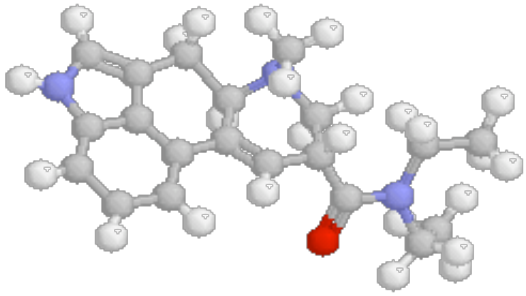
Using the Jmol viewer



You can manipulate these molecules by following the instructions below:

To adjust size, location, and orientation:

- **Size:** Hold down the shift key and drag over the molecule.
- **Location:** Hold down the shift key, double-click, and drag the molecule. (Reset by shift-double-clicking away from the molecule.)
- **Orientation:** Drag the mouse around inside the molecule window.

To bring up a popup menu:

- Click on the **Jmol** in the lower right corner or "Right click" for anywhere in the molecule window .

  The menu options will allow you to display the model several different ways. You should experiment with as many of these menu commands as you like, but **make sure to try every option under the "Render->Scheme"** menu. If you choose "Stereo Display->cross-eyed" you will see two molecules. If you make them overlap by either crossing your eyes or looking "through" the monitor you can see a 3D version of the molecule.

To measure distances:

- Double-click on one of the atoms, and then hover over another atom.
- To make the measurement permanent, double-click on the second atom.
- To cancel the measurement, move the mouse outside of the molecule window.

To measure Angles:

- Double-click on the first atom (not the middle of three atoms making the angle).
- Click on the second atom.
- Hover over the third atom. To make the angle permanent, double-click on the third atom.
- To cancel the measurement, move the mouse outside of the molecule window.