

NMR Data Acquisition and Processing Procedure






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Please **DO NOT** remove from NMR lab!

Things to Avoid when Using NMR Lab

Here's a list of stuff that I have seen that you *should not* do:

1. Do not bring a magnetic substance near to the magnet ... after all it's a *magnet* and a very powerful one at that. Screwdrivers and wrenches are death tools around an NMR magnet ... keep them away!
2. Do not put little tape 'flags' with the name of your sample on your NMR tube. If the flag is left on the tube it will stick inside the magnet for sure (Murphy's Law).
3. Do not put your sample into a depth gauge and then try to put the whole thing, gauge and all, into the magnet.
4. Do not put the spinner on *upside down* and then put sample and spinner into the magnet. There *will* be problems.
5. Do not make the mistake of thinking that just because a sample in the autosampler carousel is past the sample injection point that it has already run. The *only* way to know if it has run is to look at the ICONNMR display.
6. Do **not** pull on the autosampler carousel in order to rotate it and retrieve your sample!!! Ever.
7. If you must take un-run samples out, PLEASE also cancel the samples in ICONNMR.
8. Do not be helpful and clean the NMR tube depth gauge with acetone. The gauge is plastic and will dissolve in acetone.
9. Do not be helpful and try to fix a broken depth gauge ... there are tiny springs in the stop mechanism that will fly out if you try to take it apart, never to be found again.
10. Do not put the sample into the magnet unless the lift air is turned on. Again, you risk damaging the probe if you simply drop the sample into the magnet.
11. Do not force the tuning/matching rods to turn further than their maximum or minimum positions ... this will cause serious internal damage to the probe and render it immediately useless until repaired.
12. Do not overreach when inserting or removing a sample ... you might lose your balance and injure yourself or you might break an NMR tube with sample in it.
13. Do not forget to shut off the lift air after you are finished with the machine.
14. Do not put a sample into the magnet and begin to take data when we are filling the magnets with cryogens.
15. *YOU* are responsible for the shimming. If you cannot shim your sample try starting from scratch by reading in the standard shim file (type 'rsh' and select 'currentshim') *before* complaining to the laboratory manager. If you still cannot shim the sample satisfactorily then contact one of the NMR facility staff.

| Procedures | Commands | Notes |
|------------------------------------|---|--|
| 1. Insert sample. | <i>ej</i> → load sample → <i>ij</i> | <i>sx #</i> (load sample using auto-sampler). |
| 2. Create new data set. | <i>new</i> or <i>edc</i> | |
| 3. Read in standard parameter set. | <i>rpar</i> → choose ... | |
| 4. Read in pulses and powers. | <i>getprosol</i> | <i>gpro</i> (Macro to shorten the command). |
| 5. Check temperature setting. | <i>edte</i> → set ... | |
| 6. Lock the solvent. | <i>lock</i> → choose ... |  (lock display window). |
| 7. Tune the probe. | <i>atma</i> | |
| 8. Shim the magnet. | <i>topshim</i> | <i>Topshim gui</i> (open Topshim interface).  |
| 9. Check acquisition parameters. | <i>ased</i> | |
| 10. Adjust receiver gain. | <i>rga</i> | |
| 11. Start acquisition. | <i>zg</i> | <i>tr</i> (transfer/save data to workstation). |
| 12. Processing the data. | <i>efp</i> → <i>apk</i> () → <i>absn</i> | <i>proc</i> (Macro combining the three commands). |
| 13. Peak picking. | <i>pp</i> |  (open peak picking Interactive Bar). |
| 14. Peak integration. | <i>int</i> |  (open integration Interactive Bar). |
| 15. Plot the spectrum. | <i>plot</i> | |

* Refer to succeeding contents for detailed information of each step.

Topspin3.2 Interface

The image shows the Bruker TopSpin 3.2 software interface. The window title is "Bruker TopSpin 3.2 on SSSC-EVO as jiz258". The interface is divided into several sections:

- Menu Bar:** Located at the top, containing menus for Start, Acquire, Process, Analyse, Publish, View, and Manage.
- Tool Bar:** Below the menu bar, containing various icons for file operations (Create Dataset, Find Dataset, Open Dataset, Paste Dataset, Read Pars.) and acquisition/analysis tools.
- File Browser:** On the left side, showing a tree view of the file system. The path is C:\Bruker\TopSpin3.2\data\jiz258. The "Oct02" folder is expanded, showing subfolders like "1 - zg30", "2 - zgpg30", "3 - zg", "4 - zgig", "5 - zgpg30", and "903 - zg".
- Command Line:** Below the file browser, currently empty.
- Spectrum Window:** The main display area showing an NMR spectrum. The x-axis is labeled "ppm" and ranges from 15 to 0. The y-axis is labeled "[ref]". The spectrum shows a sharp peak at 12.4705 ppm and a multiplet between 0 and 5 ppm. The multiplet peaks are labeled with their chemical shifts: 4.6845, 3.3988, 75.4456, and 4.0005.
- Tab Bar:** Above the spectrum window, containing tabs for Spectrum, ProcPars, AcquPars, Title, PulseProg, Peaks, Integrals, Sample, Structure, Plot, Fid, and Acqu.
- Acquisition Status Bar:** At the bottom, containing controls for Amplifier Control, Acquisition information (no acquisition running), Lock, Sample, and Probe Temperature (295.0 K). The Reg. State is also shown as "On".

Topspin2.1 Interface

The screenshot displays the Bruker TOPSPIN 2.1 software interface. At the top is the **Menu Bar** with options: File, Edit, View, Spectrometer, Processing, Analysis, Options, Window, Help. Below it is the **Tool Bar** containing various icons for file operations and processing. The main window is titled "Acquisition finished: Nov03 3 1 C:\Bruker\TOPSPIN2.1\pl6 jjz258". On the left is the **File Browser** showing a directory tree with folders like "C:\Bruker\TOPSPIN2.1\pl6" and "Nov03". A red arrow points to the "jz258" folder, and another red arrow points to the "3 - zgpg" folder. The main plot area shows a spectrum with the title "13C zgpg" and "Sucrose Octa-Acetate in Benzene+CDCl3 (1 drop)". The x-axis is labeled "[ppm]" and ranges from 200 to 0. The y-axis is labeled "[rel]" and ranges from 0 to 14. The spectrum shows several peaks, with a prominent one at approximately 170 ppm. At the bottom, the status bar shows "wobb: finished", "Acquisition information: no acquisition running", "Lock" status, "VTU [Kelvin]: 298.0", and "Time: 09:18 Nov 06".

Topspin3.2

2. Create New Data Set

New...

Prepare for a new experiment by creating a new data set and initializing its NMR parameters according to the selected experiment type. For multi-receiver experiments several datasets are created. Please define the number of receivers in the Options.

NAME (folder name)

EXPNO (experiment number)

PROCNO (process number)

Use current parameters (use the same experiment setting)

Experiment **Open experiment list (rpar)** →

Options

Set solvent:

Execute "getprosol"

Keep parameters:

DIR **DIR for data** →

Show new dataset in new window

Receivers (1,2, ...16)

TITLE

Topspin2.1

New...

Prepare for a new experiment by creating a new data set and initializing its NMR parameters according to the selected experiment type. For multi-receiver experiments several datasets are created. Please define the number of receivers in the box below.

NAME

EXPNO

PROCNO

DIR **DIR for data**

USER

Solvent

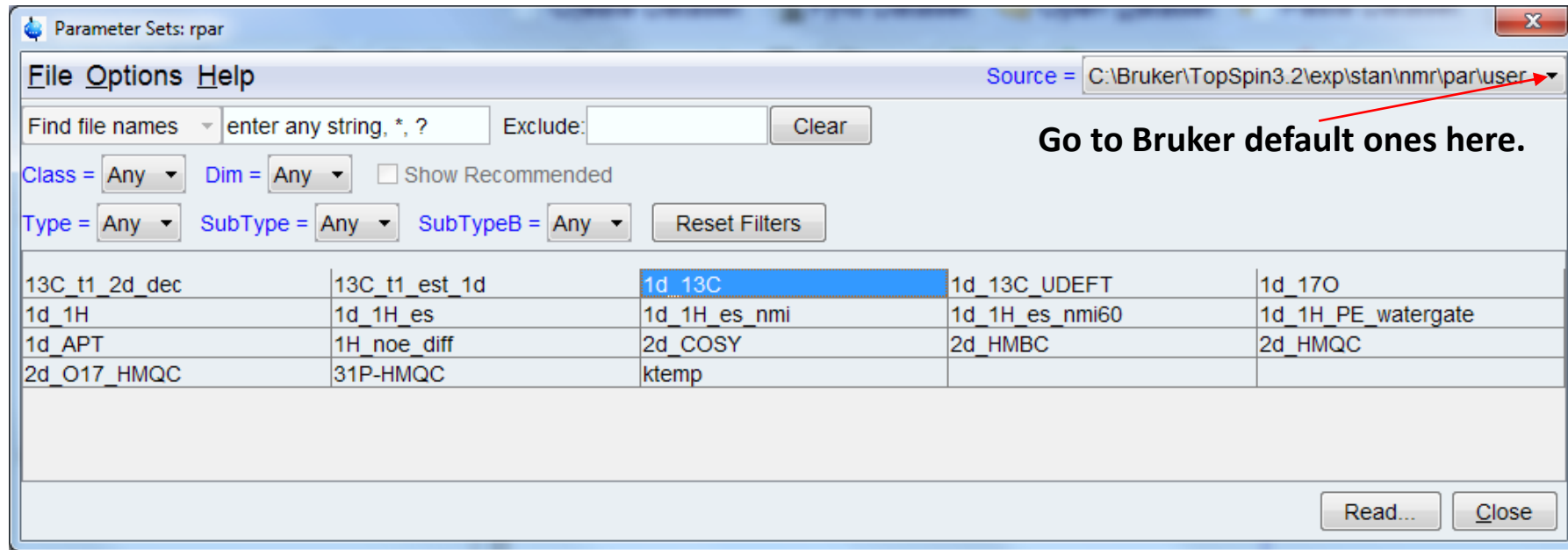
Experiment Dirs.

Experiment

TITLE **Experiment list**

Receivers (1,2, ...8)

3. Read in Standard Parameter Set



Existing Parameter Sets:

- Standard 1D: ^1H , ^7Li , ^{11}B , ^{13}C , ^{15}N , ^{17}O , ^{19}F , ^{27}Al , ^{29}Si , ^{31}P . (Format: **1d_#X**, e.g. **1d_13C**).
- Standard 2D: COSY, HMQC, HSQC, HMBC. (Format: **2d_XXXX**, e.g. **2d_COSY**).
- Other ^1H Expts: NOE, water suppression, T_1 estimate, homonuclear decoupling, etc.
- Other ^{13}C Expts: UDEFT, DEPTq, INADEQUATE, T_1 estimate, etc.

5. Set Up Variable Temperature

Temperature Control Suite

Temperature | Monitoring | Record | Correction | Self tune | Configuration | Log | Help

On Off VTU State: On **Topspin3.2**

| Channel | Regulation State | Stability | Current Temperature | Target Temperature | Heater Power |
|--|------------------|---------------|---------------------|--------------------------------|---------------------------------|
| 1 5 mm CPTXI 1H-13C/15N Z-GRD Z4... | Transient | Not Available | 294.3 K | 295.0 K (273.0 K...313.0 K) | 2.2 % (max. 5.0 % of 90.3 W) |

| | State | Gas Flow | Target Gas Flow | Standby Gas Flow |
|-----------|--------|----------|-----------------|------------------|
| Probe Gas | Steady | 699 lph | 700 lph | 0 lph |

| Accessory Channel | State | Current Power | Target Power |
|--------------------|-----------|---------------|--------------|
| 1 (Chiller) BCU | Connected | On | On |

VTU: On | Probe Temp

Edtte

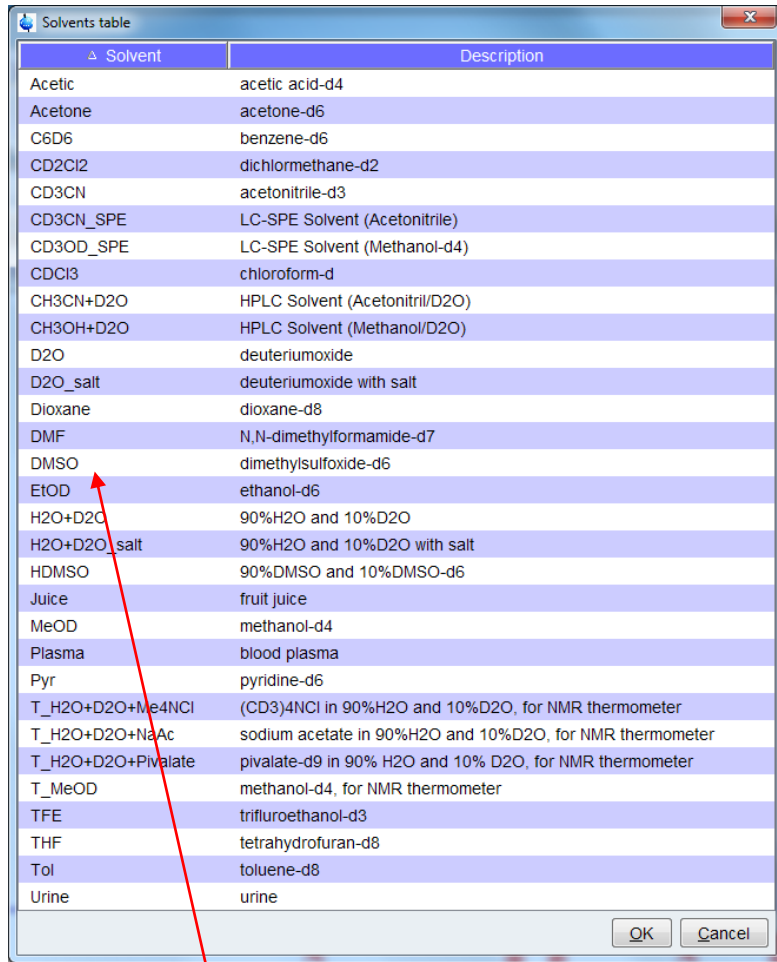
Main display | Monitoring | Corrections | Self-tune | Ramp | Recording | Aux. s... | Z44866/0043

Sample temperature

| | | |
|--------------|---------|-------------------|
| Sample temp. | 298.0 K | Topspin2.1 |
| Target temp. | 298.0 K | Change... |
| Probe Heater | On | 0.4 % |
| Gas flow | 535 l/h | - + |
| Cooling | Off | Change... |

Rec Off | BVT3200 | Exch Board

6. Lock the Solvent

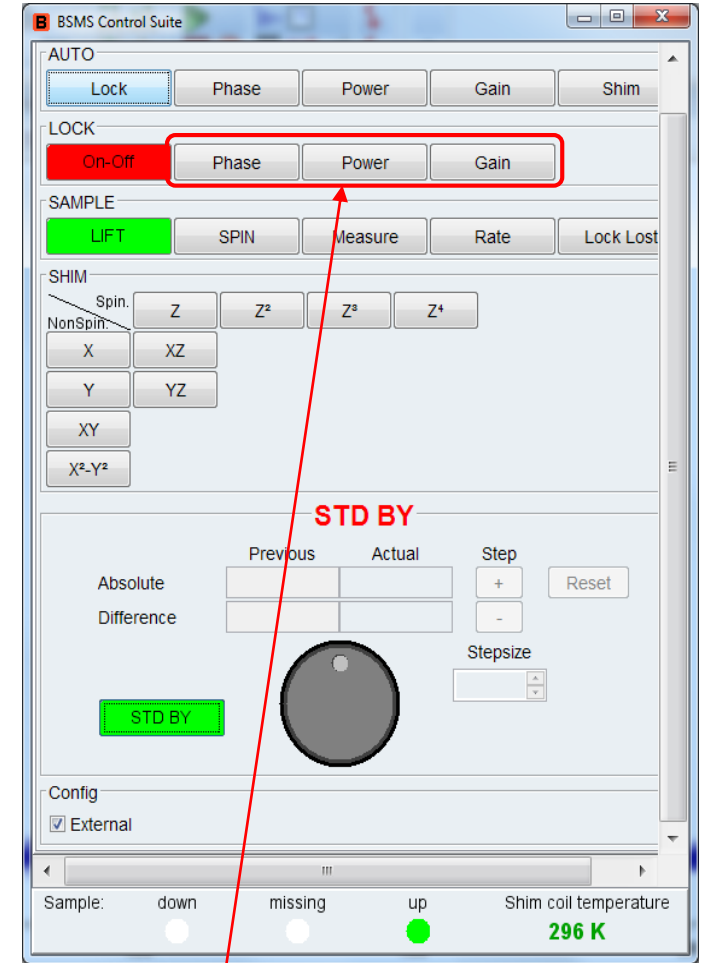


| Solvent | Description |
|--------------------|--|
| Acetic | acetic acid-d4 |
| Acetone | acetone-d6 |
| C6D6 | benzene-d6 |
| CD2Cl2 | dichloromethane-d2 |
| CD3CN | acetonitrile-d3 |
| CD3CN_SPE | LC-SPE Solvent (Acetonitrile) |
| CD3OD_SPE | LC-SPE Solvent (Methanol-d4) |
| CDCl3 | chloroform-d |
| CH3CN+D2O | HPLC Solvent (Acetonitril/D2O) |
| CH3OH+D2O | HPLC Solvent (Methanol/D2O) |
| D2O | deuteriumoxide |
| D2O_salt | deuteriumoxide with salt |
| Dioxane | dioxane-d8 |
| DMF | N,N-dimethylformamide-d7 |
| DMSO | dimethylsulfoxide-d6 |
| ETOD | ethanol-d6 |
| H2O+D2O | 90%H2O and 10%D2O |
| H2O+D2O_salt | 90%H2O and 10%D2O with salt |
| HDMSO | 90%DMSO and 10%DMSO-d6 |
| Juice | fruit juice |
| MeOD | methanol-d4 |
| Plasma | blood plasma |
| Pyr | pyridine-d6 |
| T_H2O+D2O+Me4NCl | (CD3)4NCl in 90%H2O and 10%D2O, for NMR thermometer |
| T_H2O+D2O+NaAc | sodium acetate in 90%H2O and 10%D2O, for NMR thermometer |
| T_H2O+D2O+Pivalate | pivalate-d9 in 90% H2O and 10% D2O, for NMR thermometer |
| T_MeOD | methanol-d4, for NMR thermometer |
| TFE | trifluoroethanol-d3 |
| THF | tetrahydrofuran-d8 |
| Tol | toluene-d8 |
| Urine | urine |

Choose the solvent from the list.



Check the lock level to get a sense of shimming.

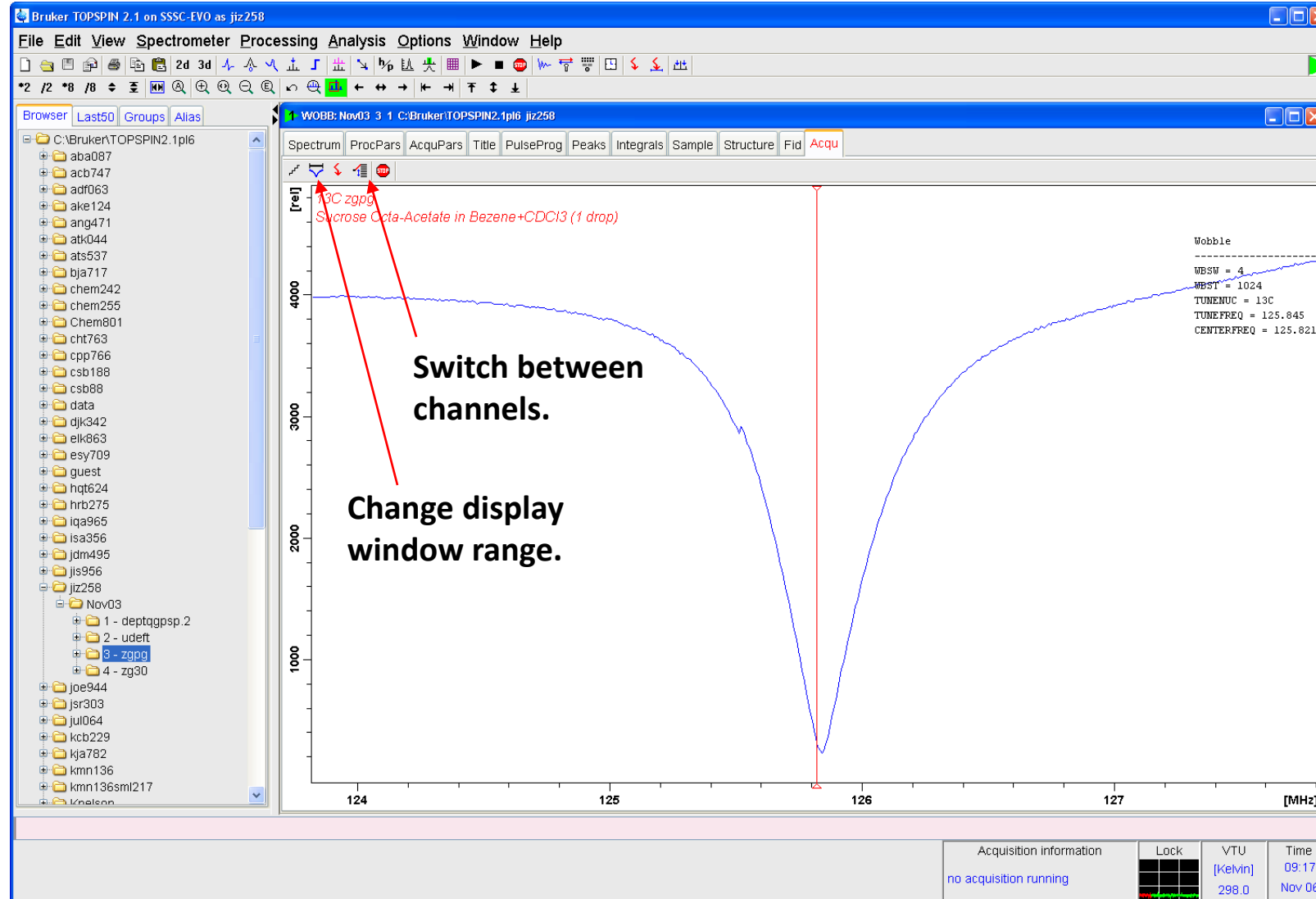


The BSMS Control Suite window shows various control parameters. A red box highlights the 'Lock' section, which includes buttons for 'On-Off', 'Phase', 'Power', and 'Gain'. A red arrow points to the 'Power' button. Below this, there are buttons for 'LIFT', 'SPIN', 'Measure', 'Rate', and 'Lock Lost'. The 'SHIM' section includes buttons for 'Z', 'Z²', 'Z³', 'Z⁴', 'X', 'XZ', 'Y', 'YZ', 'XY', and 'X²-Y²'. The 'STD BY' section includes buttons for 'Absolute', 'Difference', 'Previous', 'Actual', 'Step', 'Reset', and 'Stepsize'. The 'Config' section includes a checkbox for 'External'. The 'Sample' section includes buttons for 'down', 'missing', and 'up', and a 'Shim coil temperature' of 296 K.

Optimize these parameters if the lock signal is still weak after Topshim.

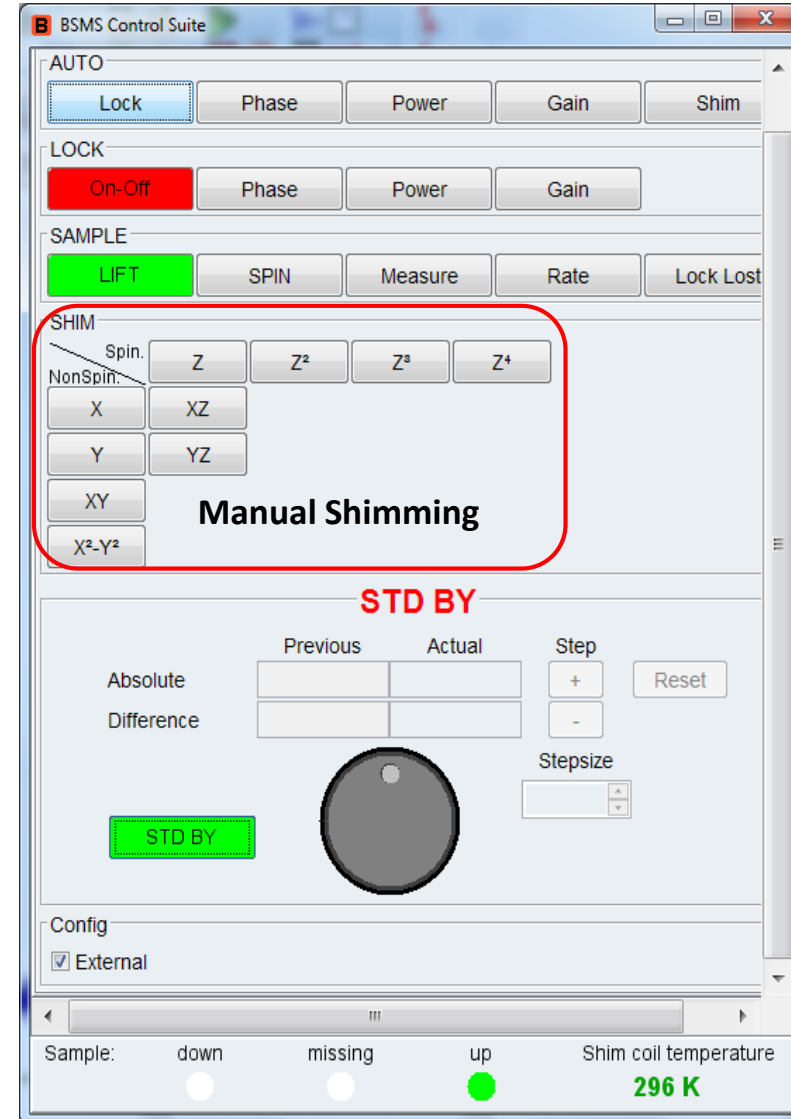
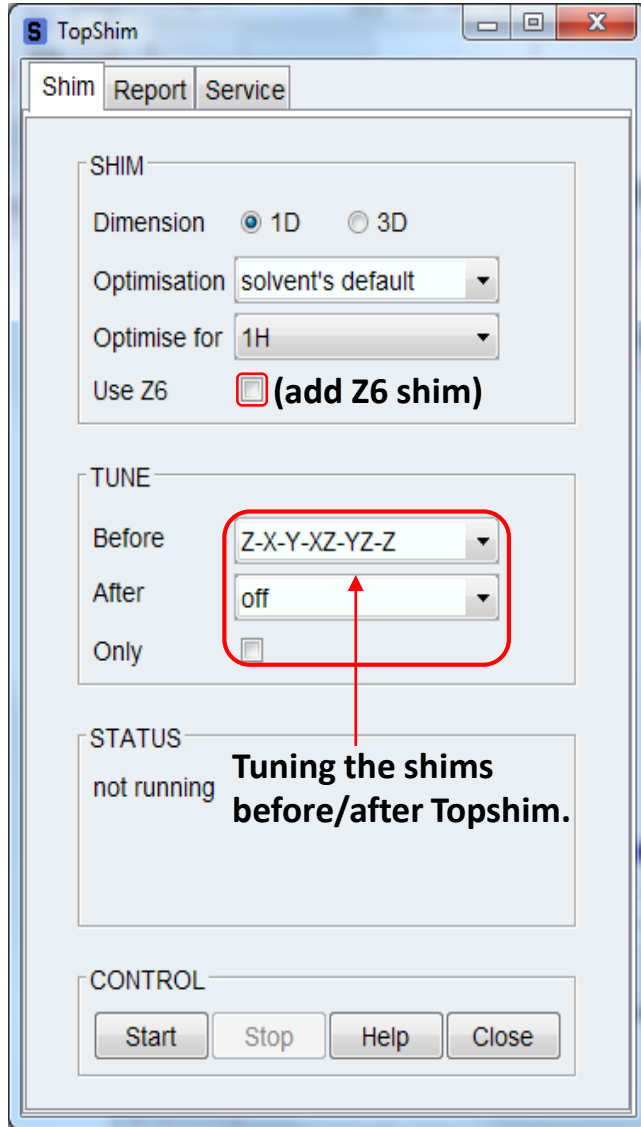
7. Tune the Probe

- Tuning and Matching are done automatically for most probes (atma).
- Use 'wobb' and manual tuning/matching if necessary.



8. Shim the Magnet

- Run 'topshim' alone is usually enough. If the shims are still not good, try 'topshim gui' as show below.



9. Acquisition Parameters

Start **Acquire** Process Analyse Publish View Manage

Sample Lock Tune Spin Shim Prosol Gain Go Options

Browser Last50 Groups

1 Oct02 1 1 C:\Bruker\TopSpin3.2\data\jiz258

Spectrum ProcPars **AcquPars** Title PulseProg Peaks Integrals Sample Structure Plot Fid Acqu

Probe: 5 mm CPTXI 1H-13C/15N Z-GRD Z44866/0043

General Channel f1

| Parameter | Value | Description |
|----------------|-------------|--|
| PULPROG | zg30 | Pulse program for acquisition |
| TD | 65536 | Time domain size (number of data points in FID) |
| SWH [Hz, ppm] | 12019.23 | Sweep width (spectrum width) |
| AQ [sec] | 2.7262976 | Acquisition time (length of FID, in seconds) |
| RG | 203 | Receiver gain |
| DW [µsec] | 41.600 | Dwell time (time interval between two data points in FID) |
| DE [µsec] | 6.50 | Pre-scan-delay |
| D1 [sec] | 1.00000000 | Relaxation delay; 1-5 * T1 (at+d1: relaxation delay) |
| DS | 0 | Number of dummy scans |
| NS | 64 | 1 * n, total number of scans: NS * TD |
| TD0 | 1 | Dimension of accumulation loop |
| SFO1 [MHz] | 600.1737063 | Frequency of ch. 1 |
| O1 [Hz, ppm] | 3706.30 | Frequency of ch. 1 (middle of the spectrum) |
| NUC1 | 1H | Nucleus for channel 1 |
| P1 [µsec] | 12.50 | F1 channel - 90 degree high power pulse (pulse and power) |
| PLW1 [W, -dBW] | 15 | F1 channel - power level for pulse (default) |

Amplifier Control Acquisition information Lock Sample Probe Temperature

no acquisition running 294.9 K

On Reg. State: ✓

12. Processing the Data (1)

The screenshot displays the Bruker TopSpin 3.2 software interface. The 'Process' menu is highlighted in red, and the 'Proc. Spectrum' option is selected. The 'Advanced' dropdown menu is also highlighted in red. The 'Reference' section is expanded, showing parameters for SI, SF, OFFSET, SR, HZpPT, SPECTYP, WDW, LB, GB, SSB, TM1, TM2, PHC0, PHC1, PH_mod, ABSG, and ABSF1. The 'Window function' section is also expanded, showing parameters for WDW, LB, GB, SSB, TM1, and TM2. The 'Phase correction' section is expanded, showing parameters for PHC0, PHC1, and PH_mod. The 'Baseline correction' section is expanded, showing parameters for ABSG and ABSF1. The 'Reference' section is expanded, showing parameters for SI, SF, OFFSET, SR, HZpPT, and SPECTYP. The 'Window function' section is expanded, showing parameters for WDW, LB, GB, SSB, TM1, and TM2. The 'Phase correction' section is expanded, showing parameters for PHC0, PHC1, and PH_mod. The 'Baseline correction' section is expanded, showing parameters for ABSG and ABSF1.

Topspin2.1

| Parameter | Value | Description |
|----------------|-------------|---------------------------------------|
| SI | 65536 | Size of real spectrum |
| SF [MHz] | 600.1700000 | Spectrometer frequency |
| OFFSET [ppm] | 16.18860 | Low field limit of spectrum |
| SR [Hz] | 0 | Spectrum reference frequency |
| HZpPT [Hz] | 0.183399 | Spectral resolution |
| SPECTYP | UNDEFINED | Type of spectrum e.g. COSY, HMQC, ... |
| WDW | EM | Window functions for trf, xfb, ... |
| LB [Hz] | 0.30 | Line broadening for em |
| GB | 0 | Gaussian max. position for gm, 0<GB<1 |
| SSB | 0 | Sine bell shift SSB (0,1,2,...) |
| TM1 | 0 | Left limit for tm 0<TM1<1 |
| TM2 | 0 | Right limit for tm 0<TM2<1 |
| PHC0 [degrees] | 169.157 | 0th order correction for pk |
| PHC1 [degrees] | -19.462 | 1st order correction for pk |
| PH_mod | no | Phasing modes for trf, xfb, ... |
| ABSG | 5 | Degree of polynomial for abs (0..5) |
| ABSF1 [ppm] | 10.00000 | Left limit for absf |

Amplifier Control: [Black Box]

Acquisition information: no acquisition running

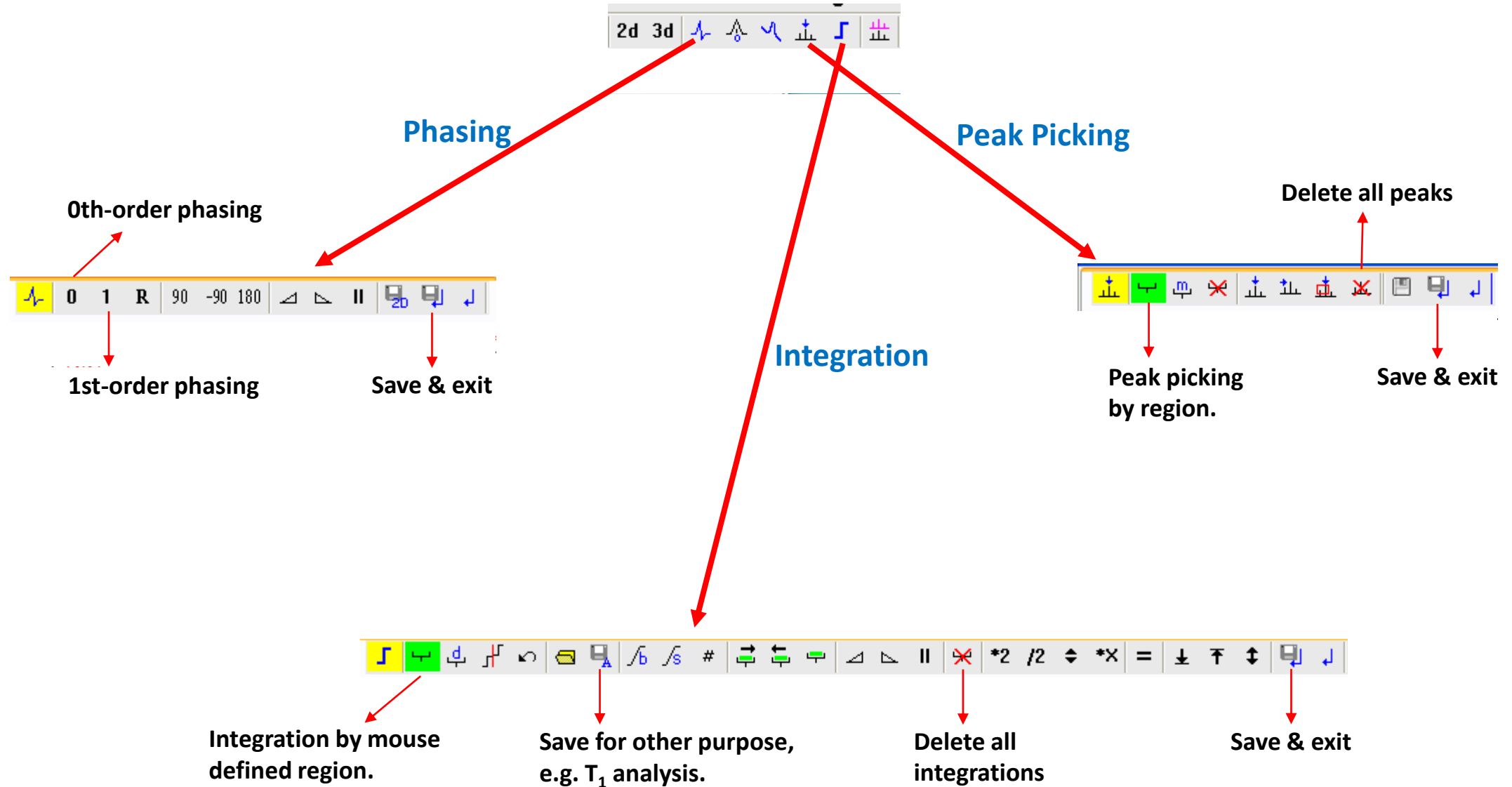
Lock: [Black Box]

Sample: [Blue Icon]

Probe Temperature: 294.9 K

Reg. State: [Green Checkmark]

12. Processing the Data (2)



15. Plot the Spectrum (1)

Bruker TopSpin (Student License)

File Edit View Processing Analysis Options Window Help

2d 3d

*2 /2 *8 /8

1

Browser Last50 Groups

- B:\NMRdata\FBR1
 - Doty-Installation
 - Nov04
 - 1 - deptqgppsp.2 - 13C DEPTC
 - 2 - zg30 - 1H zg30 / Sucrose
 - 3 - selnogg - 1H selective NO
 - 4 - selnogg - 1H selective NO
 - 5 - selnogg - 1H selective NO
 - 6 - selno - 1H selective NOE (
 - 7 - zghd.2 - 1H Homonuclear
 - 8 - zghd.2 - 1H Homonuclear
 - Oct05
 - Oct07
 - Oct08
 - Oct13
 - Oct15
 - Oct16
 - B:\NMRdata\SSSC500
 - B:\NMRdata\SSSC600

Plot Portfolio

1: Nov04 2 1 - B:\NMRdata\FBR1 - Current

1 Nov04 2 1 B:\NMRdata\FBR1

Spectrum ProcPars AcqPars Title PulseProg Peaks Integrals Sample Structure **Plot** Fid

Layout: +/1D_H.xwp

change here

Print: Default Printer Paper: A4

View: Limits: Expand

Display: Zoom

Click here to insert new elements: Standard NMR

Add more objects

1H zg30
Sucrose Octa-Acetate in Benzene+CDCl3 (1 drop)

5.646
5.635
5.812
5.793
5.772
5.685
5.674
5.657
5.618
5.508
5.331
5.311
5.310
5.291
5.027
5.000
5.000
4.993

1.872
1.867
1.860
1.776
1.735
1.697
1.680
1.608

BRUKER

Current Data Parameters
NAME Nov04
EXPHO 2
PROCNO 1

P2 - Acquisition Parameters
Date_ 20151104
Time 9.02
INSTRUM spect
PROBHD 5 mm PABBO BB/
PULPROG zg30
TD 32768
SOLVENT CDCl3
NS 2
DS 0
SWH 5000.000 Hz
FIDRES 0.192588 Hz
AQ 3.2767929 sec
RG 28.85
DN 100.000 usec
DE 6.50 usec
TE 294.2 K
D1 0.20000000 sec
TD0 1

----- CHANNEL f1 -----
SFO1 500.1325007 MHz
NUC1 1H
P1 8.86 usec
PLW1 23.01399994 W

P2 - Processing parameters
SI 65524
SF 500.1300000 MHz
WDW EM
SSB 0
LB 0.30 Hz
GB 0
FO 1.00

7.5 7.0 6.5 6.0 5.5 5.0 4.5 4.0 3.5 3.0 2.5 2.0 1.5 ppm

Position: 16.93, 19.92

15. Plot the Spectrum (2)

Bruker TopSpin (Student License)

File Edit View Processing Analysis Options Window Help

*2 /2 *8 /8

Browser Last50 Groups

- B:\NMRdata\FBR1
 - Doty-Installation
 - Nov04
 - 1 - deptqgssp.2 - 13C DEPTC
 - 2 - zg30 - 1H zg30 / Sucrose
 - 3 - selnogg - 1H selective NO
 - 4 - selnogg - 1H selective NO
 - 5 - selnogg - 1H selective NO
 - 6 - selno - 1H selective NOE (
 - 7 - zghd.2 - 1H Homonuclear
 - 8 - zghd.2 - 1H Homonuclear
 - Oct05
 - Oct07
 - Oct08
 - Oct13
 - Oct15
 - Oct16
 - B:\NMRdata\SSSC500
 - B:\NMRdata\SSSC600

1: Nov04 2 1 B:\NMRdata\FBR1

Spectrum ProcPars AcqPars Title PulseProg Peaks Integrals Sample Structure Plot Fid

Peaks

- Marks
- Labels .00
- ppm Position

Integrals

- Curve Limits...
- Labels .00
- Above X Axis
- Use for shift/scale

Axis

ppm Define...

Show scaling...

Placement

Pos. 0.30 2.82

Dim. 20.33 12.15

Axes, Grids, Curve...

Automation Actions...

1H zg30
Sucrose Octa-Acetate in Benzene+CDCl3 (1 drop)

Current Data Parameters

| | |
|---------|-------|
| NAME | Nov04 |
| EXPNO | 2 |
| F2PROC1 | 1 |

P2 - Acquisition Parameters

| | |
|---------|----------------|
| Date_ | 20151104 |
| Time | 9.02 |
| INSTRUM | axcpct |
| PROBHD | 5 mm PABBO EB |
| PULPROG | zg30 |
| TD | 32768 |
| SOLVENT | CDCl3 |
| NS | 8 |
| DS | 0 |
| SWH | 5000.000 Hz |
| FIDRES | 0.152588 Hz |
| AQ | 3.2767999 sec |
| RG | 28.85 |
| DN | 100.000 usec |
| DE | 6.50 usec |
| TE | 294.2 K |
| D1 | 0.20000000 sec |
| TD0 | 1 |

P2 - Processing parameters

| | |
|-----|-----------------|
| SI | 65536 |
| SP | 500.1300000 MHz |
| WDW | EM |
| SF | 0 |
| LE | 0.30 Hz |
| GE | 0 |
| FO | 1.00 |

5.846
5.833
5.812
5.793
5.772
5.685
5.674
5.530
5.519
5.508
5.331
5.311
5.310
5.291
5.027
5.020
5.006
4.999

1.872
1.867
1.860
1.776
1.739
1.697
1.680
1.608

2.06
1.02
1.01
1.02
1.00
1.02
6.18
1.08
25.12

7.5 7.0 6.5 6.0 5.5 5.0 4.5 4.0 3.5 3.0 2.5 2.0 1.5 ppm

Bruker Pulse Program (1)

The screenshot shows the Bruker TopSpin (Student License) interface. The main window displays the pulse program 'zg30' with the following code:

```
;zg30
;avance-version (12/01/11)
;1D sequence
;using 30 degree flip angle
;
;$CLASS=HighRes
;$DIM=1D
;$STYPE=
;$SUBTYPE=
;$COMMENT=
;$RECOMMEND=y

#include <Avance.incl>

"acqt0=-p1*0.66/3.1416"

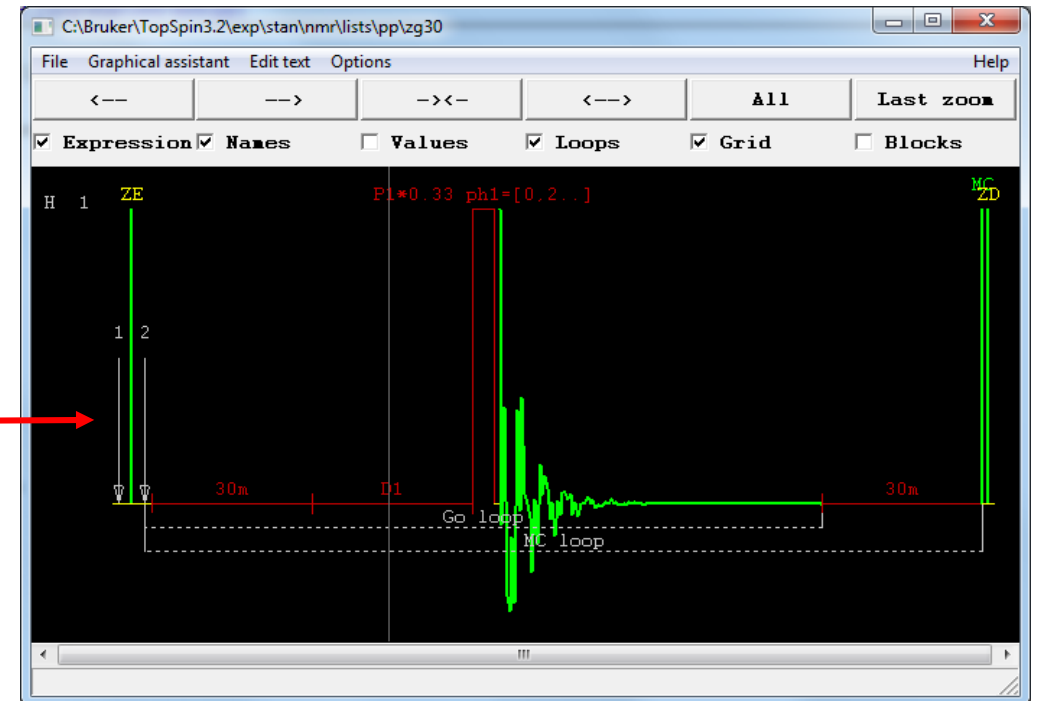
1 ze
2 30m
d1
p1*0.33 ph1
go=2 ph31
30m mc #0 to 2 F0(zd)
exit
```

Below the code, the phase list is defined:

```
ph1=0 2 2 0 1 3 3 1
ph31=0 2 2 0 1 3 3 1
```

Red boxes highlight the pulse sequence code and the phase list. A red arrow points from the pulse sequence code to the graphical assistant window on the right.

- 1 **ze** (Reset scan counter and enable the execution of dummy scans.)
- 2 **30m** (Set up a label for loop.)
d1 (Apply a delay of 'd1'.)
p1*0.33 ph1 (Apply a 30° pulse on f1 with phase list 'ph1'.)
go=2 ph31 (Execute one scan and then loop to line '2' (NS-1) times.)
30m mc #0 to 2 F0(zd) (mc macro to write data, including a disk writer (*wr*), a file increment (*if*) and memory initialization (*zd*).)
exit (The end of the pulse sequence.)



Bruker Pulse Program (2)

File Edit View Processing Analysis Options Window Help

Browser Last50 Groups

1 Oct16 4 1 B:\NMRdata\FBR1

Spectrum ProcPars AcqPars Title PulseProg Peaks Integrals Sample Structure

File: zgpg30 (C:\Bruker\TopSpin3.2\exp\stan\nmr\lists\pp)

```
"acqt0=-p1*0.66/3.1416"

1 ze
  d11 p112:f2
2 30m do:f2
  10u p113:f2
  d11 cpd2:f2
  DELTA
  4u do:f2
  10u p112:f2
  100m cpd2:f2
  p1*0.33 ph1
  go=2 ph31
  30m do:f2 p113:f2 mc #0 to 2 F0(zd)
exit

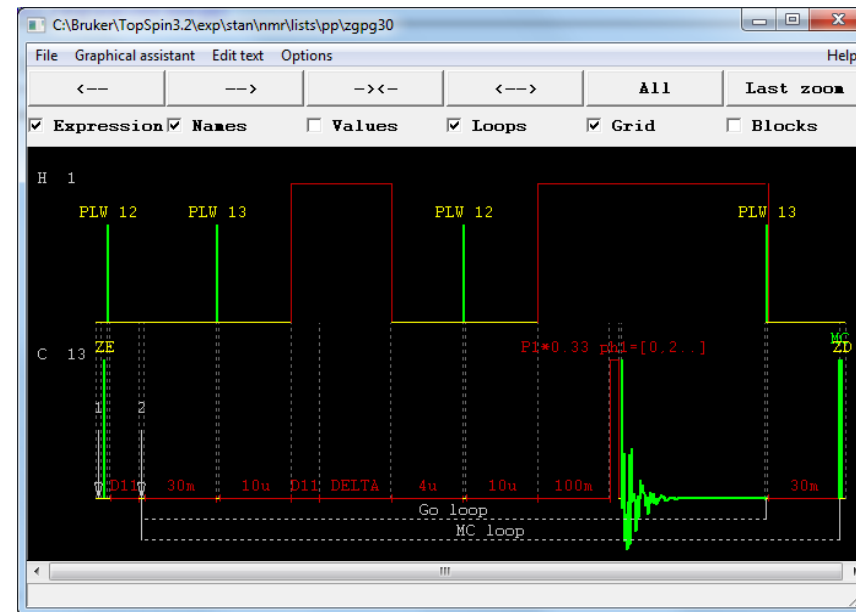
ph1=0 2 2 0 1 3 3 1
ph31=0 2 2 0 1 3 3 1
```

Turn off decoupling on f2.

Turn on CPD decoupling on f2.

Turn off decoupling on f2.

Turn on CPD decoupling on f2.



File Edit View Processing Analysis Options Window Help

Browser

1 Nov03 3 1 B:\NMRdata\SSSC500

Spectrum ProcPars AcqPars Title PulseProg Peaks Integrals Sample

File: zgpg (C:\Bruker\TopSpin3.2\exp\stan\nmr\lists\pp)

Description of Parameters

```
;p11 : f1 channel - power level for pulse (default)
;p112: f2 channel - power level for CPD/BB decoupling
;p113: f2 channel - power level for second CPD/BB decoupling
;p1 : f1 channel - high power pulse
;d1 : relaxation delay; 1-5 * T1
;d11: delay for disk I/O [30 msec]
;ns: 1 * n, total number of scans: NS * TD0
;cpd2: decoupling according to sequence defined by cpdprg2
;pcpd2: f2 channel - 90 degree pulse for decoupling sequence
```