M winmostar tutorial

Modeling Molecule Organic Molecule

V11.5.6

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About This Document

- This manual is a tutorial demonstrating use cases for Winmostar V11.
- For those using Winmostar V11 for the first time, please consult <u>Beginner's Guide</u>.
- For those who wish to explore the details of each feature, please refer to <u>Winmostar User Manual.</u>
- If you are unable to proceed with the operations as outlined in this manual, please first consult <u>Frequently asked questions</u>.
- If your issue is not resolved through the Frequently Asked Questions, for the purpose of information accumulation and management, please contact us from <u>Contact</u>. Attach files generated at the time of the issue and provide steps to reproduce the problem.
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Overview

- Winmostar provides four methods for creating organic molecules:
 - A. Inputting structural formulas
 - B. Import SMILES
 - C. Importing files created by other software or obtained from various databases
 - Supports formats like pdb, mol, mol2, cif, xyz, sdf
 - D. Directly modeling 3D molecular structures
- In this tutorial, we will introduce each method using the following molecules as examples.



A. Inputting structural formulas (Benzene)

- A. Click File | New File, New Project, or Edit | Reset Structure.
- B. Click **Draw Molecule**, then click on the phenyl group button.



C. Click near the center of the window to generate a benzene ring.

Build Molecule in 2D Mode

Image: Second seco



D. Click **OK** at the bottom right of the window to display the 3D structure of benzene.



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B. Import SMILES (Benzene)

A. Copy the SMILES string for Benzene (c1ccccc1) from <u>Wikipedia</u>. (Be mindful of uppercase and lowercase letters.)



B. Import SMILES (Benzene)

- B. Click File | New File, New Project, or Edit | Reset Structure.
- C. Olick **Import SMILES** and paste the SMILES string into **Enter SMILES** field.

)n Tools Window Help	Milles – 🗆 X
	Enter SMILES: c1ccccc1
% % Import SMILES	O Use OpenBabel
	Use Balloon
	Import Close

D. Click **Import**, then click **OK**, and the 3D structure of Benzene will appear.



C. Import File (Caffeine)

- A. Click File | New File, New Project, or Edit | Reset Structure.
- B. Click File | Import File, select caffeine.dat from the Samples folder one level above, then click Open.

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Note: You can perform the same operation by dragging and dropping a file from Explorer into Winmostar.

C. Click **Discard and Load** to display the 3D structure of caffeine.



D. Directly modeling (Isooctane)



Structural Formula

3D Model

D. Directly modeling (Isooctane)

- A. Click File | New File, New Project, or Edit | Reset Structure.
- B. Select '-CH3' under **Fragment**, and click **Replace marked atom with fragment** five times to create n-pentane.



C. After adjusting the camera angle by dragging, click on each of the three hydrogen atoms indicated by the arrows in the figure, then **click Replace marked atom with fragment**. Repeat this process to create isooctane.



Note: You can perform an equivalent operation to 'Replace with Fragment' more easily by directly Shift+Ctrl+right-clicking on an atom.

D. Directly modeling (Isooctane)

If only 'Click' is mentioned, it refers to left-clicking.

D. Clicking <u>A</u> Quick Optimization automatically adjusts bond lengths and angles to reasonable values.



E. To explicitly rotate a dihedral angle, click both atoms at the ends of the bond you want to rotate, then click **Modify Selected Group | Rotate Around Axis (2 Marked atoms)**. After that, drag over the molecular structure to rotate the dihedral angle.





Structural Formula

3D Model

If only 'Click' is mentioned, it refers to left-clicking.

- A. Click File | New File, New Project, or Edit | Reset Structure.
- B. Select '-C6H5' under **Fragment**, and click **Replace marked atom with fragment** two times to create Biphenyl.



C. Right-click on the hydrogen atom shown in the diagram below and click **Delete Atom**.



If only 'Click' is mentioned, it refers to left-clicking.

D. Right-click on the hydrogen atom shown in the diagram below and click **Change Element to | C 6.**



E. Sequentially click Solution on the two carbon atoms indicated by arrows in the diagram below, then click **Add/Change Bond**.



F. Click on the carbon atom shown in the diagram below and then double-click **H** Add **Hydrogen to Maked Atom**.



G. Clicking <u>A</u> Quick Optimization automatically adjusts bond lengths and angles to reasonable values.





- A. Click File | New File, New Project, or Edit | Reset Structure.
- B. Select '-C5H4' under **Fragment**, and double-click **Replace marked atom with fragment**.



C. Sequentially click on the two hydrogen atoms indicated by arrows in the diagram below, then click **Edit | Build Ring** and finally click **_____ Quick Optimization**.



If only 'Click' is mentioned, it refers to left-clicking.

D. Select '-CH3' from **Fragment**, for the three hydrogen atoms indicated by the arrows in the figure, click each atom followed by clicking **Replace marked atom with fragment**, and repeat this process.



E. Sequentially Ctrl+click on the two hydrogen atoms indicated by arrows in the diagram below, then right-click on one of the atoms and click **Change Element to | O 8**.



If only 'Click' is mentioned, it refers to left-clicking.

F. Click **Select | Invert Selection**, then sequentially Ctrl+click on the four hydrogen atoms indicated by arrows in the diagram below. Right-click on one of the atoms and click **Change Element to | N 7**.



G. Right-click on the hydrogen atom shown in the diagram below and click **Delete Atom**.



Supplement: Changing Bonds

- To change the bond order (such as single or double bonds), sequentially click on the two atoms at either end of the bond and then click S Add/Change Bond.
- However, keep in mind that the bond order does not affect the results of quantum chemical calculations and first-principles simulations. Therefore, it is not problematic for these calculations if the bond order is not accurately represented.



G. Directly modeling (Uric acid)





Structural Formula

3D Model

G. Directly modeling (Uric acid)

- A. Start with the structure from F. Directly modeling (Caffeine) .
- B. Right-click on the hydrogen atom shown in the diagram below and click Add Hydrogen to Marked Atom.





C. Right-click on the hydrogen atom shown in the diagram below and click **Change Element to | O 8**.



G. Directly modeling (Uric acid)

D. Sequentially click on the atoms indicated by arrows in the diagram below in the order of the numbers, then click **Modify Selected Group | Delete**, and finally click **Delete**.



E. Repeat the procedure in step D to remove the remaining two methyl groups.



Supplement: Registration of Fragments

The molecules modeled can be registered as user-defined fragments (substituents). As an example, the registration procedure for a tert-butyl group is shown below.

A. Model isobutane and click on the hydrogen atom indicated by the arrow.

B. Click Edit | Select Fragment| Save Fragment



The position of the hydrogen atom selected here will be set as the starting point of the substituent.

C. Enter 'T-BUTYL' in **Enter Name of the Fragment** and click **OK**.







Troubleshooting and Additional Resources

• For detailed information on each feature, please refer to Winmostar User Manual.



- If you are unable to proceed as instructed in this guide, please first refer <u>Frequently asked questions</u>.
- If FAQs do not resolve your issue, for the purposes of information accumulation and management, please contact us through <u>Contact</u>, detailing the steps to reproduce the issue and attaching any generated files at that time.