

Ligand Preparation

Proper preparation of 3D, all-atom ligand structures is critical to modeling tasks. The preparation involves the following tasks:

1. Add hydrogen atoms.
2. Filter out unsuitable molecules based on their properties.
3. Remove unwanted molecules, such as water, small ions.
4. Neutralize charged groups, then generate ionization and tautomeric states with Epik
5. Generate stereoisomers, particularly if stereochemical information is missing.
6. Generate low-energy ring conformations.
7. Remove any badly prepared structures.
8. Optimize the geometries.

This sheet summarizes ligand preparation with LigPrep.

The screenshot shows the LigPrep dialog box with the following settings and annotations:

- Use structures from:** File
- File name:** s/zone1/dyall/ligprep/examples.sdf
- Filter criteria file:** (empty)
- Force field:** OPLS_2005
- Ionization:**
 - Do not change
 - Neutralize
 - Generate possible states at target pH: 7.0 +/- 2.0
- Using:**
 - Ionizer
 - Epik
- Add metal binding states
- Include original state
- Desalt
- Generate tautomers
- Stereoisomers:**
 - Computation:**
 - Retain specified chiralities (vary other chiral centers)
 - Determine chiralities from 3D structure
 - Generate all combinations
 - Generate at most:** 32 per ligand
- Generate low energy ring conformations:** 1 per ligand
- Output format:** Maestro SDF

Annotations with red arrows:

- Filter molecules by functional group count or property
- Use this option to keep the charge state of the original molecule
- Generate ionization states with significant population at the given pH.
- Use this option if you have chirality information stored with the molecule
- Use this option if your structure is 3D and you want to keep its stereochemistry
- Add anionic states for binding to metals (not normally generated)
- Keep the original ionization state even if it's not the most probable.
- Limit the number of stereoisomers generated. The choice of chiralities is based on natural products.
- Generate more ring conformations if the ring is flexible and likely to change conformation on docking.

1. Choose the source of the structures from the Use structures from option menu, and supply the file name if using a file.
2. Filter the structures by property by functional group counts—click Create to set up the filter.
3. Choose the force field. You usually only need to do this if the default doesn't cover some atom types in your ligands.
4. Choose an ionization option. Use of Epik is recommended.
5. Leave Desalt selected, to remove molecules other than the ligand.
6. Deselect Generate tautomers if you don't want to generate tautomers, for example to prepare just the original structures.
7. Choose an option for generating stereoisomers.
8. Increase the number of ring conformations if you have flexible rings that are likely to change conformation.
9. Select an output file format, and start the job.