

# HDOCK SERVER

Protein-protein and protein-DNA/RNA docking based on a hybrid algorithm of template-based modeling and *ab initio* free docking.

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## Your HDOCK results for job 64d6bff35de6b

### Download Files

[Receptor PDB file](#) [Ligand PDB file](#)

[\[1\]](#) [\[2\]](#) [\[3\]](#) [\[4\]](#) [\[5\]](#) [\[6\]](#) [\[7\]](#) [\[8\]](#) [\[9\]](#) [\[10\]](#) [\[11\]](#) [\[12\]](#) [\[13\]](#) [\[14\]](#) [\[15\]](#) [\[16\]](#) [\[17\]](#) [\[18\]](#) [\[19\]](#) [\[20\]](#)

[Top 10 Predictions](#) [Top 100 Predictions](#) [All the results in a package](#)



Receptor style  
Surface ▼

Receptor color  
☒ Pure  
☐ Rainbow

MODEL No.  

Model 1

Model 2

Model 3

Model 4

Model 5

Model 6

Model 7

Model 8

Model 9

Model 10

Ligand style  
Cartoon ▼

Action  

Spin

Reset

Complex Template Information [\(Click to Show\)](#)

### Summary of the Top 10 Models

Rank	1	2	3	4	5	6	7	8	9	10
Docking Score	-355.17	-333.33	-313.83	-313.60	-304.07	-289.32	-288.44	-284.37	-283.35	-276.63
Confidence Score	0.9838	0.9751	0.9636	0.9635	0.9561	0.9419	0.9410	0.9363	0.9351	0.9264
Ligand rmsd (Å)	48.26	49.50	42.79	73.83	54.24	52.09	67.88	75.93	65.46	80.29
Interface residues	<a href="#">model 1</a>	<a href="#">model 2</a>	<a href="#">model 3</a>	<a href="#">model 4</a>	<a href="#">model 5</a>	<a href="#">model 6</a>	<a href="#">model 7</a>	<a href="#">model 8</a>	<a href="#">model 9</a>	<a href="#">model 10</a>

**Note:** The models are ranked according to the docking scores. Please click [help](#) for the explanations of evaluation metrics

Quality of Docking Structures/Input Data [\(Click to Show\)](#)

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