

FORECASTER Platform Tutorial

Self and Cross Docking using FITTED



Molecular Forecaster Inc.

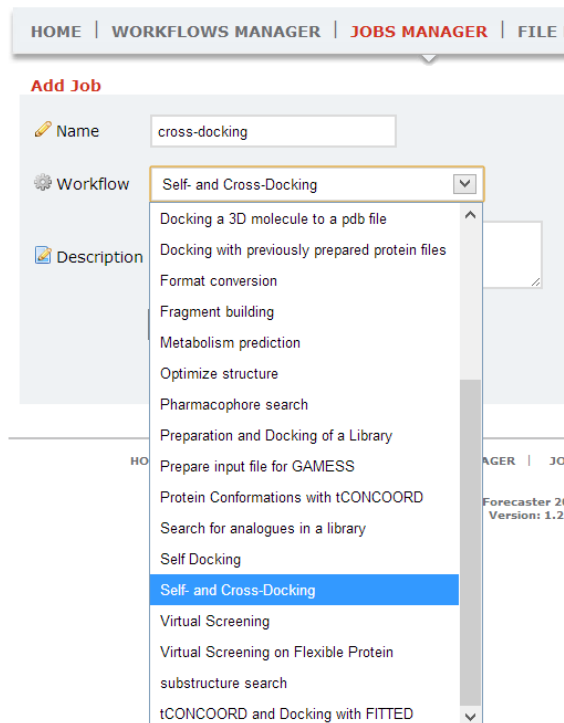
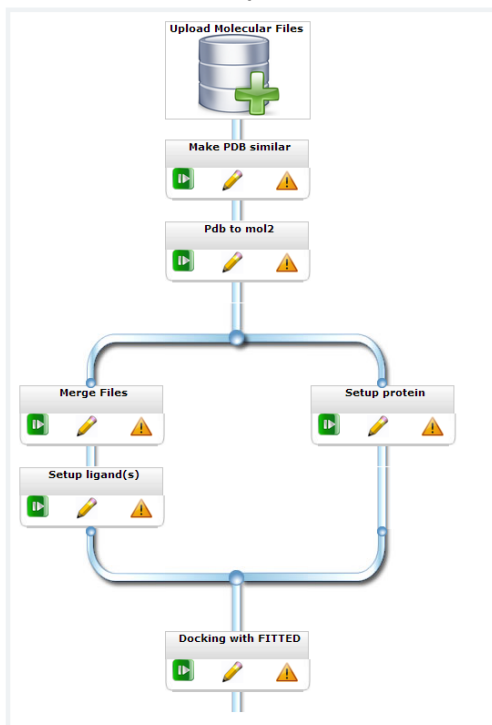
Laval, Québec, Canada

21/02/2015

Self and Cross Docking using FITTED

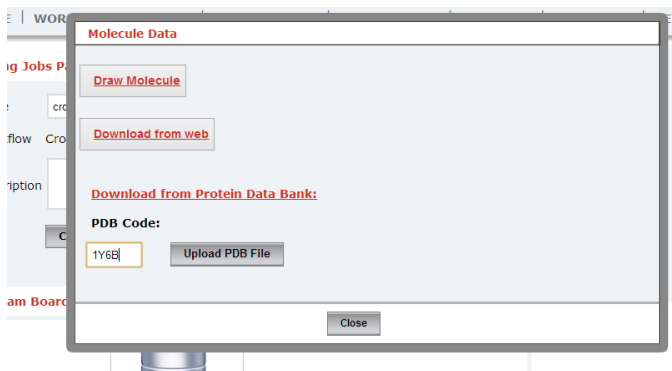
In this tutorial, we will use 3 PDB files: 1Y6B, 2P2H, 2P2I. A **cross docking** in a **rigid protein** docking mode will be done. The same workflow can be used to run a cross docking in flexible protein docking mode

1. Create a new job and select the “Self and Cross-Docking” workflow (If the workflow doesn't exist already, contact us or create it from the workflow manager).

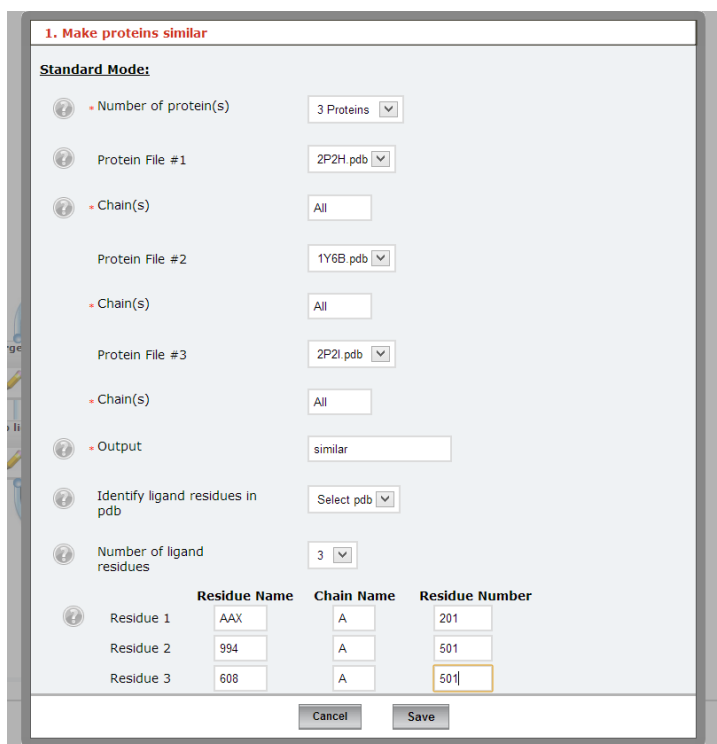


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2. Upload the PDB files by clicking on the cylinder “Upload Molecular Files”.



3. In the “Make PDB similar” box, fill in the required settings. Then click save.



	Residue Name	Chain Name	Residue Number
Residue 1	AAX	A	201
Residue 2	994	A	501
Residue 3	608	A	501

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- In the “PDB to mol2” box, fill in the aligned_mutated proteins and residues. Leave all other settings as default. Then click save.

3. Prepare protein - pdb to mol2

Standard Mode:

Number of protein(s) 3 Proteins

Protein File #1 2P2H_aligned_mutated.pdb

Protein File #2 1Y6B_aligned_mutated.pdb

Protein File #3 2P2I_aligned_mutated.pdb

Output prepare_protein

Identify ligand residues in pdb Select pdb

Number of ligand residues 3

	Residue Name	Chain Name	Residue Number
Residue 1	AAx	A	501
Residue 2	994	A	501
Residue 3	608	A	501

Re-assign hybridization No

Protonate atom No

Optimize Yes No

Iterations 5

Side-chain conformations Generate new side chain conformations Take from input file only

- In the “Merge Files” box, merge the ligand files to create a single multi-mol2 file. Don’t forget the “.mol2” extension.

3. Merge Files

SIMPLE MODE

File Type .mol2

Files for Concatenation:

- 2P2H_aligned_mutated_pro.mol2
- 2P2H_aligned_mutated_lig.mol2
- 1Y6B_aligned_mutated_pro.mol2
- 1Y6B_aligned_mutated_lig.mol2
- 2P2I_aligned_mutated_pro.mol2
- 2P2I_aligned_mutated_lig.mol2

Output File Name ligands.mol2

(should have the appropriate extension and be different from any input file names)

Cancel Save

6. Prepare the ligands within the “Setup Ligands” box.

1. Setup ligand(s) for docking

Standard Mode:

- Input File: ligands.mol2
- Output File Name (different from input file name): lig_smart
- Atomic partial charges assignment:
 - MMFF
 - Electronegativity equalization method
 - Keep input file charges

Advanced Mode: SHOW

Buttons: Cancel, Save

7. Prepare the proteins within the “Setup Proteins” box. Choose Docking to rigid protein.

Standard Mode:

- Number of protein(s): 3 Protein structures
- Protein File #1: 2P2H_aligned_mutated_pro.mol2
- Protein File #2: 1Y6B_aligned_mutated_pro.mol2
- Protein File #3: 2P2I_aligned_mutated_pro.mol2
- Macromolecule: Protein
- Number of Ligand(s): 3 Ligands
- Ligand File #1: 2P2H_aligned_mutated_lig.mol2
- Ligand File #2: 1Y6B_aligned_mutated_lig.mol2
- Ligand File #3: 2P2I_aligned_mutated_lig.mol2
- Ligand Cutoff: 7
- Output File Name (different from input file name): process_protein
- Prepare for: Docking to rigid protein
- Keep files for later use:
 - Yes
 - No

Advanced Mode: SHOW

Buttons: Cancel, Save

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8. Fill in the settings for the “Docking with FITTED” box. Pay attention to selecting “Evaluate RMSD”, the proper flexibility mode “Rigid” and set the Run Mode to “Cross Docking”.

1. Dock ligand(s) using FITTED

Standard Mode:

Input / Output parameters

Number of protein(s)	3 Protein structures
Protein Prefix #1	2P2H_aligned_mutated_pro
Protein Prefix #2	1Y6B_aligned_mutated_pro
Protein Prefix #3	2P2I_aligned_mutated_pro
Macromolecule	Protein
Ligand File	lig_smart.mol2
Output File Name (different from input file name)	docking
Evaluate RMSD	<input checked="" type="radio"/> Yes <input type="radio"/> No
Number of references for RMSD	1
Reference File [1]	lig_smart.mol2
Files from archives	<input type="radio"/> Yes <input checked="" type="radio"/> No
Number of references for RMSD	1
Reference File [1]	lig_smart.mol2
Files from archives	<input type="radio"/> Yes <input checked="" type="radio"/> No
Binding Site Cavity	2P2H_aligned_mutated_pro_BindSite_flex.mol2
Interaction Sites	2P2H_aligned_mutated_pro_IS_flex.mol2
Minimum match with the IS	0.00
Pharmacophore (constraints)	<input type="radio"/> Yes <input checked="" type="radio"/> No
Protein flexibility mode	Rigid
Scoring function	RankScore5
Run Mode	Cross-Docking

Advanced Mode: SHOW

Cancel Save

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9. Once the docking is complete, the complete results can be found in docking-results.txt and the docking.sdf contains the docked poses.