**Reminder Sheet for Gemini-200 NMR Operation**

**KEYBOARD COMMANDS** *FUNCTION KEYS* (KNOBS)
**lower case** and **#** stand for your specific values

1. Type **LOGIN** <enter>, **name** <enter>, **password** <enter>
2. **E** - eject standard ($CHCl_3$ in $CDCl_3$). **I** - insert sample.
3. **LK**: interactive lock. *PF3* - Lock off. Set (LGAIN) and (LPOWER) to card values for lock solvent, adjust field (Z0) for zero frequency signal, *PF4* to lock.
4. **SHIMI**: interactive shim. *PF5* and adjust (LPHASE) for maximum lock level, then *PF1* and adjust (Z1) and (Z2) for maximum lock level.
5. **SETUP(nucleus, solvent)** Nucleus: **H** or **C** Solvent: **CDCL3, D2O, ACETON,** or **DMSO**
6. **GO** - starts data collection. When complete: **DF** - displays FID, (VF) adjust FID vertical scale. **WFT** - Weighted Fourier Transform.
7. **F** - displays full spectrum. (VS) - vertical scale. **APH** - apply automatic phasing.
8. If phasing is still not right: **QP** - quick phase: Put cursor (CR) on rightmost peak, adjust (RP) to phase rightmost and (LP) to phase leftmost peak, then **DS** to apply correction.
9. Expand region of reference peak: *PF3* toggles among one cursor (CR), two cursors (LCR) and (RCR), and no cursor. *PF4* expands the region defined by two cursors. (SP) - move display window right / left. (WP) - expand and contract display window.
10. Set reference: *PF3* to get one cursor, place on reference peak. **NL** - centers cursor on nearest line. **RL(#P)** - sets line to # ppm reference. **F** - back to full spectrum.
11. Integration: **CZ** - clears integration markers *PF1* - displays integral. Use (CR) and *PF7* to mark beginning and end of each integral region, *PF10* to blank. Adjust (IS) - integral scale. **INS = 1** **DLI** - display list of peak areas. To normalize integral, **INS = #**, where **# = (peak area) / (number of H's)** and **(peak area)** is taken from the list for a peak of known number of H's. **DLI** to verify that selected integral has desired value. **DS** *PF1* – to redisplay spectrum and integrals
12. Peak List: *PF6* - adjust (TH) to set threshold for peak lists. **DPF** - display ppm values on screen. **LL** - print a peak list on the printer.
13. Add title: **TEXT('title')** where **title** describes your sample, your name, etc. **DS** *PF1*
14. Plot Spectrum: Make sure paper is loaded in plotter. Repeat step 9 above to expand desired region of spectrum, (VS) to adjust vertical scale (or use **VSADJ**).
    To plot typical spectrum: **PL PSCALE PIRN PPF PAP PAGE** <return>
    **PL** - plots spectrum and integrals (if displayed); **PSCALE** - plots ppm scale; **PIRN**- plots normalized integral areas; **PPF**- plots peak ppm values on plot; **PAP** - prints parameters with title or **PLTEXT** - prints title only; **PAGE** – sends plot data to the printer
15. **E** - eject sample. **I** - insert standard ($CHCl_3$ in $CDCl_3$).
    Repeat step 3 above with standard sample so lock is stable and on-scale.
16. Type **LOGOUT** <enter>

**Other Options:**

Retrieve Shims: **RTS (filename)** **SU** (see corkboard for most recent shim file)
Abort Acquisition: **/A** - abort acquisition. Largest completed multiple of **BS** is available.
Floppy Disk: **FORMAT(DSK5)** - format a new 5 1/4" floppy disk. **SVF(DSK5.filnam)** - save FID to floppy disk as "FILNAM". **RT(DSK5.filename)** - retreive FID.