1D NMR VnmrJ Quick Guide
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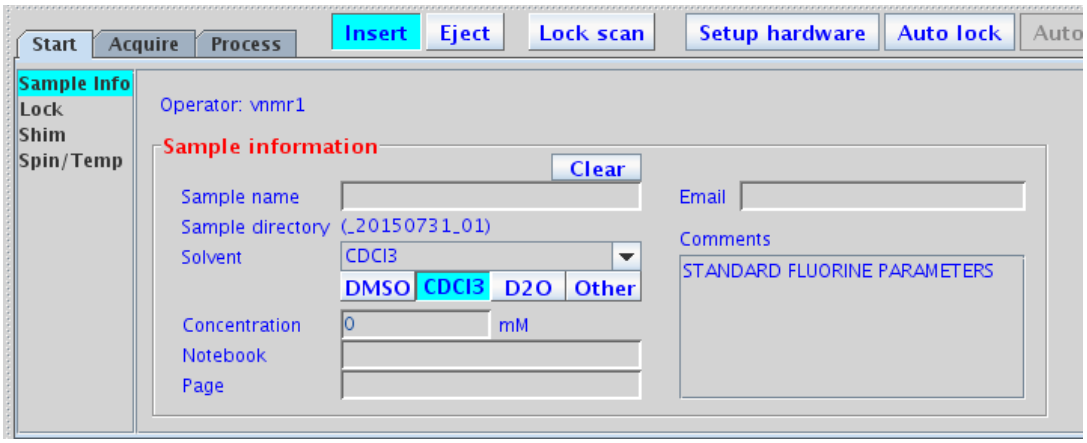
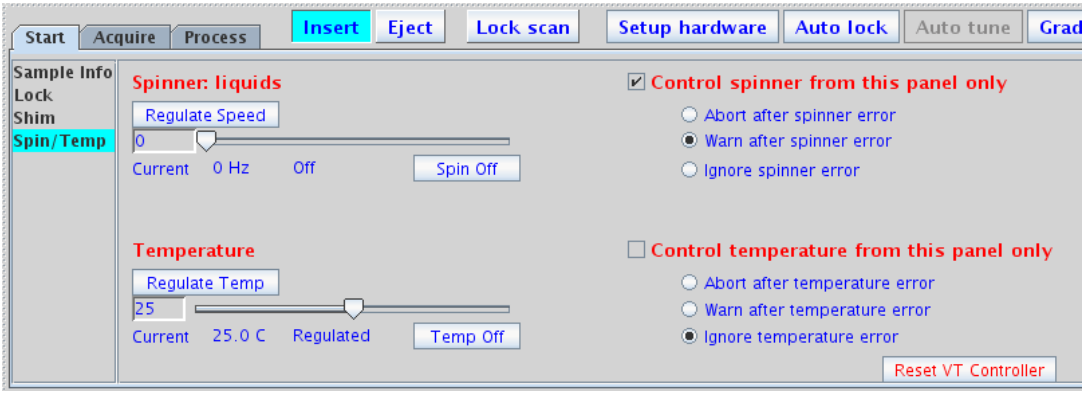
1) Getting started

- Log on using your Username and Password.
- Click on the VnmrJ Desktop Icon.
- Type *e* <Ent>. Place sample in spinner. Gauge properly. Place on top of magnet. Type *i* <Ent>.
- Click **Experiments**=>**Proton** (*or desired expt.*) type *su* <Ent>.
- In the bottom Parameter Panel, select the **Start** tab and the **Standard or sample info** page.



- Choose your solvent from the **Solvent** dropdown menu.
- Add your text to the **Comment** field.

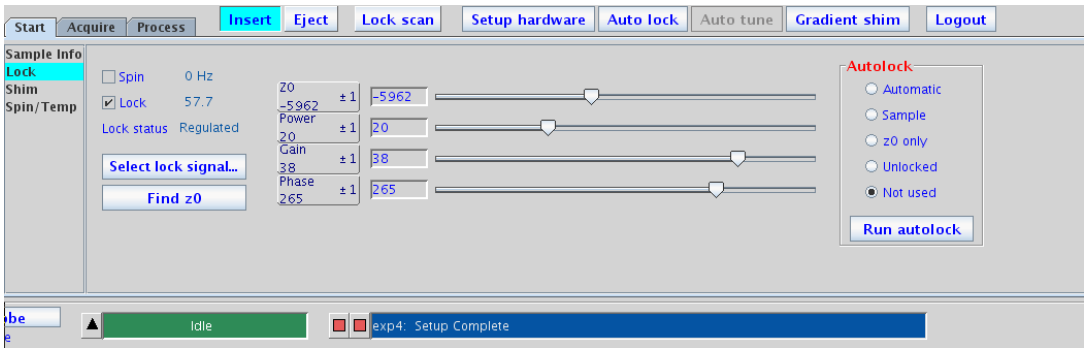
- Check spinning. If you want to spin the sample. Go to start menu, left side Spin/Temp section to regulate spinning speed



- Set up the temperature if you are planning to run an experiment at higher temp (max Temp = 65C)

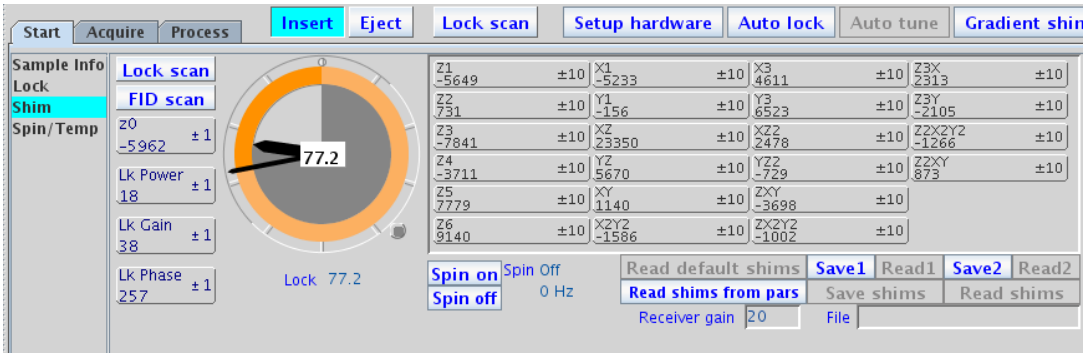
2) Lock

- Type **Lock**
- Wait for the message Idle in the message box at the bottom of the panel



3) Shimming

- Go to start shim
- Adjust Z1, and Z2 until the lock signal is max

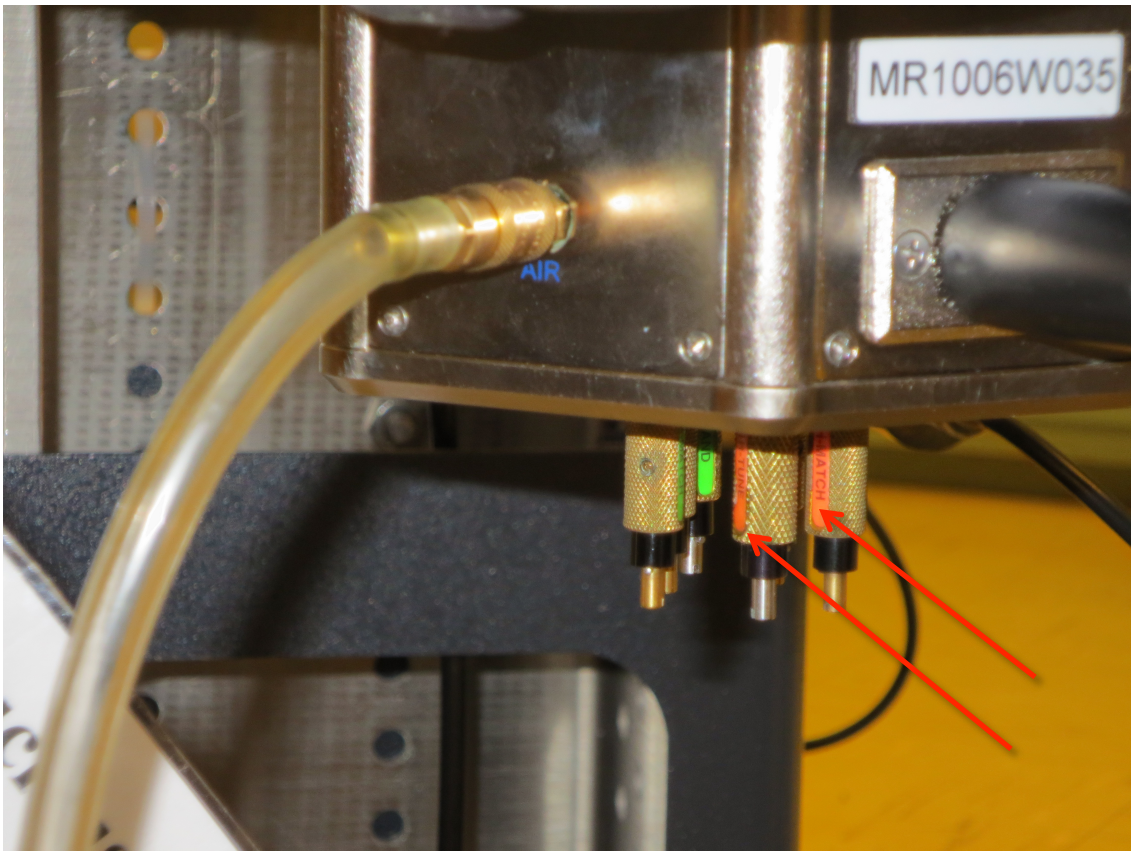


4) Tunning

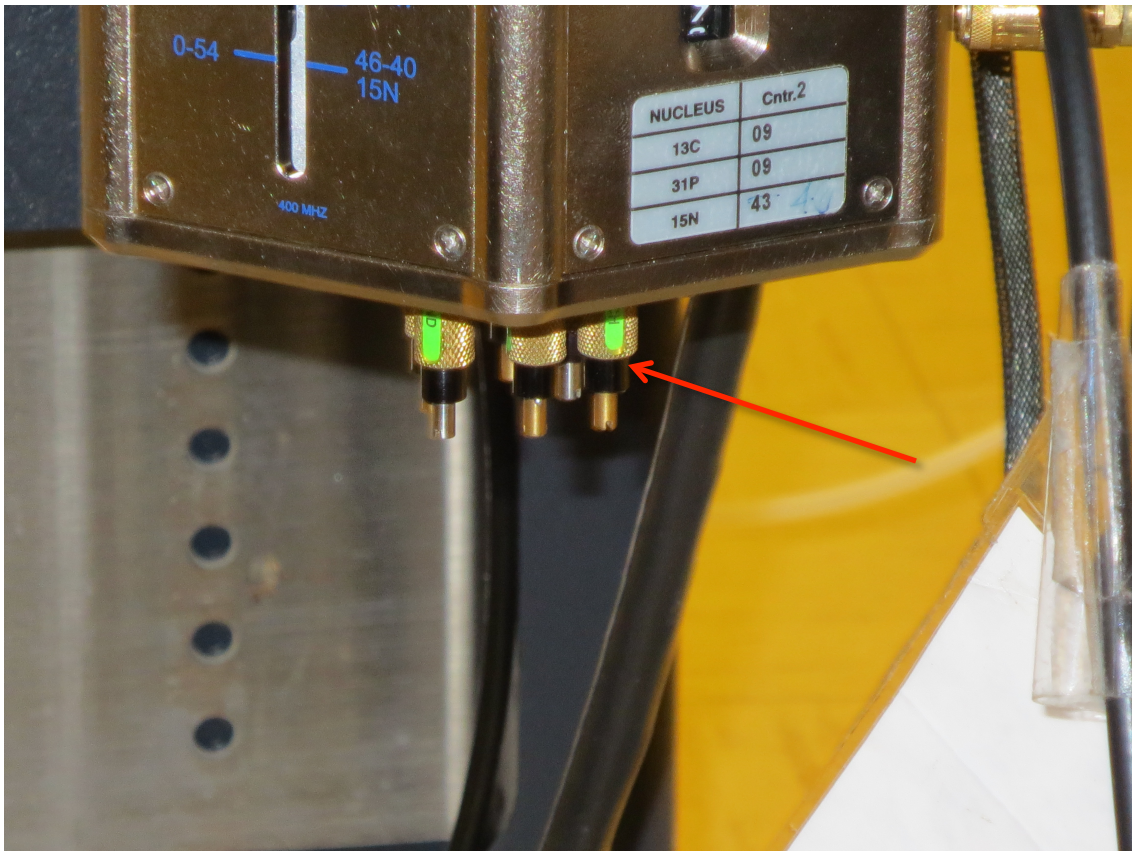
- Type *su* <Ent> tune via the pre amp, press the chan bottom

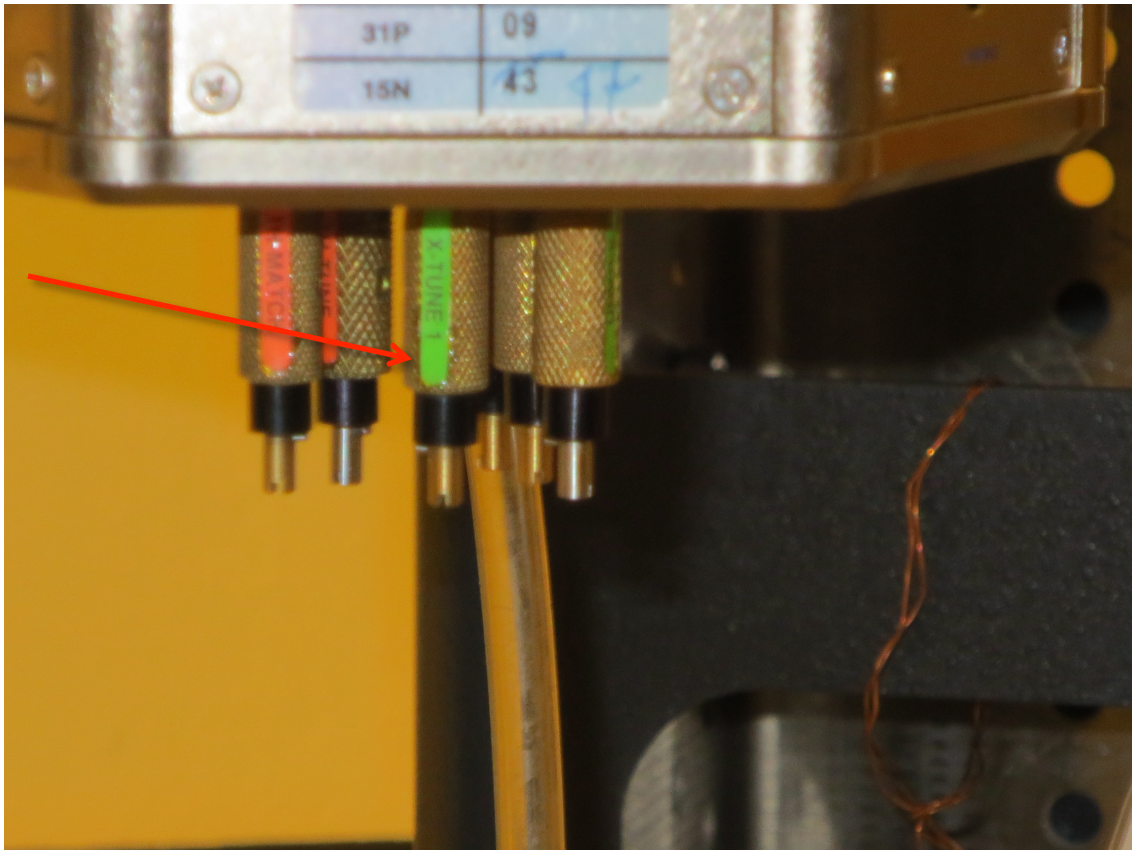
- Take the probe cable from pre amp (right side) and attach it to probe in ‘tune interface’’

- channel 1 is proton, the matching and tuning rod has an orange labeling, tune and match until you see small number like 001 which is shown in the above picture.



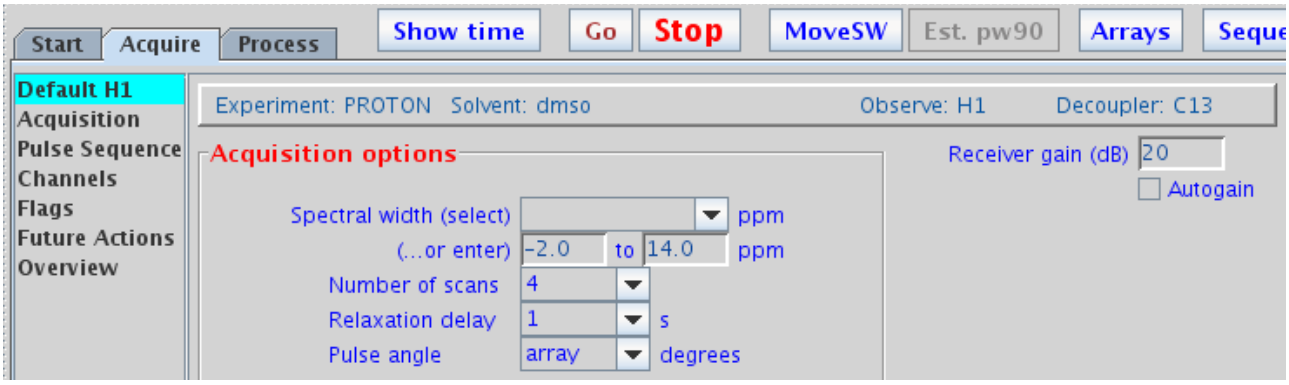
- For ^{13}C acquisition, channel 1 is ^{13}C and channel 2 is ^{1}H, ^{13}C rods are green. Turn match 4 and tune 1 rods


0-54
46-40
15N
400 MHz
NUCLEUS
Cntr.2
13C
09
31P
09
15N
43


31P
09
15N
43
X-TUNE

5) Acquiring your spectrum

- Select the **acquire** tab and the **default** page



- Chose your parameters, or type
- *nt* (number of scan*)* = desired number
- *d1*(delay between scans) = desired number
- *bs* (block size) = desired number
- *Type ga* or *go* or click on GO bottom
- Message :BS# completed
- Type *wft* to process
- When complete *f full aph vsadj* <Ent>

6) Referencing your spectrum:

- locate your solvent peak
- Click the **Cursor** icon and place red cursor line on top of solvent peak.
- Type *nl rl(<your solvent ppm>p)* <Ent>. For example, for $CDCl_3$ you would *type nl rl(7.24p)* <Ent>.

7) Integrating your spectrum (not for 13C NMR)

- Click the **Full spectrum** icon and click the **Integral** icon
- Type *cdc dc cz* <Ent>
- Expand around first desired integral region.
- Click **Resets** icon (it has scissors).
- Use a *left* mouse click for each integral reset point. If you make a mistake, use the *right* mouse button to undo last reset point. To restart, type *cz* <Ent>.
- Click the **Hand** icon and drag the spectrum to next region, click **Resets** icon, left click your next points, repeat for every region.
- When complete, click **Full spectrum** icon.

8) Plotting your spectra

- Typical example, *pl pscale ppf pir pltext page* <Ent>
- Type *ds*<Ent, expand desired plot regions, and repeat plot command

Common Plotting Commands:

pl	plot spectrum
pscale	plot scale
pir	plot integral regions
ppf	plot peak frequencies
pll	plot line list with freqs in Hertz
pltext	plot text
pltext(150,150)	plot text in top right (*use with pll*) *pap* plot all parameters
page	send plot to printer

Icon Guide:

 **Full Spectrum**

 **Magnifying Glass (Zoom)**

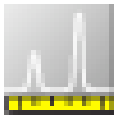
 **Hand Icon (Pan & Scan)**

 **Integral Resets**

  **Cursor**

 **Phasing**

 **Threshold**

 **Display Scale**

VNMR Basic Commands		
Command	***Description***	***Typed Example***
nt	**number of transients**: Sets the number of transients (scans) to be acquired. You should always select a multiple of 4 (e.g. 4, 8, 128). The larger the number of scans, the better the signal to noise.	*nt=16* : default setting for 1H,CDCl3
bs	**block size**: Directs the acquisition computer, as data are acquired, to periodically store a block of data on the disk.	*bs=8* : sets the block size to 8 scans.
ga	**submit experiment to acquisition and FT the result**: Performs the experiment described by the current acquisition parameters and Fourier transforms (*wft*) the result.	*ga*
wft	**weight and Fourier transform 1D data**: Performs a Fourier transform on one or more 1D FIDs with weighting applied to the FID.	*wft* : used if you stop the acquisition prior to completion or when loading a saved FID.
aph	**automatic phase of rp and lp**: Automatically calculates the phase parameters lp and rp required to produce an absorption mode spectrum and applies them to the current spectrum.	*aph* usually gives well phased spectra
f, full	**full**: Sets the horizontal and vertical control parameters to produce a display on the entire screen.	*f* or *full*
vsadj	**Automatic vertical adjustment**: Automatically sets the vertical scale, vs, in the absolute intensity mode so that the largest peak is at the requested height.	*Vsadj* : resets the vertical scale to fit on the screen
dscale	**Display scale below spectrum or FID**.	*dscale*
aa	**abort acquisition**: immediately aborts the acquisition.	*aa*
sa	**stop acquisition**: stops acquisition after acquiring current transient.	*sa*
su	**submit a setup experiment to acquisition**: Sets up the system hardware to match the current parameters but does not initiate data acquisition.	*su*
svf	**Save FIDs in current experiment**: Saves parameters, text, and FID data in the current experiment to a file.	*svf('H1_070703')* : saves the FID as a file named H1_070703