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 and use your thumb to seal the shaft. Use the flashlight to check if the lowered tube is spinning.

alt tab to switch between programs. Usually PNMR is left window and NUTS is right.

The PNMR data collection program requires you to press *enter* (return) to accept but the NUTS data plotting and printing program uses *enter* (return) to cancel.

zg enter enter in PNMR (left window) to **collect data** with the default file name (pnmrfid). Wait for data collection to finish, then *alt tab* or click NUTS (right window).

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

Optional:

While holding mouse down over known peak, *sz* [value] *return* to set ppm.
Use mouse wheel to adjust peak heights so tallest sample peak reaches the top.
To phase use *qp* or *ap* (sometimes more than once) or *ph* (mouse drag) *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, *pf* turns labels off, *mh* minimum height for labeling, *dp* manually labels peaks.

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

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* and drag to select region, CTRL-E (or right click) to expand, *enter*. *mo* to inset, click *A* to add view, drag, then CTRL-F (or right click) to resume full scale. Can *mo* again to position or remove box. *Delete inset* for every new sample.