

# Screening tutorial

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In silico screening using multiple target  
screening method with MolDesk Screening

MolDesk Screening ver. 1.1.53

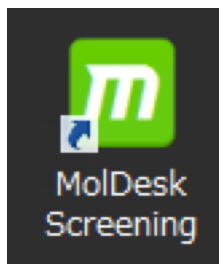
Biomodeling Research Co., Ltd.

2018/08/30

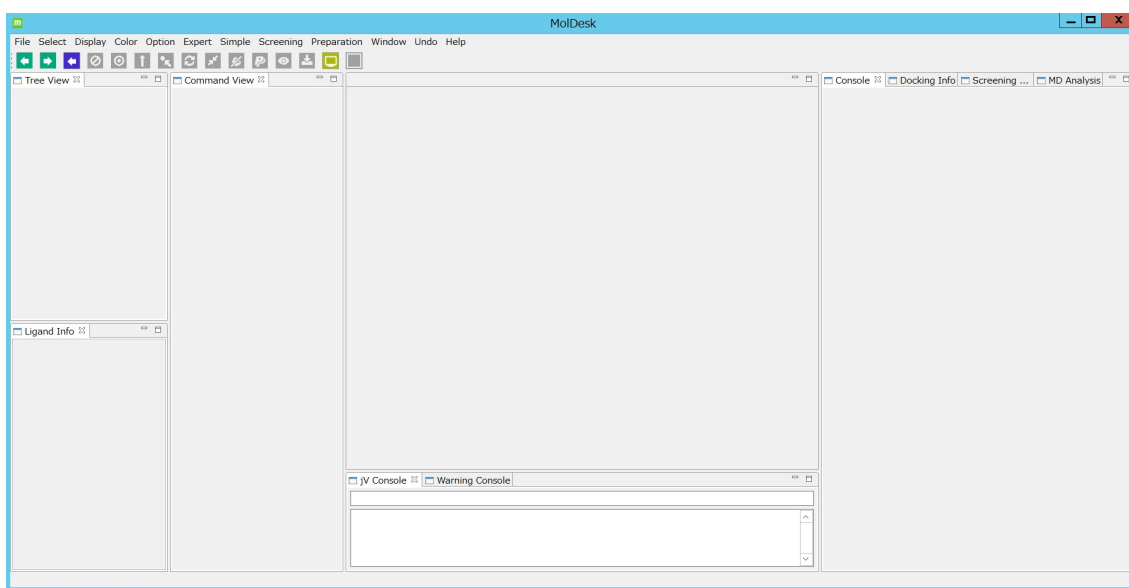
In this tutorial, we will practice how to perform screening calculation using multiple target screening (MTS) method with MolDesk Screening.

## 1. Launch of MolDesk Screening

Click on the desktop icon to launch MolDesk Screening (Fig. 1).



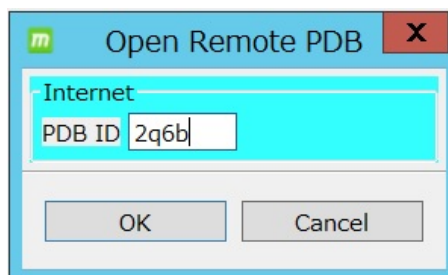
**Fig. 1** Icon of MolDesk Screening



**Fig. 2** Screenshot after the launch of MolDesk Screening

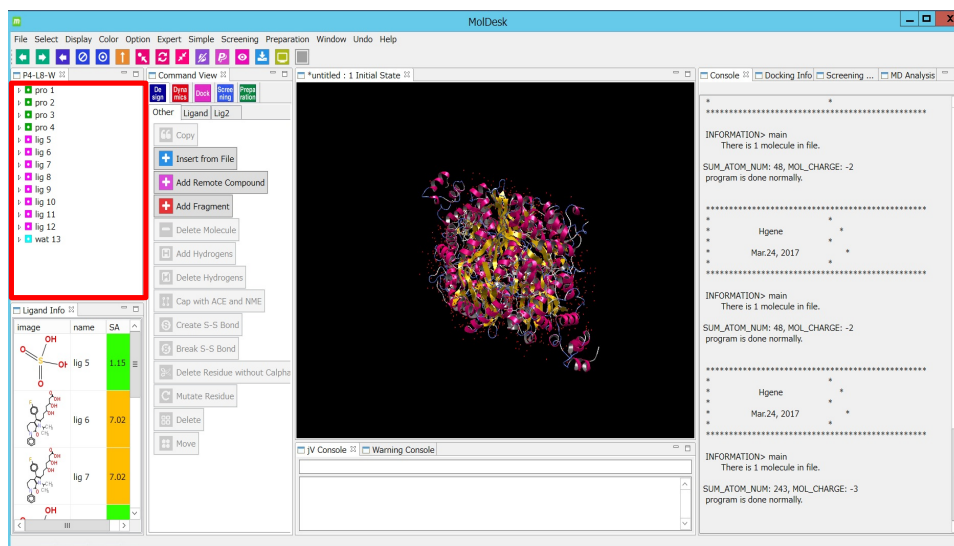
## 2. Reading a protein structure file

To load a molecule, first, click the "File"→"Open Remote PDB". A dialog box will appear. Enter a PDB ID into the dialog box. You can also read a file using "File" → "Open Molecular File". Here, please input 2Q6B (English letters may be uppercase letters or lowercase letters).



**Fig. 3 Input dialog of PDB code**

The contents of the loaded molecule can be confirmed in the window indicated by the red frame in Fig. 4 (left side of the screen). In this example, you can see that the loaded file contains four protein chains, eight ligands, and water molecules.



**Fig. 4 Screenshot after reading a molecular structure file**

### 3. Deleting molecules not to be used

You can delete selected molecules by clicking "Delete Molecule" in the Command view. Here, please select wat13 and click "Delete Molecule". Fig. 5 is the screen after removing water. Wat13 disappears from the Tree View.

In addition to water molecules, please delete pro3, pro4, lig5, lig7 to lig12 in the same way. Fig. 6 shows the screen after removing all the unnecessary molecules. Pro3, pro4, lig5, lig7 to lig12, wat13 disappear from the Tree View.

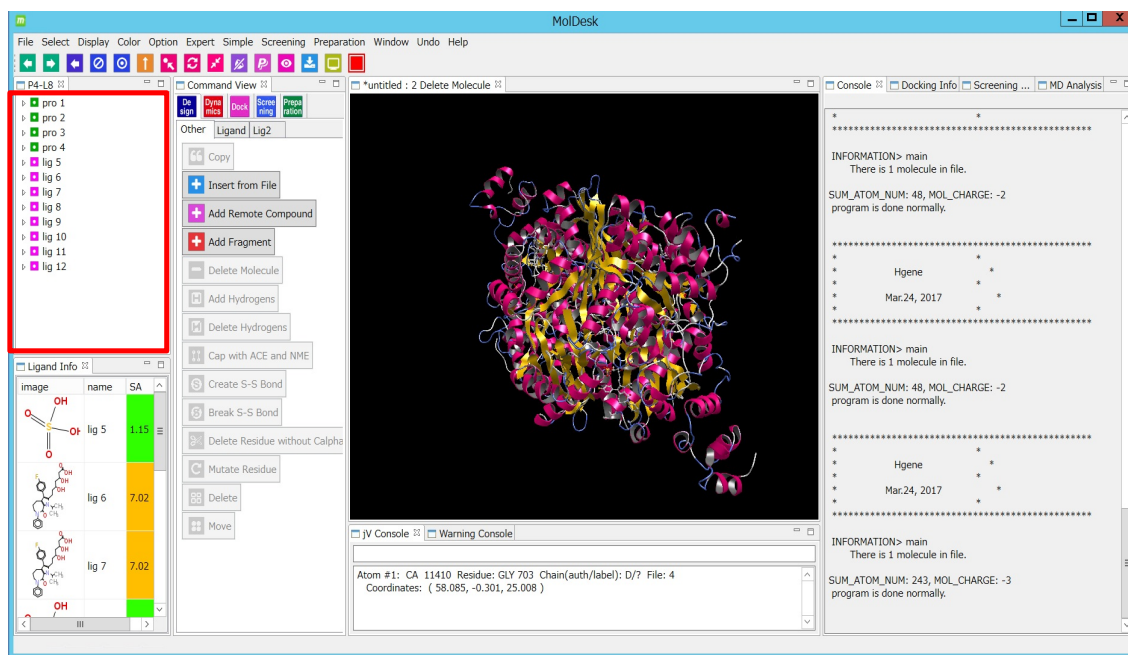


Fig. 5 Screenshot after deleting water molecules

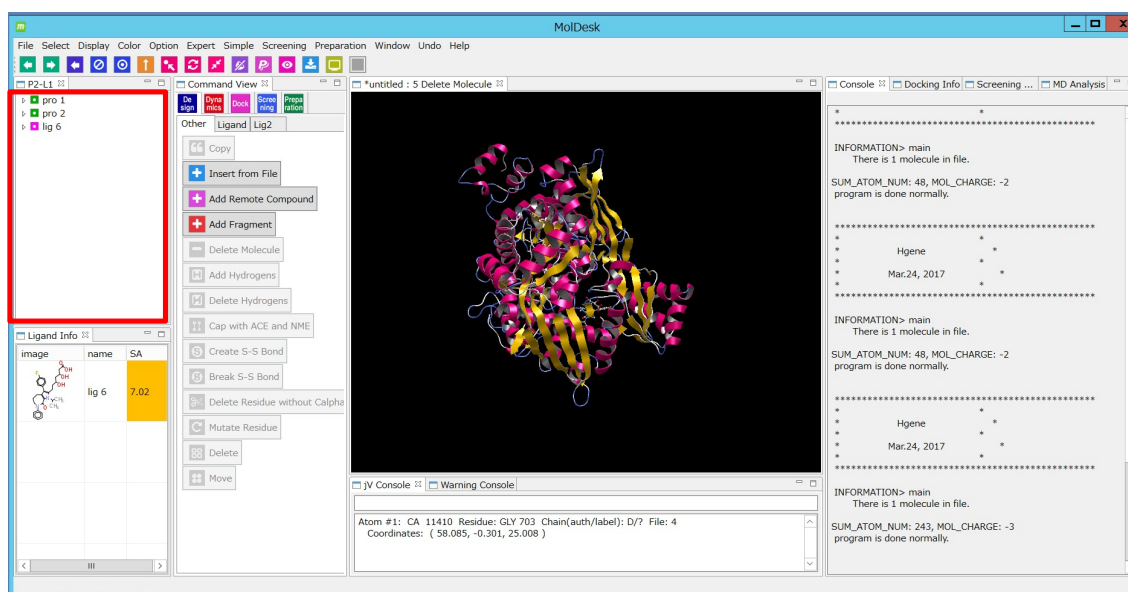


Fig. 6 Screenshot after deleting molecules not to be used

#### 4. Creating probe points

In myPresto, we must prepare probe points near the center of the site to be docked. Here, we create probe points using coordinates of the ligand molecule. Click lig6 in the Tree View and select a ligand molecule. If a tab of Command View is not in either “Dock” or “Screening”, change it and select lig6 of Tree View again. After selecting lig6, click “Make Pocket” in the Command View (Fig. 7). After clicking “Make Pocket”, red spheres will appear at the atomic coordinates of the ligand (Fig. 8). In the Tree View, point7 appears newly. Since lig6 is not used after now, here we delete lig6.

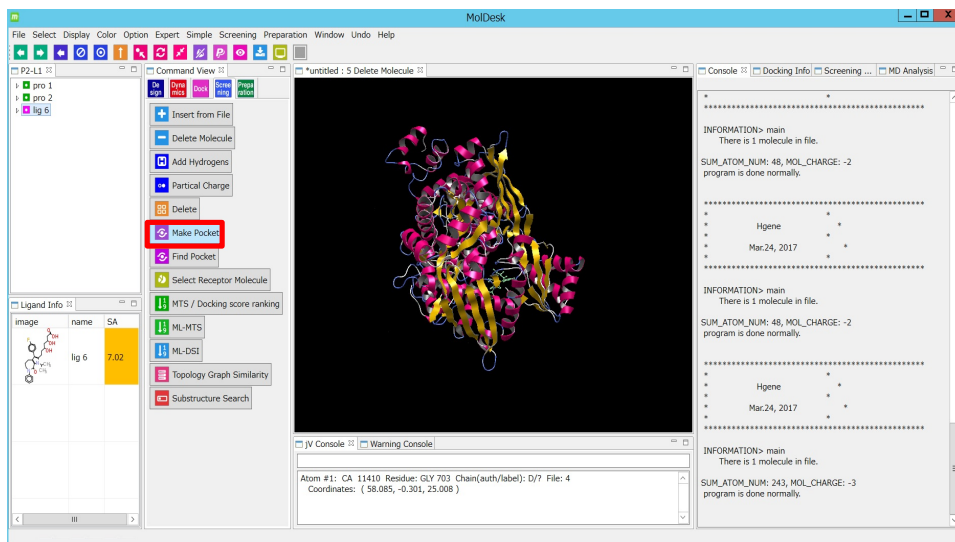


Fig. 7 Creating probe points

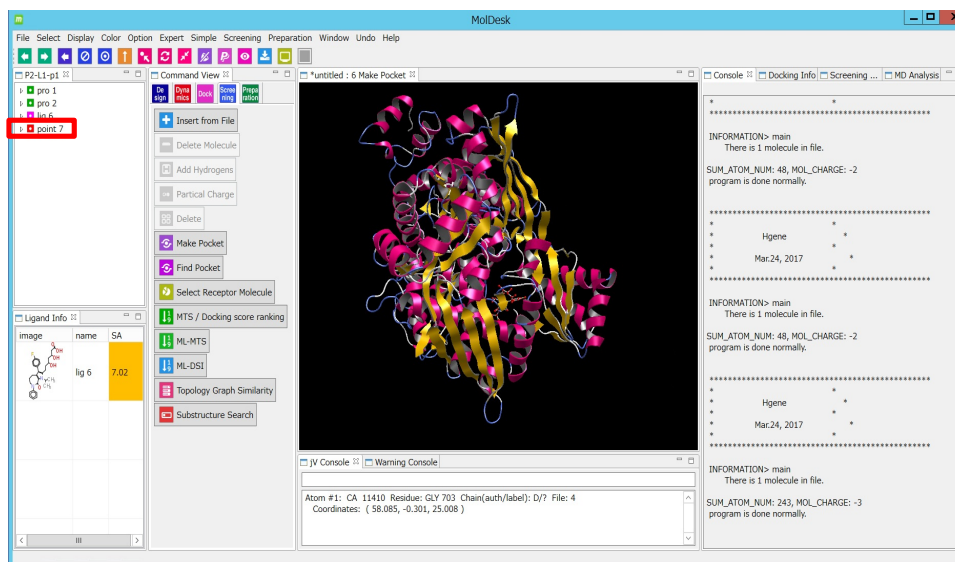
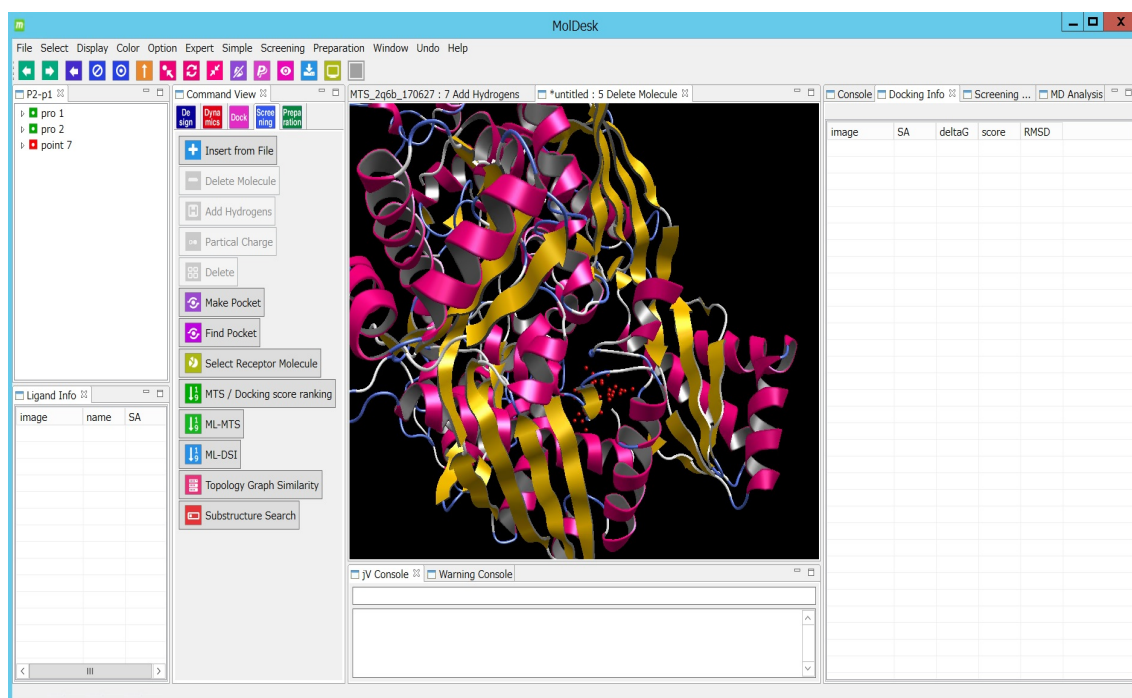


Fig. 8 Screenshot after creating probe points

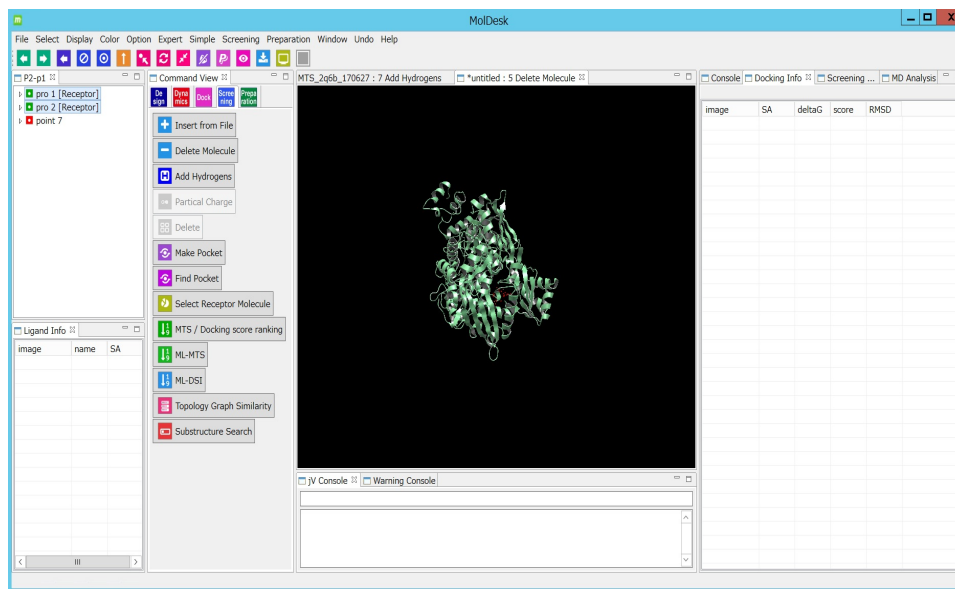
Fig.9 shows the screen after deleting ligand molecule (lig6).



**Fig. 9 Probe points for docking**

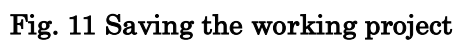
## 5. Selection of receptor protein

Here we select the receptor protein. If the Command View tab is not in Screening tab, select the Screening tab, and select pro1, pro2 in the Tree View, then click "Select Receptor Molecule". "[Receptor]" indications are added next to pro1 and pro2 in the Tree View.



**Fig. 10 Screenshot after selecting receptor molecules**

You must save the project before performing the screening calculation. Save the project using [File] -> [Save As] in the menu bar. To save the project, please create a new folder and select it. The folder name should be easy to understand and find like-MTS\_Target\_YYMMD. For example, here MTS\_2q6b\_180802 would be good.





## 7. Launch of screening calculation

Till here, preparations for screening calculation are already completed. We can start screening calculations. Click "MTS / Docking score ranking" in the Command View (Fig.

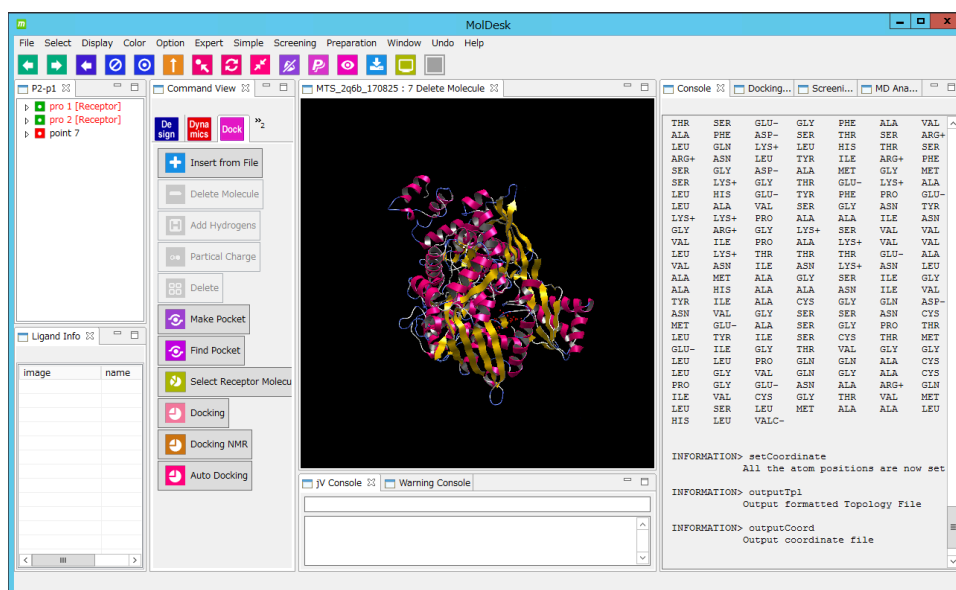


Fig. 12 Starting MTS/Docking score ranking

12).

The part surrounded by a light blue frame on the left side of Fig. 13 (Previous input) is used when using repeated screening. In the initial screening, set the yellow frame part (New input). If a hit compound is available, you can draw a graph of AUC showing screening performance from the order of the hit compound by clicking Select mol2 files of Compounds and registering the mol2 file.

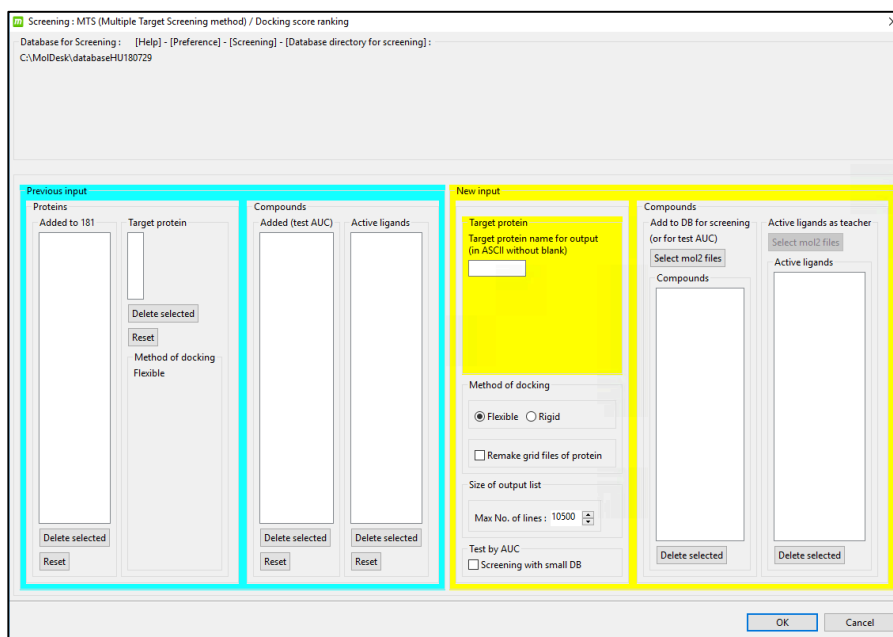
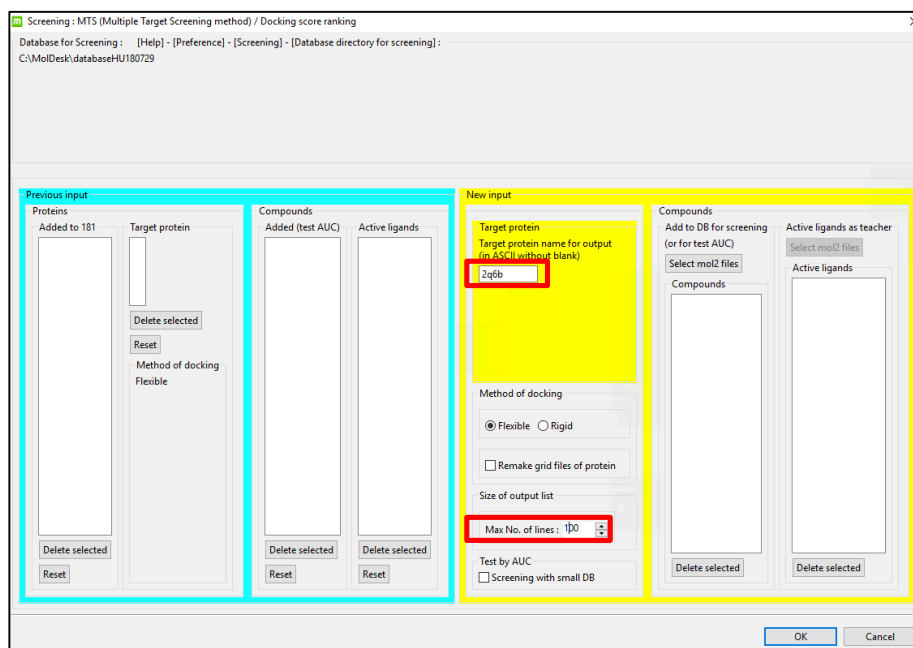


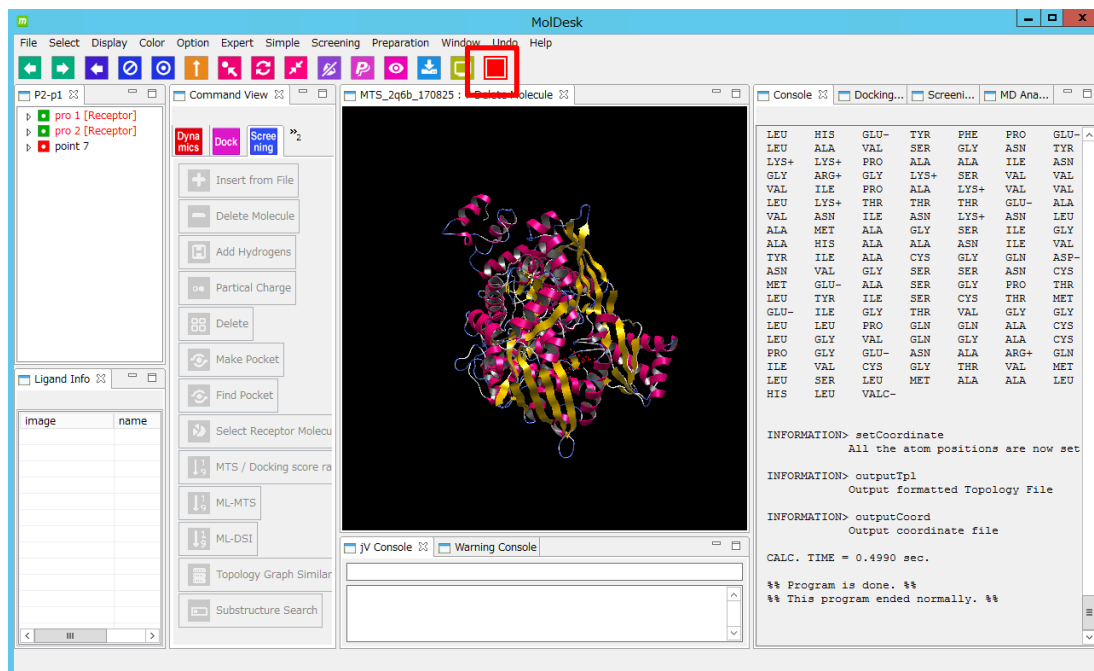
Fig. 13 Dialog box for the setting of MTS/Docking score ranking

Here, enter the target code (2q6b in this case), set 100 at the “max no. of line” in the dialog box. (100 is selected for this tutorial to save calculation time), and press OK (Fig. 14). Click OK to start screening calculations.



**Fig. 14 Setting for MTS/Docking score ranking**

Calculation can be stopped by clicking the “Stop Task” icon indicated with a red square frame in Fig. 15.



**Fig. 15 Stop Task icon to stop calculations**

## 8. Operation after screening calculations

When the screening calculation is completed, compound information is displayed in the "Screening Info" (Fig. 16). When selecting a compound in the Screening Info, the docking pose of the selected compound is displayed (Fig. 17).

Not available

### **Fig. 16 Screenshot after completing screening calculation**

You can hide probe points by selecting point7 (Point 9 in Fig. 17 but point 7 is correct) and selecting "Hide atoms" from the right-clicked menu. Also, select pro1, pro2 and choose "Space Filling" from Display on the menu bar to display the protein surface. With molecules selected in the Screening Info, pressing the up or down cursor keys instantly switches compounds.

Not available

### **Fig. 17 Screening Info**

Not available

**Fig. 18 Receptor protein drawn with space filling**

Screening Info shows many profiles about top ranking compounds. (Fig. 19)

Not available

**Fig. 19 Screening Info**