JEOL Delta acquisition and Jason processing

New NMR software

13th June 2024

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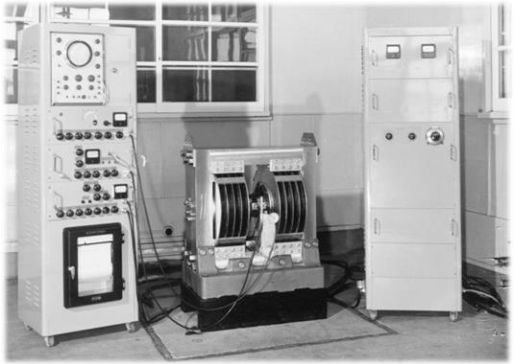
JEOL UK Demo Lab nmrapps@jeoluk.com

Some highlights of JEOL NMR history

1956
JNM-1 (32MHz commercial NMR)



1972
JNM-FX60 (Fourier Transformed NMR)

1981
JNM-GX400

(First automated NMR)

1985: First autotunable probe

1996: First Windows NMR software

2005: First Mac NMR software

2016: First liquid state autotunable probe with both double and triple resonance modes

2002
JNM-ECA series

(Modular NMR with sequencers and full automation)

2014
JNM-ECZ series

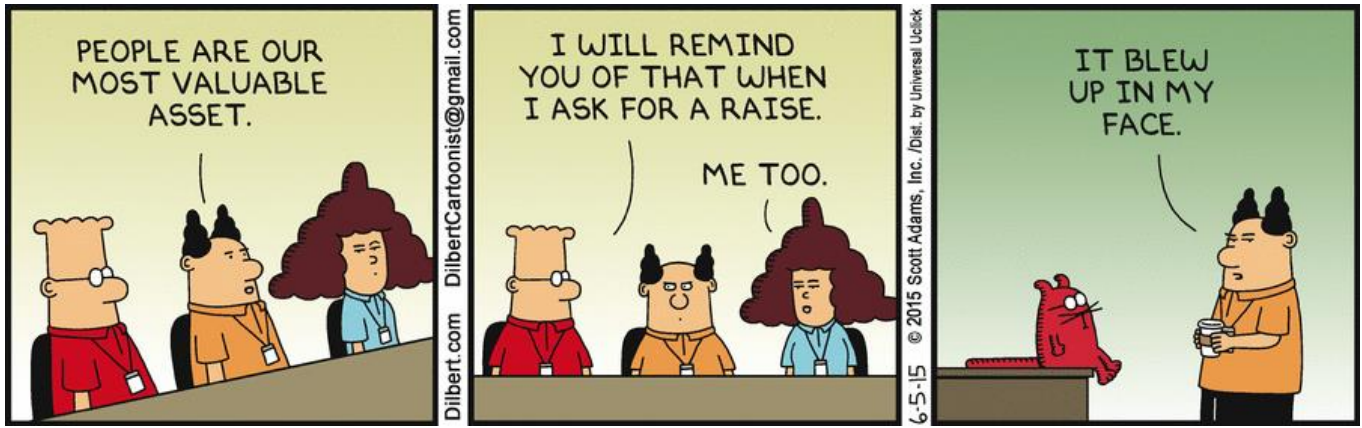
(Transceiver system)

And in 2021 …

JEOL ECZL spectrometer

see NMR in a new light

User management



Automation setup

Flexible configuration of defaults and privileges for different users, including:

Variable temperature, Solids mode, Data folder, Email address, **user operators**, **user profiles,** multiple backup structure as per user, project, date, etc.

Automation setup

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Variable temperature, Solids mode, Data folder, Email address, user operators, …

Usage reports, logs, statistics and billing:

JEOL Instrument:	Virtual_spectrometer			
Usage Log Report:	1-AUG-2022 - 18-AUG-2022			
User	Cost Center	Active(min)	Rate/Hr	Active Charge
Botana	<blank>	63	0.00	0.00
console	<blank>	0	0.00	0.00
Delta	<blank>	200	0.00	0.00
demo	<blank>	35	10.00	5.83
tesT	<blank>	2	0.00	0.00
		300		**5.83**

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Usage reports, logs, statistics and billing:

Detailed output:

* Breakdown of folder 'demo'														
Operation Began	Operation End	Duration	Duration/day	Username	Job Name	Experiment Began	Experiment End	Experiment Duration	Experiment Duration/day	Experime	Project Na	Folder	Filename	Job Result
14-12-22 23:14	14-12-22 23:14	0 days 00:(	0.00037037	demo	Proton	14-12-22 23:14	14-12-22 23:14	0 days 00:00:18	0.000208333	proton.jxp		demo	test1_1H	FINISHED
15-12-22 10:19	15-12-22 10:19	0 days 00:(	0.000208333	demo	Proton	15-12-22 10:19	15-12-22 10:19	0 days 00:00:08	9.25926E-05	proton.jxp		demo	sample1_1H	FINISHED
21-01-23 21:46	21-01-23 21:46	0 days 00:(	0.000300926	demo	Proton	21-01-23 21:46	21-01-23 21:46	0 days 00:00:18	0.000208333	proton.jxp		demo	aa1_1H	FINISHED
* Breakdown of folder 'organometallic/PhD_1'														
Operation Began	Operation End	Duration	Duration/day	Username	Job Name	Experiment Began	Experiment End	Experiment Duration	Experiment Duration/day	Experime	Project Na	Folder	Filename	Job Result
29-06-23 9:38	29-06-23 9:38	0 days 00:(	0.000243056	test	1H	29-06-23 9:38	29-06-23 9:38	0 days 00:00:10	0.000115741	proton.jxp		organome	sampl3_PROTON	FINISHED
* Breakdown of folder 'organometallic/PhD_2'														
Operation Began	Operation End	Duration	Duration/day	Username	Job Name	Experiment Began	Experiment End	Experiment Duration	Experiment Duration/day	Experime	Project Na	Folder	Filename	Job Result
16-12-22 19:21	16-12-22 19:22	0 days 00:(	0.000196759	test2	1H	16-12-22 19:21	16-12-22 19:22	0 days 00:00:10	0.000115741	proton.jxp		organome	fds_PROTON	FINISHED

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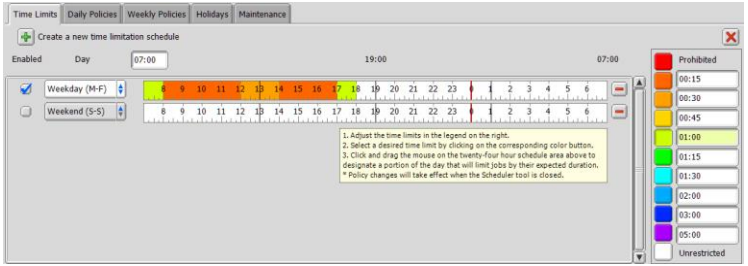
		300		**5.83**

Custom time limitations:



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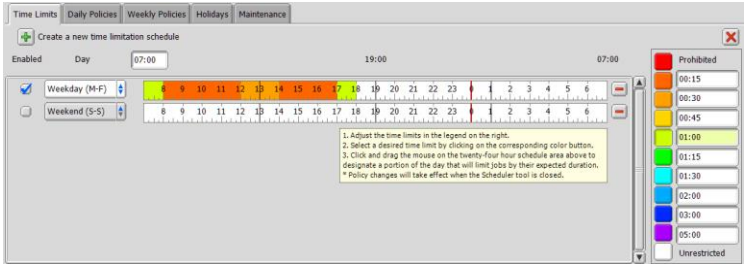
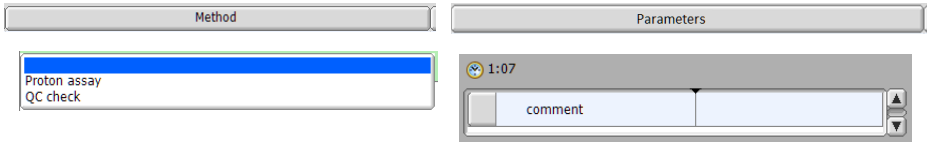
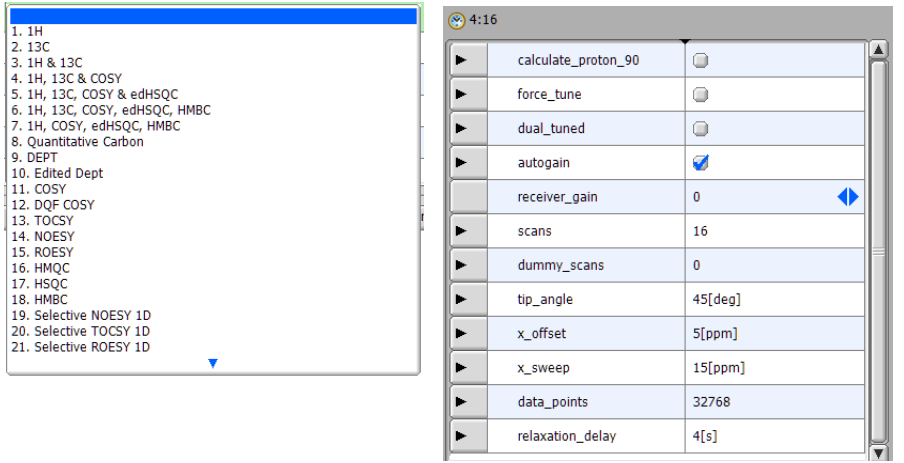


Fully customizable methods for each user

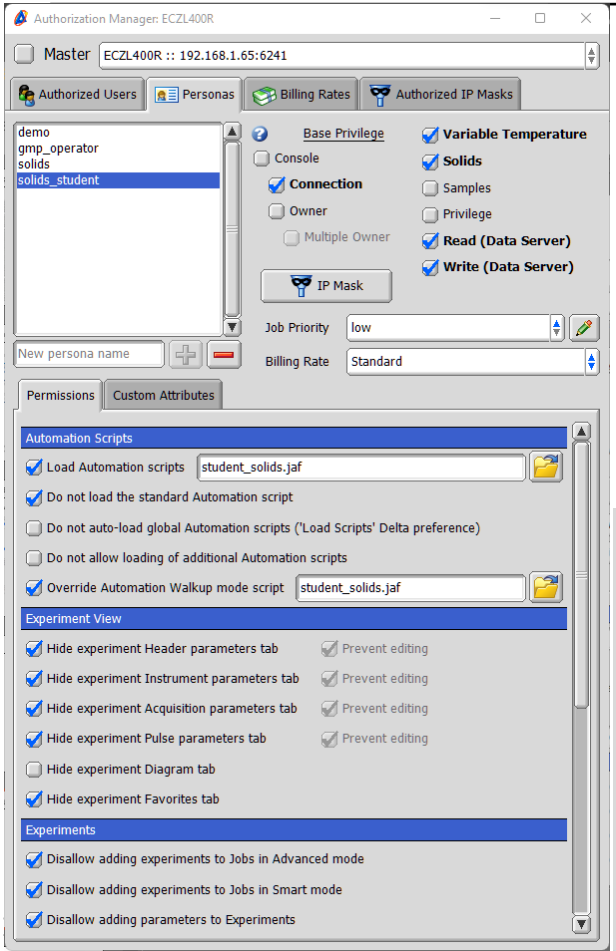
User 1

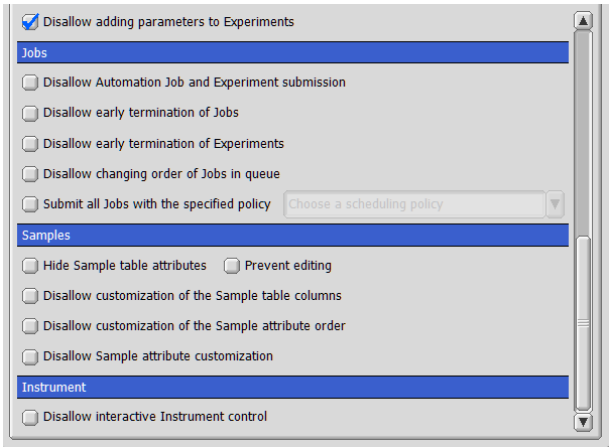


User 2

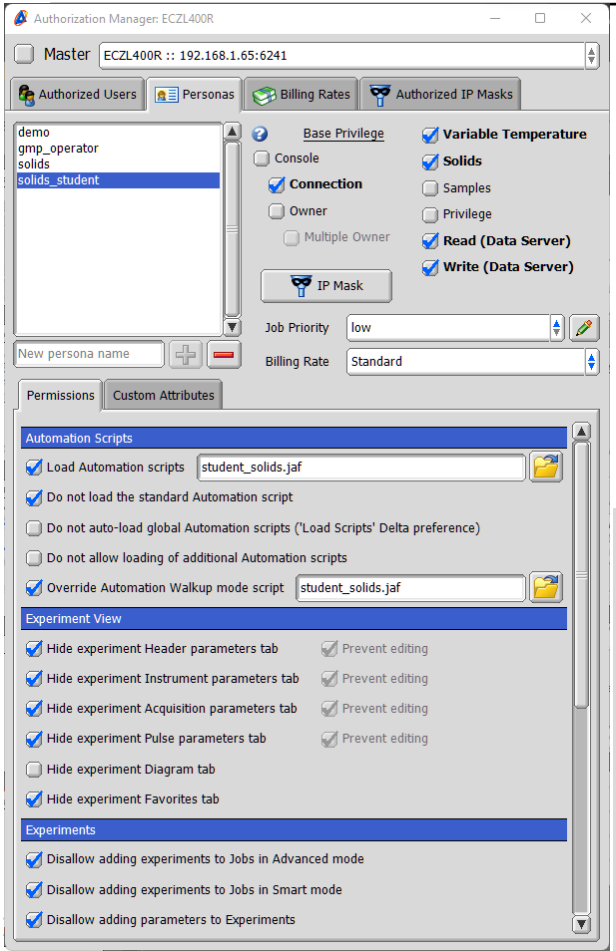


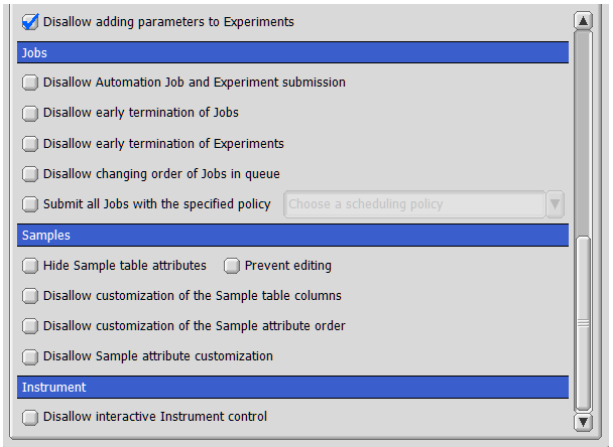
Persona manager

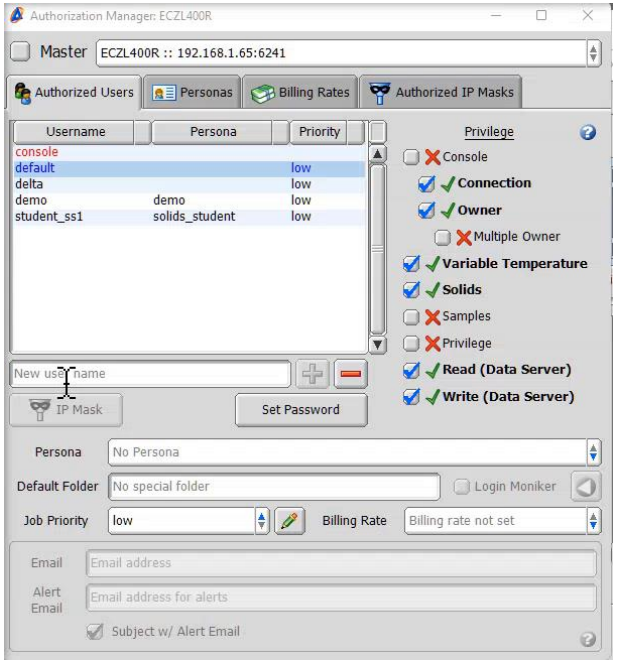




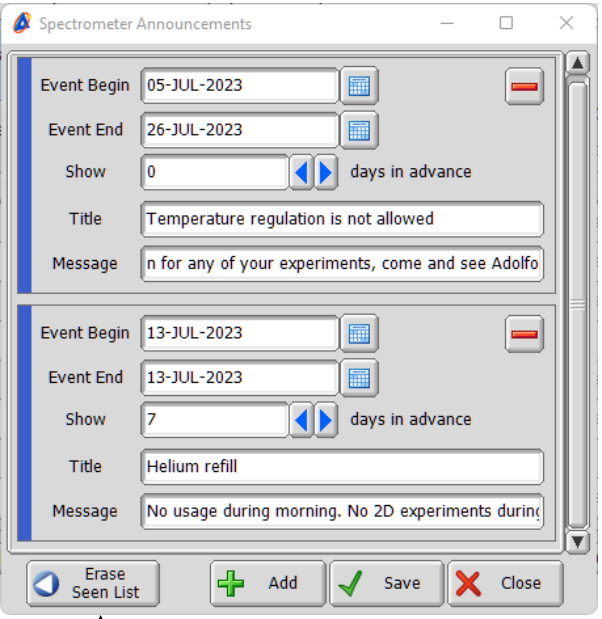
Persona manager







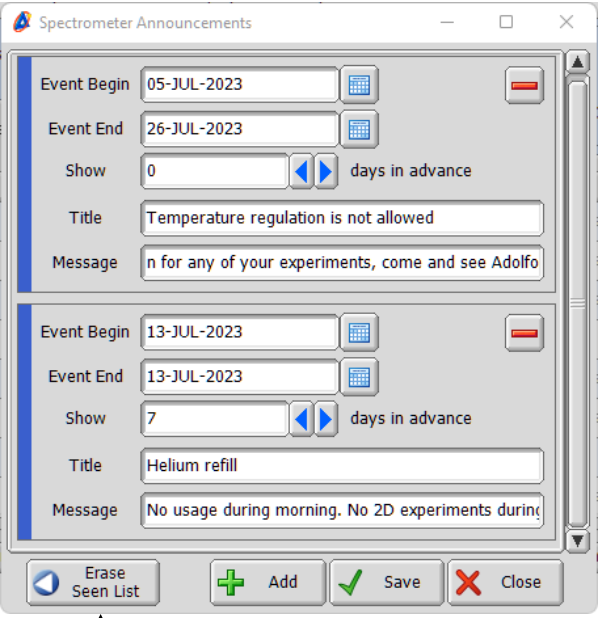
Announcement editor

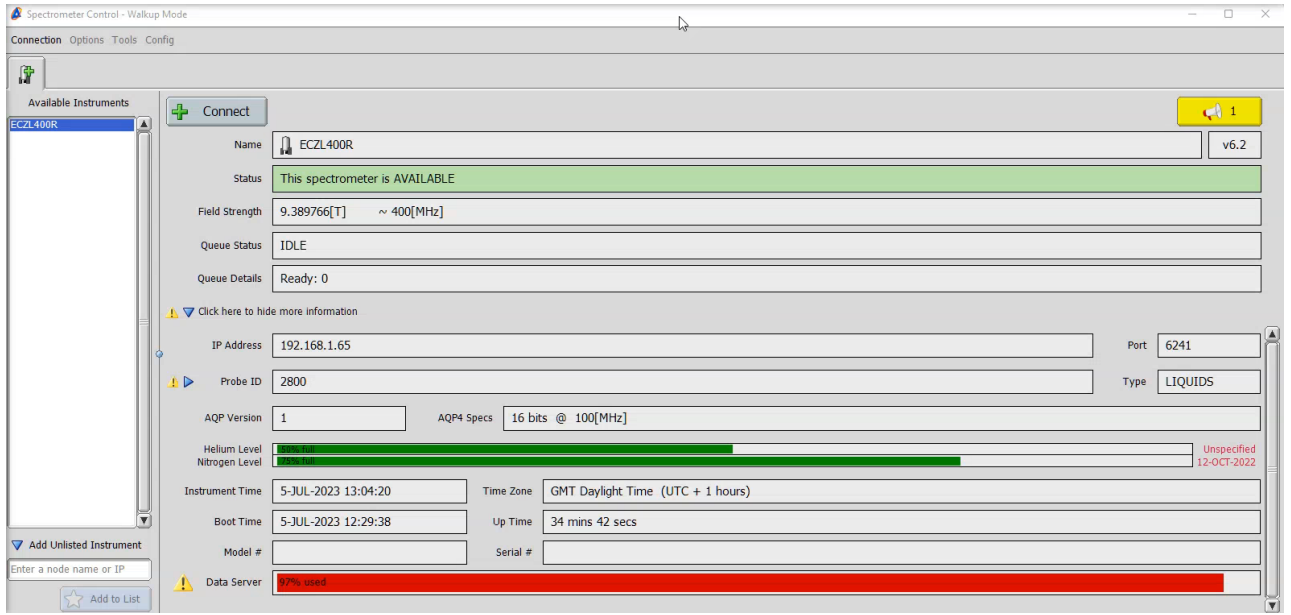


Announcements show up only on first login once the announcement is active.

Push this button to show again.

Announcement editor





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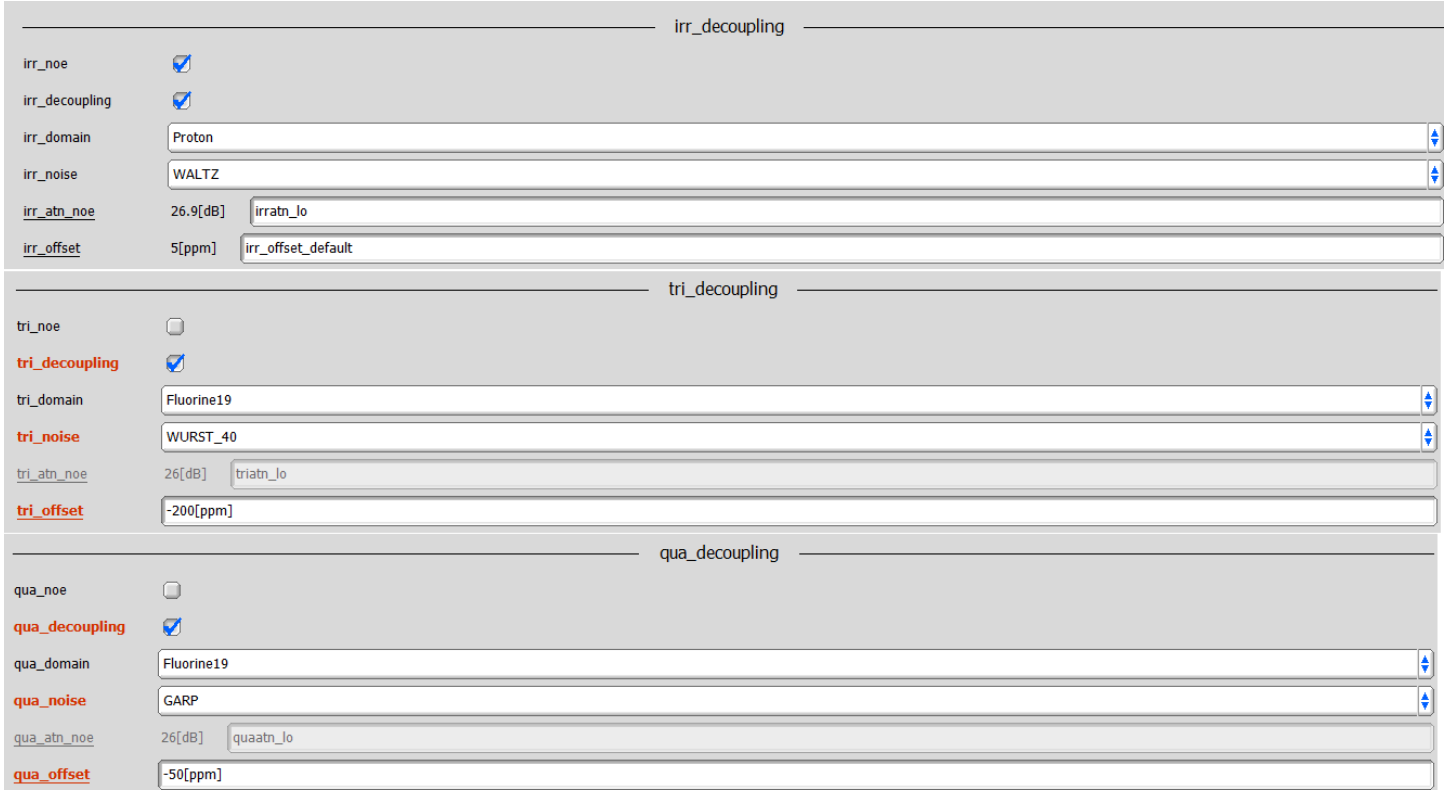
Push this button to show again.

Manual use

~~Manual use???~~

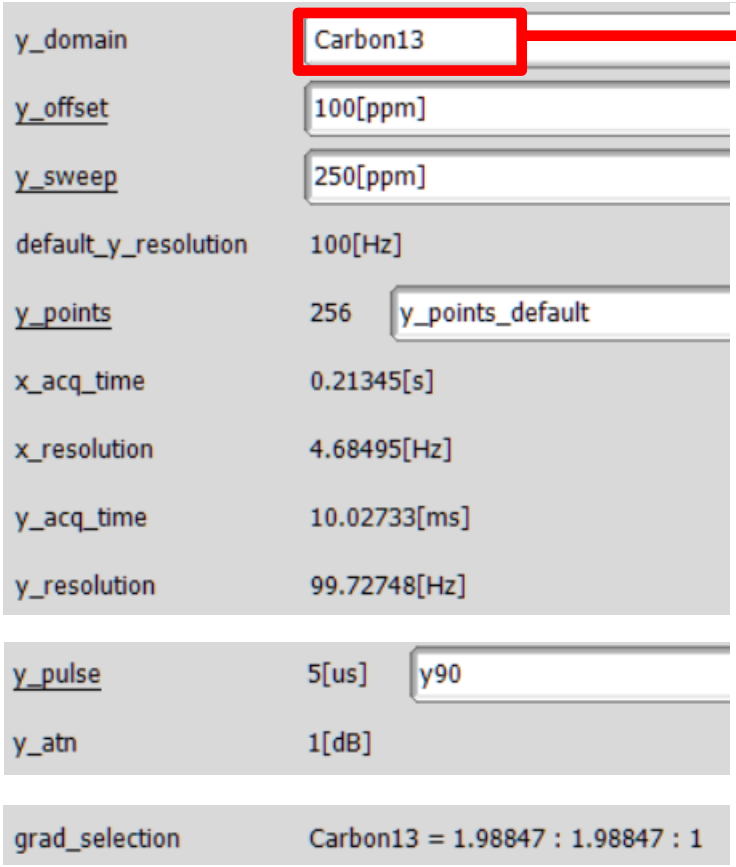
Non-routine use

Easy multiple decoupling setup



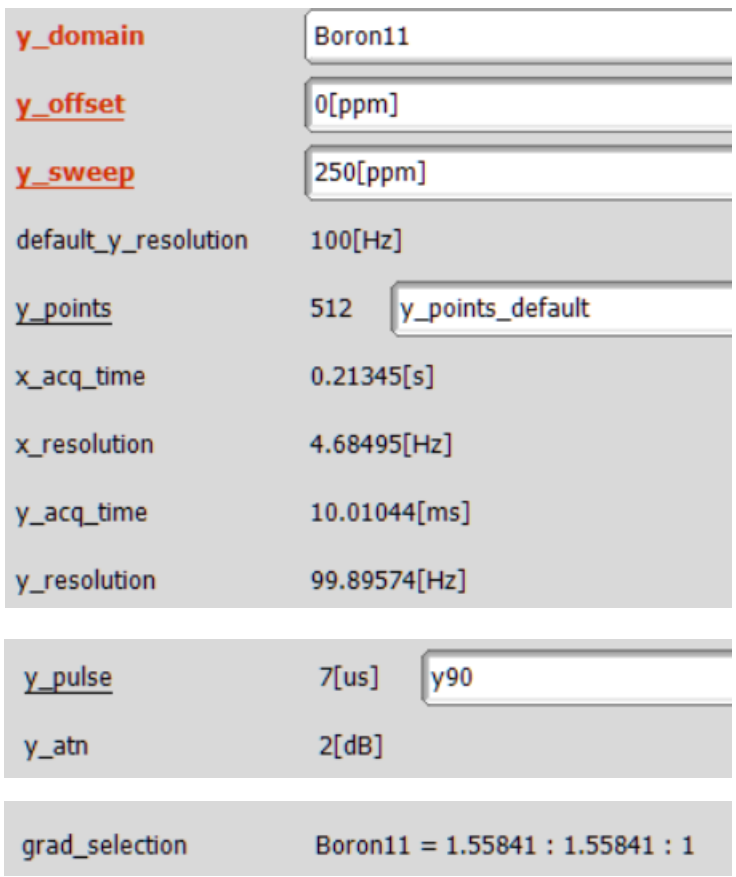
Just choose nuclei and offsets (and decoupling schemes)
No need to recalculate pulses

HMBC ^{1}H-^{13}C to HMBC ^{1}H-^{11}B



Only change the nucleus.

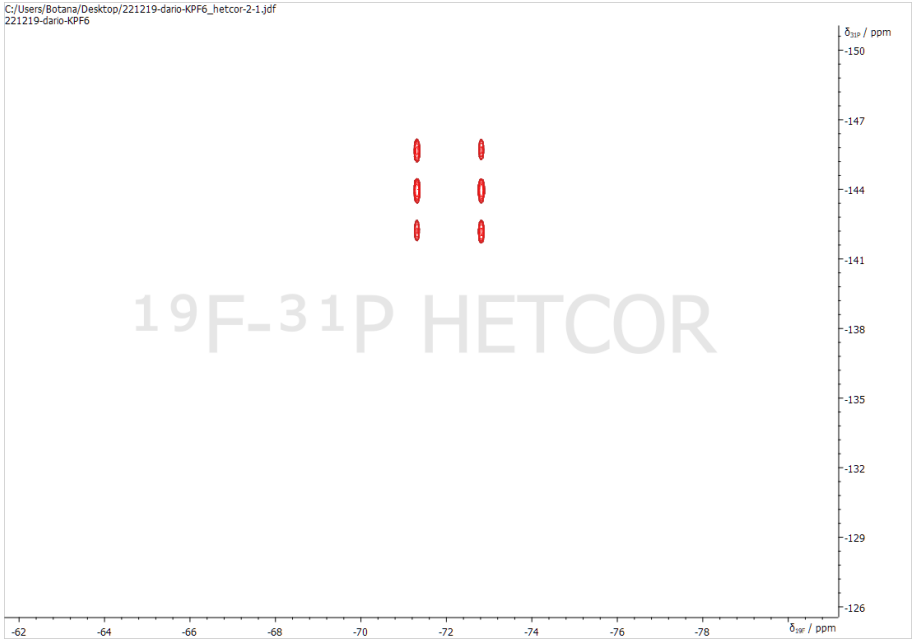
Other related parameters will be automaticall y calculated!



^{19}F-^{31}P and ^{31}P-^{19}F HETCOR!

Data kindly provided by Dario Rothauer and Ulrich Haunz, University of Konstanz

Universität Konstanz



Automation use

Spectrometer control Interfaces

Walkup

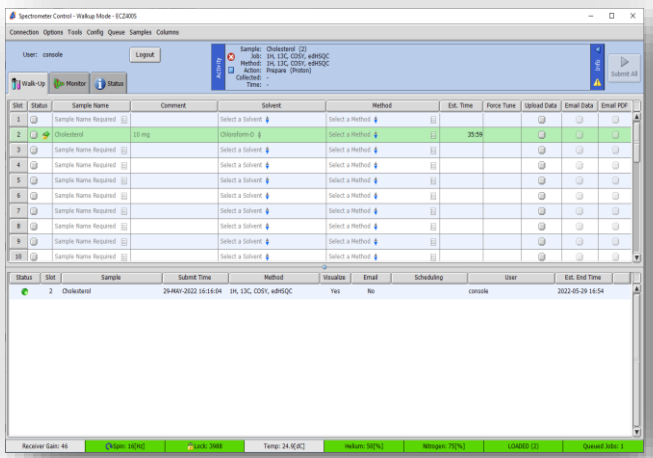
- User accessible Methods defined by administrator
- Select slot, put sample information, select the method, and then Go!

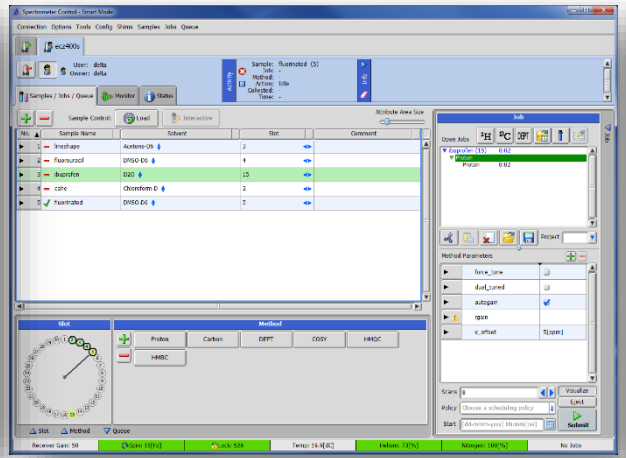
Smart

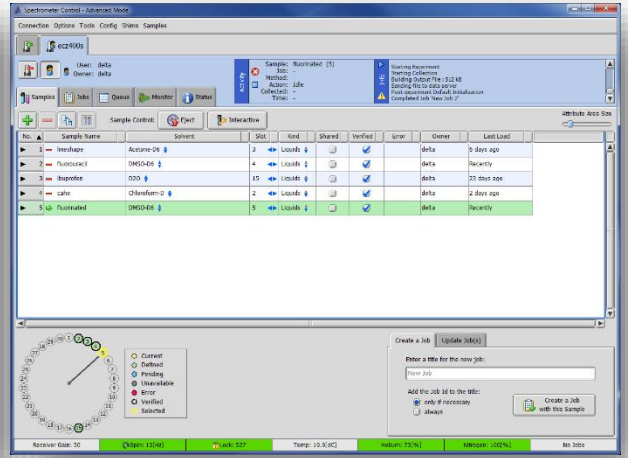
- Method shortcuts defined by user as buttons
- Define sample information, select the method, and then Go!

Advanced

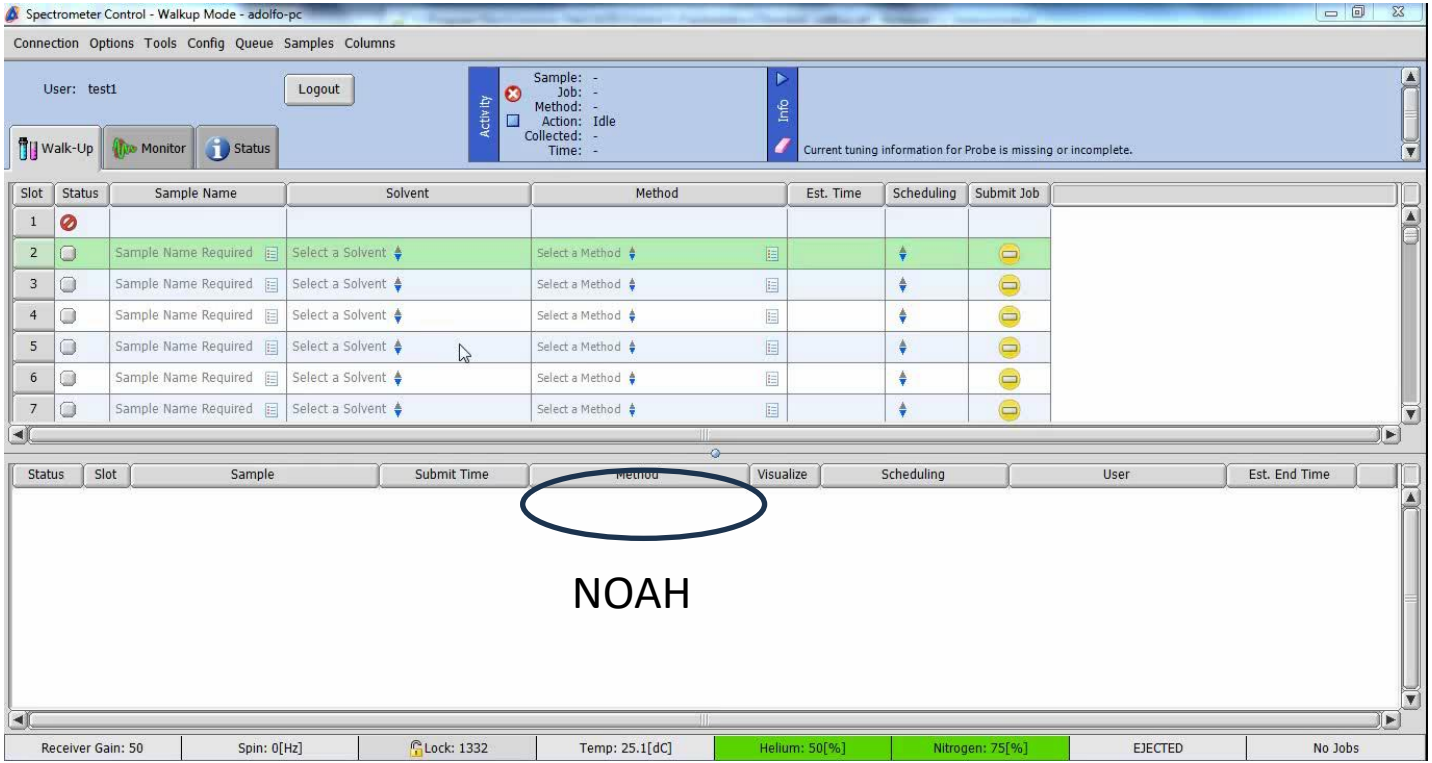
- Easy access to all functions
- Suitable both for continuous work on a sample and for sample batch submission







Walkup mode

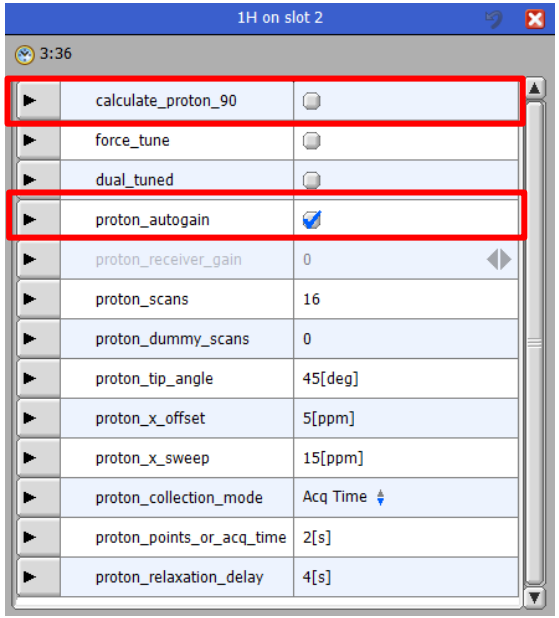


On-the-Fly Parameter Optimization

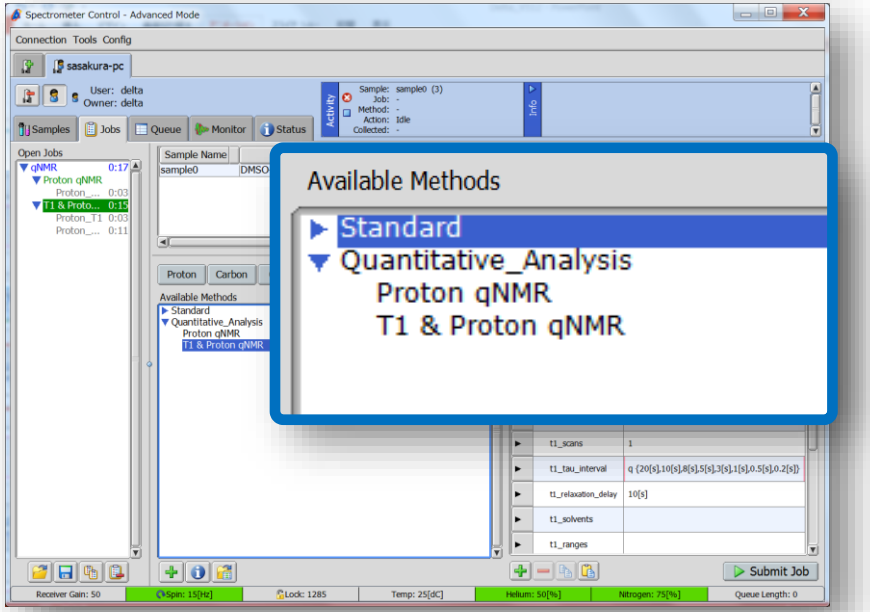
JEOL Delta acquisition software provides a variety of tools for on-the-fly parameter optimization of acquisition parameters, including:

- Fully automated probe tuning and gradient shimming
- Automatic adjustment of receiver gain (autogain)
- Automatic calibration of 90-degree pulse for each sample
- Automatic optimization of F_1/F_2 spectral windows in 2D methods
- Automatic optimization of offset (e.g. for presaturation) in solvent suppression methods
- Automatic determination of signal-to-noise ratio in 1D carbon experiments

Parameter panel for ^1H method showing calculate 90-degree pulse and automatic receiver gain adjustment (red boxes)



Automation scripts



T_1 & qNMR (^{1}H,^{13}C,^{19}F, etc.)

Automatic 90 pulse calibration, T_1 measurement first, then automatically extract the T_1 values to set the relaxation delay of the qNMR experiment

^{1}H T_1 & CPMAS

Run T_1 measurement first (IR or SR), then automatically extract the T_1 value to set the relaxation delay of CPMAS

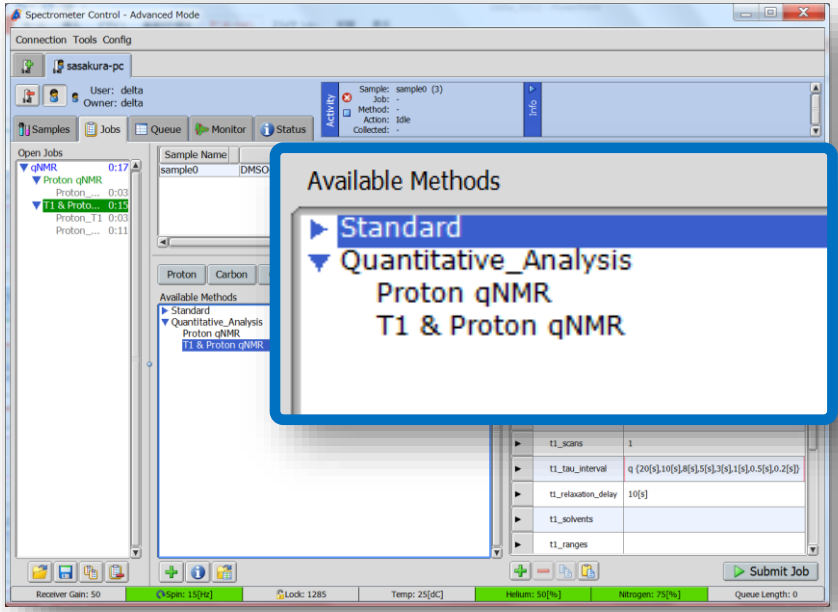
Automation for both solid and liquid samples

- **Use the same sample changer for solids and liquids**
- Routine SS-NMR measurements, same as solution NMR.
- Compatible with Narrow Bore Magnets
- **-100ºC to +220ºC**
- **Auto tuning and magic angle adjustment**
- Up to 100 samples
- **1 mm** (0.8uL @ 80kHz) **, 3.2 mm (49uL @ 22 kHz) and 8 mm** (~600uL @8kHz)

Introducing rotor in rotorcarrier

Bench spinner

Automation scripts



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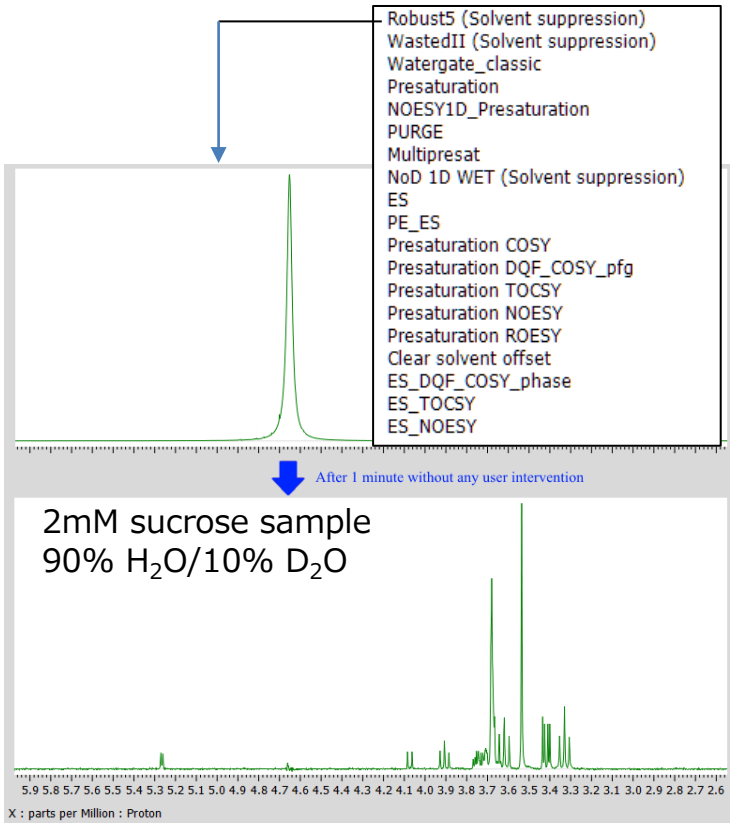
^{1}H T_1 & CPMAS

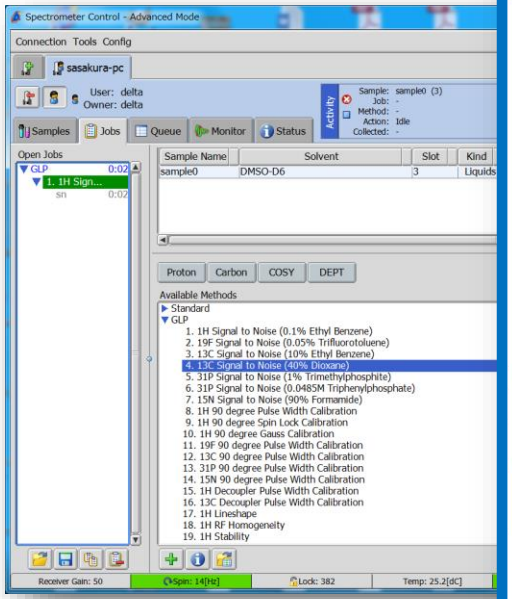
Run T_1 measurement first (IR or SR), then automatically extract the T_1 value to set the relaxation delay of CPMAS

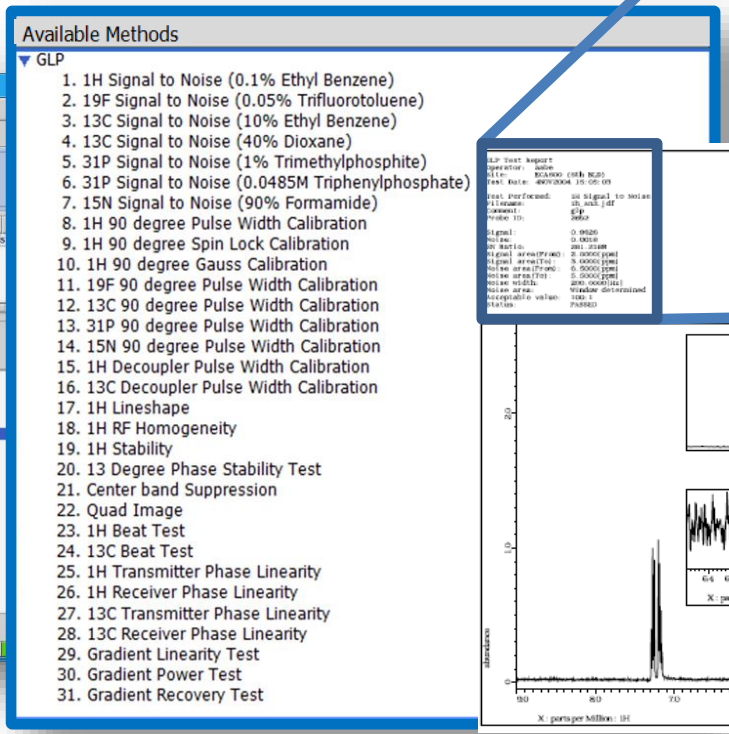
Solvent suppression

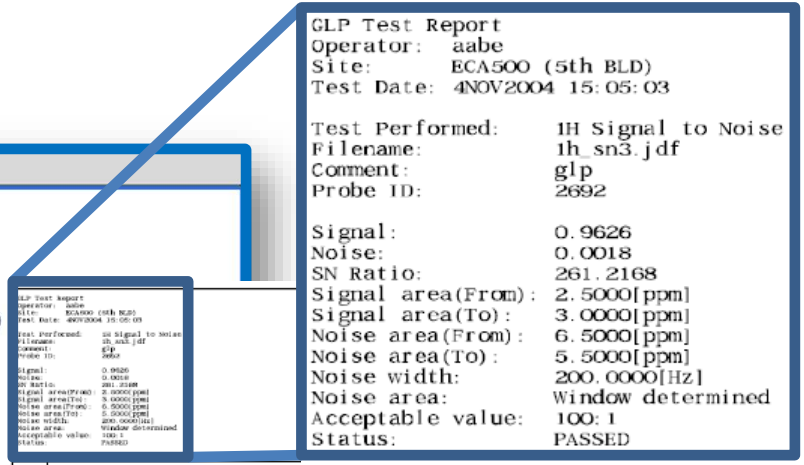


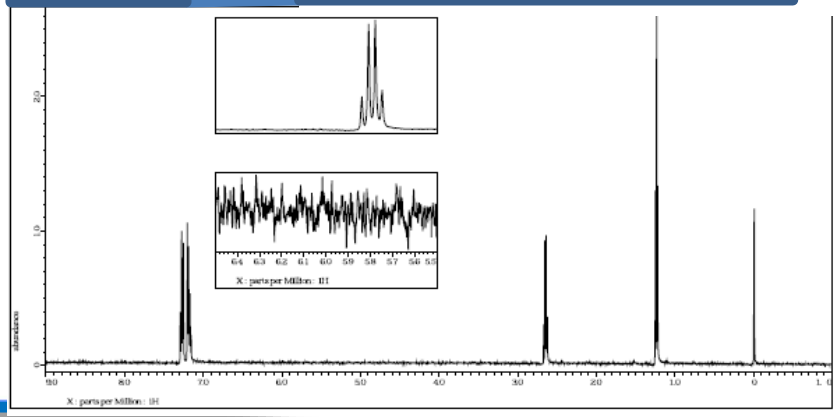
System suitability (GLP) tests

The GLP methods can verify the performance of the NMR machine periodically









DOSY steps (automatic_setup)

1. Automatic setting of chosen sample parameters (temperature, temperature delay, shimming, tuning*,…)
2. Automatic estimation of diffusion coefficient using SEGWE with the **solute MW**

User input in bold

Self-Diffusion and molecular weight (SEGWE)

- Approximation for the correlation between molecular weight and self-diffusion coefficient
- More advanced than previous estimations such as $r_H \propto \sqrt[3]{MW}$
- Takes into account the molecular interactions of solvent and solutes
- **Calculator available, input: temperature, solvent and MW or D**

$$D = \frac{k_B T \left(\frac{3\sqrt[3]{\frac{MW_S}{MW}}}{2} + \frac{1}{1+\sqrt[3]{\frac{MW_S}{MW}}} \right)}{6\pi\eta\sqrt[3]{\frac{3MW}{4\pi\rho_{eff}N_A}}}$$

k_B : Boltzmann constant

T: temperature

η: viscosity

ρ_{eff}: effective density of the molecule (packing effects, geometry, solvation and flexibility)

MW : molecular weight of the molecule

MW_S: molecular weight of the solvent

N_A: Avogadro number

R. Evans et al, *Angew. Chem. Int. Ed.* (2013), 52: 3199–3202
R. Evans et al, *Anal. Chem.* (2018), *90* (6), 3987–3994
R. Evans, *Prog Nucl Magn Reson Spectrosc* (2020), 117, 33-69
https://www.nmr.chemistry.manchester.ac.uk/?q=node/432

Calculating DOSY parameters (Stejskal-Tanner equation)

$$S = S_0\, e^{-D\gamma^2\delta^2G^2\Delta'} \qquad \delta = \sqrt{-\frac{ln\,{}^{S}/_{S_0}}{D\gamma^2G^2\Delta'}}$$

S : signal amplitude [0.1 S_0]

S_0: signal amplitude without diffusion [S_0]

D : diffusion coefficient [SEGWE]

γ : gyromagnetic ratio (dependent on *x_domain*) [γ_H]

δ : gradient pulse width (***delta*** *or* ***smallDelta***)

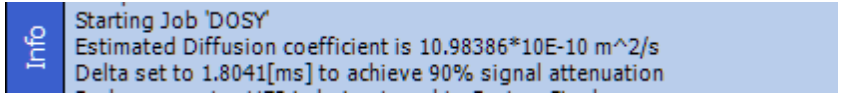
G : gradient amplitude (***g***) [maximum usable gradient strength]

Δ' : corrected diffusion time

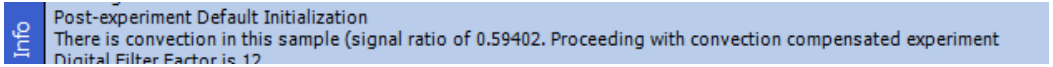
Δ : diffusion time (***diffusion_time***) [0.1 s]

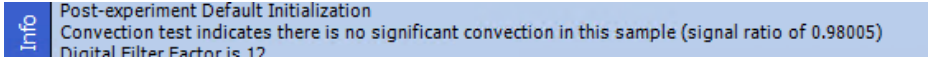
DOSY steps (automatic_setup)

1. Automatic setting of chosen sample parameters (temperature, temperature delay, shimming, tuning*,…)
2. Automatic estimation of diffusion coefficient using SEGWE with the **solute MW**
3. Automatic determination of gradient length to achieve 90% signal attenuation (0.1 s diffusion time and maximum usable gradient strength)



4. Automatic determination of 90 degrees pulse and setup (**optional**)
5. Automatic determination of sample convection (**optional**), by evaluating if a delay imbalance of 30ms leads to a signal loss of more than 20%.





6. Automatic acquisition of DOSY with/out convection compensation
7. Automatic DOSY plot automatically generation

User input in bold

Results from automatic_setup (Quinine + Geraniol + Camphene)

MW set to 324

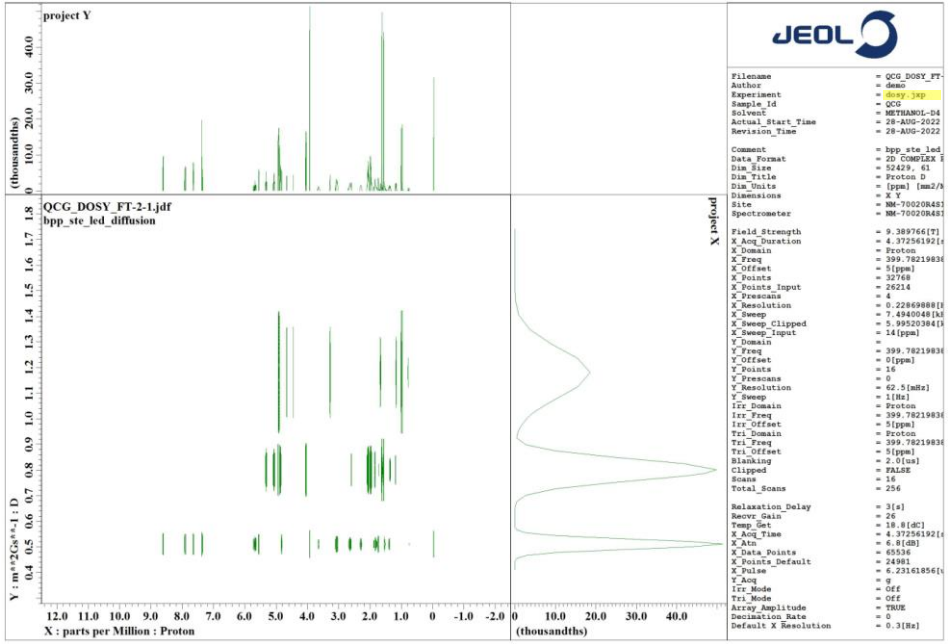
Info

Reached Lock State 'AUTOLOCK'
Estimated Diffusion coefficient is 7.78834*10E-10 m^2/s
Delta set to 2.14247[ms] to achieve 90% signal attenuation

1H 90 degree pulse width for QCG estimated as 6.12549[us]

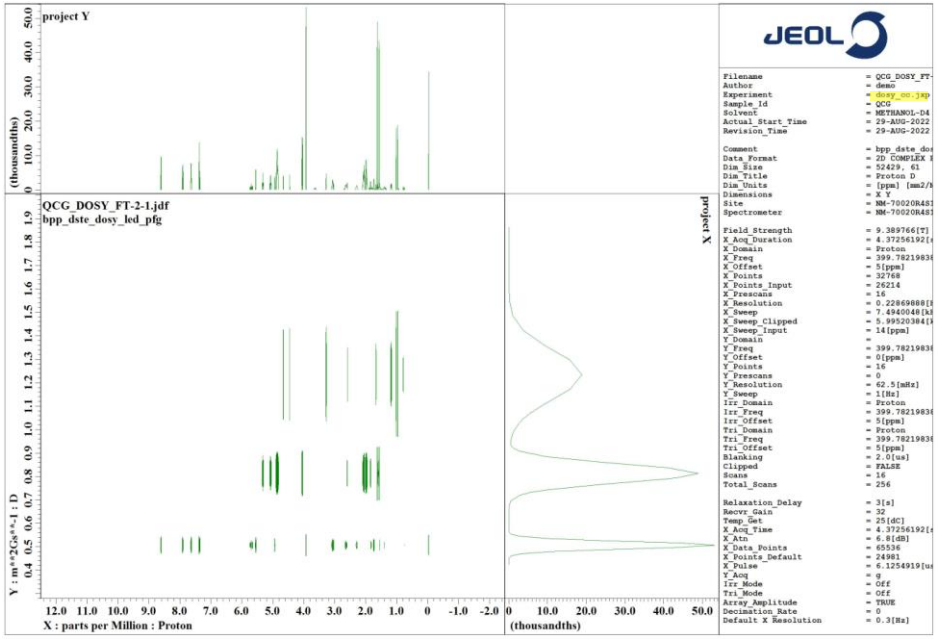
Room temperature

Convection test indicates there is no significant convection in this sample (signal ratio of 0.9784)



25C

There is convection in this sample (signal ratio of 0.35024. Proceeding with convection compensated experiment

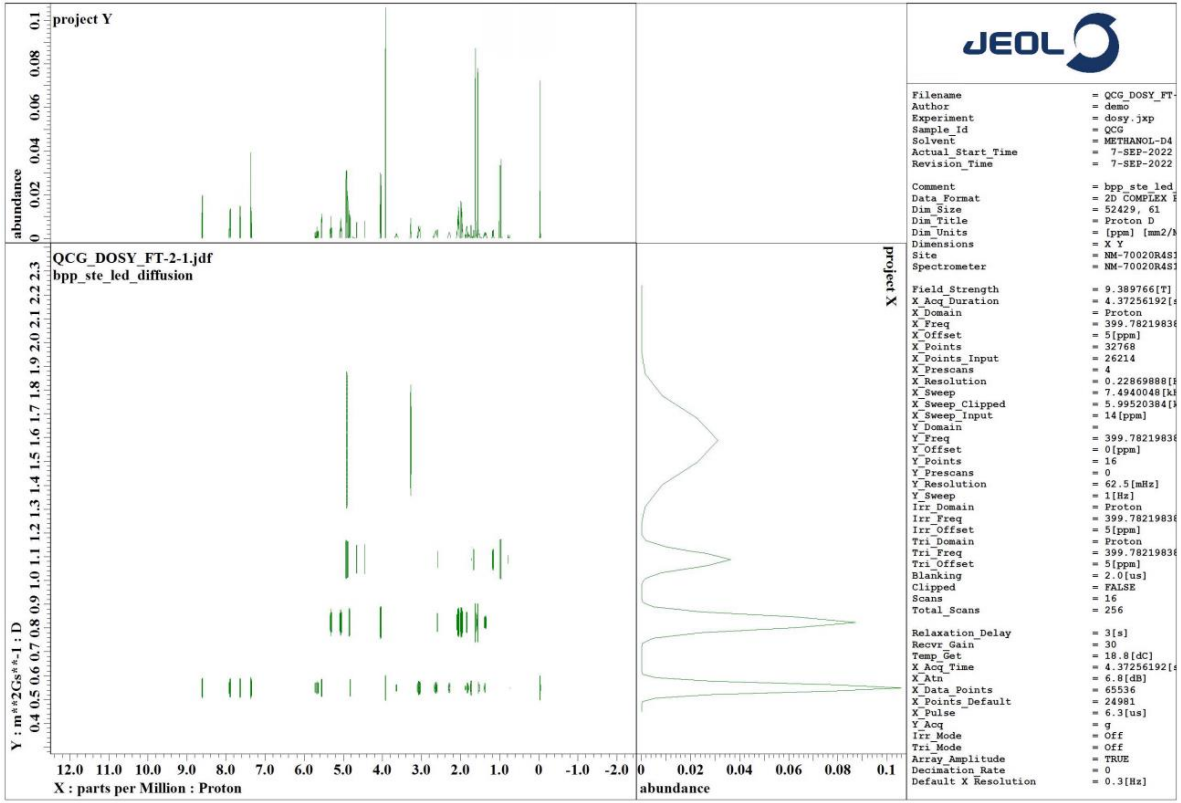


Results from automatic_setup (Quinine + Geraniol + Camphene)

MW set to 136

Info

Reached Lock State 'AUTOLOCK'
Estimated Diffusion coefficient is 11.71103*10E-10 m^2/s
Delta set to 1.74719[ms] to achieve 90% signal attenuation



JEOL

Filename	= QCG_DOSY_FT-
Author	= demo
Experiment	= dosy.jxp
Sample_Id	= QCG
Solvent	= METHANOL-D4
Actual_Start_Time	= 7-SEP-2022
Revision_Time	= 7-SEP-2022
Comment	= bpp_ste_led
Data_Format	= 2D COMPLEX
Dim_Size	= 52429, 61
Dim_Title	= Proton D
Dim_Units	= [ppm] [mm2/
Dimensions	= X Y
Site	= NM-70020R4S
Spectrometer	= NM-70020R4S
Field_Strength	= 9.389766[T]
X_Acq_Duration	= 4.37256192[
X_Domain	= Proton
X_Freq	= 399.7821983
X_Offset	= 5[ppm]
X_Points	= 32768
X_Points_Input	= 26214
X_Prescans	= 4
X_Resolution	= 0.22869888[
X_Sweep	= 7.4940048[k
X_Sweep_Clipped	= 5.99520384[
X_Sweep_Input	= 14[ppm]
Y_Domain	=
Y_Freq	= 399.7821983
Y_Offset	= 0[ppm]
Y_Points	= 16
Y_Prescans	= 0
Y_Resolution	= 62.5[mHz]
Y_Sweep	= 1[Hz]
Irr_Domain	= Proton
Irr_Freq	= 399.7821983
Irr_Offset	= 5[ppm]
Tri_Domain	= Proton
Tri_Freq	= 399.7821983
Tri_Offset	= 5[ppm]
Blanking	= 2.0[us]
Clipped	= FALSE
Scans	= 16
Total_Scans	= 256
Relaxation_Delay	= 3[s]
Recvr_Gain	= 30
Temp_Get	= 18.8[dC]
X_Acq_Time	= 4.37256192[
X_Atn	= 6.8[dB]
X_Data_Points	= 65536
X_Points_Default	= 24981
X_Pulse	= 6.3[us]
Y_Acq	= g
Irr_Mode	= Off
Tri_Mode	= Off
Array_Amplitude	= TRUE
Decimation_Rate	= 0
Default X Resolution	= 0.3[Hz]

PDF automatically generated after clicking the Submit Job button with the DOSY automation method

Note PDF printout is generated using multivariate analysis, results can be misleading

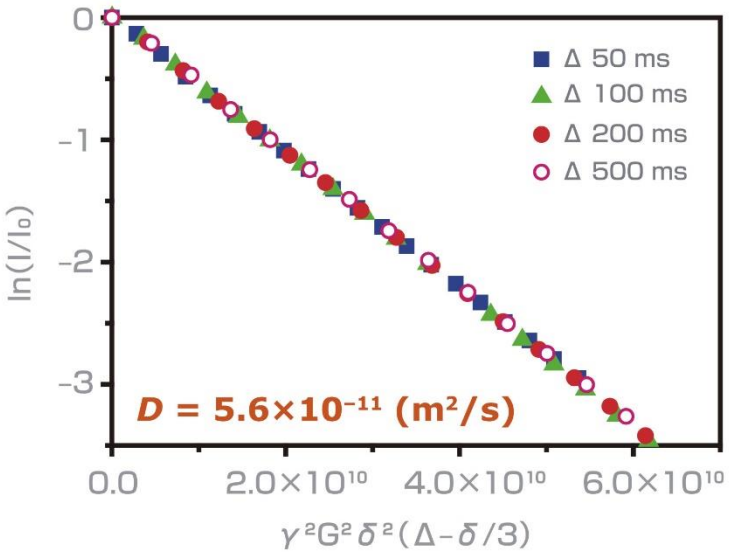
Further analysis with other methods is recommended, particularly for more complex samples

JEOL Diffusion probe

- Narrow bore
- Air cooled
- -70 to 120 °C
- 1200G/cm at 30A
- 2000G/cm at 50A

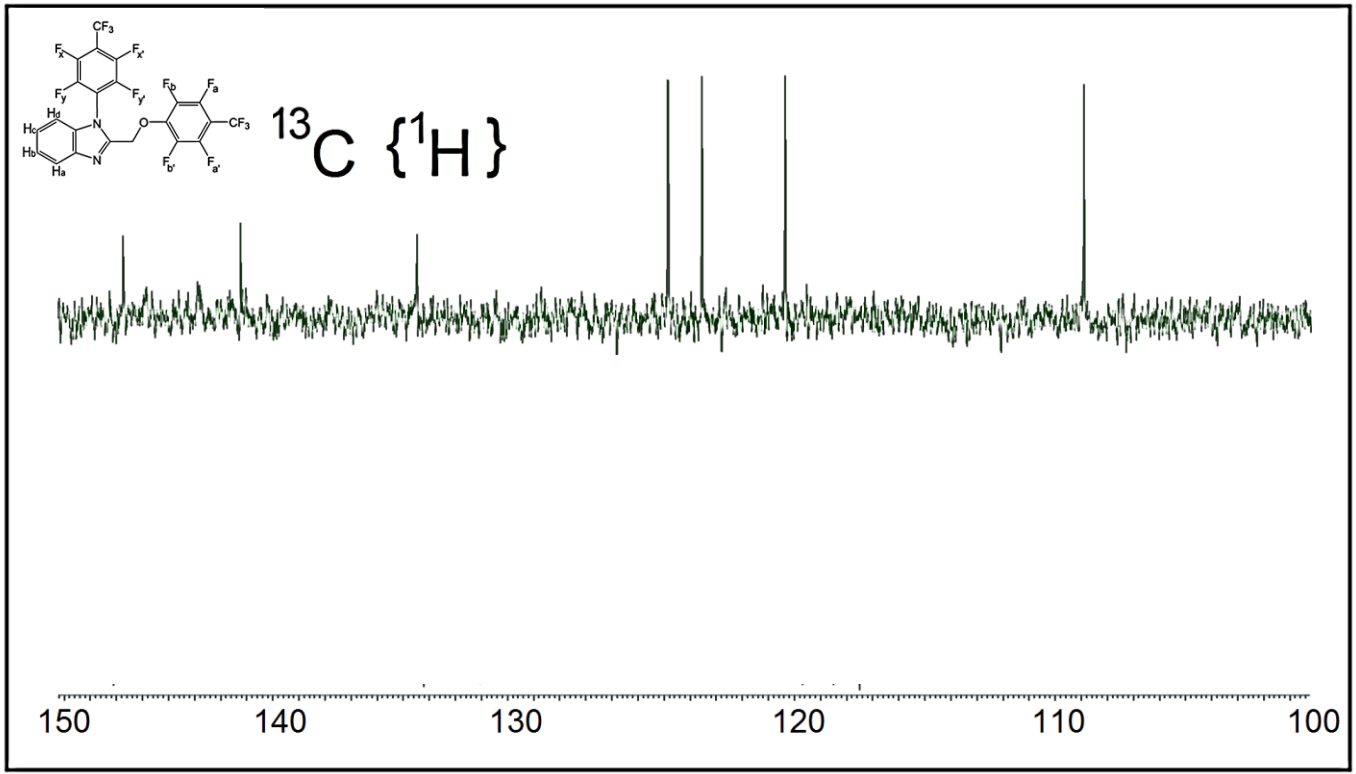
50A PFG amplifier

Analysis of Li diffusion in solid-state electrolyte



Data courtesy:
Y. Hashimoto, N. Horiike, and H. Shobukawa, Asahi Kasei Corp

JEOL-ECZ-500 2 channels with Royal HFX Probe (Aug 2017)

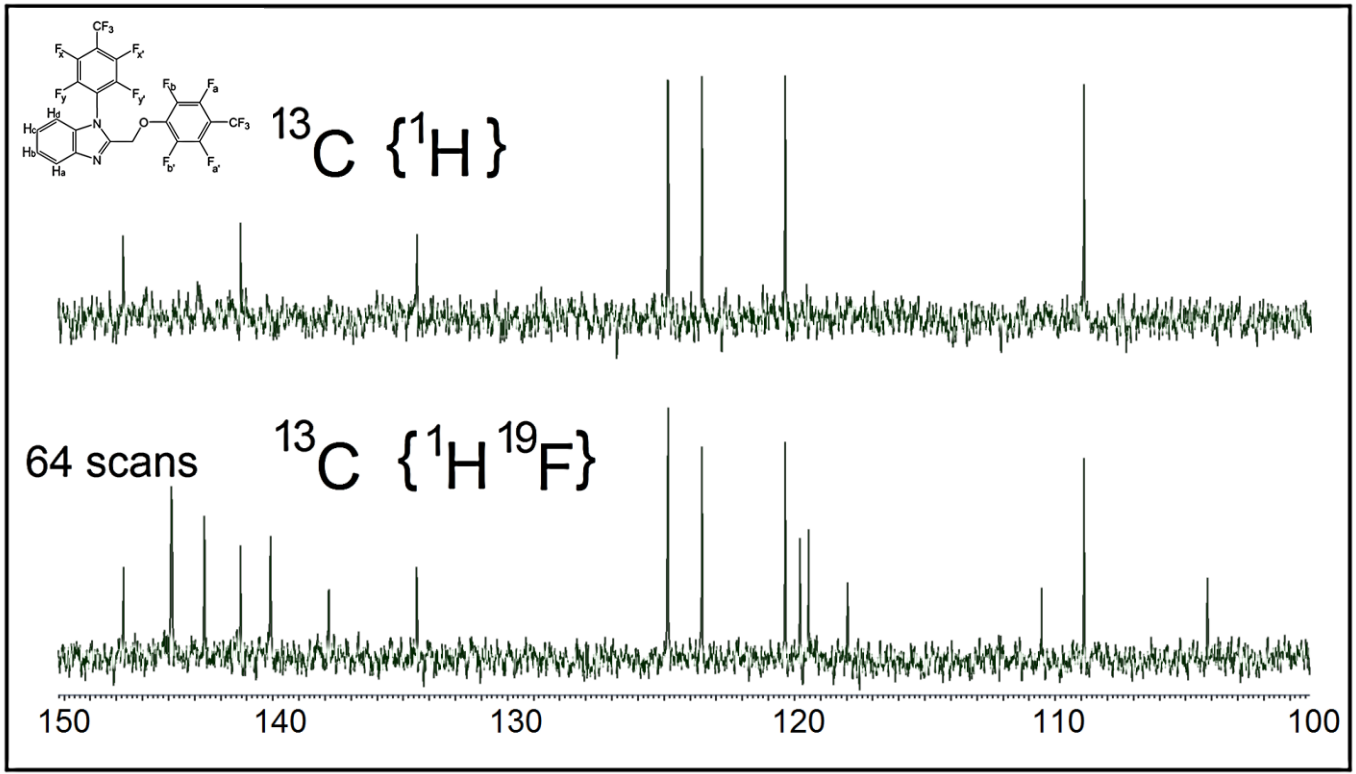


https://doi.org/10.1002/mrc.4947

Dr. Mark Edgar

Solutions for Innovation JEOL

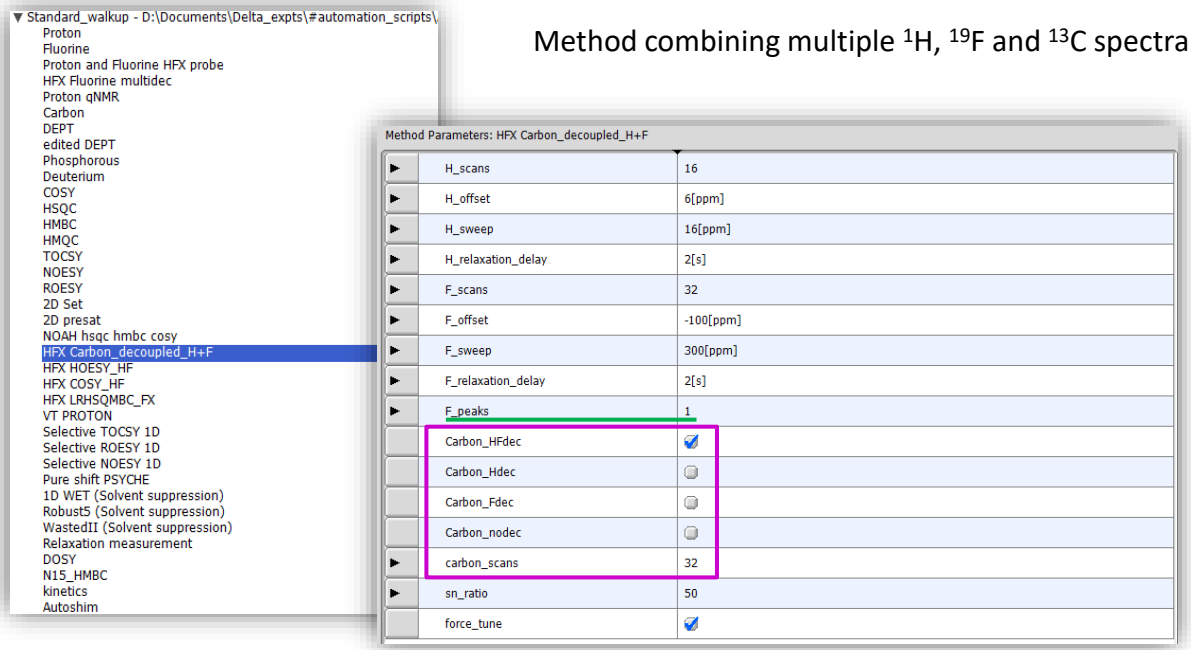
JEOL-ECZ-500 2 channels with Royal HFX Probe (Aug 2017)



https://doi.org/10.1002/mrc.4947

Dr. Mark Edgar

HFX experiments in automation



Method combining multiple ^{1}H, ^{19}F and ^{13}C spectra with/out decoupling

1. Runs ^{1}H

2. Runs ^{19}F

3. Runs $^{19}F\{^{1}H\}$ centered on "F_peaks" tallest fluorine signals

4. Runs $^{1}H\{^{19}F\}$ with decoupling centered on tallest fluorine peak

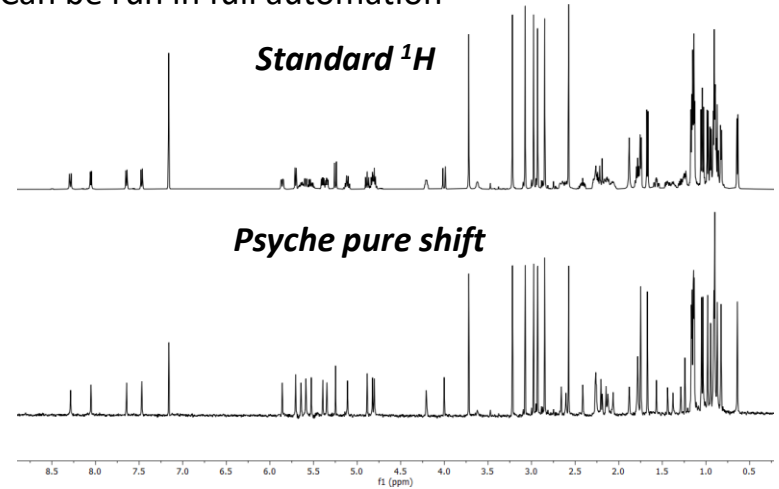
5. Runs choice of $^{13}C\{^{1}H,^{19}F\}$, $^{13}C\{^{1}H\}$, $^{13}C\{^{19}F\}$, ^{13}C *(with decoupling centered on tallest fluorine peak)*

More single click experiments

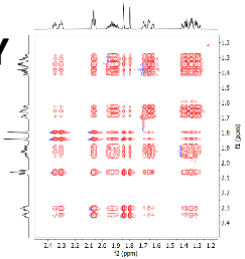
PSYCHE PURE SHIFT (homonuclear broadband decoupling)

A single line for each peak in the spectrum

Can be run in full automation

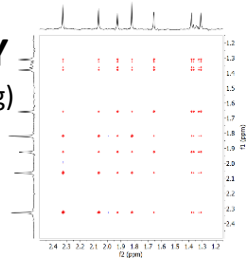


TOCSY

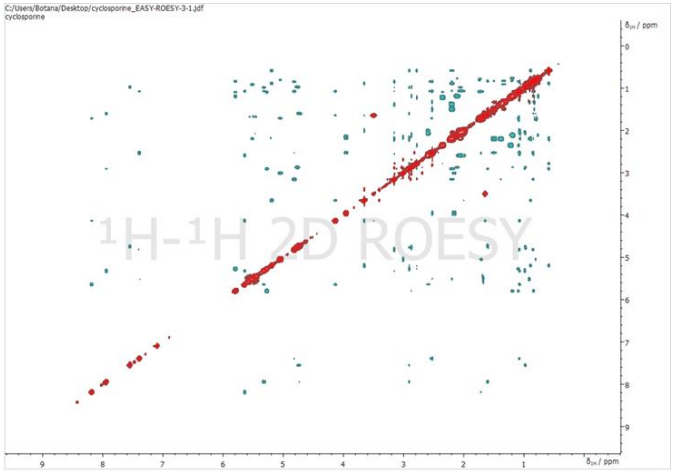


PSYCHE- TOCSY

(covariance processing)



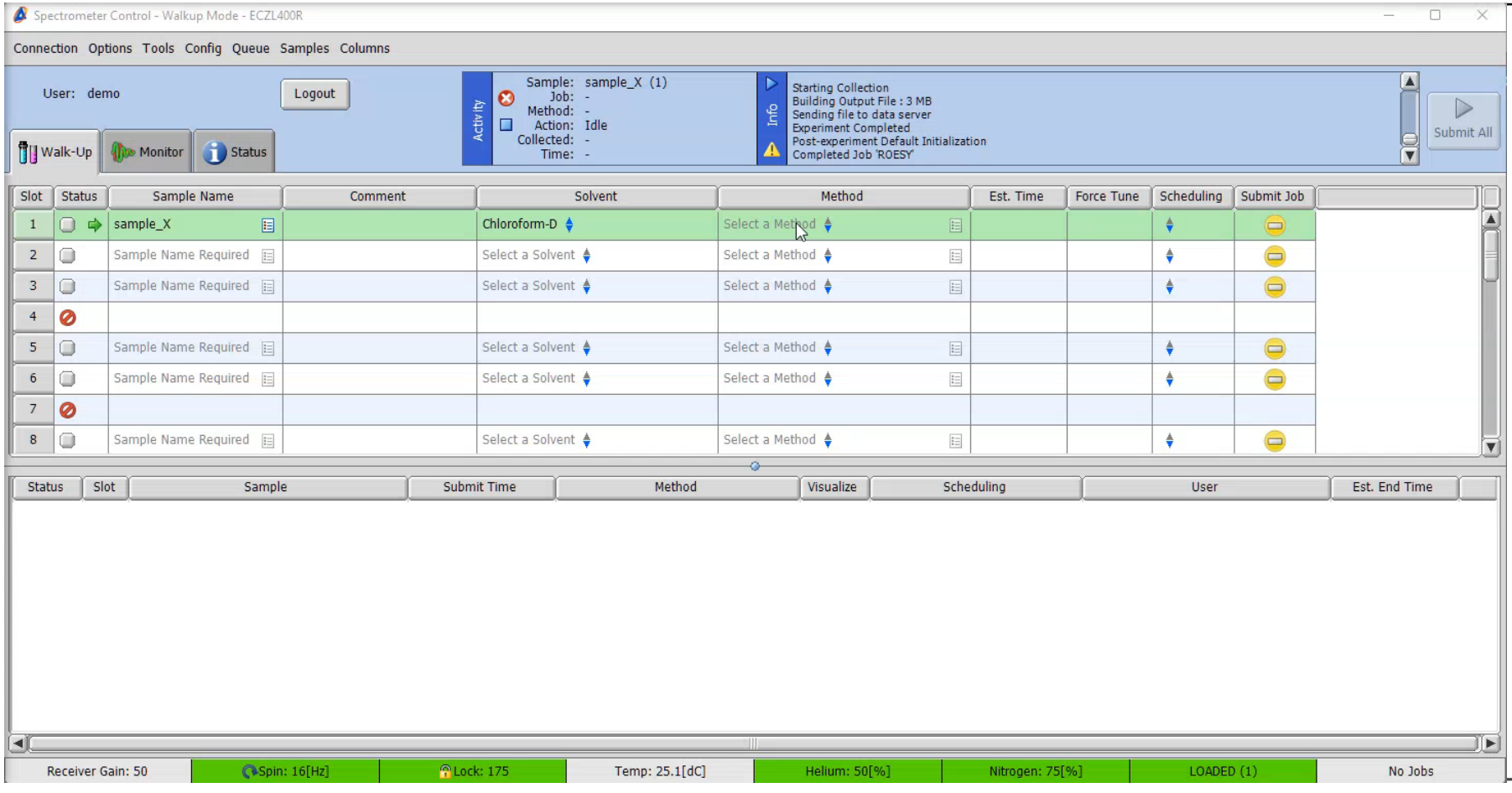
Off-resonance ROESY (EASY-ROESY)



Automatically:

- Set spin-lock RF field dependent on magnet field strength
- Set spin-lock angle to 60 degrees
- Calculate off-resonance shift as per spin-lock RF strength, angle and magnet field
- Set offset frequency of spin-lock pulses

IPAP–HSQMBC: Measurement of long-range heteronuclear coupling constants



IPAP–HSQMBC: Measurement of long-range heteronuclear coupling constants

Two complementary in-phase (IP) and anti-phase (AP) data are separately recorded from a modified HSQMBC experiment and then added/subtracted to provide spin-state-selective α/β–HSQMBC spectra. The magnitude of ${}^{n}J_{XH}$ can be directly determined by simple analysis of the relative displacement between α- and β-cross-peaks.

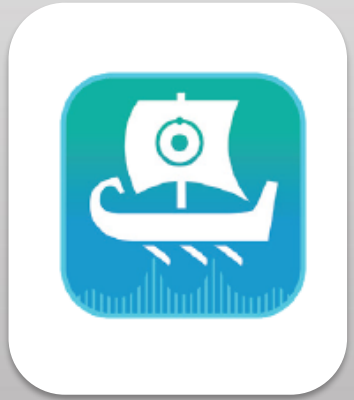
S. Gil et al./Journal of Magnetic Resonance 207 (2010) 312–321

What the automation is doing:

```
EXPERIMENT pip_hsqmbc_ip IS
    COLLECT "pip_hsqmbc";
    SET ipap_flg        = FALSE;
END EXPERIMENT;

EXPERIMENT pip_hsqmbc_ap IS
    COLLECT "pip_hsqmbc";
    SET ipap_flg        = TRUE;
END EXPERIMENT;

SET pip_hsqmbc_add = pip_hsqmbc_ip + pip_hsqmbc_ap;
SET pip_hsqmbc_sub = pip_hsqmbc_ip - pip_hsqmbc_ap;
```



Jason software

- **Vendor agnostic**
- Easy reports
- Windows and Mac OS X versions
- Subscription based
- Agile release cycle (new release every 3 months)
- Automated structure verification

JASON Software Development Team

Vadim
Zorin

Iain
Day

Yibiao
Li

Hiroshi
Endo

Yuko
Igarashi

Naoto
Seki

Nikolay
Larin

Peter
Kiraly

Rachel
Brignall

Nader
Amin

Ronil
Sedani

Maximillian
Reinhart

Saeko
Suzuki

1 Customer Support
1 Developer

Very Agile team

The request:

orward

Wed 08/05/2024 23:21

I am trying to link both the y axis and x-axis on a proton - proton correlated 2D spectrum to a 1D proton spectrum.

On a proton-proton correlation like a noesy and linking the noesy to the proton, moving the cursor on the noesy spectrum along the x axis shows the cursor on the relevant proton peak on the proton spectrum. However, moving it in the Y-axis direction and keep it stationary on the x-axis position quite understandably does not move the cursor on the proton spectrum.

The response:

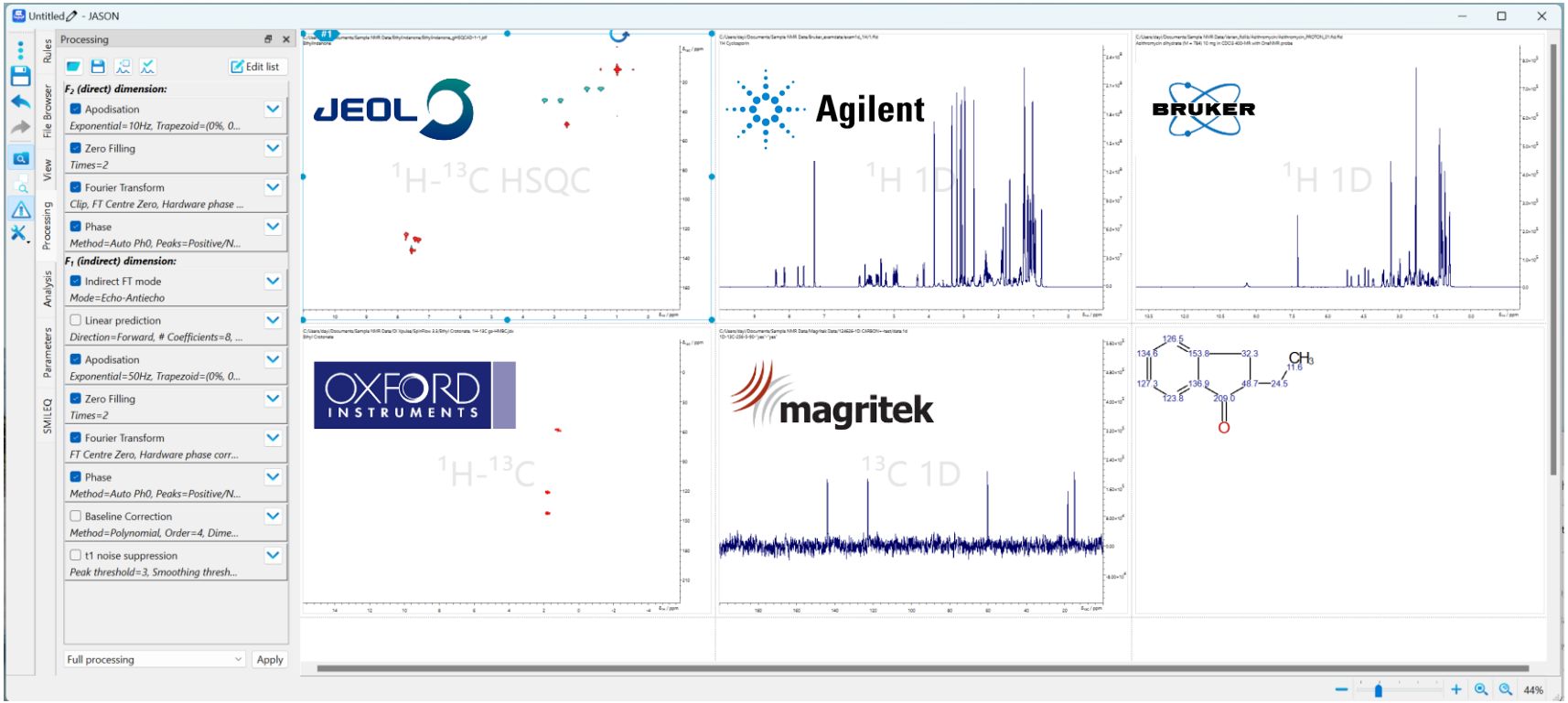
rward

Thu 09/05/2024 14:54

Thanks again for your email. We had a quick discussion and Vadim has already added this feature to the development version of JASON! It should be available from version 4.1.7300

Vendor Agnostic

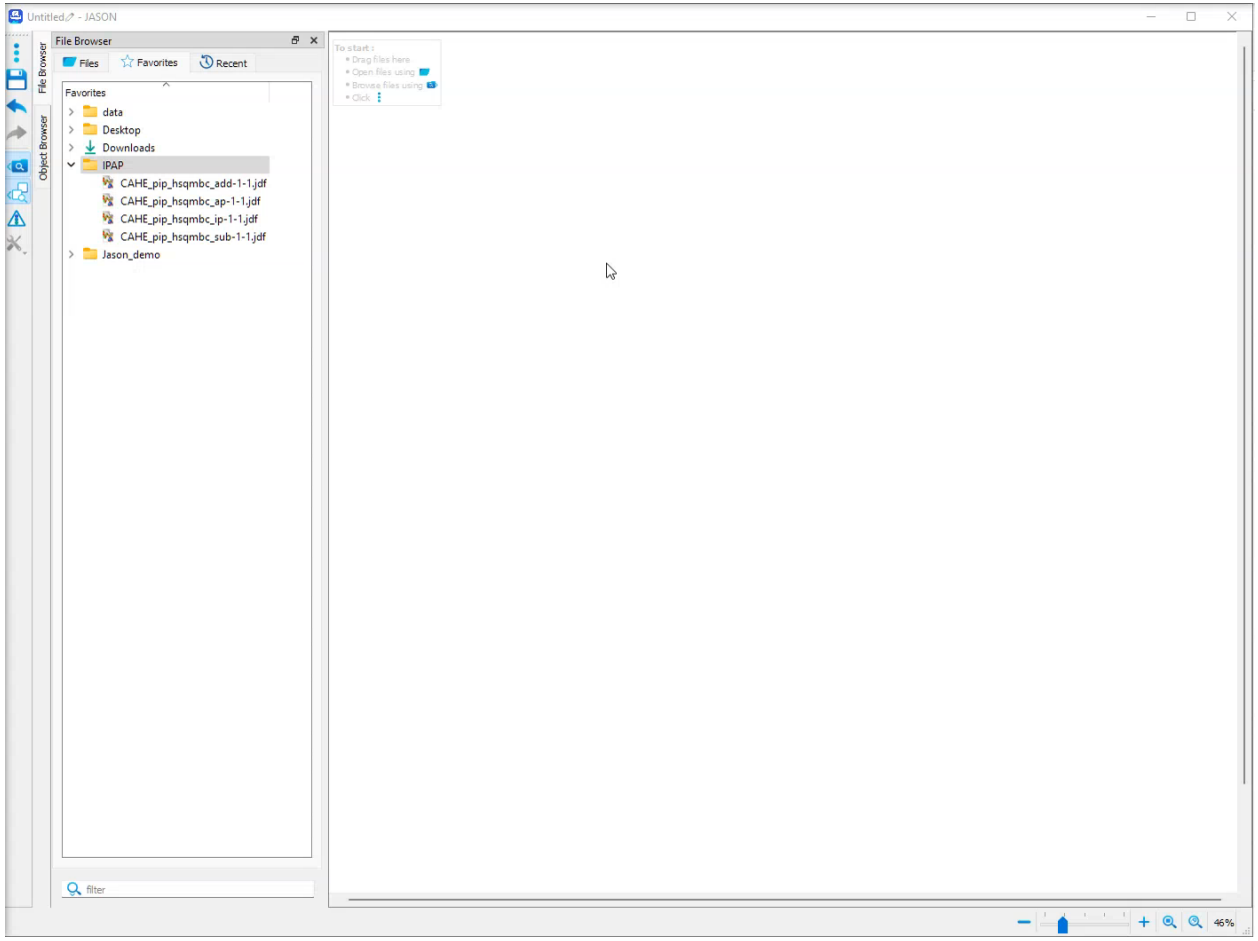
- Redeploy and synchronize any data/reports around the **WYSIWYG canvas**
- Data and metadata stored in standard **HDF-5 format**, accessible with any HDF-5 reader.



Findable, Accessible, Interoperable, Reusable

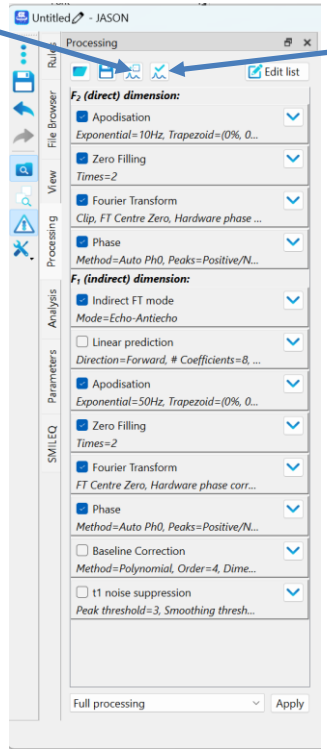
Stacking IPAP-HSQMBC spectra

- IPAP-HSQMBC experiments acquired in Delta Walkup mode
- Addition and subtraction datasets automatically obtained in Delta automation. If not present, they can be generated with Jason.
- Overlay or stack vertically, horizontally or diagonally multiple 1D or 2D spectra
- Easily change layout and colours
- Easily measure distances



Powerful Processing Engine

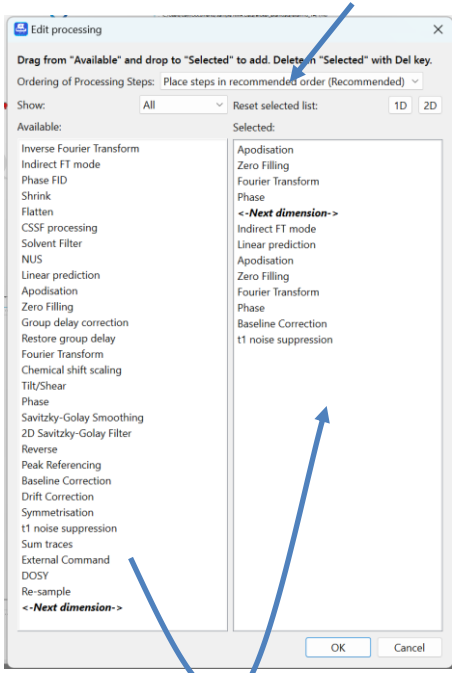
Raw data



Recommended processing

Automatic experiment recognition

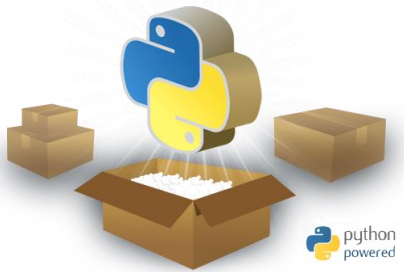
Expert vs guided mode



Drag and drop

- External command enables further processing with other programs such as scripts made in Python, R or Matlab
- BeautifulJason enables calling a background instance of Jason from your Python scripts to integrate the power of Jason in your workflows
- Free tool:

```
pip install beautifuljason
```



Beyond Python

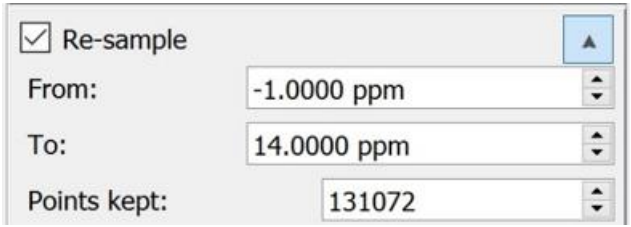
The problem

Dear Application Team,

I have been faced with a task that seems to have been beyond my field of expertise. After two days of struggle, I'm slowly losing hope for completion. It requires me to convert several thousands of 1H NMR spectra into a suitable format, which will then be used as an input for machine learning. The format I need at this stage is a vector containing only normalized intensities for individual points.

The first step is to process the spectra into a form in which each spectrum will have the same range of chemical shifts (for example, from 10 ppm to -1 ppm) and an identical number of points so that each point in each vector always corresponds to

Solution: Step 1



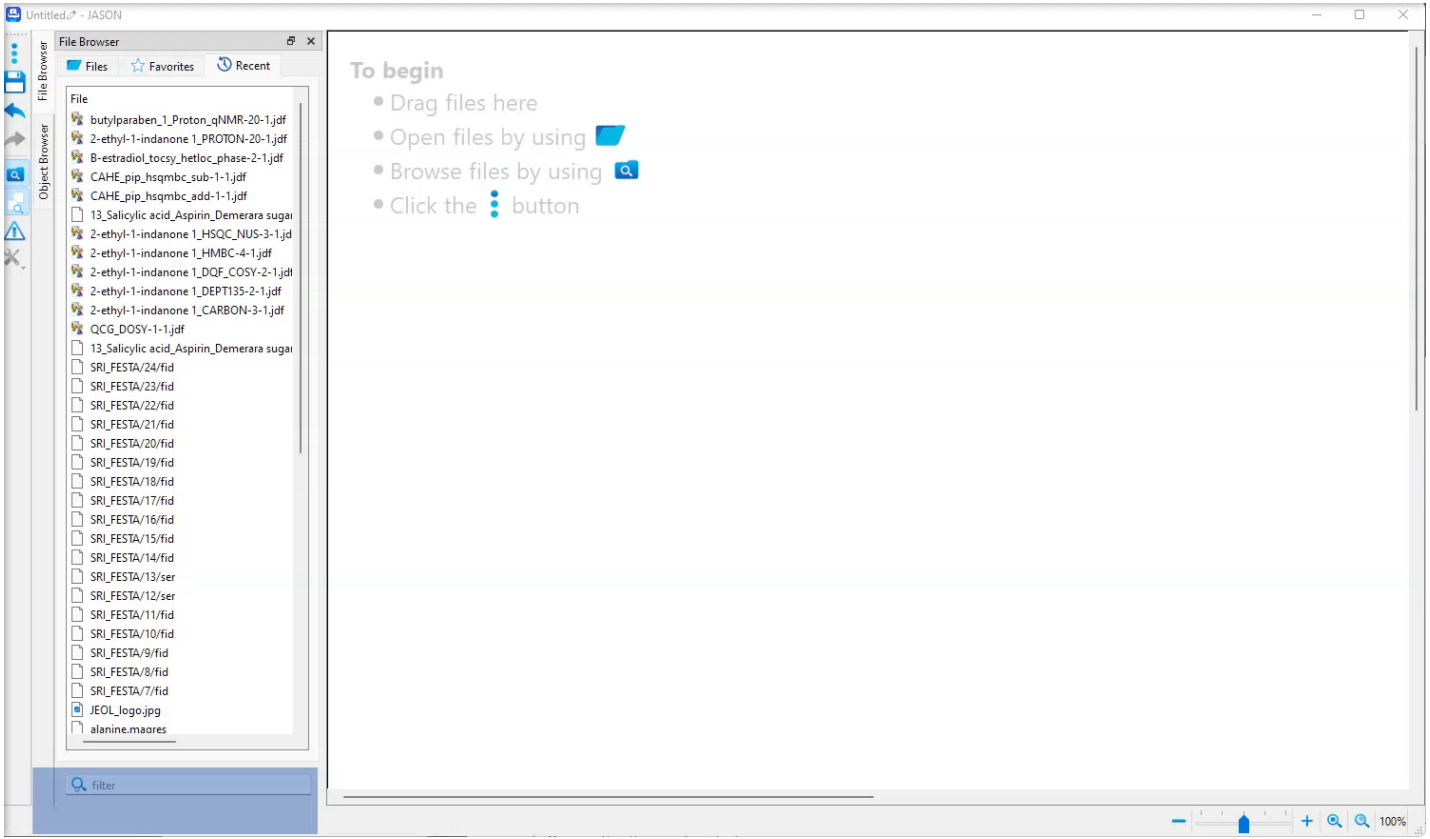
From and **To** specifies the range of the spectrum which will be kept. If the spectrum doesn't contain datapoints in some part of the requested region then zero intensity points will be used in place of the missing data. Values of from and to are automatically swapped internally if needed, a region can be specified in any order.
Points kept defines the exact number of points which will be used within the above specified region. Linear interpolation is used to convert the existing data points to the new digital resolution of the spectrum.

Solution: Step 2

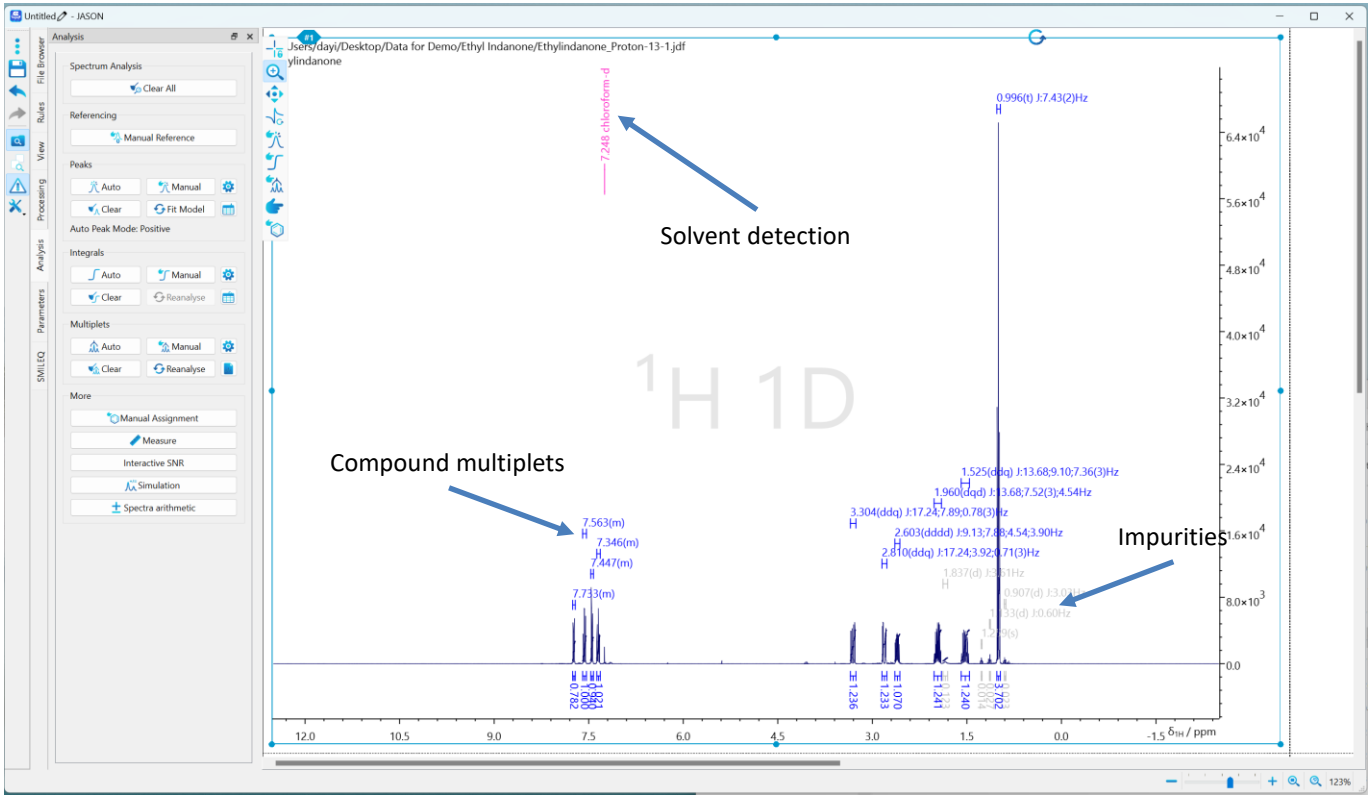
```
for %%f in (*.jdf) do (
 %jason_path% --headless "%path%\%%f" "%path%\kp_process1d.jjp" -s "%path%\%%~nf.jjh5" -s "%path%\%%~nf.csv"
)
```

Automated structural assignment

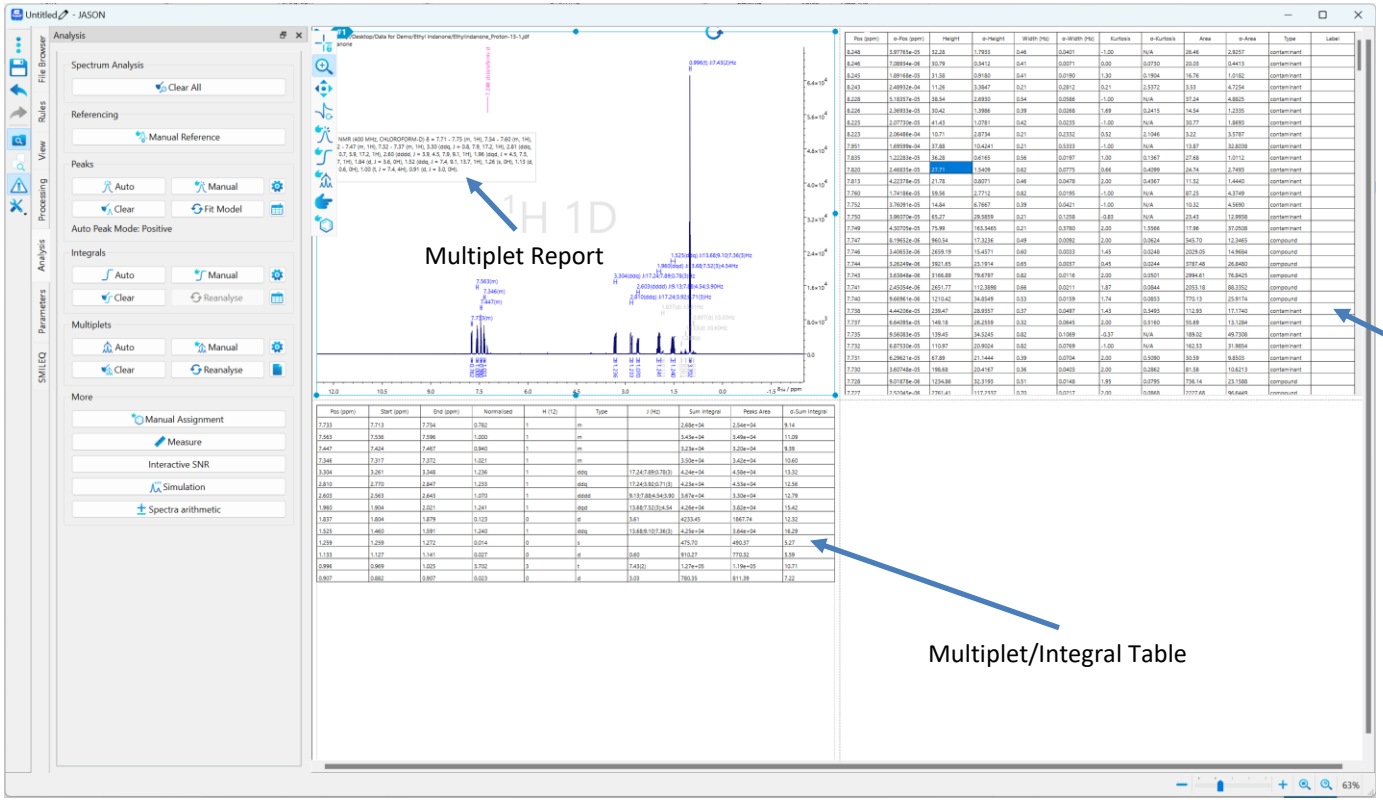
- **Molecular drawing tools** (Reads/writes .mol and .sdf files)
- ^{1}H and ^{13}C (for now) **chemical shift prediction** on the fly
- Hybrid approach:
  - Neural Network based on NMRShiftDB and JEOL Natural product DB
  - HOSE code-like approach for unfamiliar molecules
- **Automatic structural assignment** and drag-and-drop manual assignment
- Accurate simulate systems with up to 20 spins coupled
- Automatic peak picking, integration, J-coupling analysis, multiplet analysis. Drag-and-drop manual reformulation of multiplets



Automated Analysis

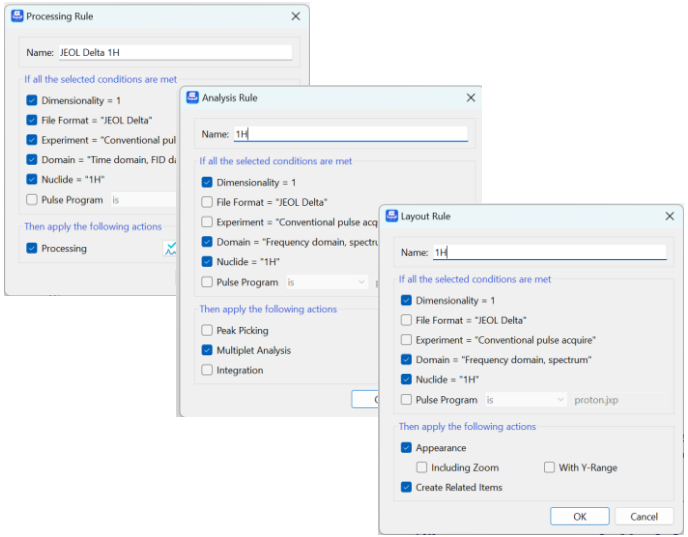


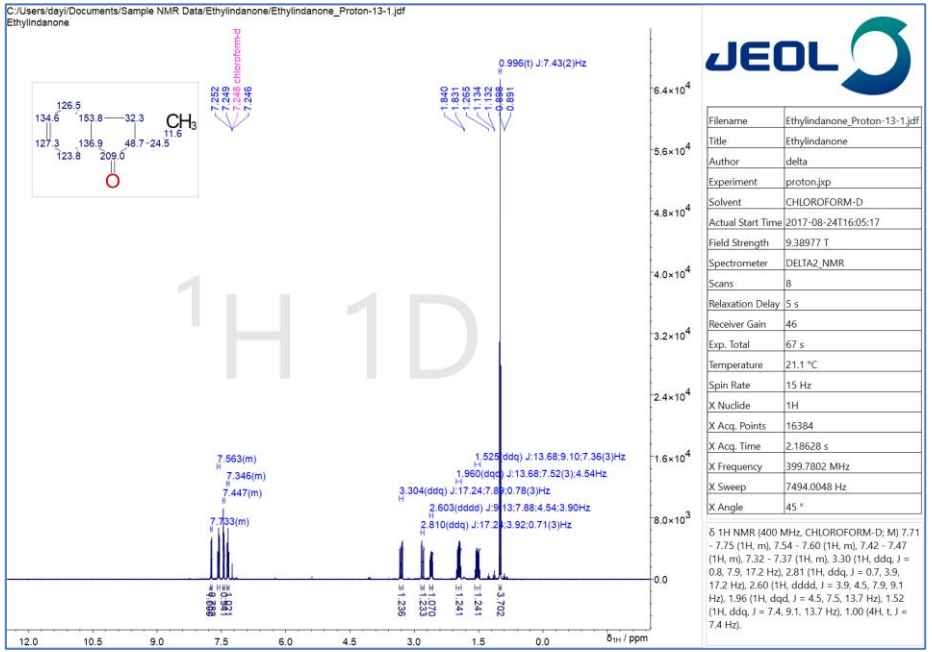
Reporting



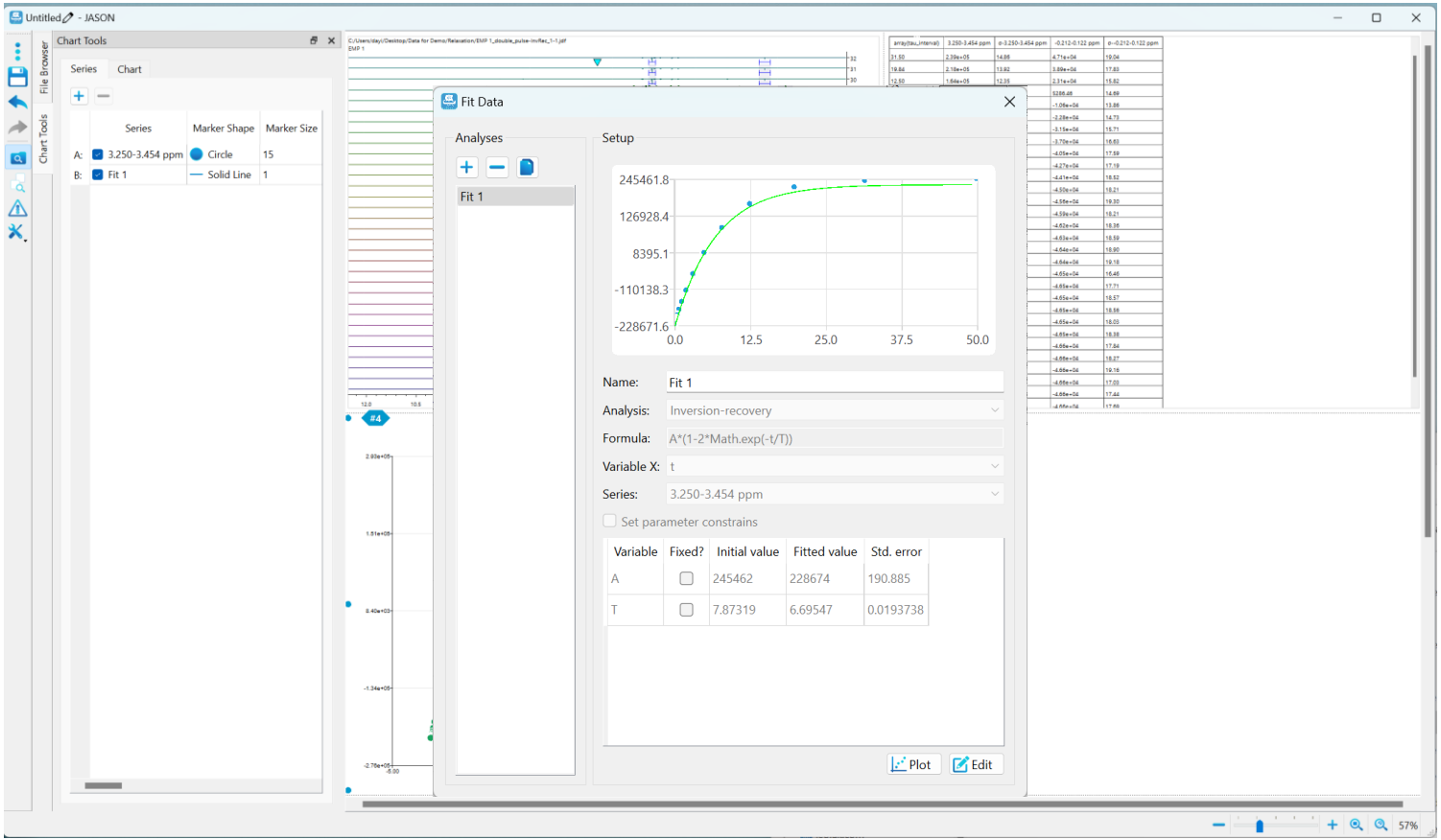
Rules!

- Control your processing, analysis and layout automatically
- Produce consistent reports to department or company format
- Annotations linked to spectral placement



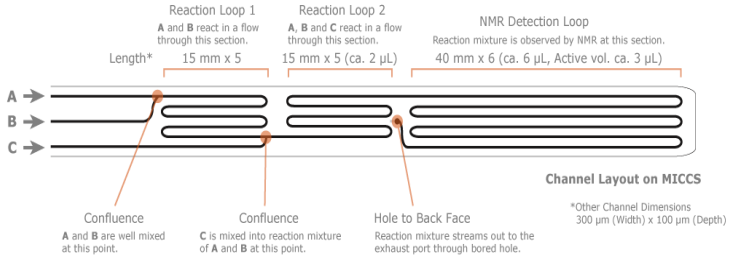


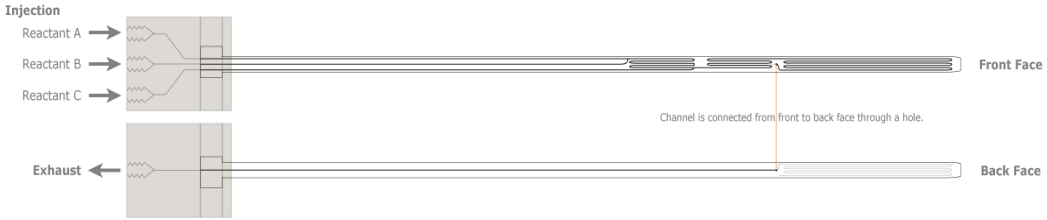
Charts and Fitting



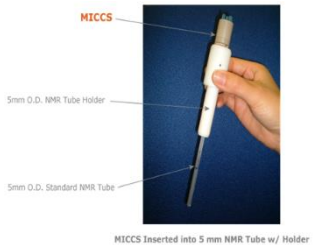
Reaction monitoring with MICCS

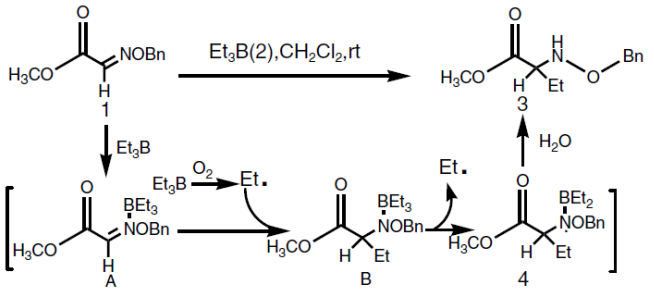
MIcro **C**hanneled **C**ell for **S**ynthesis monitoring



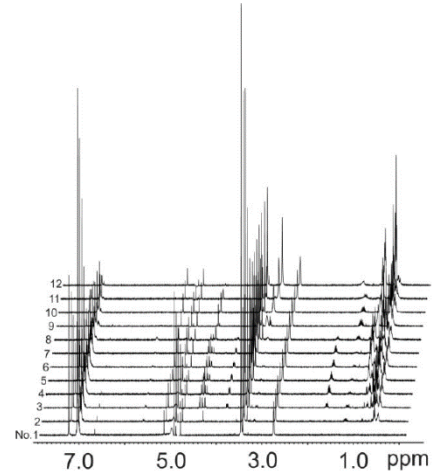


Micro Channeled NMR Cell Design



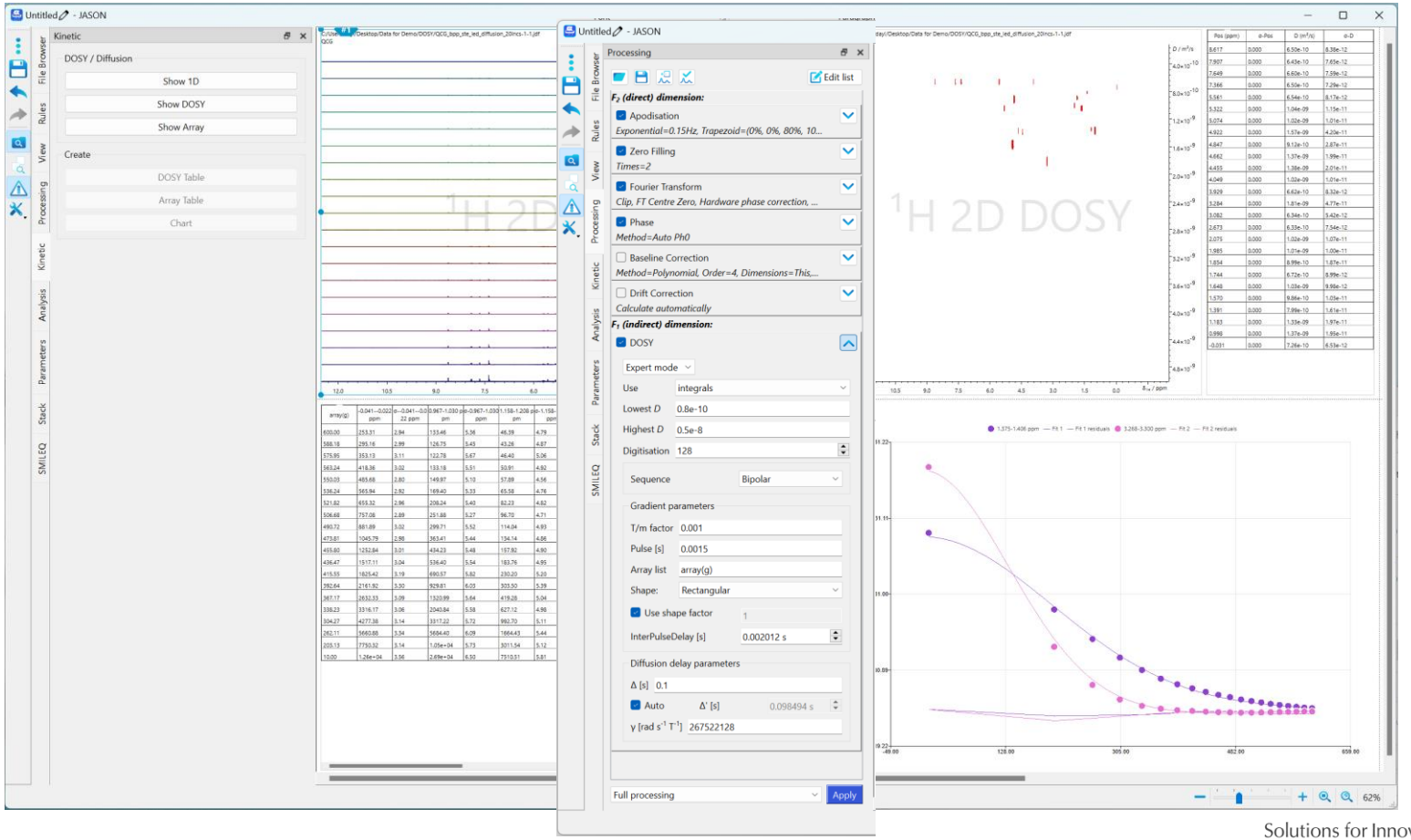


Oxime ether and triethylborane reaction



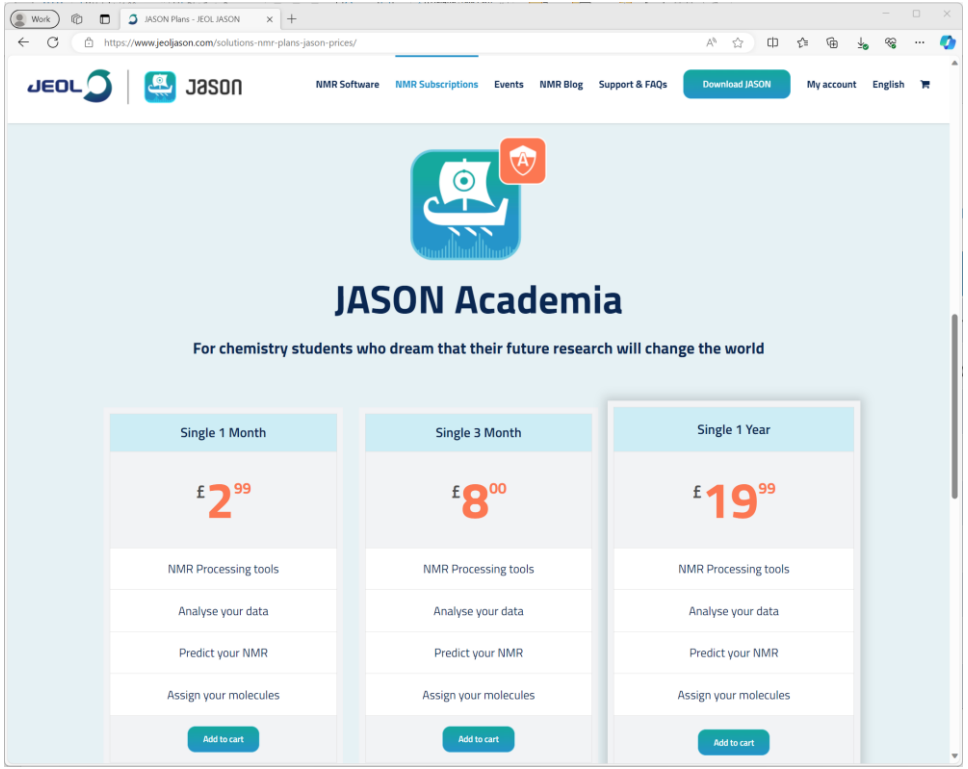
Takahashi et al., *Anal Sci.* 2007 Apr;23(4):395-400

DOSY Processing



JASON Licensing

- JASON uses a subscription model
- Benefits for the user include:
  - Frequent updates
    - Bug fixes every month
    - New features every 3 months
  - Easier support, you always have the latest version
- Pricing around “consumables” level
- Discounts for large userbase and campus licences



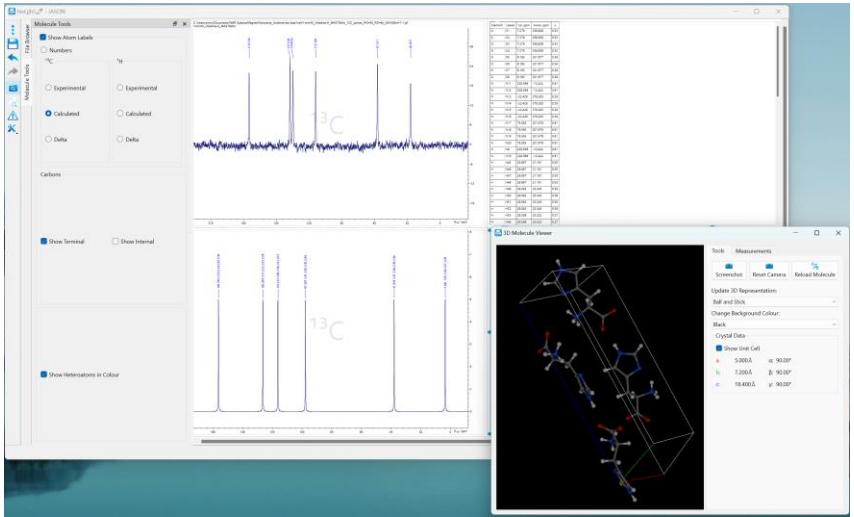
~ 41 NZD

Plugins

MAGRES for solid state NMR / NMR crystallography

Free!

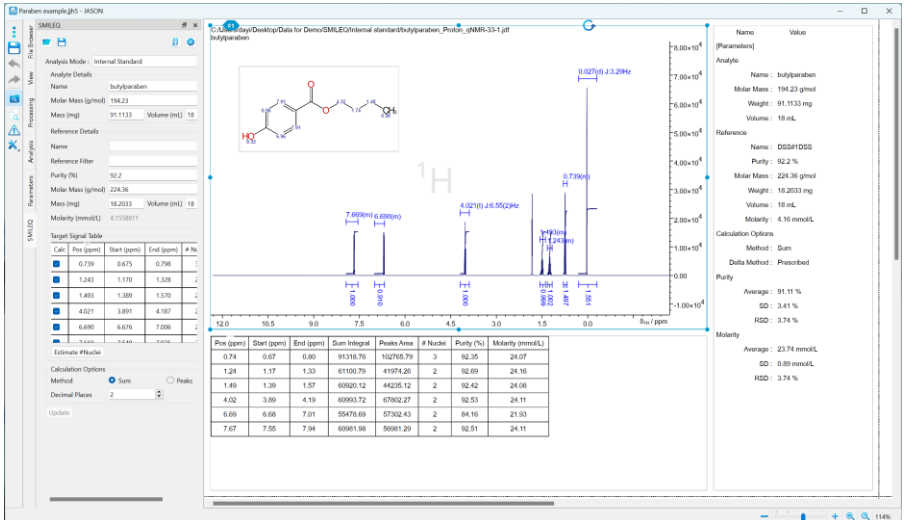
- Reads .magres output from CASTEP or QuantumESPRESSO
- View crystal structure
- Create 1D and 2D simulated spectra
- Option to include 2nd-order quadrupolar shift
- RMSD alignment with experimental data
- 3D visualization, easy distance and angle measurements



qNMR with SMILEQ

207 NZD /year

- Internal or External standard methods
  - PULCON and SOLCOR corrections
- Report generation
- Batch mode for multiple repetitions
- ISO 24583 compliant uncertainty reporting
- Seamless integration with JEOL Delta



JEOL webinars (https://www.jeol.co.jp/en/news/seminar/webseminar/movie_index.html)

Webinar	Link
An Introduction to NMR: Practical Aspects	https://attendee.gotowebinar.com/register/6221243905175906829
Speeding up NMR: NUS and NOAH	https://attendee.gotowebinar.com/register/5215973618176042256
An Introduction to Pure Shift NMR	https://attendee.gotowebinar.com/register/7480233097627308048
Introduction to JEOL Delta: Processing of 1D NMR data	https://attendee.gotowebinar.com/register/3743196484819939856
An Introduction to Solid-State NMR	https://attendee.gotowebinar.com/register/1588889267810221067
Natural Products identification through JEOL systems	https://attendee.gotowebinar.com/register/987608140196536078
An Introduction to JEOL Delta pulse programming	https://attendee.gotowebinar.com/register/4684449906779482894
Main aspects and applications of FAST MAS Solid-State NMR	https://attendee.gotowebinar.com/register/3947946440960288782
Elucidating nano-crystalline structure by combining microED and solid-state NMR	https://attendee.gotowebinar.com/register/5151154110240940816
Delta processing part 2: quantitative NMR	https://attendee.gotowebinar.com/register/591245194184783115
Assignment strategies in NMR pt1: 1D NMR and coupling	https://attendee.gotowebinar.com/register/7874168324236508685
NMR application in battery research	https://attendee.gotowebinar.com/register/7305723011972237583
Gradient Shimming: Theory and Practice	https://attendee.gotowebinar.com/register/5291489178361927691
A Synergy between Cryo-EM and NMR	https://attendee.gotowebinar.com/register/7623552241737432588
Assignment strategies in NMR pt2, 2D NMR	https://attendee.gotowebinar.com/register/2012768594452261388
Solid-State NMR Tutorial: Sample Packing, Standard Samples & Sample Spinning	https://attendee.gotowebinar.com/register/8621407423140093454
Ethyl Indanone: a user's perspective of the new JASON software	https://attendee.gotowebinar.com/register/3360923782708443918
Practical aspects of high-resolution 1H solid-state NMR at moderate MAS rate	https://attendee.gotowebinar.com/register/3873886639811883023
Your data in JASON: file formats and external access	https://attendee.gotowebinar.com/register/2441061364881739019
Selective Excitation of Overlapping Multiplets	https://attendee.gotowebinar.com/register/3213601326619561742
NMR Crystallography of Dynamically Disordered Solids	https://attendee.gotowebinar.com/register/3995403572903868683
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An Introduction to JASON NMR Processing Software using a number of worked examples	https://connect.acspubs.org/CENWebinar_JEOL_11_10_21
An Introduction of Delta NMR Data Processing Software ver.5	https://vimeo.com/755875413/1e71d583b0
Fluorinated Small Molecules at NMR -Simplifying Structure Elucidation of Fluorinated Small Molecules-	https://vimeo.com/755891713/a56376c521
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SMILEQ Plugin in JASON Software for Automated Quantitative NMR System	https://vimeo.com/755880107/efb95e2646
NMR Techniques to Determine Local Structure and Ion Dynamics in Lithium Ion Batteries	https://www.bigmarker.com/azonetwork/NMR-Techniques-to-Determine-Local-Structure-and-Ion-Dynamics-in-Lithium-Ion-Batteries
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Introduction to solid-state NMR: half-integer quadrupolar nuclei	https://www.jeol.com/events_seminars/webinars/2023/20230707_01_movie.php
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