

BRUKER AC 200 NMR SPECTROMETER
DEPT 90 OR DEPT 135 ACQUISITION WITH DISNMR SOFTWARE

Users should be knowledgeable and efficient at ^{13}C acquisition before performing DEPT experiments. The procedure for DEPT 90 or DEPT 135 acquisition is very similar to ^1H acquisition. The differences are listed in order, below.

- D.2. Type **RJ DEPT90.001 [return]** to load default DEPT 90 parameters (CDCl_3 solvent). Type **RJ DEPT135.001 [return]**, instead, to load default DEPT 135 parameters (CDCl_3 solvent).
- D.3. If the "H" light on the console is lit, type **II [return]** to initialize the interface. The "H" light will turn off. The "X", "decoupler CW" and "decoupler gate" lights will turn on.
- D.5. Type **PJ DEPT90.001 [return]** to load default DEPT 90 processing and plotting parameters (CDCl_3 solvent) in block #2. Type **PJ DEPT135.001 [return]**, instead, to load default DEPT 135 processing and plotting parameters (CDCl_3 solvent).
- H.1. Type **AU DEPT.AU** to start the data acquisition. The ZG command is not used, because DEPT is an automated pulse-sequence program.
- I.4 The deuterated solvent resonance(s) will not appear in a DEPT spectrum. To set the PPM scale properly, refer to the corresponding broad-band ^1H -decoupled ^{13}C spectrum, and choose any peak that can be seen unambiguously in both the ^{13}C and DEPT spectra. Use that peak's chemical shift in the broad-band ^1H -decoupled ^{13}C spectrum as the reference peak in the DEPT spectrum. As before, use the **G** command within EP to set the reference peak.