

## Easy Directions for ACD NMR Processor Program

There are in general 3 different ways to accomplish the tasks below: (1) use the menus at the extreme top of the screen, (2) use the task bar above the spectrum, (3) mouse right click anywhere on the spectrum to bring up a simple list of the tasks to be accomplished. As I use the program more and more I have become partial to using the mouse right click.

1. Import the first file into the program
2. Perform a Fourier Transform (or default transform) on the FID.
3. Do a horizontal zoom and use mouse to select region of interest from left peak to right peak
4. You may or may wish to do a phase correction to make the peaks symmetrical. There are several options. Some work better than others on a particular spectrum. Once you are finished accept the changes.
5. Select the Peak Picking option, then click on Auto to label shifts of peaks. Accept.
6. Click on Integration, then select Options. Under options look at the bottom under "Reference" and click on "Internal Standard". Let the internal standard range from 4-5 ppm and let the value equal 10. (After you do this once it should store this setting for the other spectra.) Click OK and then select Auto to get an integration of the other major peaks. If you have a very small peak you may need to do a "manual" integration and select the peak. Accept the changes.
7. Choose Annotation and click on a peak to annotate. A dialog box will come up. Name the pyrophosphate peak (far right peak) and the ortho peak that comes from the hydrolysis if it is present and the ortho internal standard (far left peak).
8. Save the spectrum so if you want to redo anything in the future you can.
9. Print the spectrum. You will get a chance to give the spectrum a title and to include other comments.

Now do this for each of the other spectra. You will find it goes very fast.