Analyze your docking results:

Analyze | **Download** | **Delete Job**

Table | 3D View

Table

Rank	File ID	Compound	Affinity ❓	Total Energy ❓	vdW Energy	Elec. Energy
1	2d844d7d75	⌄ ligand 1	-4.964	-101.415	-0.634	-0.170
		⦿ run 5	-4.964	-101.415	-0.634	-0.170
		○ run 5	-4.964	-101.412	-0.659	-0.139
		○ run 11	-4.977	-101.388	-0.670	-0.155
2	2d1105f87c	⌄ ligand 1	-4.644	-26.614	-0.456	-1.264
		○ run 9	-4.644	-26.614	-0.456	-1.264
		○ run 4	-4.641	-26.603	-0.416	-1.291
		○ run 4	-4.638	-26.599	-0.384	-1.317

« | 1 | »

3D View

Use your mouse to drag, rotate, and zoom in and out of the structure:

`r` auto view   `shift + left_mouse + drag` zoom   `ctrl + right_mouse + drag` rotate

Table   3D View

« 1 »

3D View

Use your mouse to drag, rotate, and zoom in and out of the structure:

r *auto view*   shift + left_mouse + drag *zoom*   ctrl + right_mouse + drag *rotate*

bond: [ARG]401 B.NH2 - [ARG]401 B.HH22 (protein_4295a59bc8_prep.pdb)

bond [TYR]182:A:CD1 - [TYR]182:A:CE1 (protein_4295a59bc8_prep.pdb)

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