Anasazi EFT60 Nuclear Magnetic Resonance Spectrometer

Solution height must be 4.0 cm.

Remove previous sample by opening top door (lift front edge), holding in the *launch* button and catching tube. (Be ready when the tube pops up!) Place tube in spinner, and adjust the height using front gauge. Place spinner and tube in sample shaft. If sample does not go down (you should hear a pop when it successfully reaches the bottom), bend the toggle labeled *lower* to lower sample, then straighten the toggle switch.

alt tab to switch between programs

The PNMR blue screen data collection program requires you to press *enter* (return) to accept a value but the NUTS white screen program for plotting spectra and printing uses *enter* (return) to cancel the command.

zg enter enter in the blue screen to collect data with the default file name (pnmrfid).

Wait for data collection, then *alt tab*.

a0 enter in the white screen to **import and Fourier transform** data from the default file (*ga bc ft qp fb l ^m ^f*).

While holding mouse down over known peak, *sz* [value] *return* to set ppm.

Optional:

Drag right slider to adjust peak heights so tallest sample peak reaches the top.

ap to autophase or *ph* (left and right mouse phase) *enter* or *zo* (select left area) *0 enter zo* (select right area) *1 enter pe* (left and right mouse phase) *enter*.

a8 (no enter) to **integrate** (*ai id z*)

Click within a region then *v* [integer] *enter* to set the region integral value.

enter enter to leave integral mode.

Optional:

Drag far left slider to adjust integral scale.

Drag near left slider to adjust vertical zero.

c to clear all regions and start again.

Double click to left of peak and single left click to right of peak to add new region.

a9 (no enter) to **print** (*zo f ^m ^e pl*).

Normal response is *12 tab -.5 enter* for proton or *250 tab -10 enter* for carbon.

pp updates and labels peak positions, *mh* minimum height for labeling, *dp* manually labels peaks, *pf* turns labels off.

These directions assume that someone has set the nucleus (*nu H1* or *nu C13*) *fo* and *shim*. Computer password for NMR USER is *beloit1*.

For longer runs, use *b*lock *a*veraging with *p*eak *r*egistration instead of *zg* above

bapr enter enter 24 enter enter

(*ns 256,* filename my_bapr, 24 blocks, no shimming and collect at least one block, *lb 1*) *Alt tab* to white screen, *a1, zo*, drag to select a single strong isolated peak, *0 enter*, CTRL-F12 to select my_bapr and process. Can examine while still collecting data.

Inset plots: *zo* to select region, CTRL-E (or right click) to expand, *enter*, *MO* to inset. Click *A* to add view, drag, then CTRL-F to resume full scale (adjust vertical scale with slider). Can *MO* again to position or remove box. *Delete inset* for every new sample.