

Introduction to Molecular Modeling using ArgusLab

[ArgusLab](http://www.arguslab.com) is a free molecular modeling package that runs under Windows (and only under Windows). It is installed on all public computers in Shoker Science Center (an icon should be on your desktop), and you may also download it for personal use from www.arguslab.com/downloads.htm. (Of course, you can't install it on a public computer at Bluffton University; you don't have permission for that!)

By the end of this tutorial, you will know how to build molecules in ArgusLab an atom at a time, or using template structures; how to change atom and bond types; and how to use previously-saved structures as starting points for building new structures.

Note:

ArgusLab may freeze, or may even freeze your computer, unless you *turn off video hardware acceleration* on your computer. To do this,

1. Right-click on your Windows desktop and select "Properties".
2. Select the "Settings" tab and click the "Advanced" button at the bottom right. A new window will open.
3. Select the "Troubleshoot" tab in the new window. Move the slider labeled "Hardware acceleration" to "None".
4. Click "OK," and click "OK" to make the "Properties" window go away.

In practice, you will probably find that you can have video hardware acceleration turned on at a low level, but be aware (if things freeze up for you) that this is what is happening.

Chirality, chiral molecules and chiral centers

Any object that is not identical to its own mirror image is *chiral*. Two easy macroscopic examples are your hands: your right hand is the mirror image of your left (unless you're missing fingers), but your right hand is not identical to your left (you can't easily get it into a left glove, for example). Therefore your hands are chiral objects.

Molecules can be chiral too; we will look at a few examples in this exercise. Within molecules, individual atoms can be *chiral centers* if they have **four different substituents**; this can include lone pairs, as we will see. Molecules with chiral centers have *stereoisomers* that differ only in the arrangement of groups around each chiral center.

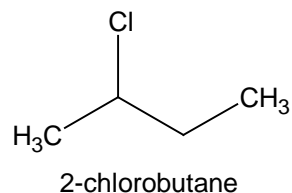
We will build the following chiral molecules and examine their stereoisomers:

- 2-chlorobutane
- Alpha-methylbenzylamine (that is, 1-phenylethanamine)
- Tartaric acid, which has **two** chiral centers.

A note: you should create a separate directory on your H-drive labeled "ArgusLab" or something similar. Save all ArgusLab files to this directory. You want to do this because ArgusLab computations create extra files that you may later want to delete, and having them all in a single directory makes this easier.

2-chlorobutane. Open ArgusLab and click the “Create New Molecule” button at the upper left.

ArgusLab defaults to “no bonds drawn,” but that’s not the way we want it. So click the button just to the left of the dumbbell-shaped buttons in the second row. (On mouseover it should say, “Automatic bonds are OFF. Click to turn ON.”)



Now *right-click* on the molecule window; an atom will appear (the default is carbon). Move the mouse a little and *right-click* again; another atom will appear, bonded to the first atom. Add two more atoms to the chain in this way.

(If you forgot to turn on automatic bonds, you can get bonds by *left-clicking* on the first atom to highlight it, then *left-clicking* on the atom you want the bond to go to. Continue to create bonds in this way until all bonds have been formed.)

When you have drawn four atoms, bonded in a straight (or zigzag) line, click the yellow arrow button in the second row. This turns off the builder mode.

Now look for the “H” buttons in the top row. The leftmost “H” will say “Add hydrogens” when you mouse over it. Click this button; hydrogens will appear on your molecule. Now click the pliers button (“Clean geometry”).

Now we will convert our model of butane into 2-chlorobutane.

Right-click on one of the hydrogen atoms on the second carbon and select “Change atom” and then “Cl [s], Cl chlorine.” Now clean the geometry again by clicking the pliers button.

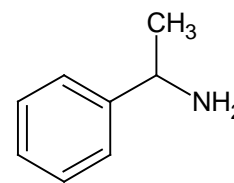
Before the cleanup is performed, ArgusLab will ask you to save your file. Name it “2-chlorobutane.” You have just built your first chiral molecule! But... is it R or S?

To find out, select the “Label” menu and click “Atom label settings.” Select the “Chiral centers” radio button at the bottom, then click “OK.” Now, from the Label menu, select “All atoms.” Your chiral center will now be labeled either (R) or (S). Convince yourself that the label is correct by using the “steering wheel” method.

Now open a new molecule window. Click “Create new molecule” and under the “Window” menu, select “Tile.” In the new window, build the mirror image of your first molecule. Set the labels to show chiral centers and turn on labeling in your new molecule. Does it have the opposite (R/S) designator as your first molecule? If so, satisfy yourself that the two are indeed mirror images. (Ignore variations in methyl group conformations; your chiral centers should be mirror images!)

Close the two molecule windows.

Alpha-methylbenzylamine. Open a new molecule window. On the left-hand side of your screen will be three tabs; select “Rings” and click on the benzene ring (see the structure of α -methylbenzylamine and select the ring that looks like that.) Right-click in the molecule window to make the ring.



α -methylbenzylamine

The ring will be a bit odd-looking, and all atoms will be selected; to make it look more normal (and allow us to continue to build), click on the yellow arrow button. Now right-click on one of the hydrogen atoms and “Change atom” to “C [sp³], C_3 tetrahedral.”

Select the “pencil dot” button, and left-click on your new carbon atom to select it. Turn on automatic bonds if you haven’t already, and left-click away from the selected atom to create another carbon atom. Now click the “add hydrogens” and “clean structure” buttons. Save your file as “a-methylbenzylamine.”

Right-click one of the hydrogens on your CH₂ group, and change it to “N [sp³], N_3 tetrahedral.” Add hydrogens and clean the structure again. Save it. Now create a copy by selecting “Save as…” from the file menu.

Create a new window. Rather than build the mirror-image from scratch, we will make it from the copy of our first α -methylbenzylamine model.

Under the File menu, select “Open” and choose one of your methylbenzylamine models. (If you choose the one that is already open, you will get an error message. If you do, just open the other file.) Now select “Window”, then “Tile” so you can see them both onscreen. To give yourself more room onscreen, you may want to turn off the “pencil benzene” button (“Turn off the build menu”). If you do this, you will need to tile your windows again. For each window, select the “four-arrows” button in the top row (“Center the molecule in the window”).

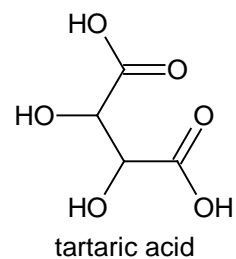
For one of your models, do the following sequence:

1. Select the “H eraser” button (“Delete hydrogens”).
2. Right click on the nitrogen atom and delete it.
3. Select the left-hand “H” button (“Add hydrogens”).
4. Turn your molecule so that it’s a mirror image of the other (except for the missing nitrogen). Then change a hydrogen into a nitrogen to make it a true mirror image, and click “Add hydrogens” again.
5. Clean the structure and save.

Using the “steering wheel” method, assign each window “R” or “S”. Now turn on chirality labels in both windows. Were you correct?

Tartaric acid. This molecule has *two* chiral centers; see whether you can identify them in the drawing.

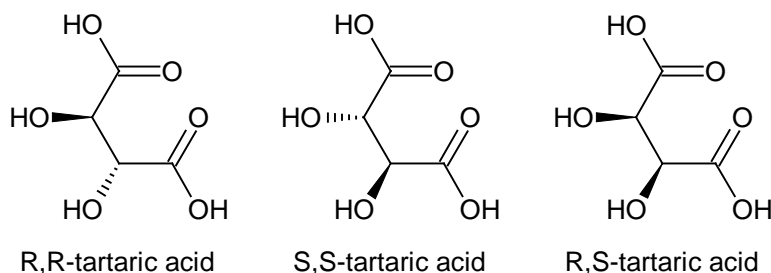
To build our first tartaric acid model, we begin by building a **6-atom** chain. This is to accommodate the four carbons, with one oxygen on each end. Build a chain of six carbon atoms, and select the yellow arrow button to turn off the build mode.



Build the carbonyl groups. Right-click an end atom, and change the atom to “O [sp²] > O_2 trigonal, non-aromatic.” Do the same with the other end atom.

Right-click the carbon next to **each** of our new oxygen atoms, and change it to “C [sp²] > C_2 trigonal, non-aromatic.” Now right-click the **bond** between carbon and oxygen and select “Double.”

You should now have a chain that looks like this: O=C–C–C–C=O. Click “Add hydrogens.” (If you get two hydrogens on one of your end carbons, it means you forgot to change its type. Click “Delete hydrogens” and change the carbon atom as directed in the last paragraph.) After adding hydrogens, change each of the end hydrogens to an oxygen “O [sp³] > O_3 tetrahedral” and add hydrogens again. Clean the geometry and save your structure as “butanedioic acid” because that’s what it is.



There are three isomers of tartaric acid. Build each isomer from your model of butanedioic acid by changing two hydrogens to OH groups; use chiral labeling to confirm that you have made what you think you have made.

Compare the three isomers in three windows. Two of them are mirror images of each other; one is not. Which is the odd structure out? Which structure has a mirror plane such that half of it is the mirror image of the other half?

To hand in:

Name each structure file with the correct chiral designation and e-mail your structure files to the instructor for grading.