HDOCK SERVER

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

[**Huang Lab**] [**HDOCK**] [**Help**] [**Output example**]

Your HDOCK results for job *63d146f7a7ab6*

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
Cartoon

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	-307.74	-275.70	-275.32	-274.20	-268.03	-262.37	-258.40	-249.66	-248.31	-242.52
Confidence Score	0.9591	0.9251	0.9246	0.9230	0.9138	0.9044	0.8973	0.8801	0.8772	0.8642
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)