



Sep 08, 2020

Ligand docking using Patchdock for Biochemistry I

In 1 collection

Chris Berndsen¹¹James Madison University**1** Works for me This protocol is published without a DOI.Chris Berndsen
James Madison University

PROTOCOL CITATION

Chris Berndsen 2020. Ligand docking using Patchdock for Biochemistry I. **protocols.io**
<https://protocols.io/view/ligand-docking-using-patchdock-for-biochemistry-i-bd27i8hn>

COLLECTIONS ⓘ

 **Biochemistry I methods**

LICENSE

————— This is an open access protocol distributed under the terms of the [Creative Commons Attribution License](#), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited

CREATED

Mar 21, 2020

LAST MODIFIED

Sep 08, 2020

PROTOCOL INTEGER ID

34623

PARENT PROTOCOLS

Part of collection

[Biochemistry I methods](#)

MATERIALS TEXT

molecule visualization program
a ligand file in .pdb format
a receptor/protein file in .pdb format
internet connection

BEFORE STARTING

Have PDB file of protein and ligand

Docking setup

- 1 Navigate to [Patchdock](#)

1.1



Molecular Docking Algorithm Based on Shape Complementarity Principles
[\[About PatchDock\]](#) [\[Web Server\]](#) [\[Download\]](#) [\[Help\]](#) [\[FAQ\]](#) [\[References\]](#)

Type PDB codes of receptor and ligand molecules or upload files in PDB format

Receptor Molecule:	<input type="text"/>	(PDB:chainId e.g. 2kai:AB) or upload file:	<input type="button" value="Choose File"/> No file chosen
Ligand Molecule:	<input type="text"/>	(PDB:chainId e.g. 2kai:I) or upload file:	<input type="button" value="Choose File"/> No file chosen
e-mail address:	<input type="text"/>		
Clustering RMSD:	<input type="text" value="4.0"/>		
Complex Type:	Default <input type="button" value="v"/>		
<input type="button" value="Submit Form"/> <input type="button" value="Clear"/>			

Be sure to give receptor and ligand in the corresponding order!

Advanced Options:
[\[Show\]](#) [\[Hide\]](#)

Receptor Binding Site:	<input type="button" value="Choose File"/> No file chosen	upload receptor binding site file
Ligand Binding Site:	<input type="button" value="Choose File"/> No file chosen	upload ligand binding site file
Distance Constraints:	<input type="button" value="Choose File"/> No file chosen	upload distance constraints file
<input type="button" value="Submit Form"/> <input type="button" value="Clear"/>		

- 2 In **Receptor molecule**: Provide your PDB file as a RCSB code OR upload a .PDB file



The receptor molecule is your protein/biomolecule and is generally the larger of the two molecules.

- 3 In **Ligand molecule**: Provide your PDB file as a RCSB code OR upload a .PDB file.



If you do not have the ligand file, you can create one from information from PubChem and YASARA.

- 4 Under **Clustering RMSD**: Set to 1.5 for protein-small molecule binding, 4 for protein-protein or protein-DNA docking.

- 5 Provide your email address.

- 6

Under **Advanced Options**: You can specify a binding site if you have one identified from Uniprot, COACH, BLAST or some other source.

- 6.1 The binding site location is provided as a .txt file with the following format:

```
88 L
89 L
90 L
91 L
92 L
93 L
95 H
96 H
```

101 H
102 H

The number indicates the amino acid number, the letter indicates the molecule name in the receptor PDB file (usually A).

Note: If the binding site file is not accepted, remove the letters and try again.

- 7 Record your submission settings and add new rows as needed.

Receptor code/file	
Ligand code/file	
Clustering RMSD	

- 8 Press Submit Form and wait 24 to 72 hours.

Analysis of docking

- 9 Open the results email to go to the table of solutions. This table contains several important pieces of information or files.

- **Solution No:** Number of the solution
- **Score:** Geometric shape complementarity score. The more steric clashes the lower the score. The solutions are sorted according to this score.
- **Area:** Approximate interface area of the complex.
- **ACE:** Atomic contact energy or the energy required to transfer the molecule from water to protein site
- **PDB file of the complex:** The predicted complex structure in PDB format.



For more about the score see:

Duhovny D, Nussinov R, Wolfson HJ. Efficient Unbound Docking of Rigid Molecules. In Gusfield et al., Ed. Proceedings of the 2nd Workshop on Algorithms in Bioinformatics(WABI) Rome, Italy, Lecture Notes in Computer Science 2452, pp. 185-200, Springer Verlag, 2002

For more about the ACE/Atomic contact energy see:

Zhang C, Vasmatzis G, Cornette JL, DeLisi C. Determination of atomic desolvation energies from the structures of crystallized proteins. J Mol Biol. 267(3):707-26, 1997

- 9.1 Record the values for the top 5 hits. Add rows as needed. You can also download the entire solutions table using a link below the table.

Solution number	Score	Area	ACE

- 10 Below the table is an option to download the top X hits. Change the number to be between 5 to 10 and obtain the file.

10.1 Name the file as

proteinname_ligandname_patchdock.zip

Replace proteinname with the receptor name, the ligandname with the ligand name.

Upload the file to OSF and provide the link to this file as note on this step.

Visualization of docking results

- 11 Extract the .zip file.

- 12 Open all of the hits in a single window of a molecule visualization protein. YASARA will be used in this instance.

12.1

ATOM PROPERTIES

Number:
Name:
Element:
Occupancy: % BFactor:
Residue:
Object:

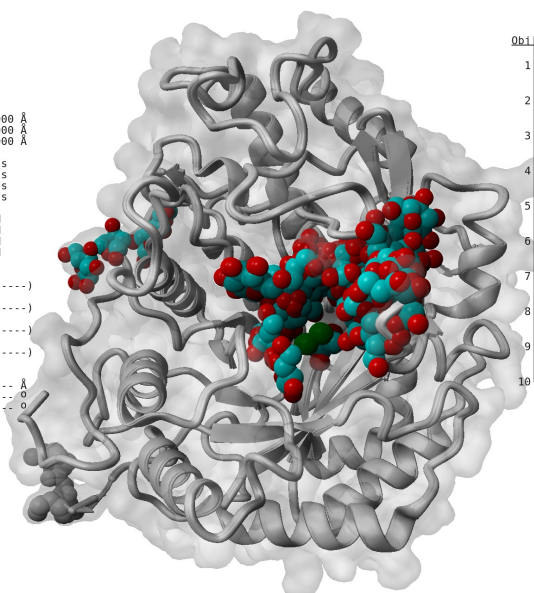
Position: X = 000000.00000 Å
Y = 000000.00000 Å
Z = 000000.00000 Å

Speed: X = 0000000000 m/s
Y = 0000000000 m/s
Z = 0000000000 m/s
Total = 0000000000 m/s

Active X = 0000000000 fN
Forces: Y = 0000000000 fN
Z = 0000000000 fN
Total = 0000000000 fN

Bonds:
1) Type to ---- (-----)
Length ---- Å
2) Type to ---- (-----)
Length ---- Å
3) Type to ---- (-----)
Length ---- Å
4) Type to ---- (-----)
Length ---- Å

Marked Distance: ---- Å
Marked Angle: ---- °
Marked Dihedral: ---- °



SCENE CONTENT

Obj	Name	Vis	Act	Atom
1	docking_res	Yes	Yes	1
2	docking_res	Yes	Yes	3980
3	docking_res	Yes	Yes	7959
4	docking_res	Yes	Yes	11938
5	docking_res	Yes	Yes	15917
6	docking_res	Yes	Yes	19896
7	docking_res	Yes	Yes	23875
8	docking_res	Yes	Yes	27854
9	docking_res	Yes	Yes	31833
10	docking_res	Yes	Yes	35812

All 10 docking results shown with proteins as ribbon with a transparent surface and docked ligands as spheres colored by element.

- 13 In the example results in 12.1 most of the solutions cluster in the same area suggesting good complementarity in this region. If not specified before, the list amino acids in this region can be used to specify a receptor site and the docking repeated to refine the placement.

14 YASARA users only!

With all the solutions loaded, press the space bar to bring up the command window and type the commands shown below. The # indicates explanations that are not typed in the window.

```
# Remove all objects except 1
RemoveObj 1
```

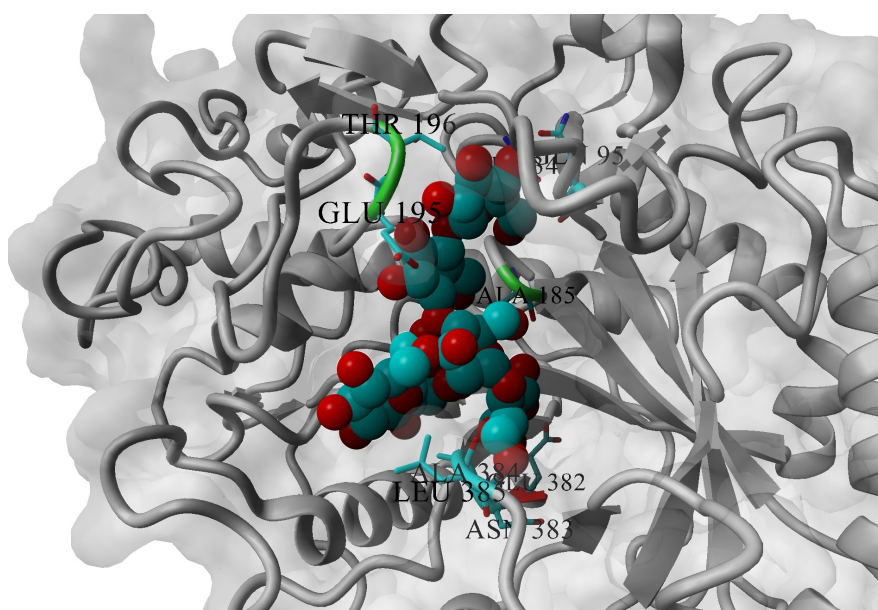
```
# Color protein grey
ColorRes protein, grey

# Select amino acids less than 3 angstroms from the ligand <-- you need to know
# ligand name. Click on the ligand and look at res name at top right
SelectRes protein with distance <3 from ligandname

# Show, color, and label all amino acids interacting with ligand
ShowRes selected
ColorRes selected, element
LabelRes selected, Format = "RESNAME RESNUM", Height = 1.0, Color = Black, X = 0, Y = 0, Z
= 0
```

Remember to replace the ligand name in the SelectRes command with the name of your ligand in YASARA.

14.1 An example result from the commands in Step 14.



- 15 Analyze the amino acids that interact with the ligands and record the interacting amino acids using a table with the format below. If desired add tables or rows to the table below to keep results in this protocol.

Amino Acid name (Glu, Asp, etc.)	Amino acid number	Type of weak interaction	Interacting group in the ligand