

myPresto GUI Free software

myPresto Portal

Ver.1.1.90

Quick manual

Japan Biological Informatics Consortium

Contents

1. Quick manual	3
1.1. Project.....	3
1.2. Creating a project.....	4
1.2.1. [File] - [Open Molecular File]	5
1.2.2. [File] - [Open Molecular File as list (Numerous Molecules)]	6
1.2.3. [File] - [Open Remote mmCIF / PDB]	8
1.2.4. [File] - [Open Project]	9
1.3. Saving the project.....	10
1.3.1. [File] - [Save as].....	10
1.4. 3D display of molecular structure	11
1.4.1. Mouse operation	11
1.4.2. Selection of molecules, chains, residues, and atoms	11
1.4.3. Selection of display model	12
1.4.4. How to color	13
1.5. Dock.....	13
1.5.1. Read mmCIF / PDB files over the internet	14
1.5.2. Fully automatic docking	15
1.5.3. Select receptor and ligand molecules	15
1.5.4. Create a pocket.....	16
1.5.5. Confirmation of results.....	19
1.6. MD calculation in water	20
1.6.1. Read mmCIF / PDB files over the internet	20
1.6.2. Fully automatic MD calculation.....	21
1.6.3. Confirmation of MD calculation result.....	28
1.7. GROMACS : MD calculation Trajectory Analysis	29
1.7.1. [Preference] - [Molecular dynamics] settings.....	29
1.7.2. Trajectory Analysis	30
1.8. Compound 2D editor.....	31
1.8.1. Start JChemPaint	31
1.9. Remove feature restrictions	32

1. Quick manual

1.1. Project

myPresto Portal processes data on a project-by-project basis.

As a general rule, one project will be created for each file entered with [File]-[Open Molecular File].

The project should be in the directory set in the Default Project Directory of [Help]-[Preference]-[8. Other].

MoldeskProject00000

MoldeskProject00001

MoldeskProject00002

...

Is created as.

The above Default Project Directory directory is the system default tmp directory, which differs for Windows, Linux, and MAC, so check where it is stored.

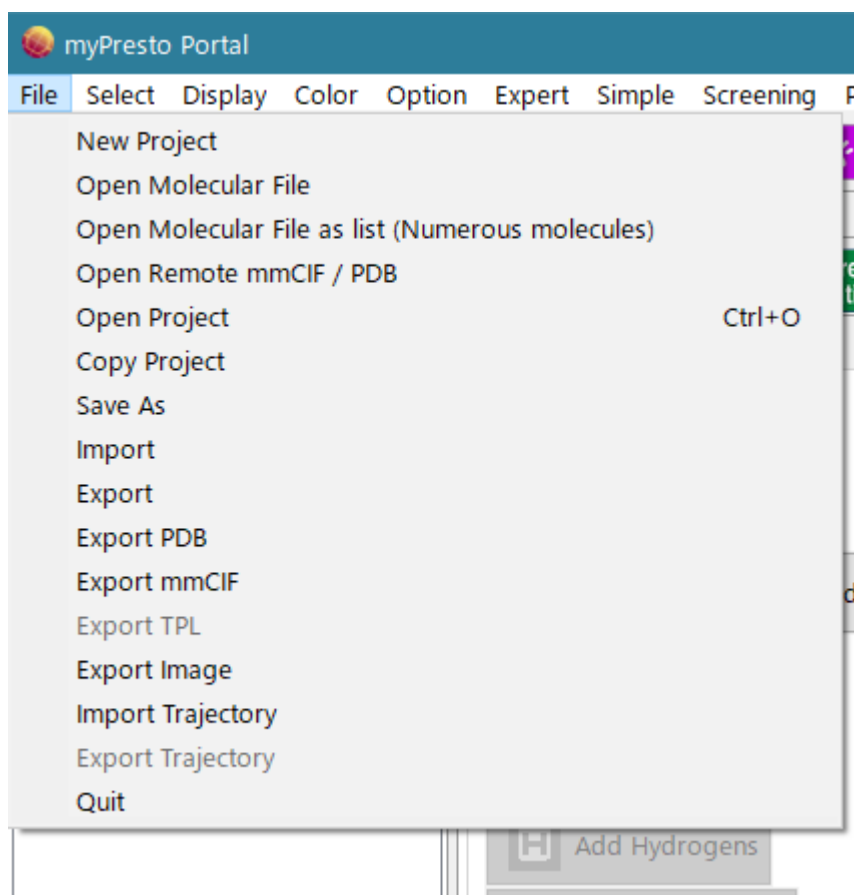
[Help]-[Preference]-[8. Other]

Please verify.

If the user changes the Default Project Directory in [Help]-[Preference]-[8. Other], the screen prompting you to save the project will disappear when the program ends.

We recommend changing to a directory (folder) with sufficient disk space.

1.2. Creating a project



There are seven menus related to creating a project.

[File] - [New Project]

[File] - [Open Molecular File]

[File] - [Open Molecular File as list (Numerous Molecules)]

[File] - [Open Remote mmCIF / PDB]

[File] - [Open Project]

[File] - [Import]

[File] - [Import Trajectory]

Of these

[Open Molecular File]

[Open Molecular File as list (Numerous Molecules)]

[Open Remote mmCIF / PDB]

[Open Project]

This section explains.




1.2.1. [File] - [Open Molecular File]

Reads the specified file and creates a new project.

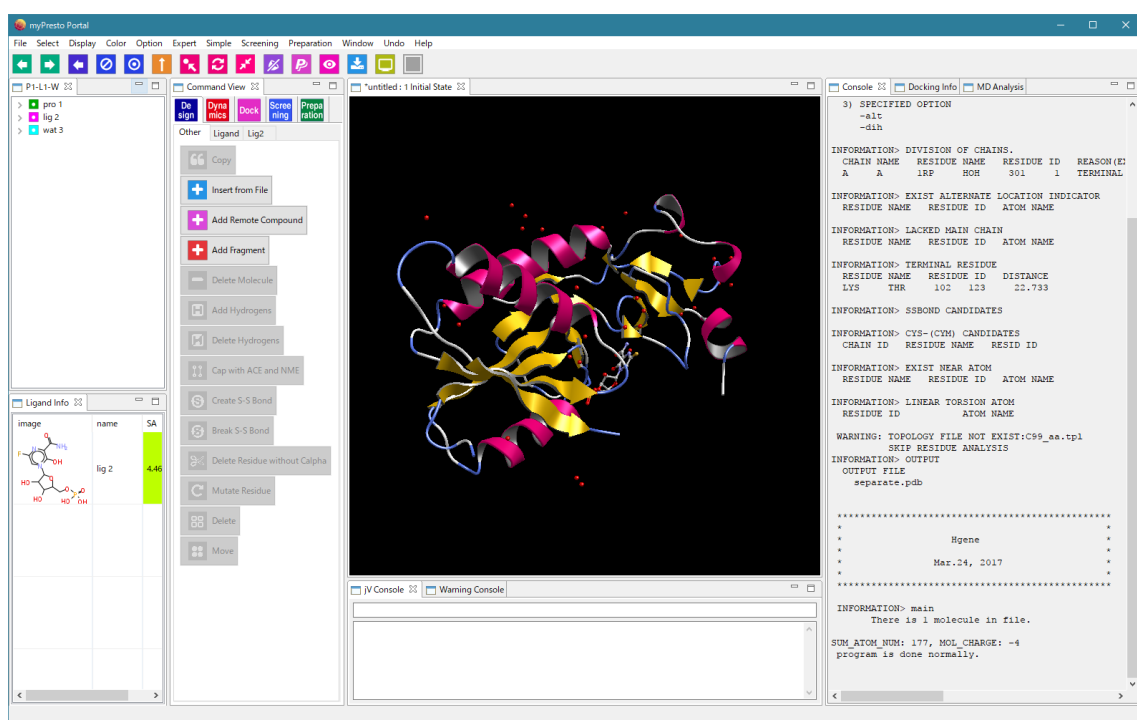
There are five file formats that can be entered: PDB / mmCIF / Sybyl Mol2 / MDL SDF / MDL MOL / SMILES. The file extensions should be as shown in the table.

If the extension is different, change the extension before entering.

File	File extension
PDB	.pdb / .ent
mmCIF	.cif
Sybyl Mol2	.mol2 / .sm2 / .SM2 / .ml2
MDL SDF	.sdf
MDL MOL	.mol / .mdl
SMILES	.smi / .SMI / .smiles / .SMILES

- If the input file is a mmCIF file or pdb file, hydrogen atoms are missing, so it is necessary to add hydrogen atoms with  [Add Hydrogens] as appropriate.
 - If you want to detect and process the terminal residues of a protein molecule, perform  [Cap with ACE and NME] before adding a hydrogen atom. If a hydrogen atom is added first, an OXT atom will be added to the N-terminal and the NME terminal cannot be added.
- If the input file is a mol2 file, if the mol2 file contains charge information, that information is read, but even if the charge information is not included, the charge calculation is not performed automatically.
 - If you read a mol2 file that does not have charge information, use  [Partial Charge] to calculate the charge as appropriate.

When you load the file, the molecular structure will be displayed on the 3D screen.



At this point, the project name has not been given yet.

When saving the project name with "1.3.1 [File] - [Save As]" described later, save it with the project name.

1.2.2. [File] - [Open Molecular File as list (Numerous Molecules)]

Reads files containing more than 10,000 molecules at high speed. It can be used as a **molecule viewer for files containing large numbers of molecules**.

Since a large number of molecules are loaded as a list, a new project will not be created at the time of loading.

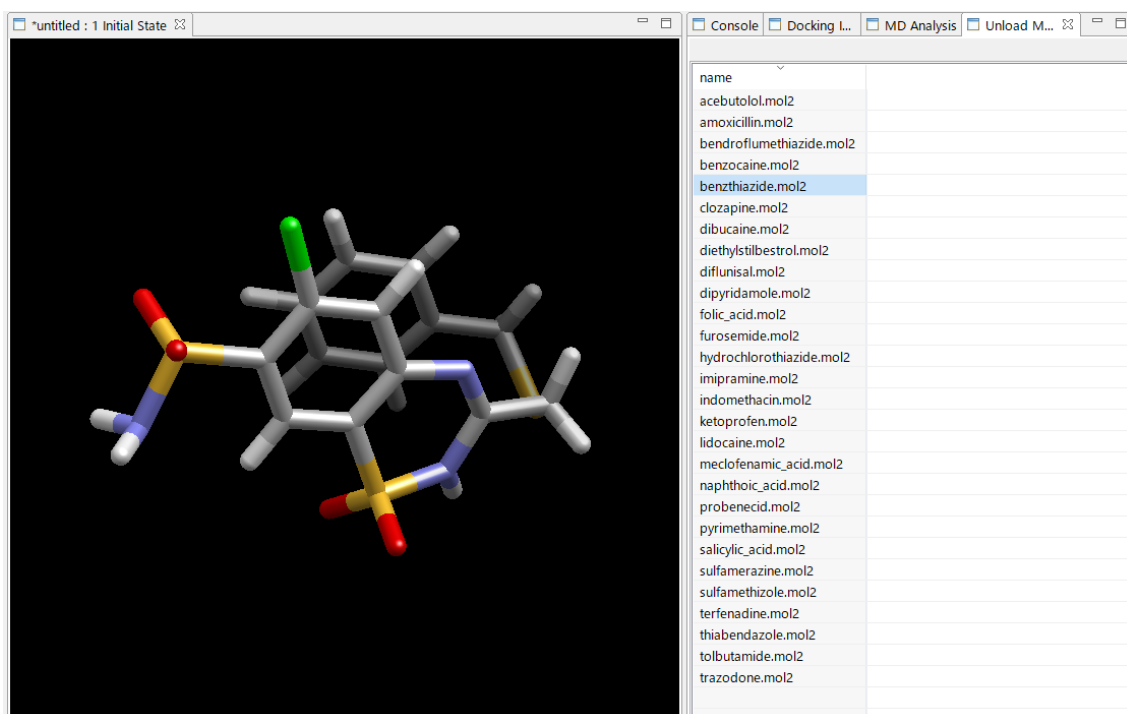
There are four file formats that can be entered: PDB / Sybyl Mol2 / MDL SDF / MDL MOL.

File	File extension
PDB	.pdb
Sybyl Mol2	.mol2
MDL SDF	.sdf
MDL MOL	.mol

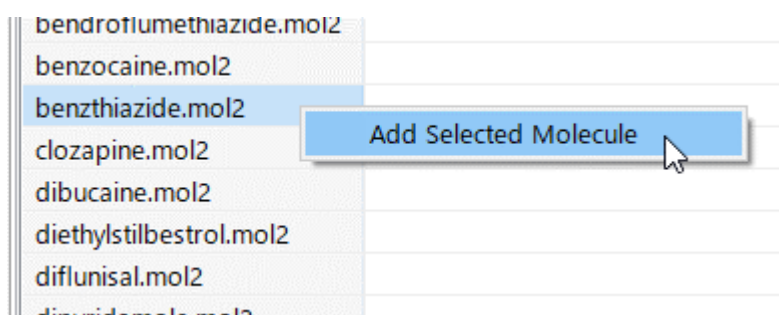
- The file extension must be as shown in the table. If the extension is different, change the extension before entering.

Example of loading MolDesk Basic-> sample-> mol2-> multi28.mol2.

This file contains only 28 molecules, but read it as a list as follows:



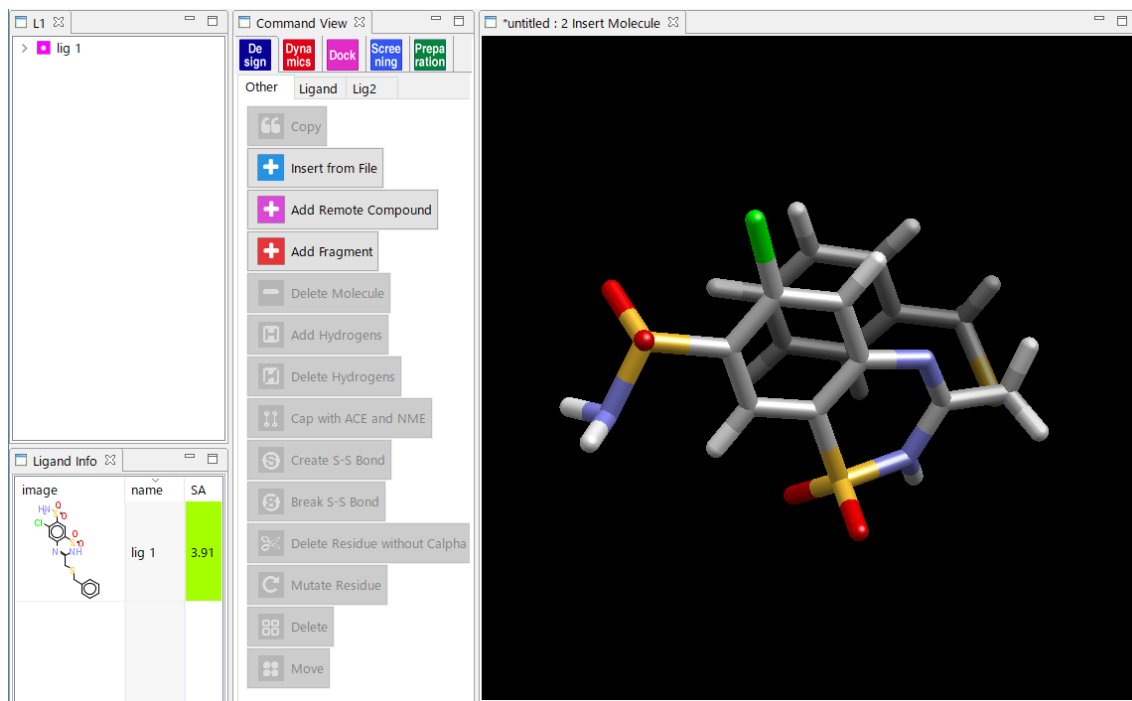
Click the molecule name in the list to display the molecule in 3D as shown above.



Right-click on the molecule name in the list to display the Add Selected Molecule menu. If you click this, you can import the molecule as a project, and the molecule you imported will be added to the tree display.

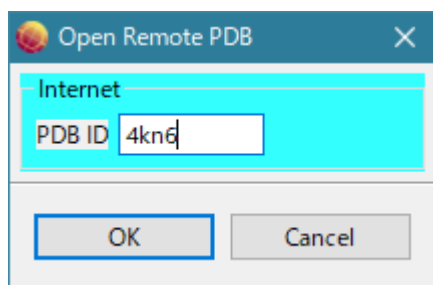
Only then will the project be created.

✖ Before importing molecules with the [Add Selected Molecule] menu, only the molecules are displayed and no project is generated.



1.2.3. [File] - [Open Remote mmCIF / PDB]

Download mmCIF and PDB files via the internet. Import the mmCIF file and create a new project.



Example: Read PDB ID "4kn6"

1.2.4. [File] - [Open Project]

Projects saved with [File]-[Save As] in the past,

Or, it is in the directory set in Default Project Directory of [Help]-[Preference]-[8. Other].

MoldeskProject00000

MoldeskProject00001

MoldeskProject00002






...

Open.

Select the existing project folder (including the original and work folders directly under it) and click OK.

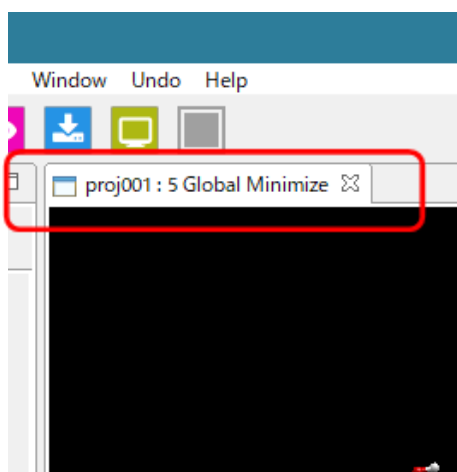
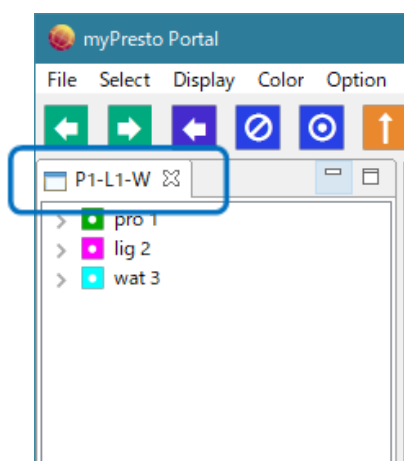
The tab name on the tree display screen (blue frame "P2-L1-W" in the figure below) indicates the number of proteins and compounds.



P is a protein chain, L is a compound, W is water of crystallization, and M is a metal / ion.

On the tree display screen,  is protein,  is compound,  is water,  is glycan and  is metal / ion.

The last command you operated can be confirmed from the tab name on the 3D screen (red frame "proj001: 5 Global Minimize" in the figure below).

The tab name indicates **[project name : history number execution command name]**.



The executed command can be re-executed by clicking  [UNDO] and  [REDO].

1.3. Saving the project

There are three menus for saving a project:

[File]-[Save As]

[File]-[Copy Project]

[File]-[Export]

Of these, [Save As] is explained.

1.3.1. [File] - [Save as]

Save the displayed system with a project name. The command history is also saved.

Run [File] - [Save As], select Create New Folder in the [Make PROJECT directory] dialog, and enter the folder name. This folder name will be the new project name. All the displayed system data (including command history) is saved in the created folder.

Please note that if you specify an existing folder without performing [Create new folder], the following folders and files will be output directly under the folder.

Original folder

Work folder

cif and pdb files downloaded via internet

* If you are interested in the details of the files stored in the project, please refer to the MolDesk Basic Manual.

1.4. 3D display of molecular structure

1.4.1. Mouse operation

You can operate the rotation and movement of molecules with the mouse on the 3D screen.

Operation	Mouse operation
X-axis (left-right axis) rotation Y-axis (vertical axis) rotation	Left drag
Z axis (depth direction axis) rotation	Shift + right drag (Left and right direction)
Move in the X-axis (left and right) direction Move in Y-axis (up and down)	right drag
Move in the Z-axis (depth) direction (enlarge / reduce)	Shift + left drag Or wheel rotation

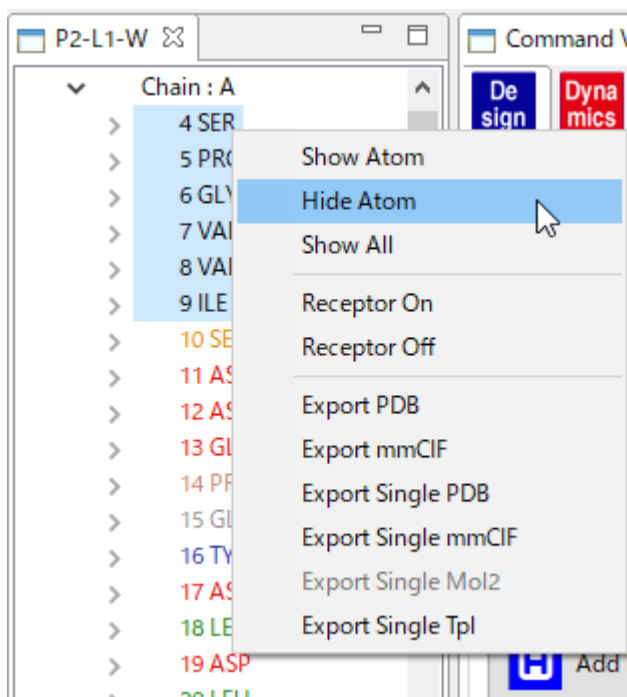
* For MAC, left click = click

Right click = [Command] + click

1.4.2. Selection of molecules, chains, residues, and atoms

Molecules, chains, residues, and atoms are selected with the mouse, but the operations differ between the 3D screen and the tree display screen.

Operation	3D screen	Tree display screen
Multiple selection	Ctrl + click	Ctrl + click
Continuous multiple selection	—	Shift + click
Residue selection	Double click	Click residue name
Select chain	Triple click	Click chain name
Molecule selection	—	Click on the molecule name

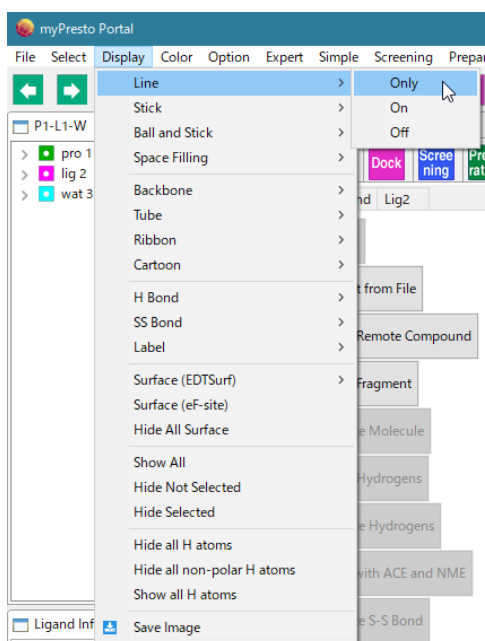


Multiple molecules, chains, residues, and atoms can be displayed / hidden at once.

Select multiple items on the tree display screen and right-click Select [Show Atom] or [Hide Atom].

Unhide with [Show All] to show everything.

1.4.3. Selection of display model



Select molecules, chains, residues, atoms, When you select a model in the [Display] menu, You can change the display model to Line, Stick, etc.

The meanings of the options are as follows.

[Only] : This display model alone will display in 3D.

[On] : Apply this display model to other display models Overwrite.

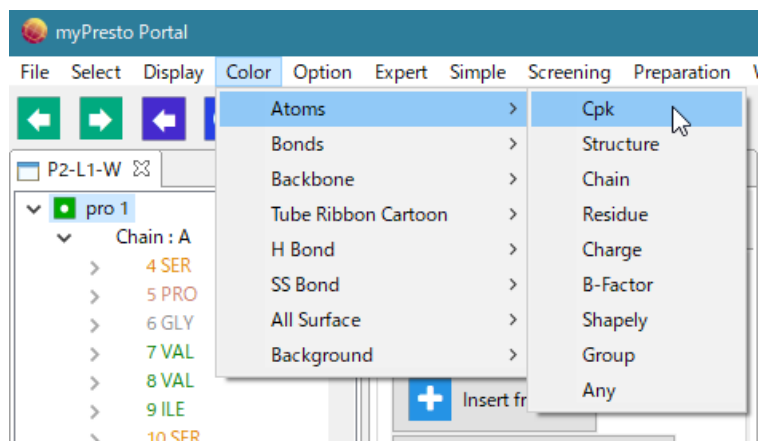
[Off] : Erase this display model.

Please refer to the following site for other display models.

<https://www.moldesk.com/moldesk-basic-commands/#Display>

1.4.4. How to color

You can change the color of molecules, chains, residues, and atoms.



Select a molecule, chain, residue, or atom, and then select a color from the [Color] menu to change the color.

You can also change the color and transparency of all molecular surfaces at the same time with [Color]-[All Surface].

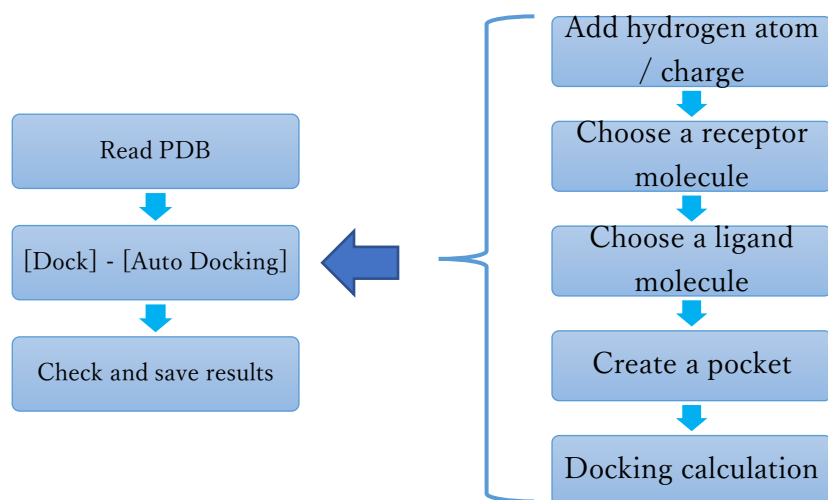
For details on each item in the [Color] menu, refer to the following sites.

<https://www.moldesk.com/moldesk-basic-commands/#Color>

1.5. Dock

Here is an example of executing the simplest docking calculation using fully automatic docking.

The procedure is as follows.



A pocket (probe point) must be generated before the docking calculation.

There are the following methods for pocket generation.

How to generate a pocket:

1. How to make the coordinates of the molecule the probe point of the pocket itself.
It is used when the correct structure of the combined state is known. Let the ligand molecule be the probe point.
Select molecules other than proteins. Multiple selections are possible.
2. How to generate a pocket probe point on the surface of a molecule
Select a molecule containing a protein or nucleic acid molecule. Multiple selections are allowed.
The user can specify the position or the search can be done automatically.

To create a pocket, you need to select a molecule that has its coordinates as the probe point (or creates a probe point on its surface).

After the pocket formation is complete, specify the receptor and ligand molecules to be used in the docking calculation.

Multiple receptor molecules can be selected, including proteins. The molecule of the ligand is one compound or glycan.

In myPresto Portal, a group of receptor molecules (must contain at least one protein or nucleic acid molecule) and a ligand molecule (one compound or glycan) can be strictly specified and calculated.

✖ In myPresto Portal, the molecular weight of compounds (ligands) that can be docked is limited to 400 Da.

1.5.1. Read mmCIF / PDB files over the internet

Refer to "1.2.3 [File] - [Open Remote mmCIF / PDB]" and read PDB ID 1m17 from the Internet as test data.

This protein is the EGFR tyrosine kinase domain, which contains the molecule of the anticancer drug Erlotinib. It is added.

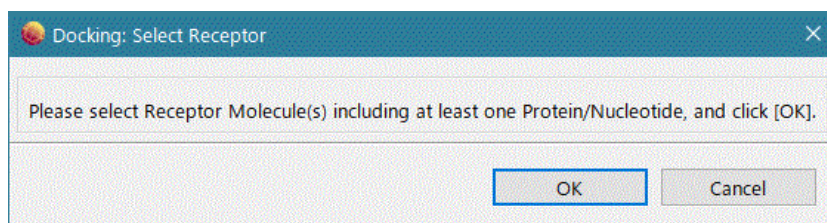
1.5.2. Fully automatic docking


Select  [Dock] -  [Auto Docking]

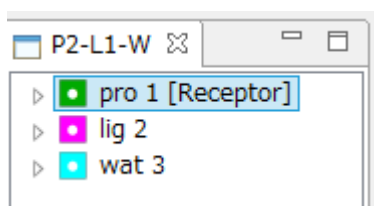
First, missing hydrogen atoms (in dissociated state in water) are automatically added to all molecules, and all compounds or glycans are charged with Gasteiger. Molecules other than compounds or glycans are charged based on the force field selected in [Help] - [Preference]-[Molecule] - [tplgeneX].




1.5.3. Select receptor and ligand molecules

When charging is complete, a message dialog will appear prompting you to select a receptor.



In this example, select  pro1 on the tree view screen and click [OK].

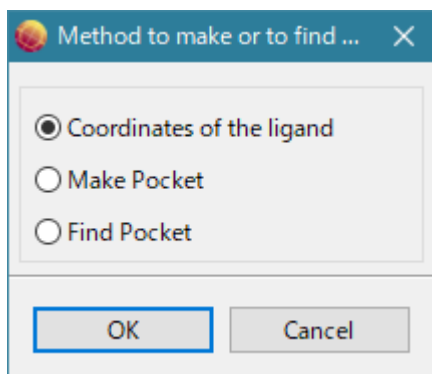


Because  pro1 was recognized as a receptor, The notation of  pro1 changes to  pro1 [Receptor].

The receptor molecule must contain at least one protein or nucleic acid molecule. It may contain compounds, glycans or metals.

- ✗ You can select a receptor molecule other than a protein or a nucleic acid molecule, but make sure to leave a space in the pocket where the ligand binds. Docking calculation is performed for the vacant space.

1.5.4. Create a pocket



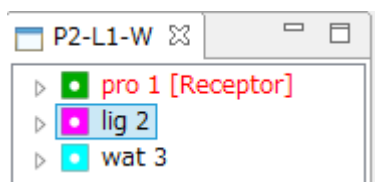
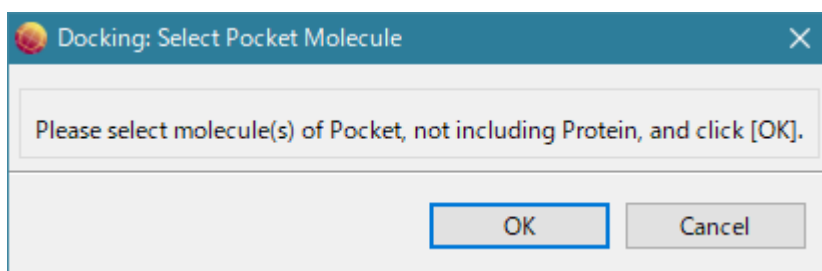
After specifying the receptor, a dialog for selecting the pocket generation method is displayed.


Since the correct structure is known in this example, select [Coordinates of the ligand] and use the coordinates of the selected ligand as the probe point of the pocket.

The description of the items in the dialog for selecting the pocket generation method is as follows.

Item	Explanation
[Coordinates of the ligand]	Makes the coordinates of the selected molecule the probe point of the pocket. You can select multiple molecules other than proteins or nucleic acid molecules and use them as probe points at once.
[Make Pocket]	Place the pocket sphere on the surface of the selected receptor and generate a pocket probe point inside the sphere.
[Find Pocket]	A pocket search is performed on the surface of the selected receptor, and multiple probe points are automatically generated in order of score.

A dialog for selecting the molecule (non-protein molecule, multiple molecules) to be the probe point of the pocket is displayed.




In this example, select  lig2 on the tree view screen and click [OK].

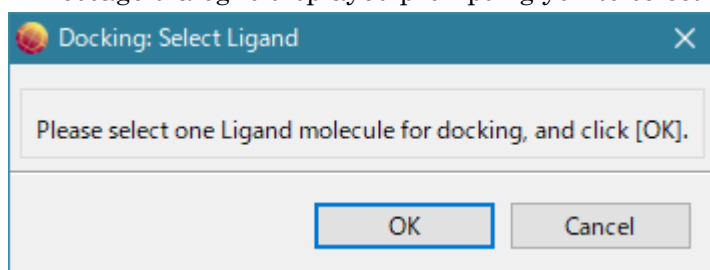
At this time, the atom of the ligand molecule becomes a red circle.


This indicates that all atoms of the ligand molecule are now pocket probe points.



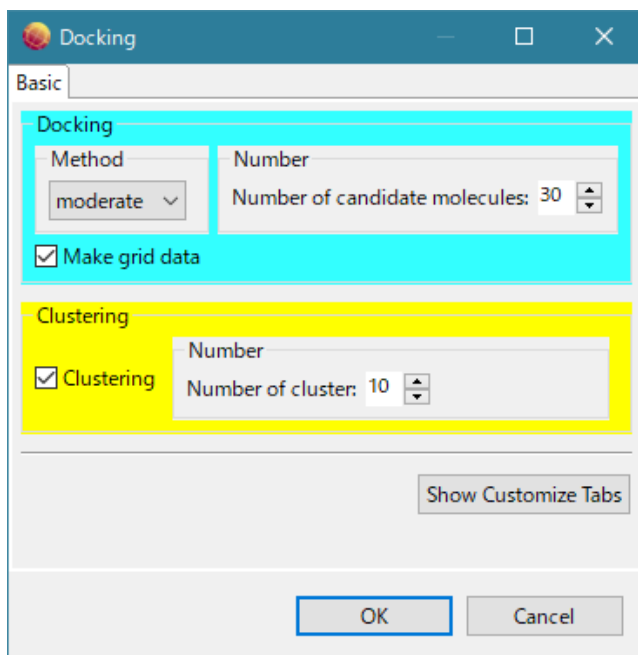
In addition,  point4 is displayed on the tree display screen, confirming that the probe point of the pocket has been added to the system.

A message dialog is displayed prompting you to select a ligand.



In this example, select  lig2 on the tree view screen and click [OK].

For the ligand, it is possible to specify a molecule different from the molecule used as the probe point of the pocket.



The docking calculation condition setting dialog is displayed.

In this example, leave the default conditions and click [OK].

Click [Show Customize Tabs] to set detailed parameters for docking calculation.

The docking calculation condition setting dialog is displayed.

Item		Explanation
Docking	Method	fast : High speed and low accuracy moderate(default) : Medium speed and medium accuracy precise : Low speed and high accuracy
	Number of candidate molecules	Number of outputs of candidate molecular structure.
	Make grid data	Grid calculation. Required for the first calculation, but can be omitted if the same receptor name and pocket are used repeatedly.
Clustering	Clustering	Structural clustering
	Number of cluster	Make the ligand atom the probe point in your pocket
Show Customize Tabs		Displays a tab for setting detailed parameters. ※Please note that when this tab is displayed, some items on the [Basic] tab cannot be changed (Cancel must be canceled and re-executed to change).

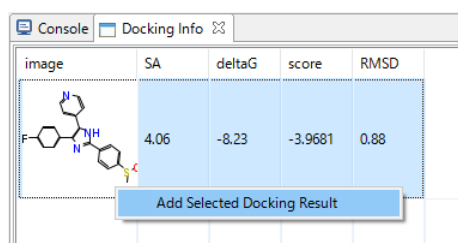
※ In myPresto Portal, the molecular weight of compounds (ligands) that can be docked is limited to 400 Da.

1.5.5. Confirmation of results

When the docking calculation is completed, the Docking Info screen lists the compound (lig3) used in the docking calculation and the 10 molecular structures predicted by the docking calculation in descending order of score.



Click the molecule on the Docking Info screen and click the $\uparrow \downarrow$ key to select the selected molecule. Displayed one by one on the 3D screen

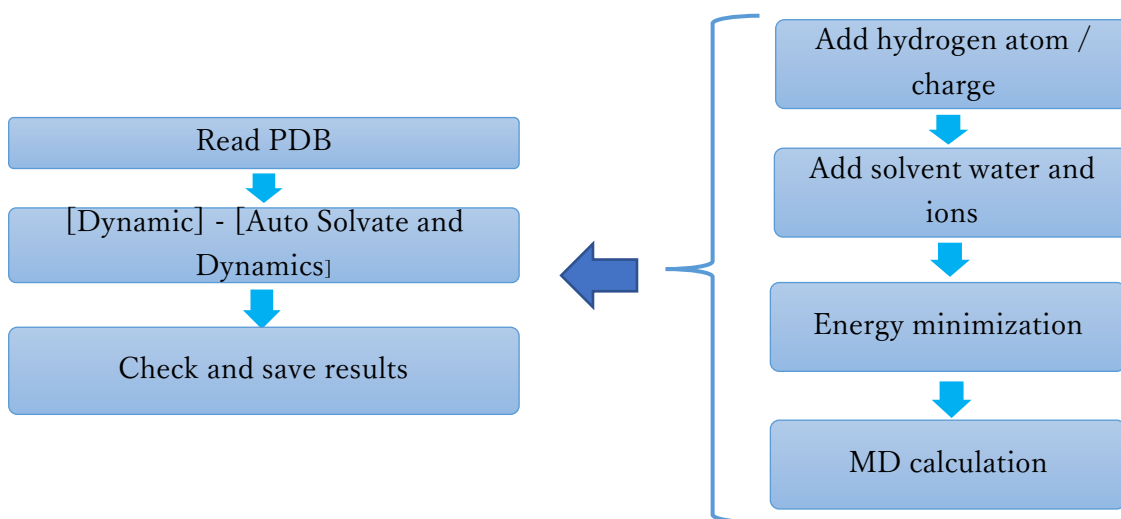


You can add a candidate structure to the Ligand Info screen by selecting the candidate structure on the Docking Info screen (Ctrl + click for multiple selection), right-clicking, and selecting "Add Selected Docking Result".

1.6. MD calculation in water

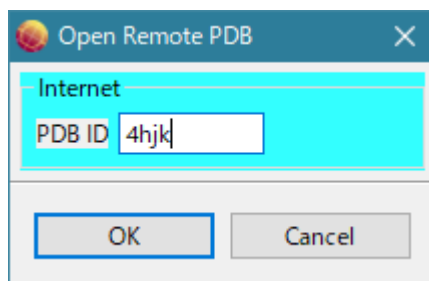
The following is an example of executing the simplest MD calculation by automated calculation.

The procedure is as follows.



1.6.1. Read mmCIF / PDB files over the internet

Refer to "1.2.3 [File] - [Open Remote mmCIF / PDB]" and read **PDB ID 4hjk** from the Internet as test data.



"4hjk" used in the example is human ubiquitin.

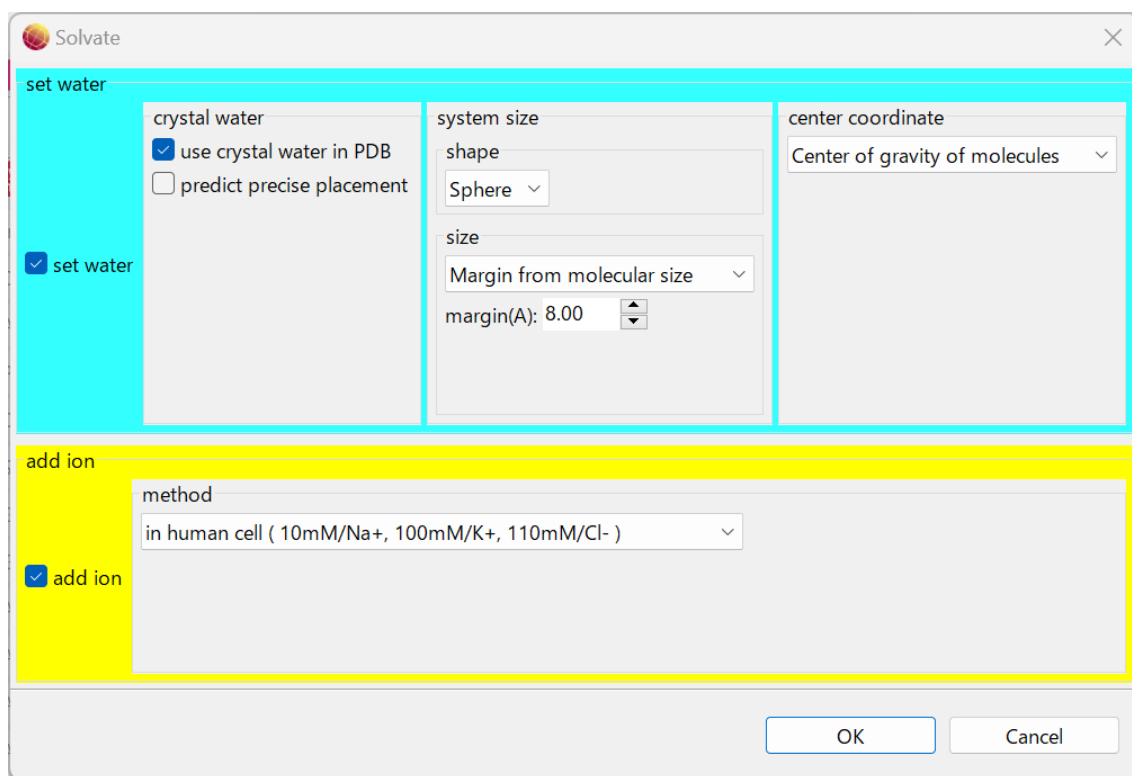
* In myPresto Portal, the total number of atoms in the system that can be calculated by MD is limited to 25,000 atoms.

1.6.2. Fully automatic MD calculation

Select  [Dynamics] -  [Auto Solvate and Dynamics].

The processing is performed in the following order.

- Missing hydrogen atoms are added to all molecules (default is dissociated state in water).
- All compounds or glycans are charged with Gasteiger.
- Molecules other than compounds or glycans add charge based on the force field selected in [Help] - [Preference] - [Molecule] - [tplgeneX].



- A dialog for selecting the water solvent and ion addition method is displayed.

In this example, the default settings are used.

About water solvent

>> The center of gravity of the system is the center of the solvent, and the size is a sphere of 8 Å from the boundary of the solute.

About Ion

>> Ion concentrations in human cells, adding Na⁺, K⁺ and Cl⁻.

The explanation of the setting items is as follows.

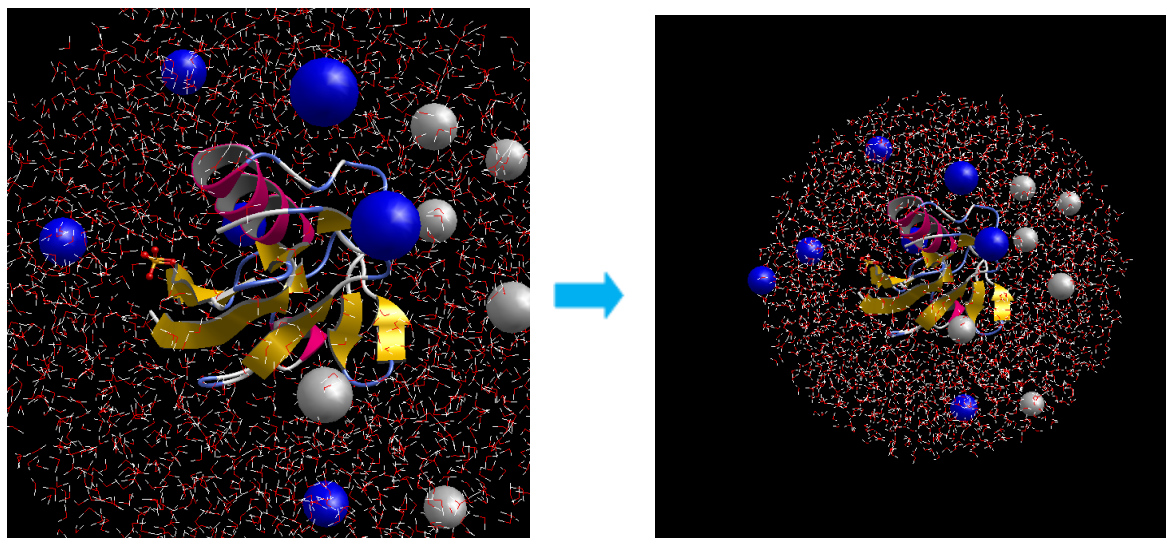
Select whether or not to set water (addition of water solvent) with the check box.


crystal water	use crystal water in PDB	Include PDB water of crystallization in the system
	predict precise placement	Produces accurate water of crystallization
shape size	Sphere	margin (Distance from solute Å)
		Radius Å
	Cube	margin (Distance from solute Å)
		x,y,z (Length directions Å)
center coordinate		Center of gravity of solute
		Setting of the central coordinate (User-specified coordinates
		Specify the central atom with a mouse click)

Select whether to add ion (Na⁺, K⁺ and Cl⁻ ion addition) or not with the check box.

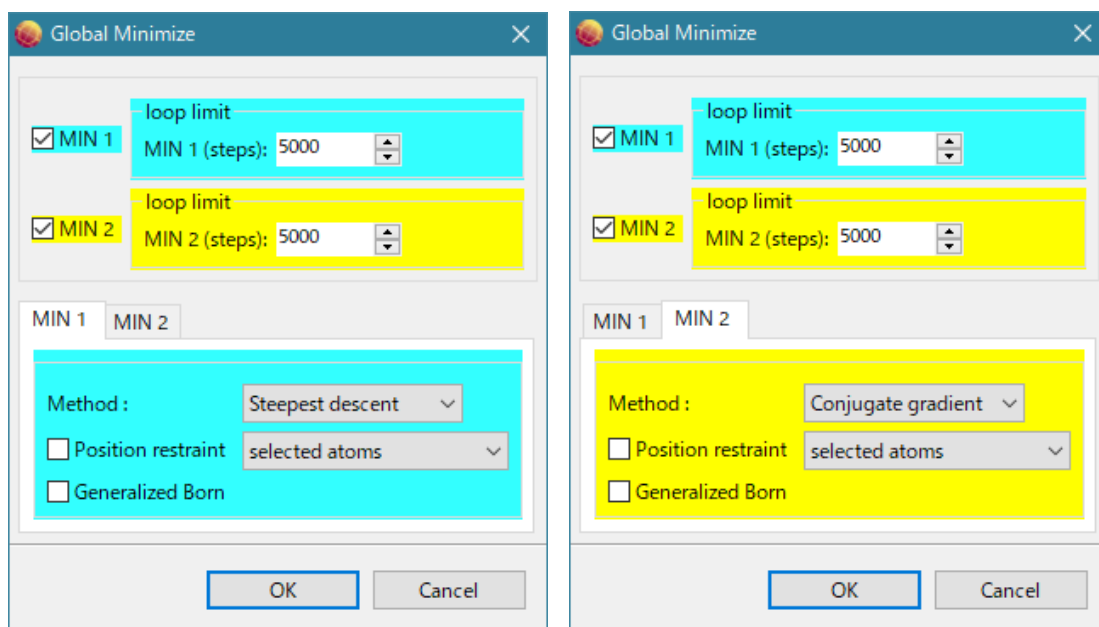
method	direct input of number of ions
	minimum number of ions to neutralization
	saline solution (0.00277/Na ⁺ , 0.00006/K ⁺ , 0.00283/Cl ⁻)
	in human blood plasma (154mM/Na ⁺ , 4mM/K ⁺ , 158mM/Cl ⁻)
	in human cell (10mM/Na ⁺ , 100mM/K ⁺ , 110mM/Cl ⁻)
	in bacteria (10mM/Na ⁺ , 200mM/K ⁺ , 210mM/Cl ⁻)
	in densities of Na ⁺ , K ⁺ and Cl ⁻ in mM
	in % densities of Na ⁺ , K ⁺ and Cl ⁻ (100mM=0.18015%)

Specify the water solvent and ion addition method and click "OK" to add the solvent water and ions.



Click  to display the entire system in the center of the screen.

The energy minimization calculation condition setting dialog is displayed.



In this example, the default is used. The meaning is as follows.

- Energy minimization calculation by cosgene is performed twice in succession.
- The first time is the steepest descent method, 5000 steps, no position constraint, no Generalized Born method
- The second time is the conjugate gradient method, 5000 steps, no position constraint, no Generalized Born method.

The energy minimization calculation can be performed twice in a row (uncheck MIN 1 or MIN 2 if you do not want to run it continuously).

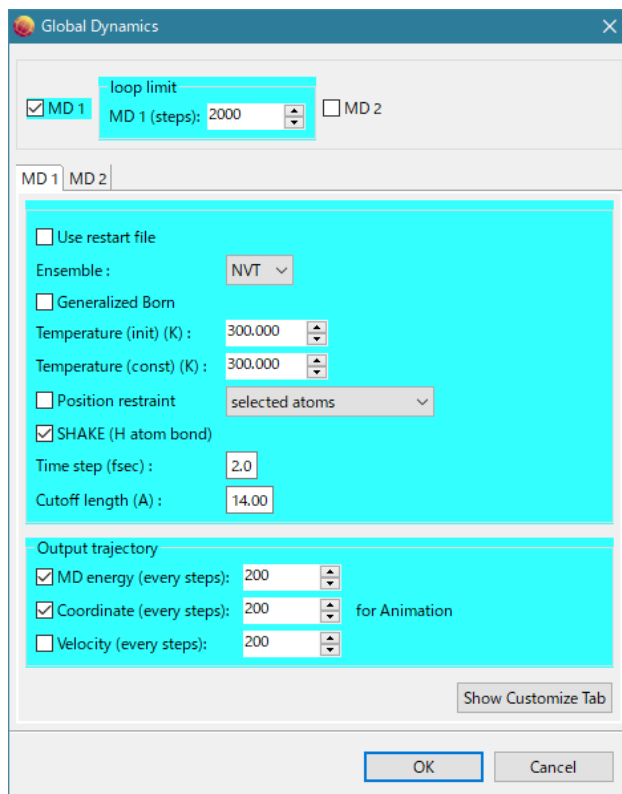
Set MIN 1 for the first run and MIN 2 for the second run.

The explanation of the setting items is as follows.

loop limit (Number of time steps) Default 5000	
Method	Steepest descent
	Conjugate gradient
Position restraint	Selected atoms (Position constrains the atom (group) specified by the user with the mouse)
	Main chain (proteins & DNA/RNA)
	Heavy atoms (proteins & DNA/RNA)
Calculated by the Generalized Born method	

When the energy minimization calculation is completed, the MD calculation condition setting dialog is displayed.

In this example, the default settings are used.



- Execute only once
- 2000 steps
- NVT ensemble
- Not calculated by the Generalized Born method
- Initial temperature 300K
- 300K constant temperature
- No position constraint
- SHAKE calculate
- Time step is 2.0 fsec
- Cutoff radius is 14.0 Å
- With energy file output (Every 200 steps)
- Trajectory file output available (Every 200 steps)
- Long-distance Coulomb force calculation by FMM method

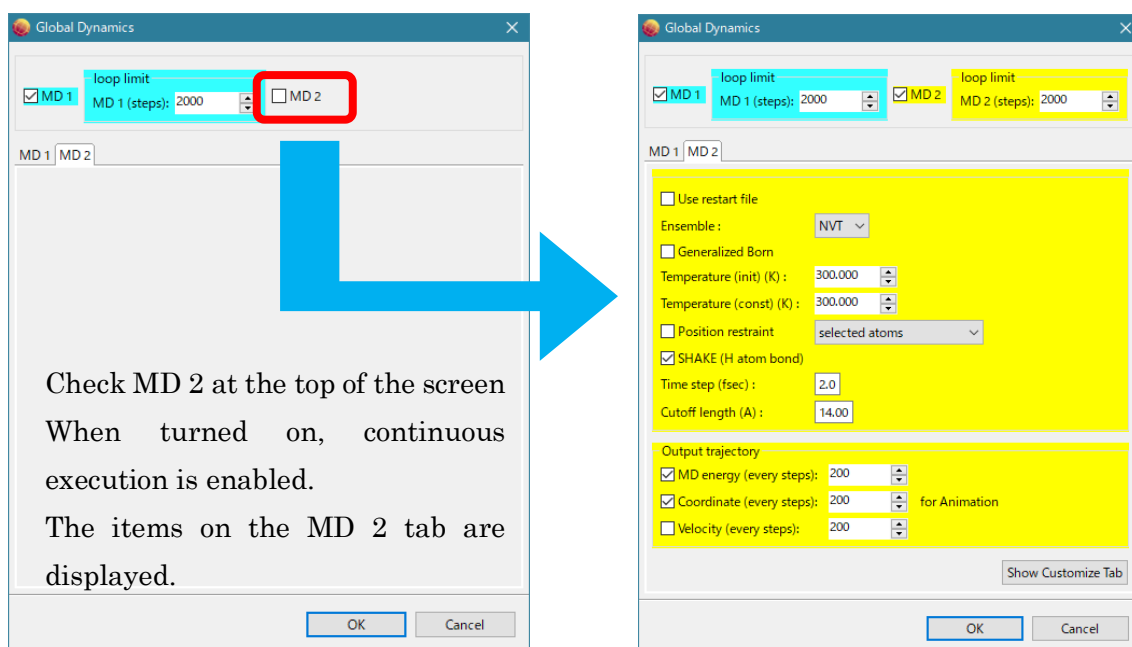
(Because the shape of the solvent water is a sphere)

- In myPresto Portal, the force field used by cosgene is set to AMBER GAFF2 for compounds or glycans and AMBER ff99SB for others (proteins, etc.). (You can change the force field with [Help] – [Preference] – [Molecule] – Force Field.)

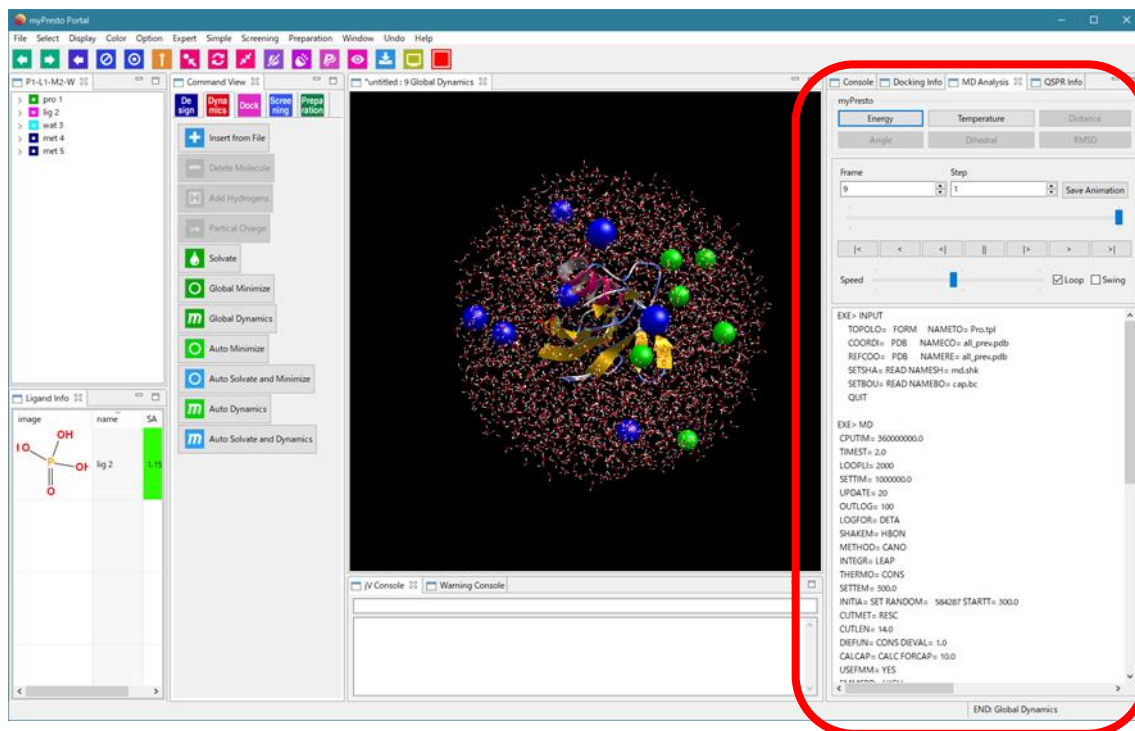
The explanation of the setting items is as follows.

Loop limit (number of time steps) Default 2000	
Use restart file Default : OFF	
Ensemble	NVT (Canonical ensemble)
	NPT (NPT ensemble)
	NVE (Microcanonical ensemble)
Calculated by the Generalized Born method	
Temperature (init)	Initial temperature K
Temperature (const)	Constant temperature K (NVE ensemble is not set)
Position restraint	Selected atoms (Position constrains the atom (group) specified by the user with the mouse)
	Main chain (proteins & DNA/RNA)
	Heavy atoms (proteins & DNA/RNA)
SHAKE Fixing hydrogen atom bonds	
Time step (fsec)	
Cutoff length (Å)	
Output trajectory	MD energy (interval between output steps for each energy value)
	Coordinate (interval between output steps of coordinates)
	Velocity (Interval between x, y, z speed output steps)

MD calculation can be executed twice in a row. Set the settings for the first execution in MD 1 and the settings for the second execution in MD 2.



When the MD calculation is completed, the buttons on the command button screen can be executed.



Refer to "1.3 Saving the project" and save the project with a name of your choice.

✖ In myPresto Portal, the total number of atoms in the system that can be calculated by MD is limited to 25,000 atoms.

1.6.3. Confirmation of MD calculation result

MD Analysis screen (red frame above) myPresto

Click the **Energy** button to display a time-varying graph of each energy.

Click the **Temperature** button to display the temperature change graph over time.

You can display a two-dimensional graph in which the video and the time axis are linked. Also, by clicking the 2D graph, you can see the video (structure) of the time of the click point.

Click the **Distance** button and then select two atoms with the mouse to display a time-varying graph of the selected two-atom distance. You can display a two-dimensional graph in which the video and the time axis are linked. Also, by clicking the 2D graph, you can see the video (structure) of the time of the click point.

Click the **Angle** button and then select 3 atoms with the mouse to display a time-varying graph of the angles formed by the selected 3 atoms. You can display a two-dimensional graph in which the video and the time axis are linked. Also, by clicking the 2D graph, you can see the video (structure) of the time of the click point.

Click the **Dihedral** button, then select 4 atoms with the mouse, and in the order you selected, 2 planes between the planes of the 1st and 2nd atoms and the planes of the 3rd and 4th atoms. Display the time change graph of the corner. You can display a two-dimensional graph in which the video and the time axis are linked. Also, by clicking the 2D graph, you can see the video (structure) of the time of the click point.

After clicking the **RMSD** button, select one molecule on the tree display screen with the mouse to display the RMSD time change graph with respect to the initial coordinates of the selected molecule. You can display a two-dimensional graph in which the video and the time axis are linked. Also, by clicking the 2D graph, you can see the video (structure) of the time of the click point.

By operating the Animation controller on the MD Analysis screen, the time change (trajectory) of atom movement is displayed in animation on the 3D screen.

By clicking the [Save Animation] button, you can output the file to an animated GIF as it is displayed. At that time, you can also set the frame time interval.

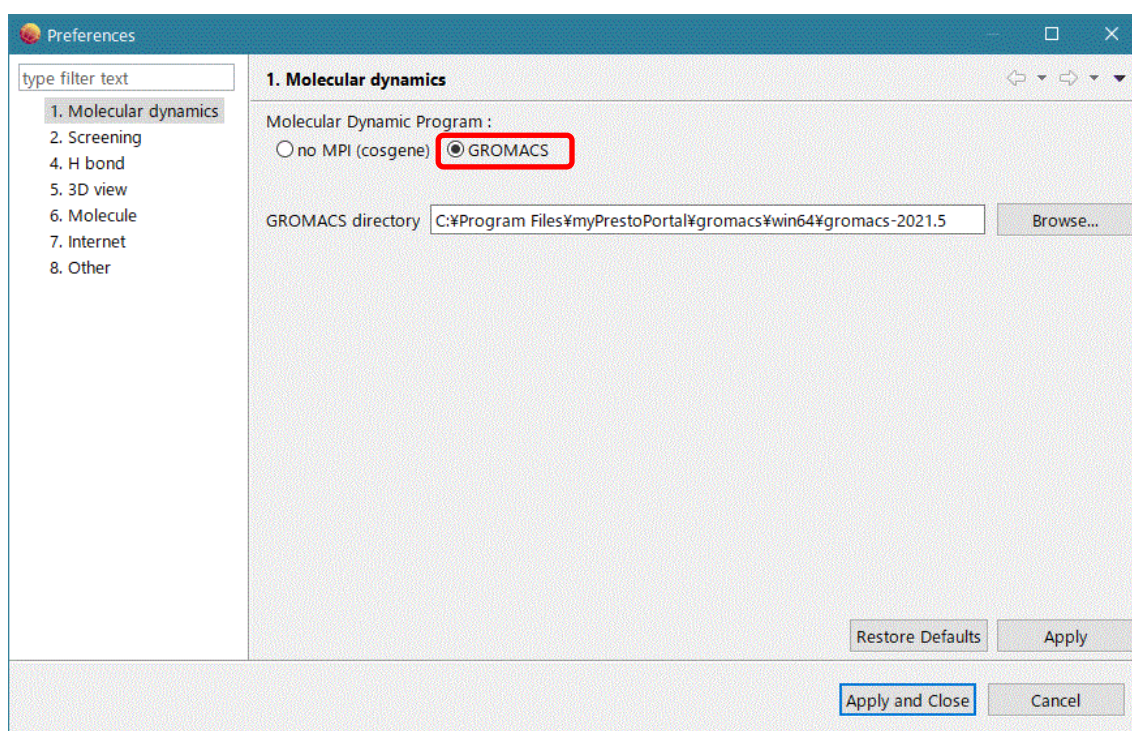
Click the [Save PDB] button to save each snapshot of the trajectory of the entire system to a PDB file.

The MD Analysis screen displays the contents of the input file for MD programs (such as cosgene).

1.7. GROMACS : MD calculation Trajectory Analysis

1.7.1. [Preference] - [Molecular dynamics] settings

On the [Help]-[Preference]-[Molecular dynamics] screen, select [GROMACS] under [Molecular Dynamic Program :] to run the GROMACS energy minimization calculations and MD calculations by GROMACS.



Here, except for Windows 10 and Windows 11, Linux and MAC, the user must install GROMACS and set the [GROMACS directory] of the installed GROAMCS. Windows 10 and Windows 11 do not require this setting since the GROMACS executable program has been implemented beforehand.

The [GROMACS directory] should be set to the directory where **share** and **bin** exist.

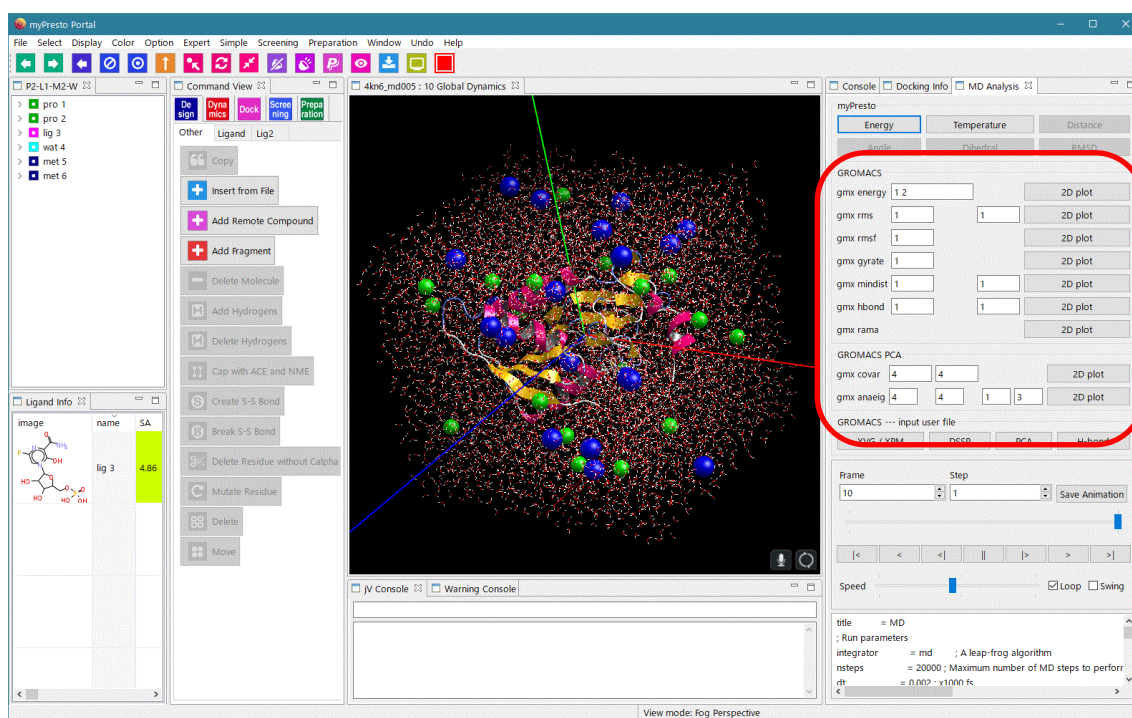
※In the current version, GROMACS is executed in **bin/gmx** without specifying the number of parallels.

If **bin/gmx** does not exist in the installation directory, GROMACS cannot be executed.

The parallel number of OpenMP and thread MPI depends on the automatic parallel number specification function of GROMACS. MPI is not used.

1.7.2. Trajectory Analysis

Perform the following trajectory analysis to display graphs with time axis linked to the video.



General

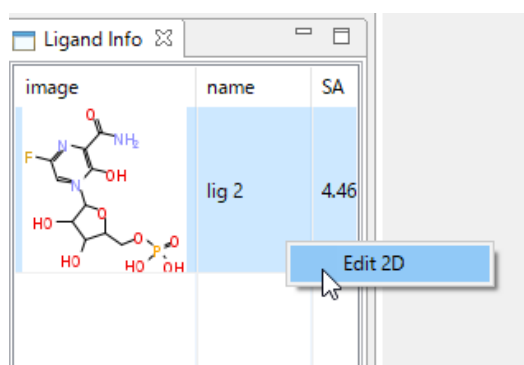
- (1) gmx energy
 - (2) gmx rms
 - (3) gmx rmsf
 - (4) gmx gyrate
 - (5) gmx mindist
 - (6) gmx hbond
 - (7) gmx rama
- PCA relationship
- (8) gmx covar
 - (9) gmx anaeig

- * Please refer to the ["MolDesk Basic Manual"](#) for details on usage.
- * For details on trajectory analysis with GROAMCS, refer to the GROMACS manual.

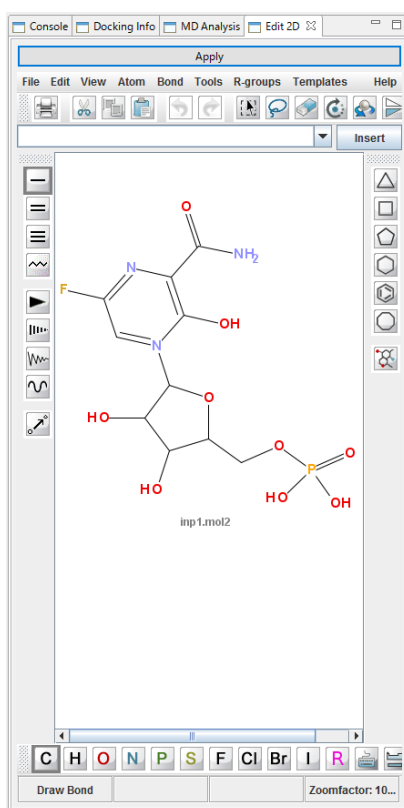
1.8. Compound 2D editor

Right-clicking on a compound or glycan on the Ligand Info screen will bring up the Edit 2D menu. Click this to enter the selected compound or glycan and launch the 2D editor JChemPaint. The version of JChemPaint is 3.3-1210 (latest version as of January 2018).

1.8.1. Start JChemPaint



Enter the selected compound or glycan to launch the 2D editor JChemPaint.



※ When the screen is small, you can drag the tab out of the myPresto Portal screen with the mouse to pull the screen out and make the screen larger.

After editing, click the Apply button at the top of the menu to three-dimensionalize the edited molecules and bring them into myPresto Portal.

For information on how to use JChemPaint, see the Help menu in JChemPaint.

1.9. Remove feature restrictions

If you want to use software that removes the functional limitations of myPresto Portal, please consider MolDesk, IMSBIO Co., Ltd.

※ IMSBIO Co., Ltd. <https://www.imsbio.co.jp/>

※ MolDesk <https://www.moldesk.com/>