



- ● Potency Determination
Quick Start

Sample Preparation

Prepare a **sample** containing the **analyte** and the internal reference standard (**reference**). The following information will be needed when setting up the potency determination experiment:

- Purity of the reference
- Weight of reference and of analyte in mg
- Structure of the analyte (mol file)
- Sample's solvent. A tip to get rid of exchangeable protons: add D_2O (50ul in 600ul dDMSO)

For each reference's integral region:

- The left and right borders in ppm
- The proton content
- The multiplicity (optional)

Optional: prepare and measure a 1H spectra of the analyte and the reference separately, in order to identify regions with no overlapping between the analyte and the reference. Overlap would lead to large errors.

Automated Potency Determination: Measurement

Start TopSpin*:



Start IconNMR with the TopSpin command: *iconc*

Add the P_PROTON experiment to the desired user:

A screenshot of the TopSpin experiment setup dialog box. A black square with the number '2' and a white arrow points to the 'Source directory' dropdown menu. The 'Source directory' is set to 'All Experiments'. The 'Experiment Name' is set to 'P_PROTON'. The 'Experiment Comment' is '1H experiment for potency determination'.

Source directory	All Experiments
Experiment Name	P_PROTON
Experiment Comment	1H experiment for potency determination

Activate *FastLane* (in the *CMC-Verification*) tab



Note:

- Refer to IconNMR reference guide for more details
- Extra license is not required when working at the spectrometer

* TopSpin 3.5pl7 or above

Automated Potency Determination: Measurement

Create a new Experiment for the holder with the sample. Give an experiment name (use letters, numbers and no spaces)

Hol...	Type	Status	Disk	Name
▼ 1	1	Available		
		Available	C:\data\amr_icon ▼	potency_sulindac_tmb ▼

Select the solvent and the P_PROTON experiment.

Solvent	Experiment
DMSO dimethylsulfoxide-d6 ▼	N P_PROTON ▼

Browse for the analyte mol file or draw the structure

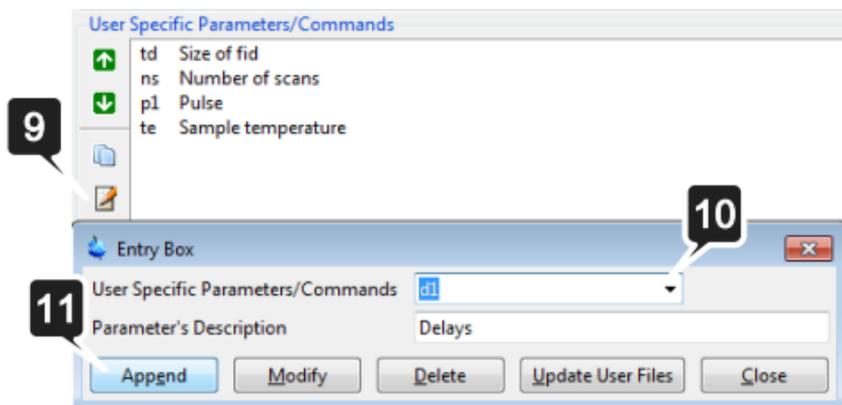
7  8

Analysis

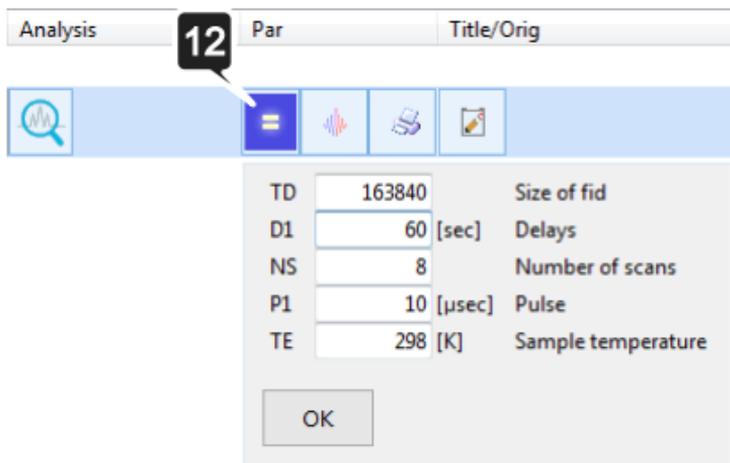
Mol File  

Change D1 Delay (default is 40s)

IconNMR configuration allows to define parameters that can be changed (9)



Then when setting up a new experiment, D1 is available by clicking on the *Par* button (12), together with the number of scans (NS):



Automated Potency Determination: Measurement

Select the Internal Reference Standard Batch to be used (13)

If maleic acid is not used as internal reference standard, then click on *R+* button (14) to create a new one. *B+* button (15) will create a batch for an already defined internal reference standard.

13

14

15

Internal Reference

maleic acid Potency: 100.00% Batch: DEFAULT

R+

B+

Enter the exact weight of analyte and internal reference standard in mg (16).

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Reference weight 10.23 mg

Analyte weight 12.54 mg

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The experiment is set-up. Click *OK*

OK

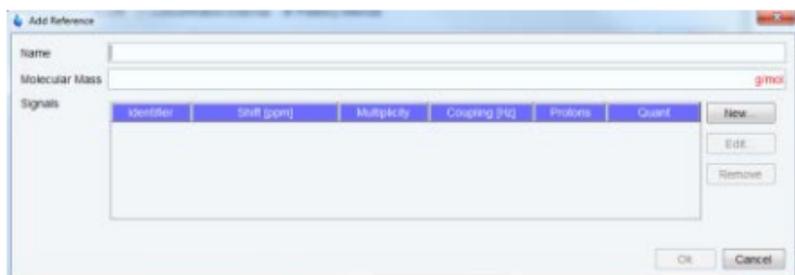
Submit the experiment

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Submit

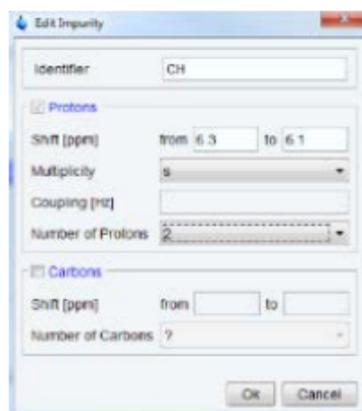
Automated Potency Determination: Measurement

Add a new reference by clicking on R+ (14)



Add the following information for the new internal reference:

- Name
- Molecular mass
- All reference integral regions by clicking on *New*



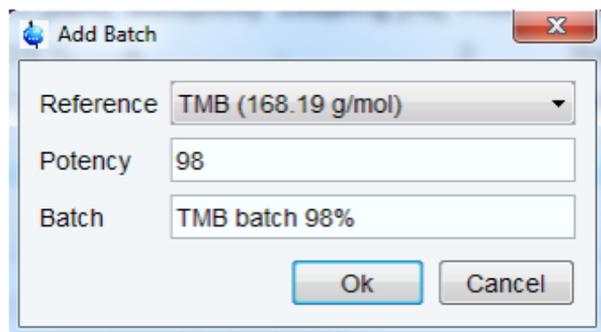
Select the integrals that will be used for



Automated Potency Determination: Measurement

Add a new Batch by clicking on *B+* (15)

- Select the reference for the new batch
- Enter a batch name
- Enter the potency of the batch



The batch is then ready to be selected for a potency determination.

Deleting a reference (19) or a batch (20) is not possible in IconNMR but possible in CMC-assist:



Note: modifications in CMC-assist qNMR settings can be discarded by clicking on *Cancel* and are stored only if the potency calculation is started

Automated Potency Determination: Analysis and Reporting

The analysis of the measured data is automatic

Open in CMC-assist with a right click in the *Preceding Experiments*

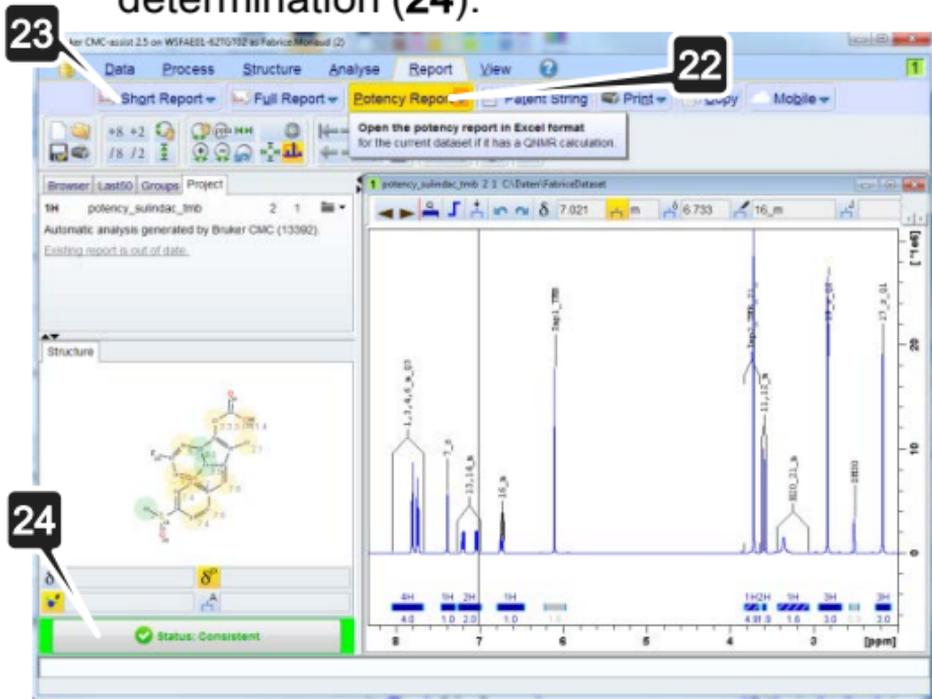
Experiment	Load	ATM	Lock	Shim
P_PROTON	✓			

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Show in TOPSPIN

Show in CMC-assist

Get the Potency excel report (22), the consistency analysis Report (23), integral regions used for potency determination (24).



Automated Potency Determination: Replicates

The average potency of several samples prepared in duplicate, triplicate... can be automatically calculated by following the steps below:

Setup the first experiment as described before. Don't submit it.

Select the replicate by selecting the first experiment with a left click (**R1**) and then, press *Ctrl* key and select the holders where the replicate samples are (**R2**).

Then right click, select *Averaging/Use selected experiments* (**R3**)

The screenshot shows a table of experiments with columns: Hol..., Type, Status, Disk, and Name. The first three rows are selected. A context menu is open over the 'Averaging' option, with 'Use selected experiments' highlighted. Callouts R1, R2, and R3 indicate the steps: R1 points to the first experiment, R2 points to the selected replicates, and R3 points to the 'Use selected experiments' option.

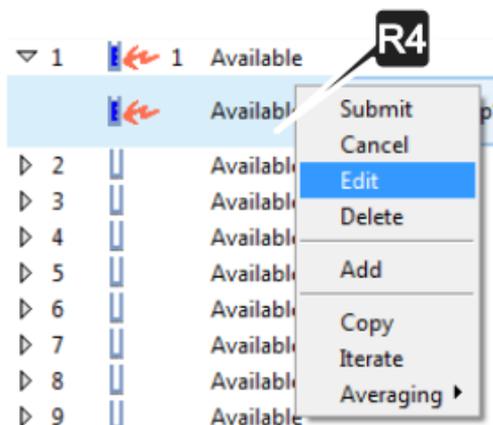
Hol...	Type	Status	Disk	Name
1	298K	Run		Potency Sulindac
2	298K	Que	C:\data\amr_icon	Potency Sulindac
3	1	Queued	C:\data\amr_icon	Potency Sulindac
4		Available		Potency Sulindac
5		Available		Potency Sulindac
6		Available		Potency Sulindac
7		Available		Potency Sulindac
8		Available		Potency Sulindac
9		Available		Potency Sulindac
10		Available		Potency Sulindac
11		Available		Potency Sulindac
12		Available		Potency Sulindac

Context menu options:

- Submit
- Cancel
- Edit
- Delete
- Add
- Copy
- Iterate
- Averaging
- Use selected experiments
- Copy settings to next

Automated Potency Determination: Replicates

Correct the analyte's and reference's weights by right click/*Edit* on each of the experiments and edit the weight as in (16).

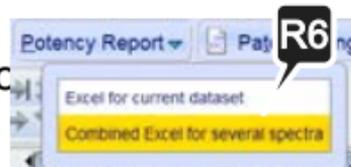


Select all replicates and submit:

Submit

When all experiments are finished, open one of them in CMC-assist as in step (21).

Open the co



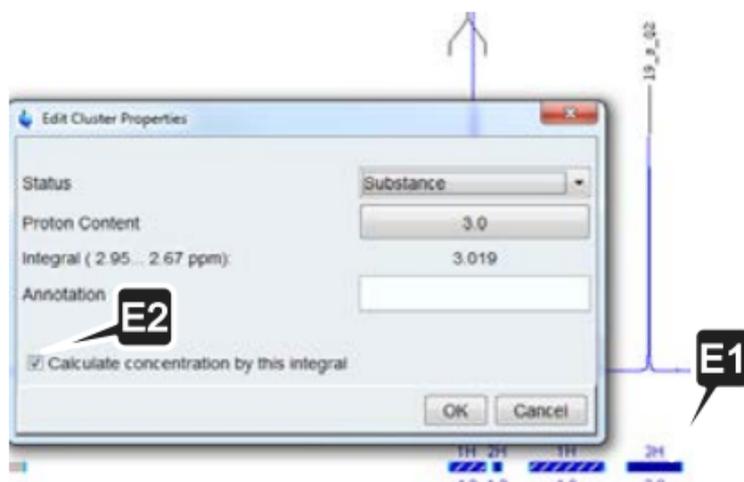
The average potency (R7)

Region 2	Averaged Area analyte	SD Area analyte	N analyte [mmol]	Potency [%]	RSD Potency [%]
1.00	1.00	0.00	0.02	98.05	
1.01	1.00	0.00	0.05	99.92	
1.00	1.00	0.00	0.02	99.70	
				99.23	0.84

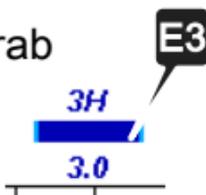
Integral Region Adjustments and Manual Report Generation

The automatically selected analyte integral regions can be modified manually and the reports updated.

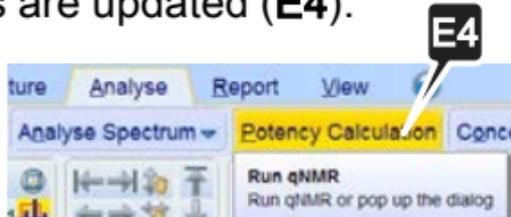
Select/UnSelect analyte integral regions: right click on a CMC-assist integral region (**E1**) and tick/untick (**E2**).



Change analyte integral regions: grab left or right borders with the mouse

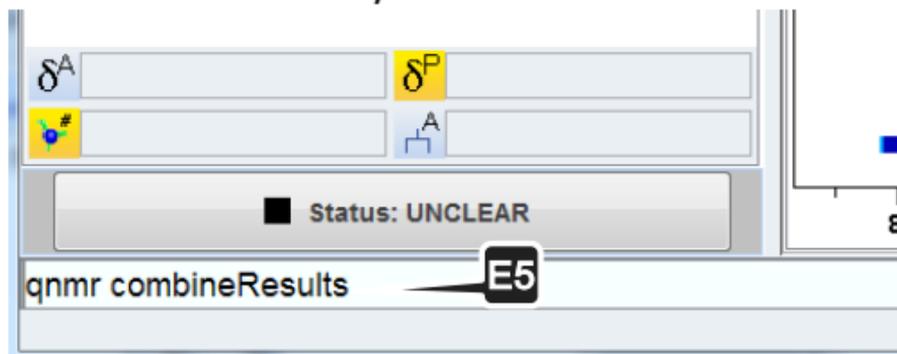


Recompute the potency, then the reports are updated (**E4**).

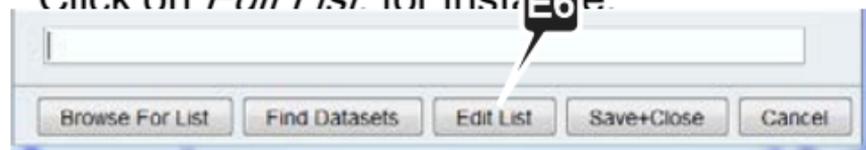


Integral Region Adjustments and Manual Report Generation

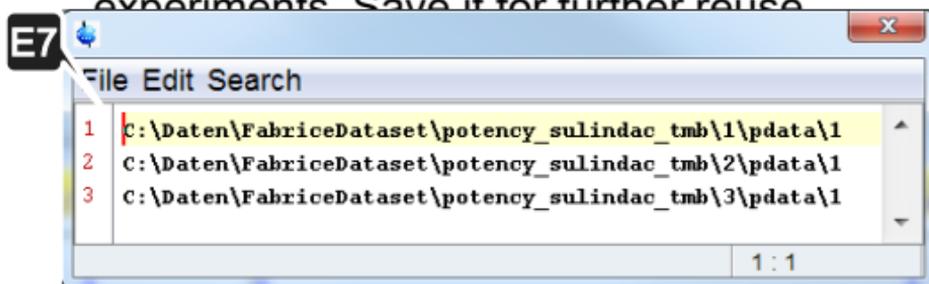
Enter command: *qnmr combineResults*



Click on *Edit List* for instance: **E6**



Copy/Paste there the paths to experiments. Save it for further reuse



Click to generate an updated combined report that override any existing one **E8**

Save+Close

Define and Use Predefined Analyte's Integral Regions

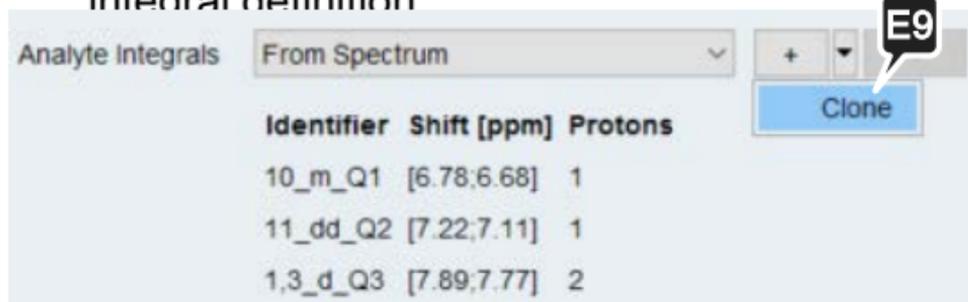
Measure first with IconNMR as described before. Open the results with CMC-assist, modify the analyte integrals (**E1 E2 E3**) that were automatically chosen.

Open Potency Calculation (**E4**)

Click on the button to edit :



The analyte's integral(s) from spectrum is the default. Selecting *Clone* (**E9**) allows to use them as a template to create and store a user defined analyte integral definition



Analyte Integrals From Spectrum

Identifier	Shift [ppm]	Protons
10_m_Q1	[6.78;6.68]	1
11_dd_Q2	[7.22;7.11]	1
1,3_d_Q3	[7.89;7.77]	2

Clone

E9

The user defined analyte integral definition is stored and can be reused using the drop down menu (**E10**)



Analyte Integrals MyAnalyteIntegralDefinition

From Spectrum

MyAnalyteIntegralDefinition

E10

● Potency Determination Quick Overview

Useful Links

- ❑ License request for using another workstation (Demo CMC-assist license)

https://www.bruker.com/nmr_license_requests.html

Learn More

- ❑ Potency determination Bruker webpage

<https://www.bruker.com/products/mr/nmr/nmr-software/software/qnmr/overview.html>

