# **HDOCK SERVER**

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

[<u>Huang Lab</u>] [<u>HDOCK</u>] [<u>Help</u>] [<u>Output example</u>]

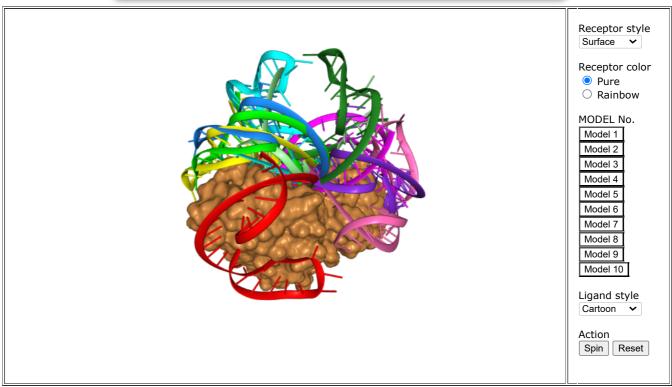
# Your HDOCK results for job 64d6bff35de6b

#### **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



## 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	model 1	model 2	model 3	model 4	model 5	model 6	model 7	model 8	model 9	model 10

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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