

**BRUKER AC 200 NMR SPECTROMETER**  
**<sup>13</sup>C ACQUISITION WITH DISNMR SOFTWARE**

Users should be knowledgeable and efficient at <sup>1</sup>H acquisition before performing <sup>13</sup>C experiments. The procedure for broad-band <sup>1</sup>H-decoupled <sup>13</sup>C acquisition is very similar to <sup>1</sup>H acquisition. The differences are listed in order, below.

- D.2. Type **RJ CARBON.001 [return]** to load default <sup>13</sup>C acquisition parameters (CDCl<sub>3</sub> 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" and "CW" decoupler lights will turn on.
- D.4. Unlike <sup>1</sup>H acquisition, O1 is not significantly solvent dependent in <sup>13</sup>C acquisitions. Therefore, leave the <sup>13</sup>C O1 value untouched. On the other hand, O2, the decoupler offset, must be set to the O1 value from the corresponding <sup>1</sup>H experiment. Change O2 and the field value if you are using a solvent other than CDCl<sub>3</sub> or benzene-d<sub>6</sub>.

<u>lock solvent</u>	<u>O2 value</u>	<u>field value</u>
CDCl <sub>3</sub> or benzene-d <sub>6</sub>	3341	7141
D <sub>2</sub> O	3825	7013
acetone-d <sub>6</sub>	4380	6853
DMSO-d <sub>6</sub>	4289	6921
methanol-d <sub>1</sub>	3340	7054

- D.5. Type **PJ CARBON.001 [return]** to load default <sup>13</sup>C processing and plotting parameters (CDCl<sub>3</sub> solvent) in block #2.
- I.6. As in <sup>1</sup>H processing, type **F** to set the frequency limits of the spectrum to be plotted. The computer will respond with its default value of F1. Type, e.g., **220 [return]**. The computer will respond with its default value of F2. Type, e.g., **-10 [return]**. The computer will respond with the corresponding ppm/cm that was set by your F limits.

- I.9. Integration is not used in routine  $^{13}\text{C}$  spectra.
- J.2. Exit the EP subroutine and type **PX [return]** to plot the spectrum. **PXB [return]** is not used because there is no integral.
- K. Return the spectrometer to default proton parameters. Type **RJ PROTON.001 [return]** to load default  $^1\text{H}$  acquisition parameters ( $\text{CDCl}_3$  solvent). Type **II [return]** to initialize the interface. The "X" and "CW" decoupler lights on the console will turn off. The "H" light will turn on. Type **2** to enter block #2. Type **PJ PROTON.001 [return]** to load default  $^1\text{H}$  processing and plotting parameters ( $\text{CDCl}_3$  solvent).