

# User's Manual

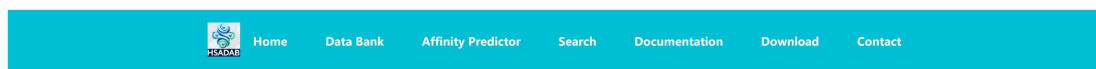
## Home page.

Our website can perform the following functions:

1. Binding data searching according to ligand SMILES (Data Bank)
2. 3D Binding Complex Structure Searching including prediction by Difusion Model and Docking (Data Bank)
3. Binding affinity prediction (Affinity Predictor)
4. Binding data searching according to other condition (Search)

There are also the quikc start link to these three functions.

# Data Bank



## Search Small Molecules in HSADab

1 Enter SMILES:

Cc2ccc(C(=O)C(C)CN1CCCC1)cc2

Submit Reset

2

3

### Search Results:

Slackam	Smile	Ligandname	Site	dol	method	parameter	pH	T	KSV	log	n	K	Ka	Kb	dH	dS	dG	Kd	Cp	pubchem	inchkey
3.36d	<chem>Cc2ccc(C(=O)C(C)CN1CCCC1)cc2</chem>	tolipirone hydrochloride	Binding of Tolipirone Hydrochloride with Human Serum Albumin: Effects on the Conformation, Thermodynamic, and Activity of HSA	10.1021/acs.molpharmaceut.7b00976	flu	None	None	298.0	49000	6.40E+12	0.93	None	None	23000	-20.5016	14.3210	-24.7693	None	None	<a href="https://pubchem.ncbi.nlm.nih.gov/compound/5511">https://pubchem.ncbi.nlm.nih.gov/compound/5511</a>	FKXKPLPLRIB-UHFFFAQYSA-N
3.36d	<chem>Cc2ccc(C(=O)C(C)CN1CCCC1)cc2</chem>	tolipirone hydrochloride	Binding of Tolipirone Hydrochloride with Human Serum Albumin: Effects on the Conformation, Thermodynamic, and Activity of HSA	10.1021/acs.molpharmaceut.7b00976	flu	None	None	303.0	40000	6.30E+12	0.93	None	None	18000	-20.5016	14.2230	-24.8111	None	None	<a href="https://pubchem.ncbi.nlm.nih.gov/compound/5511">https://pubchem.ncbi.nlm.nih.gov/compound/5511</a>	FKXKPLPLRIB-UHFFFAQYSA-N
3.36d	<chem>Cc2ccc(C(=O)C(C)CN1CCCC1)cc2</chem>	tolipirone hydrochloride	Binding of Tolipirone Hydrochloride with Human Serum Albumin: Effects on the Conformation, Thermodynamic, and Activity of HSA	10.1021/acs.molpharmaceut.7b00976	flu	None	None	310.0	35000	6.00E+12	0.92	None	None	15000	-20.5016	14.3070	-24.9360	None	None	<a href="https://pubchem.ncbi.nlm.nih.gov/compound/5511">https://pubchem.ncbi.nlm.nih.gov/compound/5511</a>	FKXKPLPLRIB-UHFFFAQYSA-N
3.36d	<chem>Cc2ccc(C(=O)C(C)CN1CCCC1)cc2</chem>	tolipirone hydrochloride	Binding of Tolipirone Hydrochloride with Human Serum Albumin: Effects on the Conformation, Thermodynamic, and Activity of HSA	10.1021/acs.molpharmaceut.7b00976	flu	None	None	315.0	30000	5.10E+12	0.93	None	None	14000	-20.5016	14.2120	-24.9785	None	None	<a href="https://pubchem.ncbi.nlm.nih.gov/compound/5511">https://pubchem.ncbi.nlm.nih.gov/compound/5511</a>	FKXKPLPLRIB-UHFFFAQYSA-N
3.36d	<chem>Cc2ccc(C(=O)C(C)CN1CCCC1)cc2</chem>	tolipirone hydrochloride	Binding of Tolipirone Hydrochloride with Human Serum Albumin: Effects on the Conformation, Thermodynamic, and Activity of HSA	10.1021/acs.molpharmaceut.7b00976	ITC	None	None	310.0	None	None	0.96	None	215000.0	None	-78.3245	-156.5626	-29.7901	None	None	<a href="https://pubchem.ncbi.nlm.nih.gov/compound/5511">https://pubchem.ncbi.nlm.nih.gov/compound/5511</a>	FKXKPLPLRIB-UHFFFAQYSA-N

## Predicted 3D Complex Structures of HSA and small molecules in HSADab

(Please enter the file name in the output table, replace ".txt")

\*(The complex modules are under development. Please use the data at your own risk.)

4

Please select an option:

☐ PLANTS\_plp ☐ PLANTS\_chemp ☐ DiffDock ☒ AlphaFold3 ☐ Chai-1 ☐ Boltz-1

Enter Structure Name: 3

Select Style: Cartoon Select Color: Secondary Structure

5

6

View Structure

Input - Custom Scripting

Enter JSmol commands...

Run Reset

JSmol tutorial for beginner



JSmol

You can directly input SMILES in the input(1) or draw the structure in the JSME web plugin(2), where the SMILES can be updated in the input(1). If the structure is in our database, it will output a table, in which we put the link to Pubchem of the small molecules. And if you want to search the

predicted 3D complex structure between the small molecules and HSA, you just need choose the method (4) and put in the filename from the table into input 5. After click view structure button (6), the docking structure will show in Jsmol web plugin (7).

# Affinity Predictor

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## ΔG Prediction Model

The affinity prediction module enables instant predictions of HSA-ligand binding affinities with a series of ML predictors, including the fingerprints-based MLP model, LGBM, RandomForest and the fine-tuned large language models. The accuracy comparison is shown below.

**1** → **SMILES:**

**3** → **Temperature:**

\*(The affinity predictions are under development. Please use the data at your own risk.)

**2** →

**4** → **Predicted Result**

Method	ΔG (kcal/mol)	Std
RF	-7.480	0.123
LGBM	-8.236	0.220
MLP	-8.456	0.222
LLM	-8.871	0.125
Ensemble	-8.261	0.505

**Physical Chemistry Properties**

Property	Value
H-Bond Donors	1
H-Bond Acceptors	4
Rotatable Bonds	7
Polar Surface Area	44.810
Stereocenters	0
LogP	4.859
Molecular Refractivity	123.237
Fraction Csp3	0.435
Rings	4
Heterocyclic Rings	2
Aromatic Rings	2
Aromatic Heterocycles	0
Spiro Atoms	0
Molecular Weight	448.394
Heteroatoms	7
Heavy Atoms	30
Total Atoms	57

You can directly input SMILES in the input(1) or draw the structure in the JSME web plugin(2), where the SMILES can be updated in the input(1). Then you should input temperature(unit is K) in the input(3). Click the “Predict” , you will see the prediction data(4). The prediction data consists of 4 kinds of machine learning model, which is a average of 3 models. Moreover, we present the physical chemistry properties.

# Search

## Condition Search

**Search Conditions:**

RemoveRemove

Search

### Search Results:

[illegible]

You can input conditions in the input(1) , where you can also add the range. Furthermore, you can click 'Add+' button(2) to add other condition Click the "Search" , you will see the searched data(3). The searched data should include the search condition.