

**Attention.....Attention.....Attention.....Attention.....Attention.....Attention**

**The previous pages are more or less the same as for the DPX200. This manual is always part of a introduction given by the supervisor of the NMR-machine. These persons are mentioned in the E-agenda when reservations have to be made.**

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In order to get the parameters for a specific NMR-experiment, like H, or C13-H decoupled etc, one has to choose from a table the correct parameterfile.

E.g. H – NMR .

Type in the command line **rpar**

Click on the specific file: AA\_orgstd1h and copy all.

The first thing which has to be done before running the experiment is **rga**.

The system automatically determines the receiver gain which will not overload the ADC.

If you need another sw or more scans ( ns ) etc., these parameternames can be given in the command line and changed to these new values.

If you want to have a quick view of the quality of the spectrum: start with ds = 0 and ns = 1 , and use the sw-01 button in the main menu of XWIN-NMR to adjust sw.

If you are satisfied, start the final experiment after setting ds = 2 and ns = even number ( 4 , 8 , 16 etc ).

Use **halt** to finish the running experiment if the S/N is good enough and still many scans should run before it stops. A message will appear in the comment line:

*zg:acquisition finished*

Use **stop** if the parameters are wrong and the experiment is not of interest.

Commands in a nutshell:

- Clean the sample tube ( should contain ~0.6 ml solvent ) position it in the spinner.
- press “**lift on/off**”
- insert the spinner with the NMR-tube in the shaft of the magnet and press “**lift on/off**”
- type **lock** in the command window
- select the **solvent** ( CDCl<sub>3</sub> , Aceton etc.) from the solvent list
- To make lock display visible, click on orange rectangle icon which is above the spectral window. Or when not visible click with right mouse button on the small lock display and choose for lock signal display. This orange rectangle will appear.
- shim** the probe by iteratively adjusting **Z**, **Z<sup>2</sup>** (fine), **Z<sup>3</sup>** (coarse).
- type **edc** In this windowform fill in your name , expno , solvent , and choose parameterfile ( 1H -> AA\_orgstd1h or 13C -> AA\_orgstd13C )
- type **rga** ( adjusting the receiver gain ).
- type **zg** ( clearing buffer and starts the NMR-experiment).

- type *ft* when the acquisition is finished or *tr* (wait a few seconds) and *ft*
- type *apk* for automatic phasecorrection.
- type *re test 1* ( to protect your data from being overwritten by the next operator ).
- switch off lock , spin and activate the lift to eject your sample.

**In case of misset shimvalues:        rsh (select) dmx300\_qnp\_chl**

If you want to acquire C13 , then this also requires selection of C13 by means of the pneumatic unit. A slider on the QNP-probe will be adjusted ( 1 should be visible on this slider ).