

Running Fluorine or Phosphorus NMR on the Varian 300

1. Login, load the **bestshim** file, and then load ^{19}F or ^{31}P parameters for your solvent. Click *Setup* and then *Nucleus, Solvent*. Select *F19* or *31P* and your solvent. Type **su**.
2. Insert your sample into the NMR as you normally would (Don't forget to turn on the eject air!).
3. Click *Acqi*, then the *Lock* tab and lock as you normally would. Adjust Z0 until you are on resonance. Note the value of Z0.
4. Click the *Shim* tab, and shim normally.
5. Click on the Lock tab again, and turn off the lock.
6. Eject your sample and insert the neat CFCl_3 or H_3PO_4 standard.
7. Do not change the Z0 value or attempt to shim on the standard.
8. Type **nt=1 gain=0**, then **ga** to acquire one scan.
9. Reference the peak to 0ppm. Click on the peak, click *Ref*, and then type **0**.
10. Eject the standard and insert your sample again.
11. Do not change the Z0 value. You should still be on resonance.
12. Do NOT turn on the lock. In order to make sure that your resulting spectrum is still referenced correctly, you want to run unlocked.
13. Type **gain = 'n'**. This turns on the Autogain.
14. Change **nt** to however many scans you wish to acquire.
15. Acquire your spectrum and save it.

Note: If the instrument status (in the Acquisition Status box) shows that you are stuck in the *Auto Set Gain* step, type **aa** to stop the process. Set **d1=10 nt=1**, and type **ga** to acquire one scan. This should set an appropriate gain for your sample. Then type **gain='y'** and **nt=1e6 bs=16**. Type **ga** to start the acquisition. After one block size (16 scans) transform your FID (type **wft**) and take a look at your spectrum. If the signal-to-noise ratio is ok, then type **sa** and save your data.

Because you are running unlocked, it is not recommended you run for an extended period of time.