

TopSpin

Data Acquisition

→ **Guided Acquisition User Interface: *TopGuide***

→ **Parameter Driven User Interface : *zg***

→ **Automation User Interface : *IconNmr***

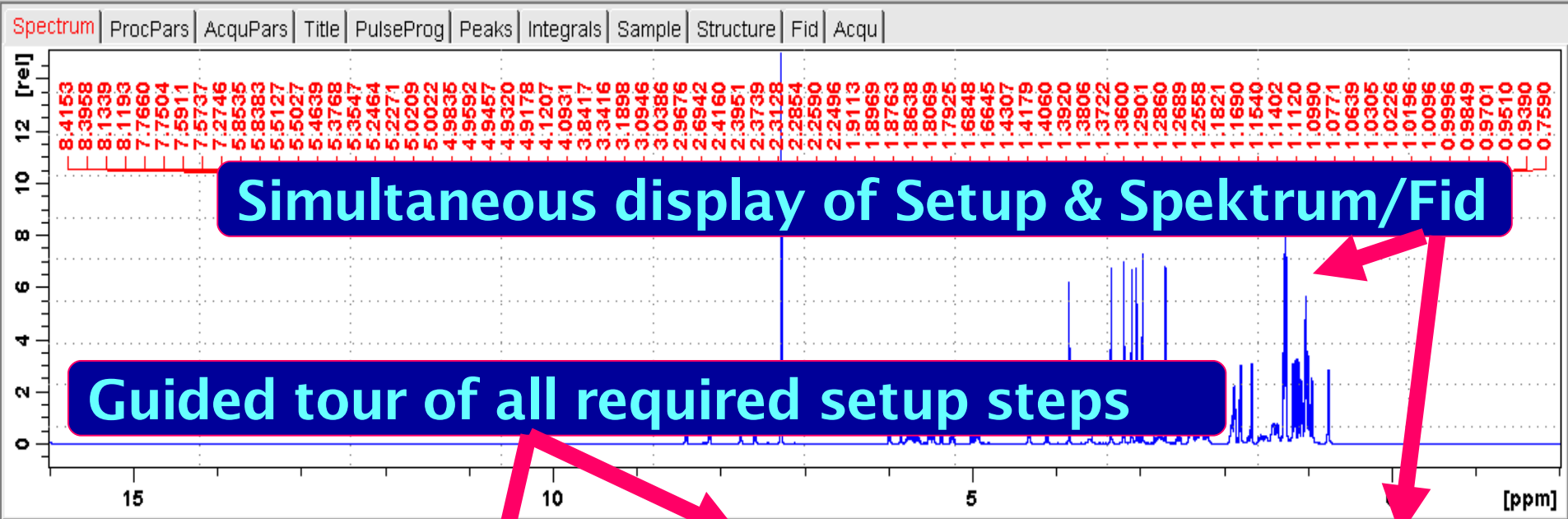
→ **Acquiring Spectra of Biomolecules: *BioTools***

→ **Controlling Spectrometer Sub-Systems**

→ **Remote Spectrometer Access**

- **Guided Acquisition User Interface for:**
 - First time users*
 - Occasional users*
 - Routine users (may skip setup steps)*
- **Supports major 2D experiments**
- **Guarantees successful spectrum acquisition**
- **Includes data processing and plotting!**

Data Acquisition: *TopGuide*



Choose Experiment...

Experiment data base: standard experiments 1D/2D

Dimension: 2-dimensional

Class: homo-nuclear

Nucleus 1: 1H

COSY
TOCSY
NOESY

GO

STOP

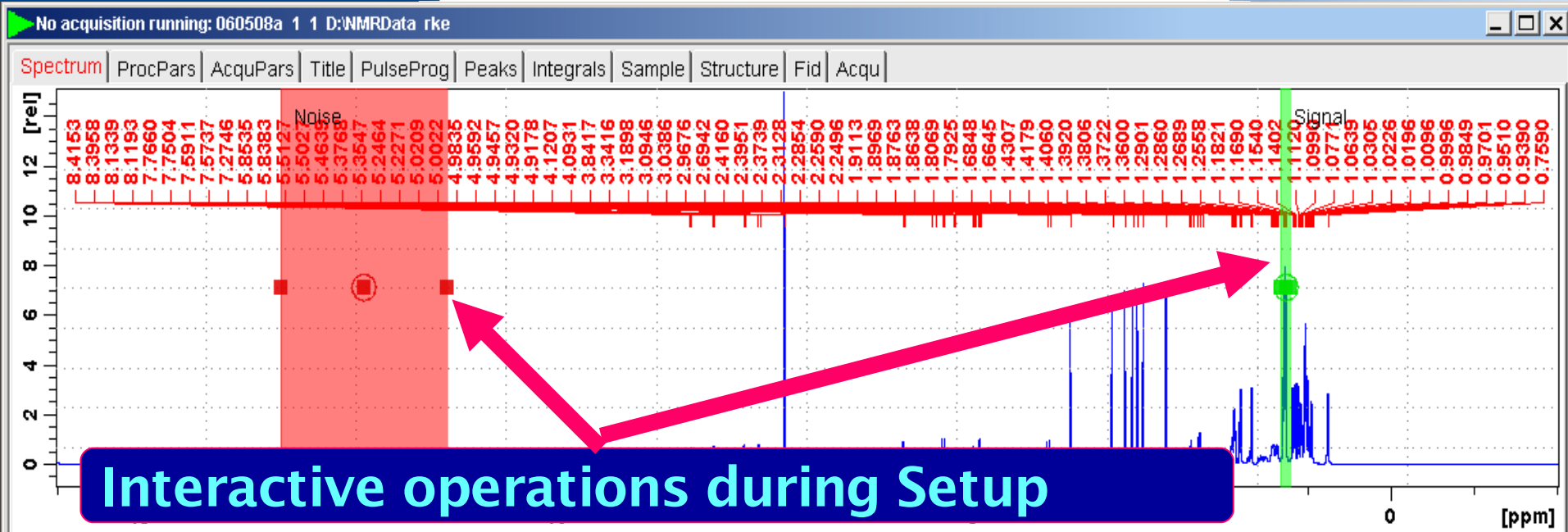
Tools icons: group of people, wrench and screwdriver

< Back | ▾ Status/Sample New experiment Next >

Tour supplemented by explanations

Select the nucleus/nuclei.
Nucleus 1 is always the observed (i.e. detected) nucleus, the other nuclei are used for decoupling and/or indirect dimensions.

Data Acquisition: *TopGuide*



Interactive operations during Setup

Define reference signal for signal to noise determination ...

Left limit of noise region	<input type="text" value="13.321"/>
Right limit of noise region	<input type="text" value="11.321"/>
Left limit of signal region	<input type="text" value="1.324"/>
Right limit of signal region	<input type="text" value="1.214"/>

Current signal/noise 5203.54



Determine the signal to noise (S/N) of your reference spectrum. The region around the highest signal (green) neglecting the solvent and a noise region (red) of up to 2 ppm are pre-selected.



You should select the signal(s) (green region) you are mainly interested in. The calculated S/N is shown above. It will be used for all further experiments with this sample to estimate a necessary NS (number of scans).



- **User Interface for:**
 - Routine users*
 - Expert users*
 - Method development*
- **Provides full flexibility and access to all software modes and hardware accessories**
- **Effective parameter optimization support**

Data Acquisition: *Parameter Driven*



The screenshot displays the Bruker TopSpin software interface. The top window shows a real-time spectrum plot with a yellow text box containing instructions. The bottom window shows the 'AcquPars' tab with various acquisition parameters.

Instructions:

- Set up acquisition parameters
- Type *zg* to start acquisition
- Observe Fid in realtime

AcquPars Parameters:

Parameter	Value	Description
PULPROG	zg	Current pulse program
AQ_mod	DQD	Acquisition mode
FnMODE	C	Acquisition mode for 2D/3D
TD	2048	Size of fid
NS	1	Number of scans
DS	8	Number of dummy scans
TD0	1	Loop count for 'td0'
SW [ppm]	13.3298	Spectral width
SWH [Hz]	6666.667	Spectral width
IN_010	0.00015000	Increment for delay D0 (F1)
ND_010	1	Number of delays in pulse program for D0 (F1)

Data Acquisition: Acquisition Status Panel



The screenshot displays the Bruker TopSpin software interface. On the left is a file browser showing a directory structure for NMR data. The main window shows a 2D NMR spectrum with green peaks. A yellow callout box with blue text reads "Acquisition and spectrometer status always visible!". A red arrow points from this box to the "Sample" icon in the status bar. Another red arrow points from the "Sample" icon to the "Time" field in the status bar. A third red arrow points from the "Time" field to the "BSMS status message" field.

Acquisition and spectrometer status always visible!

Sample

Acquisition information: no acquisition running

Fid Flash: [grid]

Lock: [grid]

Sample: [Sample icon]

POWCHK: [Red X]

Time: 12:23 Oct 18

Spooler: running: 0, queued: 0, delayed: 0

BSMS status message: Z3-2314, Autashim ✓, Locked ✓, Error

Data Acquisition: *Parameter Optimization*




2 KBr_STMAS 801 1 C:\Bruker\TOPSPIN guest

store as 2D data (ser file)
 The AU program specified in AUNM will be executed
 Perform automatic baseline correction (ABSF)
 Overwrite existing files (disable confirmation Message)
 Run optimisation in background

WDW= no
PH_mod= pk
FT_mod= fqc

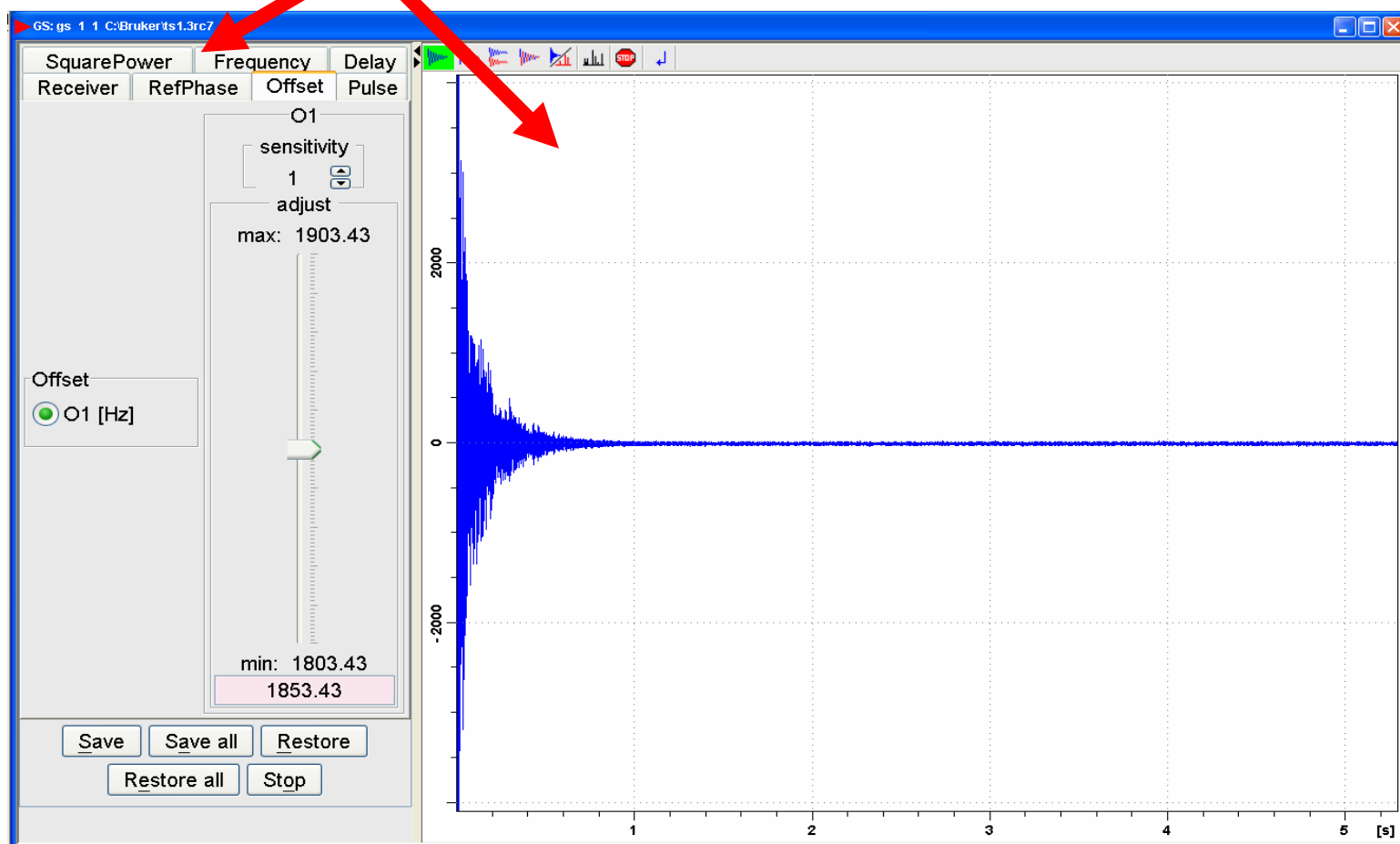
OPTIMIZE	GROUP	PARAMETER	OPTIMUM	STARTVAL	ENDVAL	NEXP	VARMOD	INC
Step by step	1	p3	POSMAX	1	8	15	LIN	.5
Step by step	1	pl2	POSMAX	4.5	7.0	6	LIN	0.5
No optimization	1	sp0	POSMAX	4.5	7.0	6	LIN	0.5
Step by step	1	p31	POSMAX	4.0	8.0	21	LIN	.2
Step by step	1	p15	POSMAX	500	5000	10	LIN	500
Step by step	1	p1	ZERO	1	12	12	LIN	1



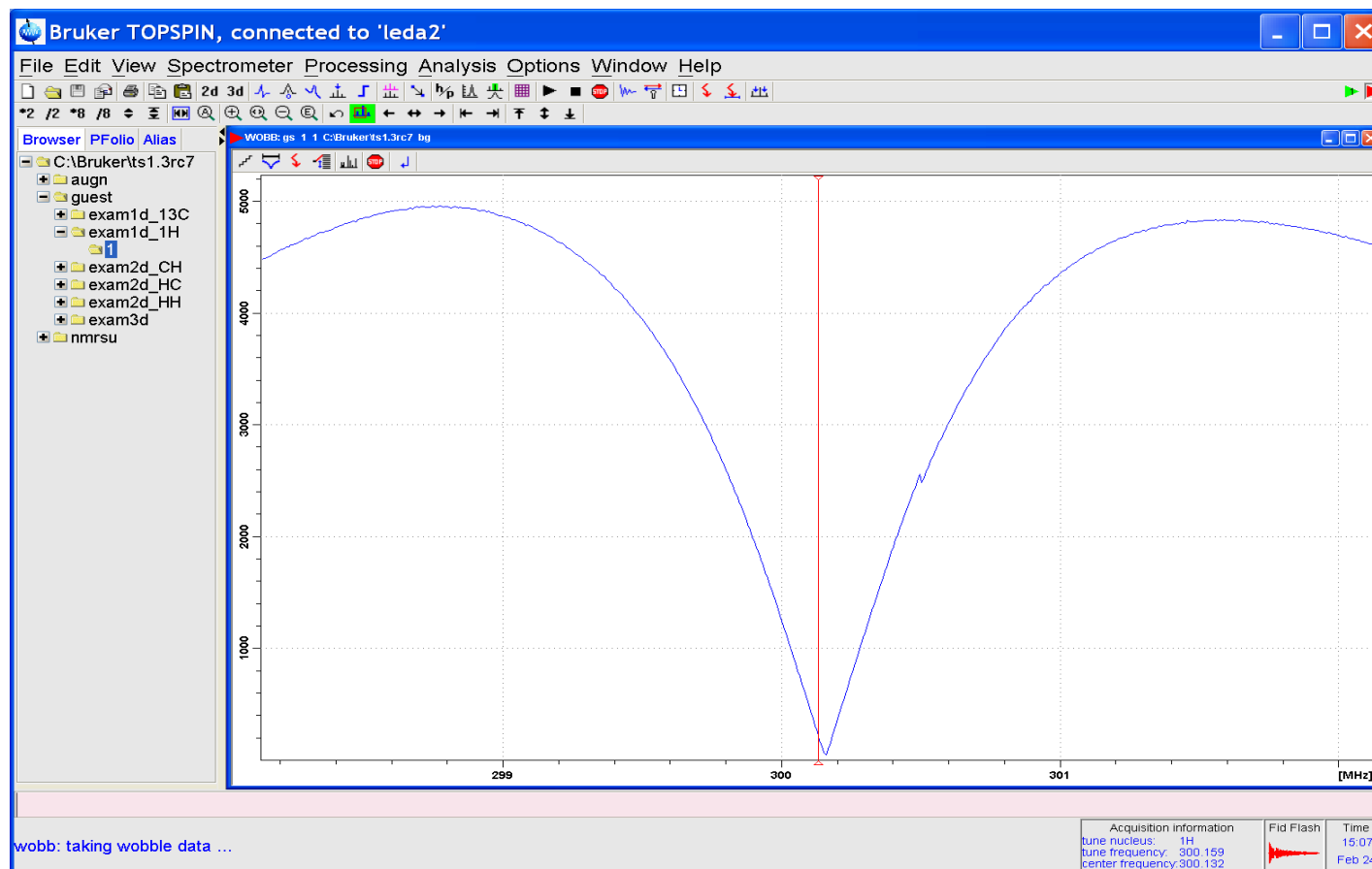
Optimize parameters by automatic variation of selected parameters over a defined range

Start optimize Skip current optimizat... Show protocol Add parameter Restore Save
Read array file Save array file as ... Stop optimization Delete parameter Help Display Dataset

Interactive parameter optimization:
Adjust parameters and watch the effect
on fid or spectrum



Optimization of wobble curve during manual tuning and matching



Graphical user interface for fully automated acquisition and processing

- **Supports sample changers and preparation robots**
- **Configurable 1-click experiment setup**
- **Multi-user support, routine users, walk-up users**
- **Spreadsheet import**
- **Priority sample support**
- **WEB interface for remote setup, incl. small screen
Pocket PC support**

Automation Interface : *IconNmr*



ICON-NMR: Automation Oct15-2004-1800-nmrsv

File Run Holder View Find Parameters Options Help

Holder	Type	Status	Disk	Name	No.	Solvent	Experiment	Par	Title / Orig	Pri	Time	User
1	6	Available	/opt/ts13b8	15102004-nmrsv	10	CDCI3	PROTON		TS13b8 Psyche		00:02:28	nmrsu
		Available	/opt/ts13b8	15102004-nmrsv	11	CDCI3	HSQCETGP		TS13b8 Psyche		00:14:35	nmrsu
		F2	/opt/ts13b8	15102004-nmrsv	10							nmrsu
		Available	/opt/ts13b8	15102004-nmrsv	12	CDCI3	HMBCGPND		TS13b8 Psyche			nmrsu
		F2	/opt/ts13b8	15102004-nmrsv	10							nmrsu
		Available	/opt/ts13b8	15102004-nmrsv	13	CDCI3	COSYGPSW		TS13b8 Psyche		00:04:06	nmrsu
		F2	/opt/ts13b8	15102004-nmrsv	10							nmrsu
		Available	/opt/ts13b8	15102004-nmrsv	14	CDCI3	HSQC GP		TS13b8 Psyche		00:14:38	nmrsu
		F2	/opt/ts13b8	15102004-nmrsv	10							nmrsu
		Available	/opt/ts13b8	15102004-nmrsv	15	CDCI3	HMQC		TS13b8 Psyche		00:57:55	nmrsu
		F2	/opt/ts13b8	15102004-nmrsv	10							nmrsu
2	8	Queued	/opt/ts13b8	15102004-nmrsv	20	C6D6	PROTON		TS13b8 Psyche		00:01:59	nmrsu
		Queued	/opt/ts13b8	15102004-nmrsv	21	C6D6	HSQCETGP		TS13b8 Psyche		00:56:44	nmrsu
		F2	/opt/ts13b8	15102004-nmrsv	20							nmrsu
		Queued	/opt/ts13b8	15102004-nmrsv	22	C6D6	HMBCGPND		TS13b8 Psyche			nmrsu
		F2	/opt/ts13b8	15102004-nmrsv	20							nmrsu
		Queued	/opt/ts13b8	15102004-nmrsv	23	C6D6	COSYGPSW		TS13b8 Psyche		00:04:06	nmrsu
		F2	/opt/ts13b8	15102004-nmrsv	20							nmrsu
		Queued	/opt/ts13b8	15102004-nmrsv	24	C6D6	HSQC GP		TS13b8 Psyche		00:56:53	nmrsu

Submit Cancel Edit Delete

Date	Time	Holder	Name	No.	Experiment	ATM	Ro	Lock	Shim	Acq	Proc	User	Disk	Title / Orig	Remarks
2004-10-17	14:02:49	7	15102004-nmrsv	55	HMQC					✓	✓	nmrsu	/opt/ts13b8	TS13b8 Psyche	
2004-10-17	13:05:30	7	15102004-nmrsv	54	HSQC GP					✓	✓	nmrsu	/opt/ts13b8	TS13b8 Psyche	
2004-10-17	13:01:05	7	15102004-nmrsv	53	COSYGPSW					✓	✓	nmrsu	/opt/ts13b8	TS13b8 Psyche	
2004-10-17	12:24:23	7	15102004-nmrsv	52	HMBCGPND					✓	✓	nmrsu	/opt/ts13b8	TS13b8 Psyche	
2004-10-17	11:26:42	7	15102004-nmrsv	51	HSQCETGP					✓	✓	nmrsu	/opt/ts13b8	TS13b8 Psyche	
2004-10-17	11:18:22	7	15102004-nmrsv	50	PROTON	✓		✓	⚙	✓	✓	nmrsu	/opt/ts13b8	TS13b8 Psyche	Shim timed out

Busy Until: Mon 22:35 | Day Experiments: 08:56 | Night Experiments: 09:34 | User: mg

Experiment setup

Sample status display

Automation Interface: *IconNmr*



Experiment setup via WEB browser
using PC or Pocket PC

ICON-NMR on TARA: Bruker

File Edit View Go Bookmarks Tools Help

https://tara:8018/template-automation.htm

BRUKER icon web

Automation - Running - Busy until : Tue 00:36 - Experiments Day : 08:56 - Night : 09:34

Help
Logout

Stop
Pause

Logged in as mg

Spectrometer: TARA: Bruker_default_av500

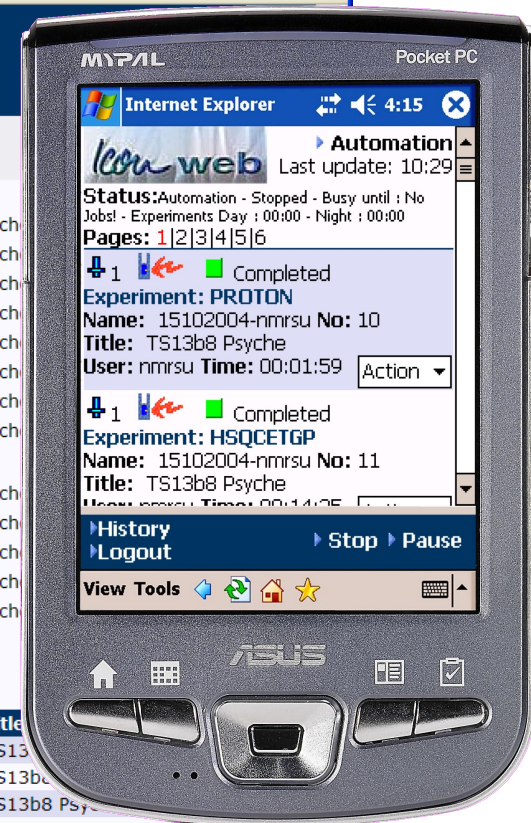
[ro acqu]	Failed	Locking	Field	Shim	Receiver	Gain	Acquire	Data	Process	Data
<input type="checkbox"/>	2		Running							
<input type="checkbox"/>	2		Running	/opt/ts13b8	15102004-nmrsu	20	C6D6	PROTON		TS13b8 Psyche
<input type="checkbox"/>	2		Queued	/opt/ts13b8	15102004-nmrsu	21	C6D6	HSQCETGP		TS13b8 Psyche
<input type="checkbox"/>	2		Queued	/opt/ts13b8	15102004-nmrsu	22	C6D6	HMBGCPND		TS13b8 Psyche
<input type="checkbox"/>	2		Queued	/opt/ts13b8	15102004-nmrsu	23	C6D6	COSYGPSW		TS13b8 Psyche
<input type="checkbox"/>	2		Queued	/opt/ts13b8	15102004-nmrsu	24	C6D6	HSQCQP		TS13b8 Psyche
<input type="checkbox"/>	2		Queued	/opt/ts13b8	15102004-nmrsu	25	C6D6	HMQC		TS13b8 Psyche
<input type="checkbox"/>	2		Queued	/opt/ts13b8	15102004-nmrsu	26	C6D6	MLEVPHSW		TS13b8 Psyche
<input type="checkbox"/>	2		Queued	/opt/ts13b8	15102004-nmrsu	27	C6D6	NOESYPHSW		TS13b8 Psyche
<input type="checkbox"/>	3		Available							
<input type="checkbox"/>	3		Available	/opt/ts13b8	Oct15-2004-nmrsu_add	10	CDCI3	PROTON		TS13b8 Psyche
<input type="checkbox"/>	3		Available	/opt/ts13b8	Oct15-2004-nmrsu_add	11	CDCI3	C13DEPT45		TS13b8 Psyche
<input type="checkbox"/>	3		Available	/opt/ts13b8	Oct15-2004-nmrsu_add	12	CDCI3	HCCOSW		TS13b8 Psyche
<input type="checkbox"/>	3		Available	/opt/ts13b8	Oct15-2004-nmrsu_add	13	CDCI3	C13CPD		TS13b8 Psyche
<input type="checkbox"/>	3		Available	/opt/ts13b8	Oct15-2004-nmrsu_add	14	CDCI3	HCCOLOCSW		TS13b8 Psyche

Submit Add Cancel Delete

Date	Time	Holder Name	Nr. Exp	ATM	Rot	Lock	Shim	Aqu	Proc	User	Title
2005-02-21	15:33:33	2	15102004-nmrsu	20	PROTON	✓	X			nmrsu	TS13b8 Psyche
2004-10-17	21:24:52	7	15102004-nmrsu	59	HCCOLOCSW			✓	✓	nmrsu	TS13b8 Psyche
2004-10-17	20:17:32	7	15102004-nmrsu	58	C13CPD			✓	✓	nmrsu	TS13b8 Psyche
2004-10-17	17:22:17	7	15102004-nmrsu	57	ROESYPHSW			✓	✓	nmrsu	TS13b8 Psyche
2004-10-17	15:58:33	7	15102004-nmrsu	56	MLEVPHSW			✓	✓	nmrsu	TS13b8 Psyche
2004-10-17	14:02:49	7	15102004-nmrsu	55	HMQC			✓	✓	nmrsu	TS13b8 Psyche
2004-10-17	13:05:30	7	15102004-nmrsu	54	HSQCQP			✓	✓	nmrsu	TS13b8 Psyche

Version: 4.0
© 2005 Bruker BioSpin
Done

tara:8018



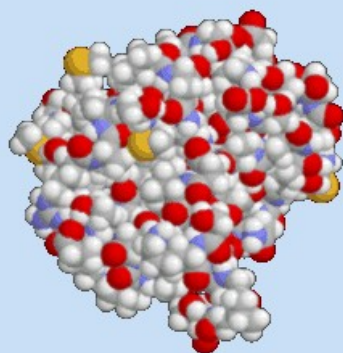
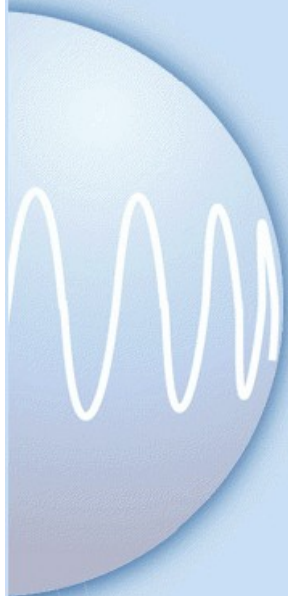
Acquisition user interface tailored for biological applications such as protein structure determination or studying protein-ligand bindings

- **Guided macro-molecule multi-experiment acquisition**
- **Automatic acquisition optimization**
- **1-click multi-acquisition launch**
- **Quick screen / scout spectral overview mode**
- **Experiment tree / operation adaptable via IconNmr.**

NMR Biotools

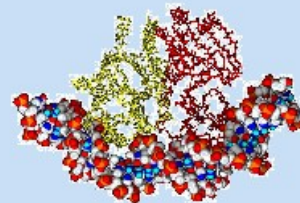
BioTools entry page

Create a New Project

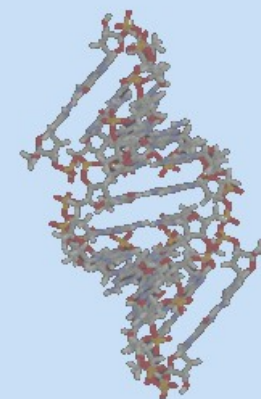


PROTEIN

Open an existing Project



PROTEIN-LIGAND



DNA-RNA

Expert Mode

Experiment tree for protein-ligand studies

NMR Biotools

Submit/Cancel Experiments from the Queue...then...

Start

Stop

Save +



ix_filtered_exps

Sample Setup

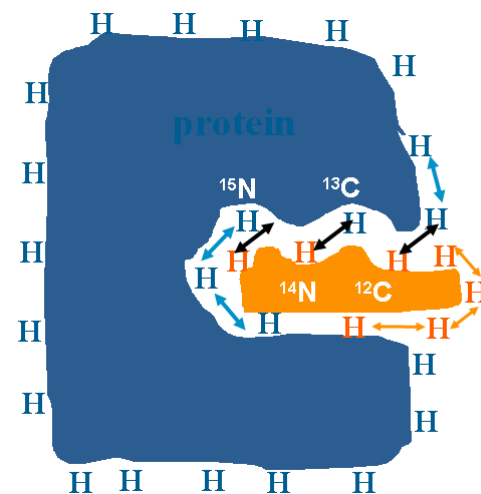
Biomolecular 1D/2D experiments

Protein/Ligand Experiments

filtered NOESY Experiments

3D (15N/13C) (f3, f1(13CEvo)) filtered NOESY Queued
3D (15N/13C) (f3, f1(15NEvo)) filtered NOESY Queued
(15N, 13C) (f1) filtered NOESY Queued
(15N, 13C) (f2) filtered NOESY Queued
3D (15N/13C) (f1, f2(13CEvo)) filtered NOESY Queued
15N double half filtered 2D NOESY Queued
(15N, 13C) (f1,f2) filtered NOESY Queued
(15N, 13C) (f1,f2) filtered NOESY (I) Queued
3D (15N/13C) (f1, f2(15NEvo)) filtered NOESY Queued

... on holder 1 (H2O+D2O)



TopSpin provides software panels to access all spectrometer sub-systems

- **Frequency routing**
- **Sample, shim, lock control**
- **Manual and automatic tuning & matching**
- **Interactive parameter optimization**
- **VTU control**
- **Magnet information system**

Visualize and configure the pulse pathway from frequency generation to the probe

frequency	logical channel	amplifier	preamplifier
BF1 300.13	MHz NUC1		
SFO1 300.131853	MHz <input type="text" value="F1"/>	<input type="text" value="FCU1/SGU1"/>	<input type="text" value="2H"/>
OFS1 1853.4	Hz <input type="text" value="1H"/>	<input type="text" value="X 150 W"/>	<input type="text" value="1H"/>
BF2 300.13	MHz NUC2		
SFO2 300.13	MHz <input type="text" value="F2"/>	<input type="text" value="FCU2/SGU2"/>	<input type="text" value="X-BB19F_2HS"/>
OFS2 0.0	Hz <input type="text" value="off"/>	<input type="text" value="H 60 W"/>	
BF3 300.13	MHz NUC3		
SFO3 300.13	MHz <input type="text" value="F3"/>	<input type="text" value="FCU3/SGU3"/>	
OFS3 0.0	Hz <input type="text" value="off"/>	<input type="text" value="X 300 W"/>	

● : cortab available

Controlling Spectrometer Sub-Systems



The *BSMS panel* allows you control sample, shims and lock by software

BSMS Control Suite

Main Lock/Level Shim Autoshim Service Log

AUTO

Phase Power Gain Lock Shim

LOCK

Lock Phase Power Gain

SAMPLE

LIFT SPIN Measure Rate

SHIM

Z X Y XY
Z² XZ YZ X²-Y²
Z³

VALUE: Z

	Previous	Actual	Step	
Absolute	6126	6269	+	Reset
Difference	4	139	-	

Stepsize: 1

STD BY

Config

External

Sample: down missing up

BSMS Control Suite

Main Lock/Level Shim Autoshim Service Log

LOCK & SPIN

Lock Phase Gain SPIN

SHIM

Z	X	Y	XY	X ² -Y ²	X ³	Y ³
Z ²	XZ	YZ	XYZ	(X ² -Y ²)Z	X ³ Z	Y ³ Z
Z ³	XZ ²	YZ ²	XYZ ²	(X ² -Y ²)...		
Z ⁴	XZ ³	YZ ³	XYZ ³	(X ² -Y ²)...		
Z ⁵	XZ ⁴	YZ ⁴	XYZ ⁴	(X ² -Y ²)...		
Z ⁶	XZ ⁵	YZ ⁵	XYZ ⁵	(X ² -Y ²)...		

VALUE

	Previous	Actual	Step	
Absolute			+	Reset
Difference			-	

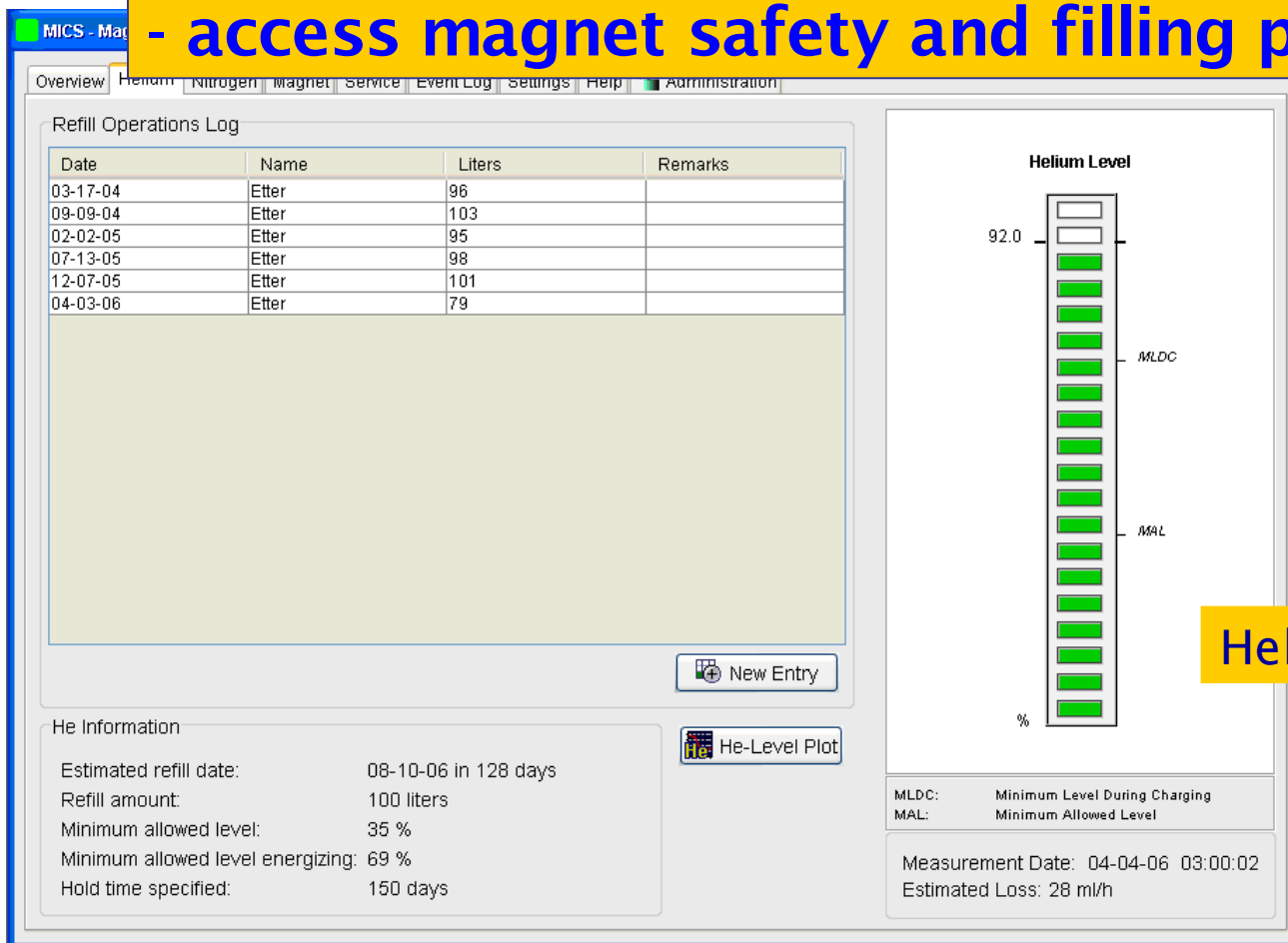
Stepsize: 0

STD BY

Sample: down missing up

Magnet Information & Control System:

- supervise Helium and Nitrogen levels
- receive automatic refill notification
- access magnet safety and filling procedures



MICS - Magnet Information & Control System

Overview Helium Nitrogen Magnet Service Event Log Settings Help Administration

Refill Operations Log

Date	Name	Liters	Remarks
03-17-04	Etter	96	
09-09-04	Etter	103	
02-02-05	Etter	95	
07-13-05	Etter	98	
12-07-05	Etter	101	
04-03-06	Etter	79	

New Entry

He Information

Estimated refill date: 08-10-06 in 128 days
Refill amount: 100 liters
Minimum allowed level: 35 %
Minimum allowed level energizing: 69 %
Hold time specified: 150 days

He-Level Plot

Helium Level

92.0

MLDC

MAL

%

Helium Watch

MLDC: Minimum Level During Charging
MAL: Minimum Allowed Level

Measurement Date: 04-04-06 03:00:02
Estimated Loss: 28 ml/h

Controlling Spectrometer Sub-Systems



MICS - Magnet Information and Control System

Overview Helium Nitrogen Magnet Service Event Log Settings Help

Events

- He refill due Notification 14 Days before
- Min allowed He level reached Warning 7 Days before
- He below minimum allowed level Alert
- Excessive He loss detected Warning
- He level measurement has failed Error

Actions

	Category	Show Dialog	Play Sound
Notification		<input checked="" type="checkbox"/>	<input type="checkbox"/>
Warning		<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
Alert		<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>

Mail Settings

Outgoing Mail Server (SMTP): smtp.bruker.com

Change

Notification settings panel



Helium level plot with estimated refill date

Automatic Shimming

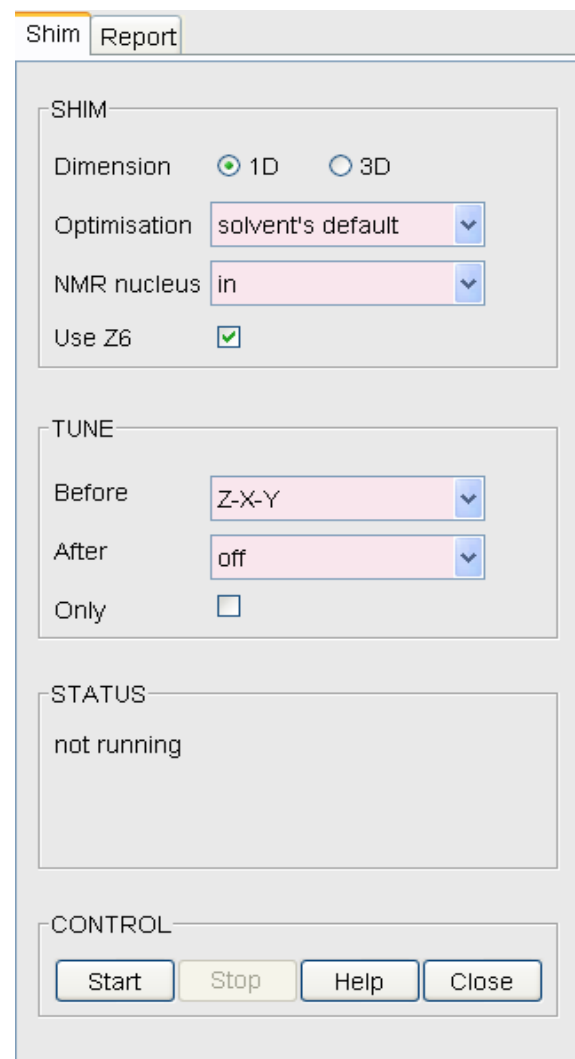
TopShim is *the* comprehensive tool for shimming:

→ Obtain excellent resolution and solvent suppression easily and fast.

→ Robust and intelligent implementation of gradient shimming.

→ Optional integrated tune functionality.

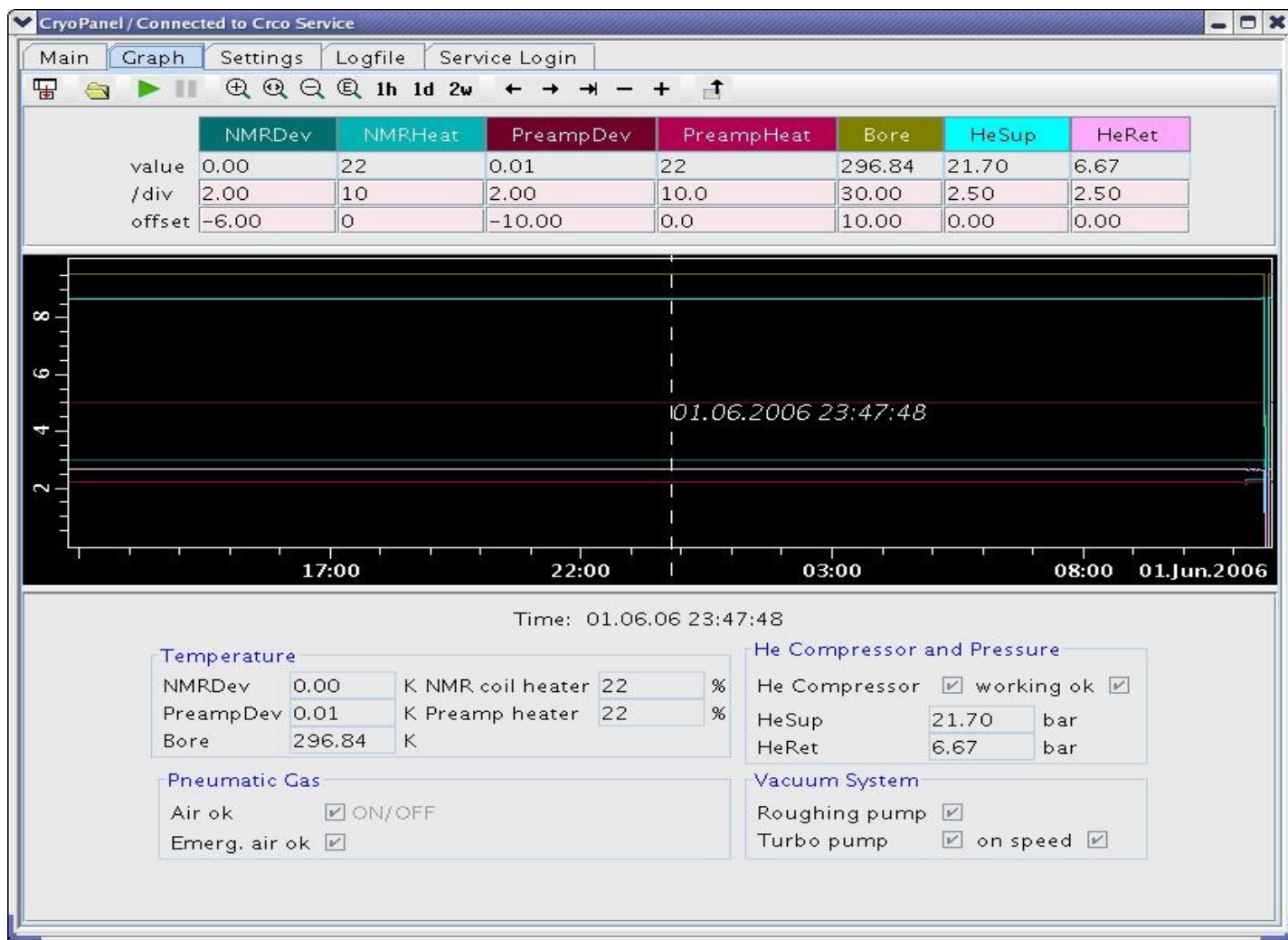
→ TopShim can be operated manually as well as during automation



The screenshot shows the TopShim software interface with the following settings:

- Shim** (selected tab) | Report
- SHIM**
 - Dimension: 1D 3D
 - Optimisation: solvent's default (dropdown)
 - NMR nucleus: in (dropdown)
 - Use Z6:
- TUNE**
 - Before: Z-X-Y (dropdown)
 - After: off (dropdown)
 - Only:
- STATUS**
 - not running
- CONTROL**
 - Start (button)
 - Stop (button)
 - Help (button)
 - Close (button)

Cryoprobe Control Panel



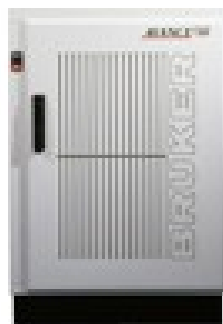
Features:

- Full spectrometer control from remote PC via network
- Several protocol possibilities:
 - telnet / SSH / X11 on Linux systems
 - Windows Terminal Server
 - VNC public domain
 - TopSpin internal protocol (no installation of 3rd party software required, high speed, no extra TopSpin license required)

Remote Spectrometer Access



Laboratory



**view fid,
lock, bsms
...**

zg, ns, ...

*Secure,
encrypted,
SSL*

Office / Home / Beach? / ...

