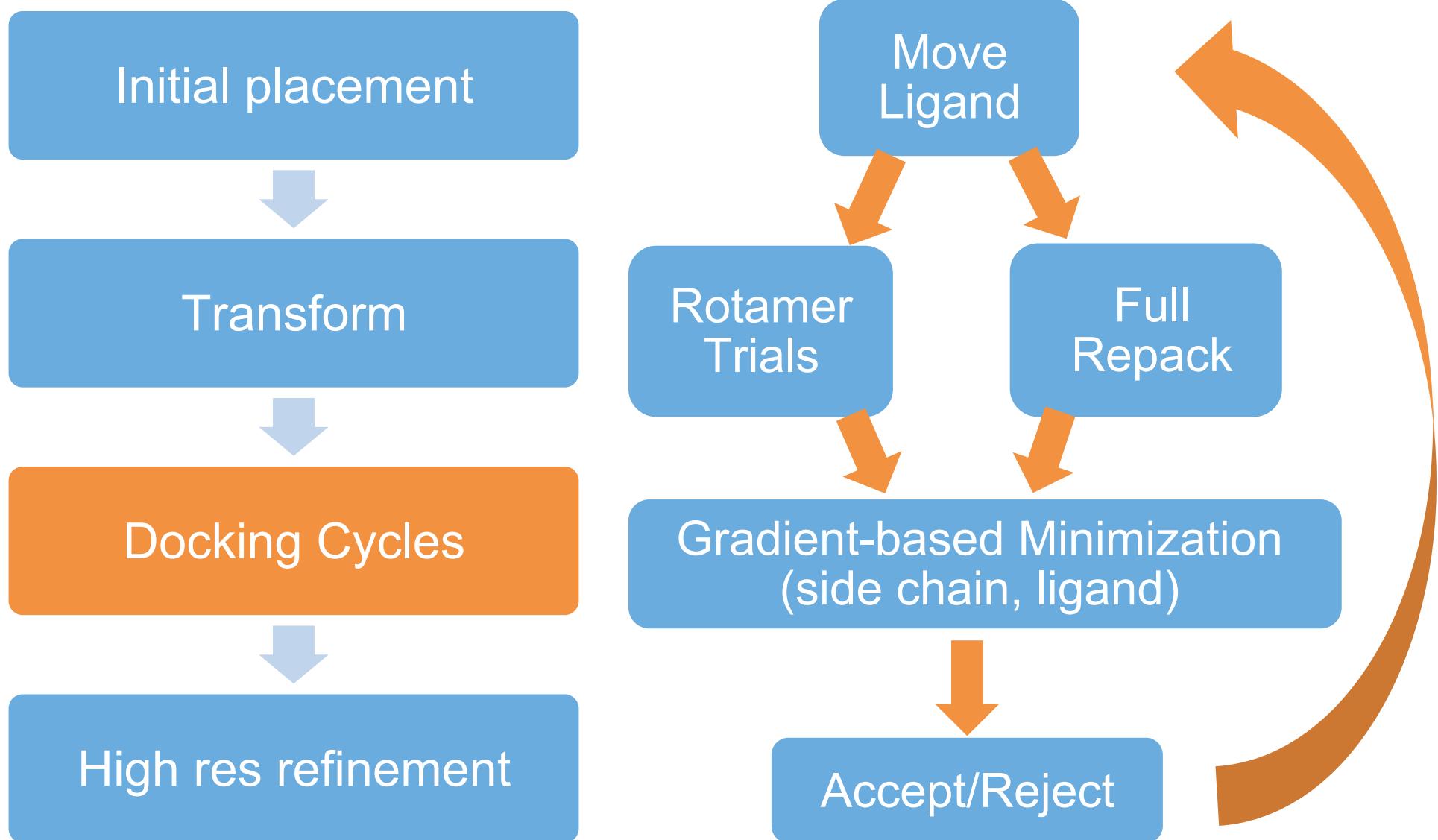
Transform

```
<Transform name=(string) chain=(string) box_size=(float)  
move_distance=(float) angle=(float) cycles=(int) repeats=(int)  
temperature=(float)/>
```

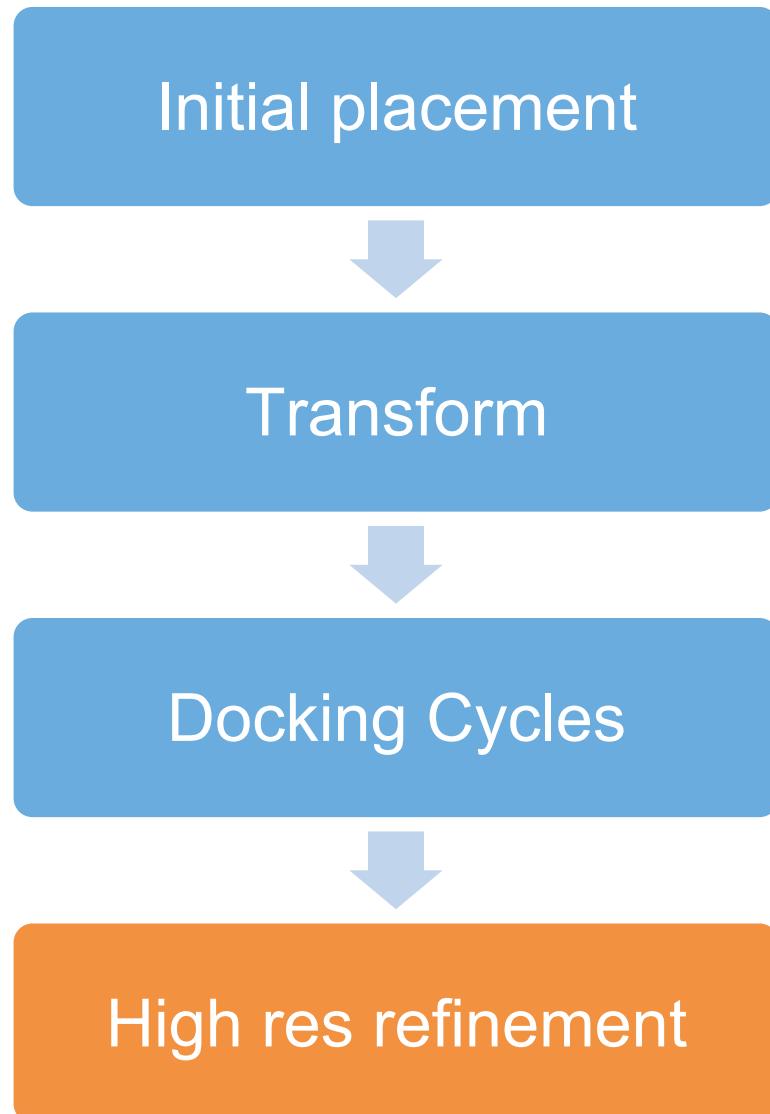
Monte Carlo transformation of ligand in grid

- Chain: Ligand chain to move
- Box_size: Distance from starting position to restrain ligand center
- Move_distance: Max translational distance of a single move
- Angle: Max angular rotation of a single move
- Cycles: Number of Monte Carlo steps to perform
- Repeats: Number of times to perform cycles from starting position
(EX: 3 repeats of 500 cycles means 1500 total steps)
- Temperature: Factor that controls determining how often an unfavorable move is accepted by Monte Carlo

RosettaLigand Algorithm



RosettaLigand Algorithm



Gradient Based
Minimization of side-
chain and backbone
torsion angles

HighResDocker

```
<HighResDocker name=(string) cycles=(int)  
repack_every_Nth=(int) scorefxn=(string)  
movemap_builder=(string) resfile=(string)/>
```

Atomistic Monte Carlo refinement of ligand and sidechain conformations

cycles: number of rotamer trials or repack steps (coupled w/small ligand movements).

repack_every_Nth: full repacks are interspersed with rotamer trials

scorefxn: Use a soft repulsive score here.

movemap_builder: movemap defined in the LIGAND AREA section

resfile: Specify what rotamer exchanges are possible (including design).

These are restricted to the defined interface region. Can be in options instead

FinalMinimizer

<FinalMinimizer name=(string) scorefxn=(string)
movemap_builder=(string)>

Minimize the structure of the docked protein/ligand complex

scorefxn: Use a hard repulsive to remove clashes

movemap_builder: movemap defined in the LIGAND AREA section

Move Maps, Interfaces, and Ligand Areas

LIGAND AREAS

- cutoff: maximum distance between C-beta atom and ligand to still be part of interface
- add_nbr_radius: accounts for ligand atom size when computing cutoff distance
- all_atom_mode: uses all ligand atoms for identifying nearby residues

INTERFACE BUILDERS

- extension_window: include “near-interface” residues for additional flexibility during backbone minimization

MOVEMAP BUILDERS

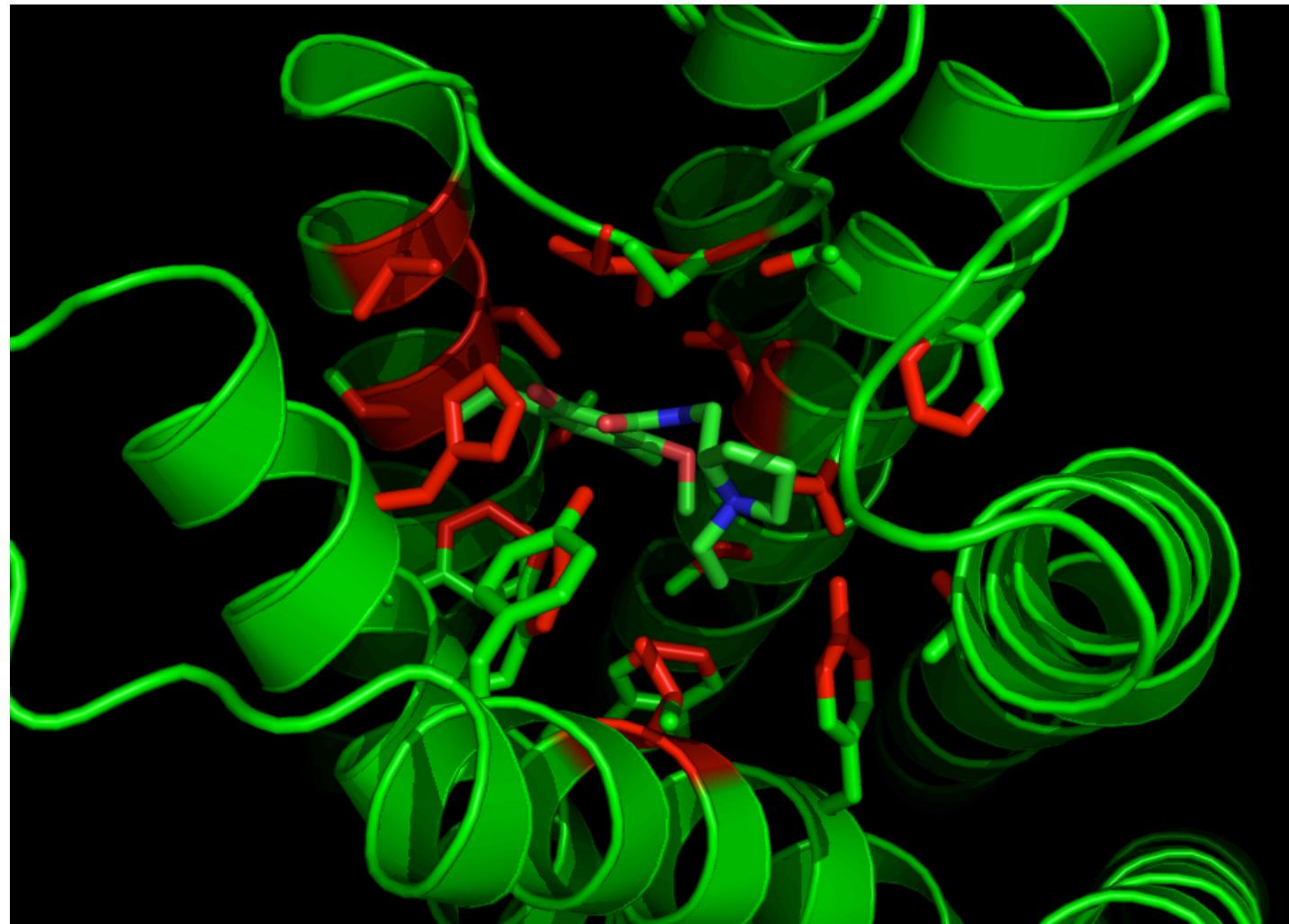
- sc_interface: residues selected for repacking and rotamer trials
- bb_interface: residues selected for backbone ϕ/ψ adjustments

Move Maps, Interfaces, and Ligand Areas

```
<LIGAND AREAS>
    <inhibitor_dock_sc chain="X" cutoff="6.0" add_nbr_radius="true" all_atom_mode="false"/>
    <inhibitor_final_sc chain="X" cutoff="6.0" add_nbr_radius="true" all_atom_mode="false"/>
    <inhibitor_final_bb chain="X" cutoff="7.0" add_nbr_radius="false" all_atom_mode="true"
        Calpha_restraints="0.3"/>
</LIGAND AREAS>
<INTERFACE BUILDERS>
    <side_chain_for_docking ligand_areas="inhibitor_dock_sc"/>
    <side_chain_for_final ligand_areas="inhibitor_final_sc"/>
    <backbone ligand_areas="inhibitor_final_bb" extension_window="3"/>
</INTERFACE BUILDERS>
<MOVEMAP BUILDERS>
    <docking sc_interface="side_chain_for_docking" minimize_water="false"/>
    <final sc_interface="side_chain_for_final" bb_interface=backbone minimize_water="false"/>
</MOVEMAP BUILDERS>
```

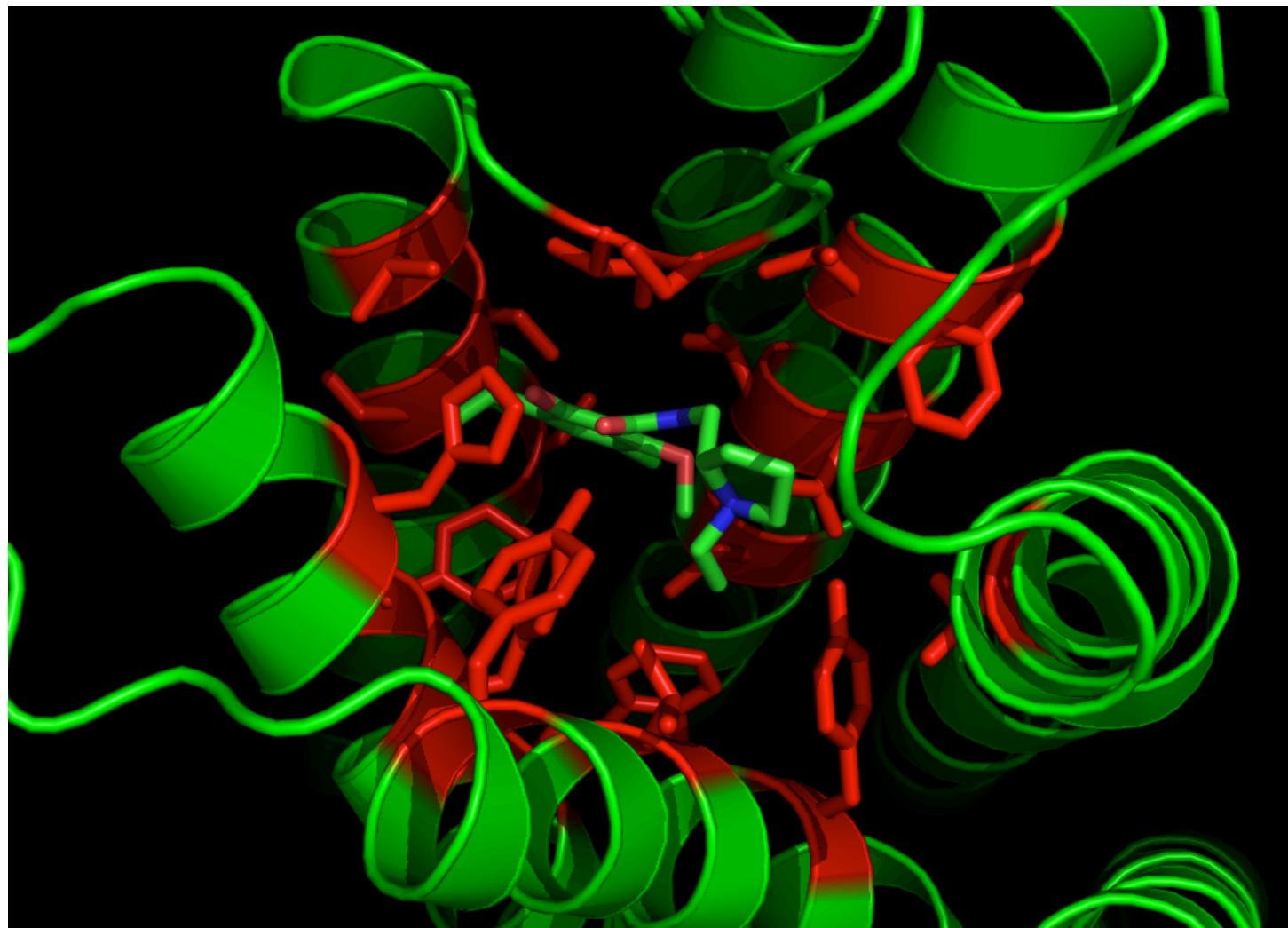
Move Maps, Interfaces, and Ligand Areas

Ligand area: identifies parameters for each ligand and identifies the atoms that are within a cutoff of the ligand



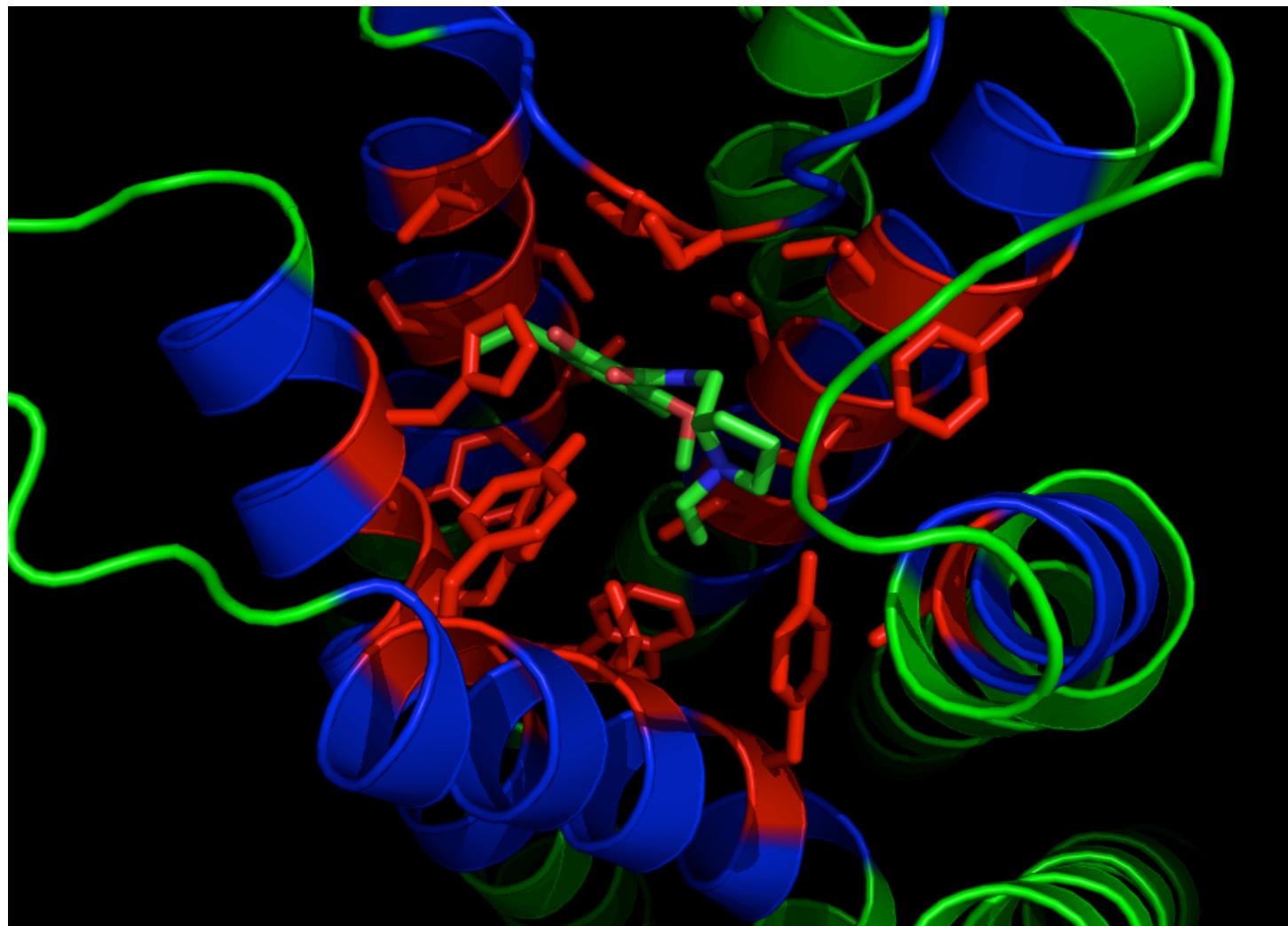
Move Maps, Interfaces, and Ligand Areas

Interface Builder: Extends those atoms to complete the residues



Move Maps, Interfaces, and Ligand Areas

Interface Builder: Extends to include surrounding residues for backbone flexibility



Move Maps, Interfaces, and Ligand Areas

Move map: identifies which residues are allowed to have backbone and side-chain movement. Typically, we have one for docking and one for minimization

Residue	Side-chain Movement	Backbone Movement
VAL 55	No	Yes
VAL 56	Yes	Yes
TYR 57	No	Yes
LEU 58	No	No

Note that these XML scripts defining Move Maps, Interfaces, Ligand Areas, etc. are set when you are running a dock. These have been benchmarked by developers so you won't be changing these.

InterfaceScoreCalculator

```
<InterfaceScoreCalculator name=(string)  
chains=(comma separated chars) scorefxn=(string)  
native=(string)/>
```

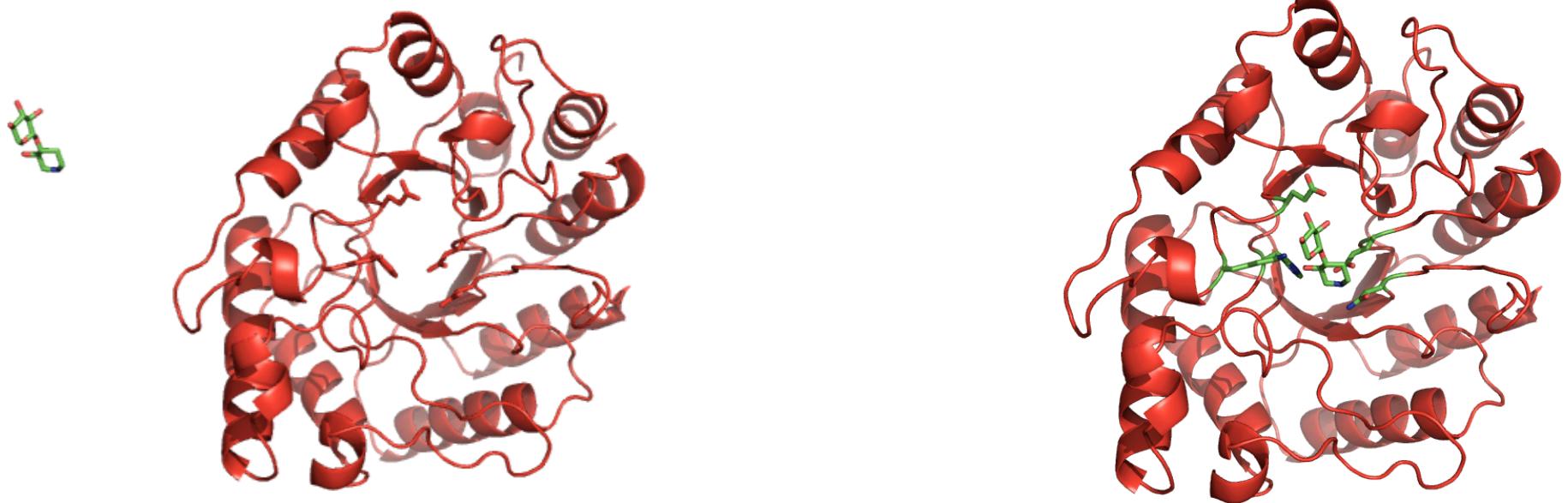
Calculates ligand-specific scores based on bound complex vs separated complex

chains: ligand chains to perform calculation for

scorefxn: Use a hard repulsive to identify clashes

native: native or “correct” structure for rms comparison if available

InterfaceScoreCalculator



$$\text{interface_delta_X} = \text{Score(Bound)} - \text{Score(Unbound)}$$

(Note: sidechains do NOT repack here)

FAQs

- How many output poses should I make?
Depends.
 - Size of active site
 - Ligand--size, rotatable bonds, etc.
- High-throughput screening?
 - Rosetta/tools/hts_tools/
 - (Deluca et al.)
- How long do docking runs usually take?
 - Not long compared to other types of runs

References

Methodology

- Fu D., Meiler. J. RosettaLigandEnsemble: A Small-Molecule Ensemble-Driven Docking Approach. *ACS Omega*, **3**(4): 3655–3664 (2018).
- DeLuca, S., Khar, K. & Meiler, J. Fully Flexible Docking of Medium Sized Ligand Libraries with RosettaLigand. *PLoS One* **10**, e0132508 (2015).
- S. Combs *et al.*, Small-molecule ligand docking into comparative models with Rosetta, *Nature Protocols* **8**, 1277–1298 (2013).
- G. Lemmon, J. Meiler, R. Baron, Ed. RosettaLigand docking with flexible XML protocols, *Methods in Mol Biol* **819**, 143–155 (2012).
- I. W. Davis, D. Baker, RosettaLigand docking with full ligand and receptor flexibility., *Journal of molecular biology* **385**, 381–92 (2009).
- K.W. Kaufmann *et al.*, Small Molecule Rotamers Enable Simultaneous Optimization of Small Molecule and Protein Degrees of Freedom in ROSETTALIGAND Docking, German Conference on Bioinformatics, pp. 148–157 (2008)
- J. Meiler, D. Baker, ROSETTALIGAND : Protein – Small Molecule Docking with Full Side-Chain Flexibility, *Proteins* **548**, 538–548 (2006).

References

Applications

- K. J. Gregory *et al.*, Probing the metabotropic glutamate receptor 5 (mGlu5) positive allosteric modulator (PAM) binding pocket: discovery of point mutations that engender a “molecular switch” in PAM pharmacology., *Molecular pharmacology* **83**, 991–1006 (2013).
- B. Allison *et al.*, Computational design of protein-small molecule interfaces., *Journal of structural biology* (2013), doi:10.1016/j.jsb.2013.08.003.
- G. Lemmon, J. Meiler, Towards ligand docking including explicit interface water molecules., *PloS one* **8**, e67536 (2013).
- G. Lemmon, K. Kaufmann, J. Meiler, Prediction of HIV-1 protease/inhibitor affinity using RosettaLigand., *Chemical biology & drug design* **79**, 888–96 (2012).
- K. W. Kaufmann, J. Meiler, Using RosettaLigand for small molecule docking into comparative models., *PloS one* **7** (2012), doi:10.1371/journal.pone.0050769.
- K. W. Kaufmann *et al.*, Structural determinants of species-selective substrate recognition in human and Drosophila serotonin transporters revealed through computational docking studies., *Proteins* **74**, 630–42 (2009).
- Regan, J. et al. Structure-activity relationships of the p38alpha MAP Kinase Inhibitor 1-(5-tert-Butyl-2-p-tolyl-2H-pyrazol-3-yl)-3-[4-(2-morpholin-4-yl-ethoxy)naphthalen-1-yl]urea (BIRB 796). *Journal of Medicinal Chemistry* **46**, 4676-4686 (2003).
- https://www.bindingdb.org/validation_sets/index.jsp

Today's Tutorial

Three possible tutorials:

1. Standard ligand docking

- I would highly suggest doing this first to get familiar with how to work with small-molecules in Rosetta

2. Virtual high-throughput screening (Deluca 2015)

- Set up a larger screen of compounds to dock against an ensemble of structures

3. RosettaLigandEnsemble (Fu 2018)

- Simultaneous docking of similar ligands

1. Standard protein-ligand docking

- Docking of eticlopride (antagonist) to Dopamine Receptor Subtype 3

Crystal Structure

Chien, E. Y. T. et al. Structure of the human dopamine D3 receptor in complex with a D2/D3 selective antagonist. *Science* 330, 1091–5 (2010)

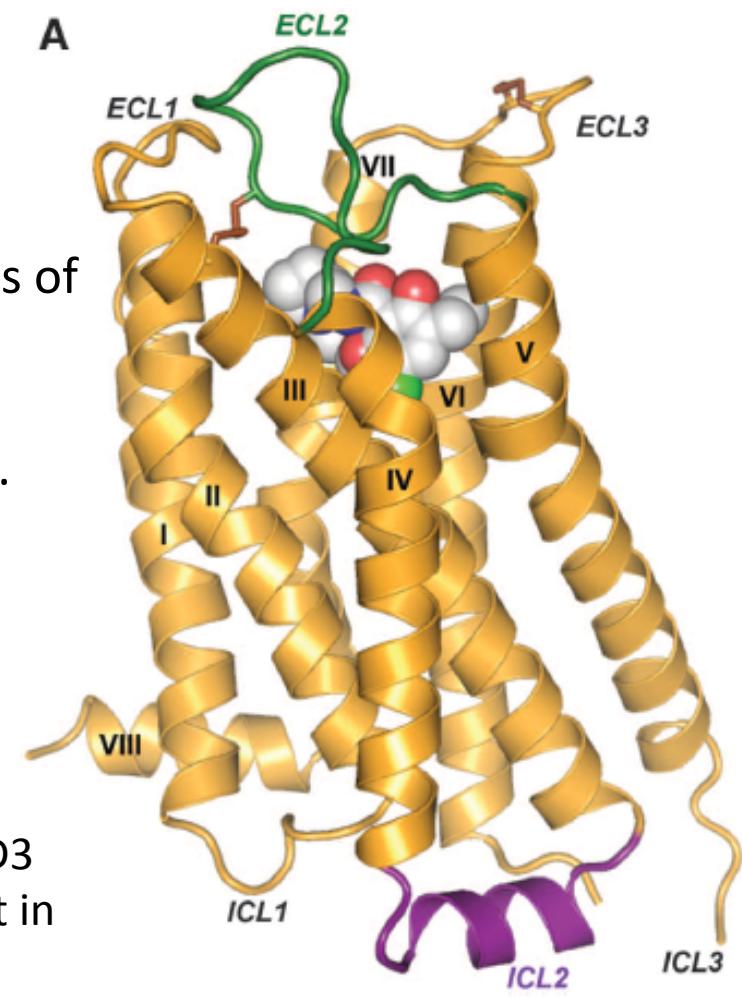
Community Assessment

Kufareva, I. et al. Status of GPCR modeling and docking as reflected by community-wide GPCR Dock 2010 assessment. *Structure* 19, 1108–1126 (2011).

Rosetta Assessment

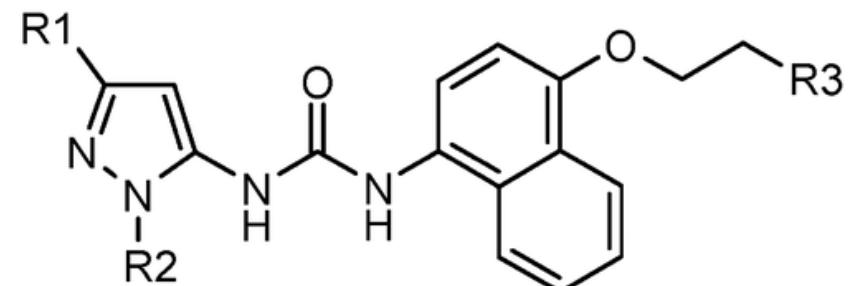
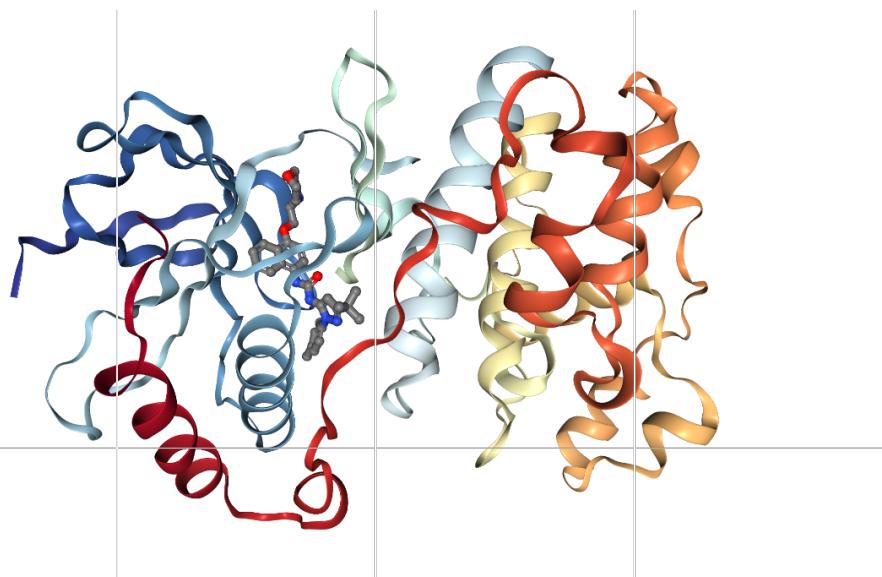
Nguyen, E. D. et al. Assessment and challenges of ligand docking into comparative models of g-protein coupled receptors. *PLoS One* 8, (2013)

Eticlopride, a D2/D3 selective antagonist in complex with D3 Receptor



2. Virtual High-Throughput Screening

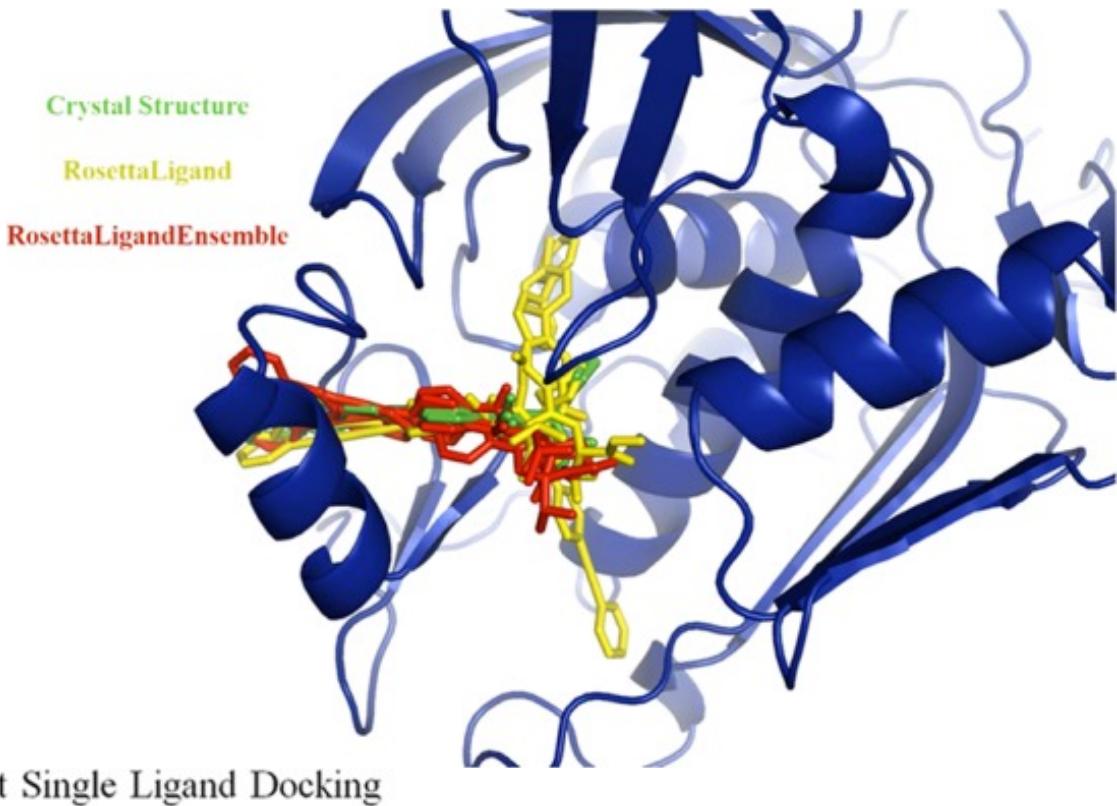
- Improvements to the low-resolution stage of ligand docking
 - Both time and performance metrics have demonstrated improved low-resolution docking using the Transform Mover (the same one that we saw in these slides)
- Protocol to set up larger screens
 - We will be setting this up on a small set of ligands that we want to dock 26 ligands against p38alpha MAP kinase
 - Original data from Regan et al (2003)
 - Dataset extracted from PDBBind Validation Sets (PDBID: 1KV2).



R1 = *t*-butyl
R2 = 4-methylphenyl
R3 = morpholine

3. RosettaLigand Ensemble

- Docking multiple similar ligand simultaneously improves structure prediction in most test cases
- *This works because we assume that similar ligands bind in a similar fashion.*
- Generally used in tandem with SAR studies



Independent Single Ligand Docking



Simultaneous Ligand Ensemble Docking



Let's get started!

`~/rosetta_workshop/ligand_docking/`

Start with `1_vanilla_docking`

Time permitting, either work through `2_vHTS`
or `3_Elbow_docking`.