

 winmostar tutorial

# Modeling Molecule Metal Complex

V11.5.6

04 January 2024

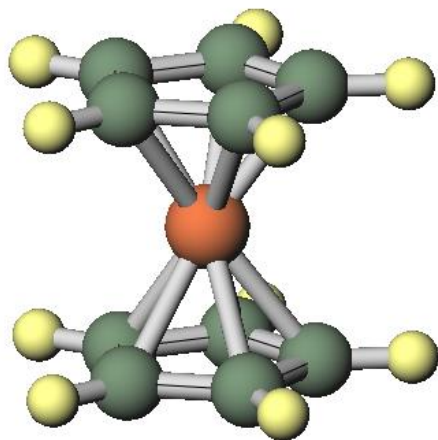
X-Ability Co., Ltd.

# About This Document

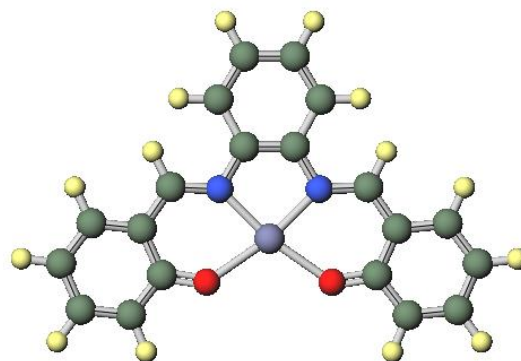
- This manual is a tutorial demonstrating use cases for Winmostar V11.
- For those using Winmostar V11 for the first time, please consult [Beginner's Guide](#).
- For those who wish to explore the details of each feature, please refer to [Winmostar User Manual](#).
- If you are unable to proceed with the operations as outlined in this manual, please first consult [Frequently asked questions](#).
- If your issue is not resolved through the Frequently Asked Questions, for the purpose of information accumulation and management, please contact us from [Contact](#). Attach files generated at the time of the issue and provide steps to reproduce the problem.
- The copyright for this document is held by X-Ability Co., Ltd. Any copying or duplication of the content in any form without the express permission of X-Ability Co., Ltd. is strictly prohibited.

# Overview

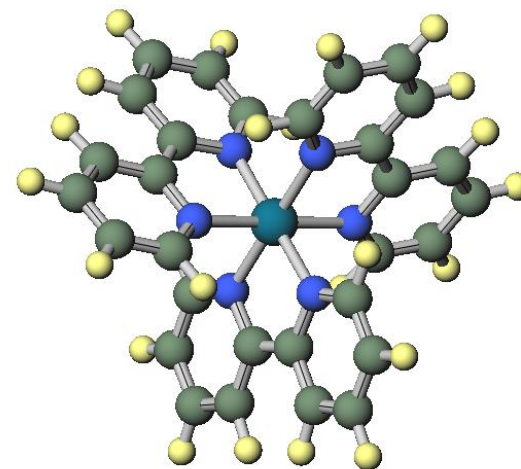
- In this tutorial, we will introduce the methods for creating the following metal complexes.
- For detailed methods on creating molecular structures, please refer to [Molecular Modeling Organic Molecules Edition tutorial](#).



Ferrocene ( $\text{FeC}_{10}\text{H}_{10}$ )



Zn(saloph) ( $\text{ZnC}_{20}\text{N}_2\text{H}_{10}\text{O}_2$ )

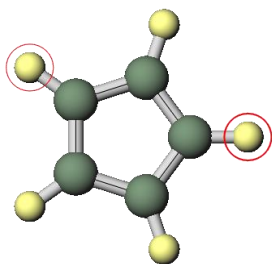


$[\text{Ru}(\text{bpy})_3]^{2+}$  ( $\text{RuC}_{30}\text{N}_6\text{H}_{24}$ )

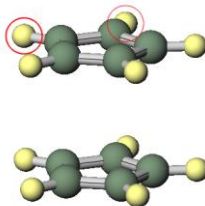
# B. Modeling of Ferrocene

Click **File | New File, New Project**, or **Edit | Reset Structure**.

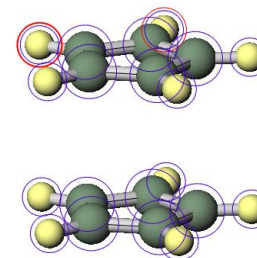
A. Change **Fragment** to **-C5H4** and click **Replace** to create a Cp ring.



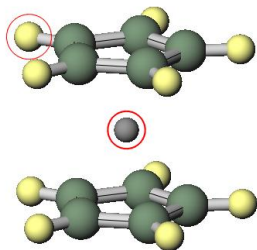
B. Follow the procedure in [Molecular Modeling Supramolecular Edition](#) to arrange the Cp rings in parallel at an interval of 3.5 Å.



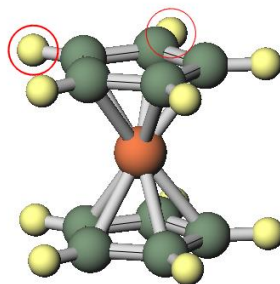
C. Click **Select | Select All**.



D. Click **Edit | Add atom | Add Dummy Atom To Center of Geometry of Selected Group**.



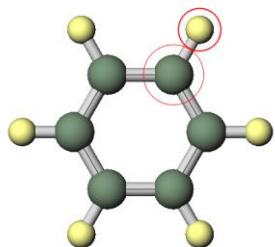
E. Change the element of the dummy atom to **Fe**, and click **Edit | Automatically Adjust Atoms/Bonds | Regenerate All Bonds**.



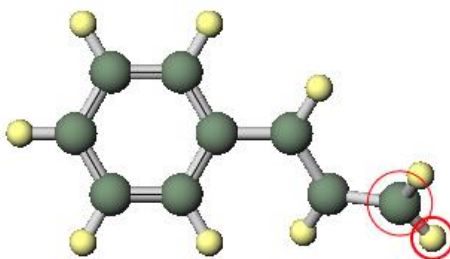
# C. Modeling of Zn(saloph)

Click **File | New File, New Project**, or **Edit | Reset Structure**.

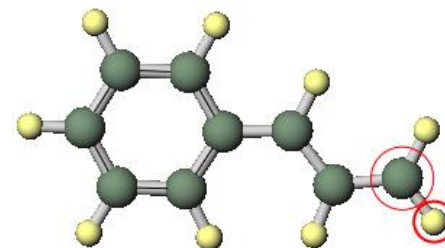
A. Change **Fragment** to **-C6H5** and click **Replace** to create a Cp ring.



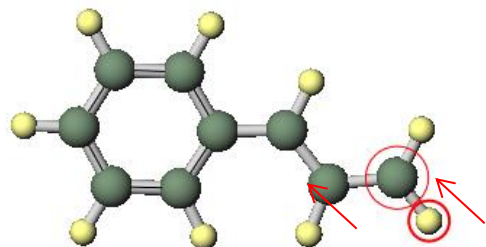
B. Click on a hydrogen atom, change **Fragment** to **-CH2**, and click **Replace** three times.



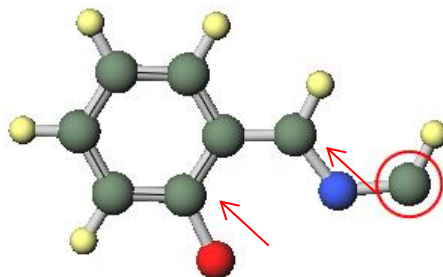
C. Click  **Quick Optimization**.



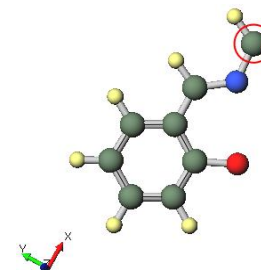
D. Right-click on each of the two hydrogen atoms shown in the diagram and select **Delete Atom** to remove them.



E. Change the elements of the two atoms shown in the diagram to **O** and **N**, respectively.

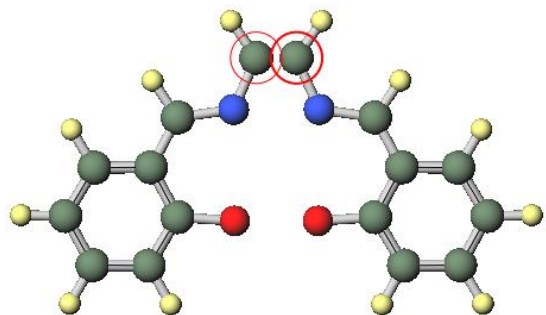



F. Change the view as shown in the diagram, then click **Edit | Adjust Axes | Set to Camera Coordinate**.

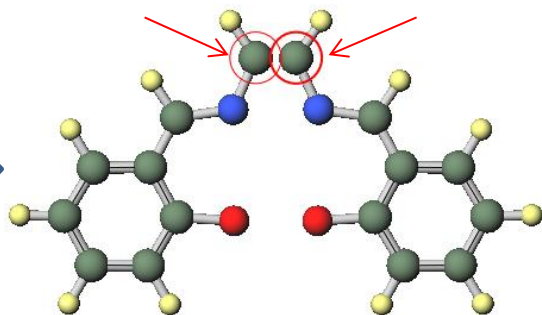


# C. Modeling of Zn(saloph)

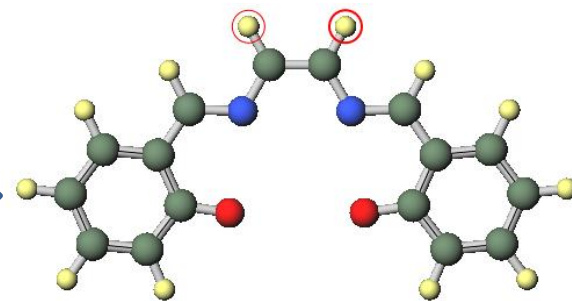
G. Click **Edit | Invert Coordinates/Chirality | Add Enantiomer.**



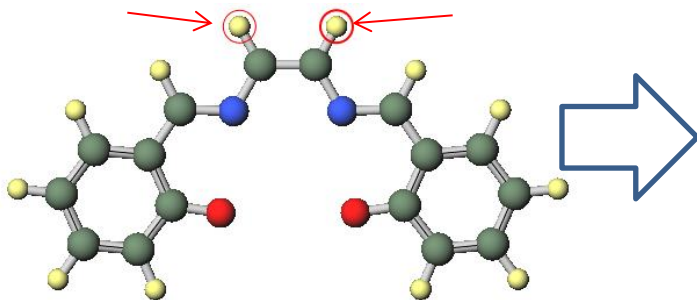
H. Sequentially click on the two atoms shown in the diagram and then click  **Add/Change Bond.**



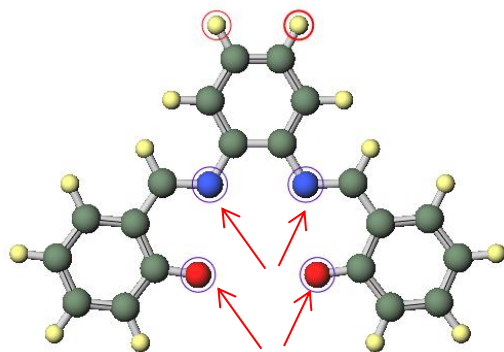
I. Click  **Quick Optimization.**



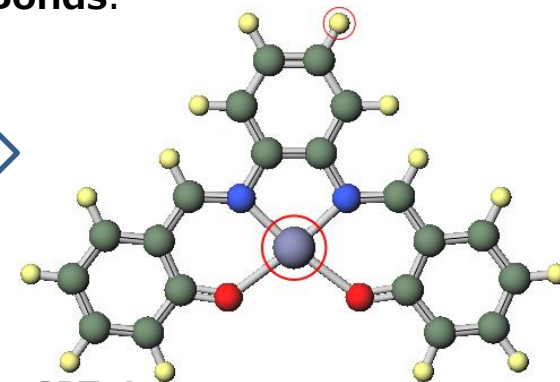
J. Sequentially click on the two hydrogen atoms shown in the diagram and then click **Edit | Build Ring.**



K. Ctrl+click on the four atoms shown in the diagram and then click **Edit | Add atom | Add Dummy Atom To Center of Geometry of Selected Group.**



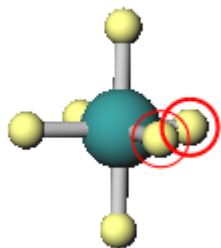
L. Change the element of the dummy atom to **Zn**, and then click **Edit | Automatically Adjust Atoms/Bonds | Regenerate All Bonds.**



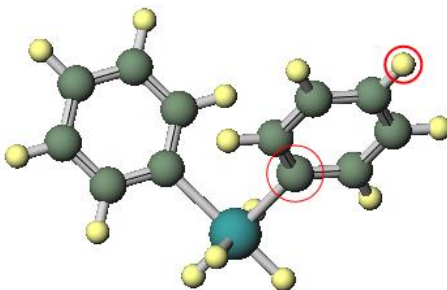
# D. Modeling of [Ru(bpy)3]2+

Click **File | New File, New Project**, or **Edit | Reset Structure**.

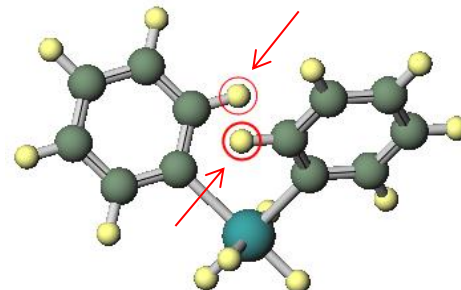
A. Change **Fragment** to **-PDH5** and click **Replace** to create a Cp ring. And Change the element of the central Pd atom to **Ru**.




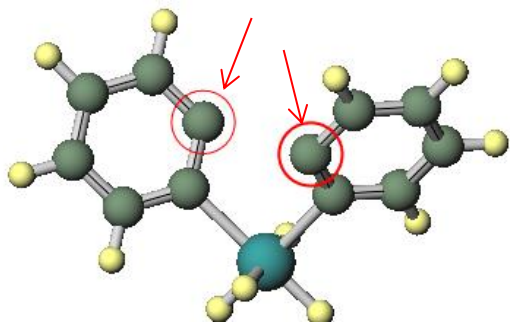
B. Change **Fragment** to **-C6H5**, and for each of the two adjacent hydrogen atoms, click on them and then click **Replace**.




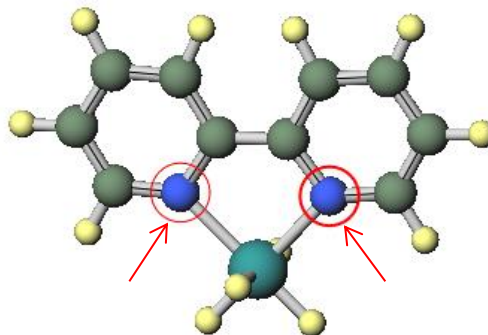
C. Right-click on each of the two adjacent hydrogen atoms of the two phenyl groups and select **Delete Atom** to remove them.



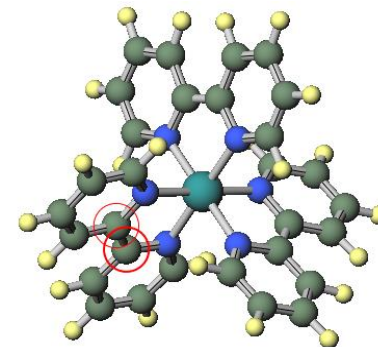
D. Sequentially click on the two carbon atoms bonded to the atoms that were deleted, and then click  **Add/Change Bond**.



E. Change the element of the carbon atoms bonded to **Ru** to **N**, and then click  **Quick Optimization**.

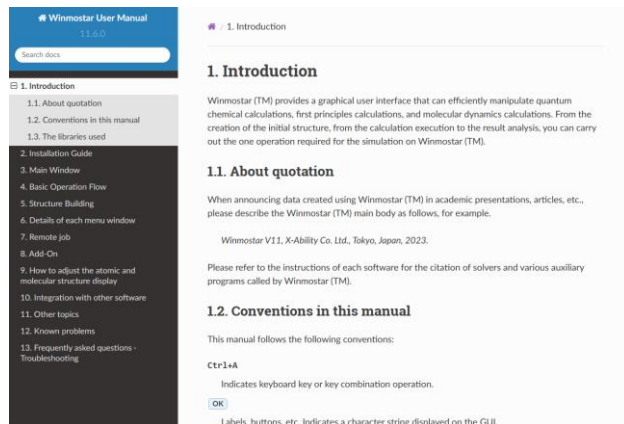


F. Repeat the steps 2 to 5 for the remaining positions twice. If a mirror image is needed, use **Edit | Invert Coordinates/Chirality**.



# Troubleshooting and Additional Resources

- For detailed information on each feature, please refer to [Winmostar User Manual](#).



## [Winmostar User Manual](#)

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