

CMC-q

- CMC-q
User Manual
Version 005



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1 Introduction

CMC-q handles data acquisition, processing, and analysis for automated batch NMR spectroscopy. It allows for a large degree of flexibility in experimental setup within a straightforward framework. CMC-q is designed to be used in conjunction with the data analysis module CMC-assist, providing a comprehensive software environment for automated batch NMR spectroscopy.

1.1 About this Manual

The User Manual describes the main aspects of Bruker's software package CMC-q. It intends to give an overview of the main aspects of the CMC-q interface, as well as provide instruction on how to set up a batch NMR acquisition with CMC-q, analyze the data, and view the results.

- **Chapter 1** provides a brief introduction to CMC-q and its intended use, as well as a description of the User Manual
- **Chapter 2** describes the installation of CMC-q, as well as how to configure the partner software IconNMR and calibrate the spectrometer for use with CMC-q.
- **Chapter 3** explains the features of the CMC-q interface. It also presents instructions on creating user-defined verification types and customized acquisition settings.
- **Chapter 4** gives step-by-step instructions for setting up a standard batch acquisition using CMC-q.
- **Chapter 5** addresses viewing, editing, and reporting the results after acquisition. It covers entire batches of results as well as individual spectra.



Please note that the figures shown in this manual are designed to be general and informative and may not represent the specific version you are working with.

1.1.1 Font Conventions

- Commands that can be entered on the command line, menus, buttons and icons that can be clicked are in **Arial bold**.
- Path, File, Dataset and Experiment names are in *Arial italic*.

1.2 Intended Use

CMC-q is a tool designed to streamline the acquisition, processing, and analysis of batches of NMR data. It is specifically tailored to facilitate compound library management with respect to structure verification as well as concentration, water content, and purity determination. These features may also be used for a variety of other applications within the fields of pharmaceutical and chemical research, e.g., for quality control of fragment libraries in the context of fragment-based screening (FBS) or the generation of reference 1D spectra for FBS.

1.3 What's New?

An expanded range of set up possibilities is now offered from within CMC-q. The new set-up dialog offers the possibility to create an SD-file from scratch or to add information to an already existing SD-file, e.g., information about the position of the sample in the sample changer from a *.csv file*. Moreover, an option was introduced to select an experiment number automatically, to avoid overwriting of data (see section [Experiment Number \[▶ 19\]](#)). In IconNMR several options are now available to create serial processing lists directly during acquisition.

1.4 CMC-q License

CMC-q requires a license for use. A license can be ordered online from: https://www.bruker.com/nmr_license_requests.html

A short instruction on installing the license file will be sent together with the license. In addition, a description how to order and install a license can be found in the **Help** menu of Topspin. Left-click on the **Help** button and select **Manuals (docs)**, afterwards click on **CodeMeter License Management**.

1.5 System Requirements

CMC-q is a batch acquisition tool with subsequent data analysis for small organic compounds in solution. Therefore, it requires a spectrometer suited for the acquisition of corresponding samples. Moreover, a sample changer is mandatory for CMC-q to operate.

2 Preparing to Use CMC-q

This chapter describes how to get started using CMC-q and gives a brief description of how to optimize your system for use with this software.

2.1 Install CMC-q

CMC-q is installed together with Bruker's NMR software TopSpin. However, CMC-q requires an additional license.

Below is a brief description of the installation of TopSpin. For further details, please read the instructions available on the installation DVD.

- Log in as Local Administrator
- Close all windows on the desktop
- Insert the DVD
- Start the Installation
 - If DVD AutoPlay is enabled, the DVD window will automatically appear
 - If this window does not appear automatically select the DVD device and double-click **install.cmd** (for Windows) or execute **install** (for Linux)
- The installation window will guide you through the installation
- After successful installation, the computer should be restarted. At this point CMC-q is installed and only requires the correct license for activation.

2.2 Configure IconNMR

IconNMR is Bruker's software tool that handles spectrometer control in automation. CMC-q is designed to work in conjunction with IconNMR to provide an efficient means of acquiring NMR data for large batches of samples. For this reason, IconNMR must be configured properly for CMC-q to be used. The IconNMR settings can be adjusted from the **IconNMR: Configuration** menu. To access this menu: type **icon** on the Topspin or CMC-assist command line and click **Configuration** in the following window. On the left hand side of the **IconNMR: Configuration** menu is the control panel. From the control panel each configuration page can be accessed.


2.2.1 Master Switches

To access the **Master Switches** menu, click **Master Switches** in the **IconNMR: Configuration** menu control panel. There are many settings in this menu that may be adjusted for individual needs, but at least the **SampleChanger/Automation Mode** must be set for use with CMC-q. Select the sample changer that is used at the spectrometer.

2.2.2 Automation Window

In this window, the user defines where CMC-q writes the External Setup File. This file is how CMC-q communicates the batch automation settings to IconNMR. Access the Automation Window via the Configuration Menu control panel.



Choose an External Setup Directory - Click the browse icon () next to External Setup Directory, and choose an appropriate directory. For example, on a windows system *C:\Temp*

2.2.3 User

The user chosen in CMC-q should have access to all of the CMC parameter sets as well as each parameter set used in a user defined verification type. Also, the user should have access to the parameters ns and ds. If no user exists with these privileges, either modify an existing user's privileges or create a new user.

New users are created from the **Additional Users** menu accessed from the control panel.

- Type the desired User ID then click **Add New**

To modify user privileges click **User Manager** from the control panel. Access to parameter sets, as well as individual parameters, is granted from this window. For detailed information on creating users and changing user privileges see the IconNMR User Manual.

2.2.4 Verification/Quantification


In the **Verification/Quantification** window some general options can be selected for CMC related products, including CMC-q. For CMC-q you can turn-on/off an email report and a print-out of the analysis results. In addition, you may select one of the available options for the automatic generation of serial processing lists.

2.3 Calibrate the Spectrometer

To determine sample concentration using CMC-q, the spectrometer must first be calibrated for the parameter set used for quantification in the verification type.

A calibration experiment is a 1D proton experiment performed on a sample of known concentration using the same parameter set to be used during the batch acquisition. Alternatively, a 1D proton spectrum without solvent suppression may be used.

2.3.1 How To Perform a Calibration Experiment

- Open Topspin by double-clicking the Topspin icon () on the desktop
- Insert a reference sample of known concentration, in any solvent, into the spectrometer
- Create a new experiment by entering **edc** on the command line
- In the **New** window, fill in the required information and click the **getprosol** option. Be sure the 90 degree pulse is properly calibrated before performing this experiment. For pulse calibration instructions, see the Topspin 1D and 2D Step-by-Step - Advanced Manual.
 - Choose the experiment to match your desired acquisition settings in CMC-q. Below are a list of the provided verification types and the corresponding 1D proton experiments to be used in the calibration experiment.
 - STANDARD_USUP: CMC_PROTON
 - STANDARD_SSUP: CMC_SINGLE
 - STANDARD_SSUP_H2O: CMC_SINGLE_H2O
 - STANDARD_DSUP: CMC_WET
 - HIGH_USUP: CMC_PROTON
 - VERYHIGH_USUP: CMC_PROTON

- If using a custom defined verification type, choose the 1D proton experiment that will be used for the quantification analysis.
- Adjust the number of scans if required for this sample. This setting does not necessarily have to be the same as what will be used in CMC-q.
- Lock, shim, tune and match the magnet before starting the experiment.
- To begin the experiment enter **xaua** on the command line. If not using a CMC experiment, be sure to set the receiver gain (enter **rga** on the command line) before starting the experiment.
- For more detailed instruction on inserting a sample into the magnet, creating a new experiment, locking, shimming, tuning and matching, see the Topspin 1D and 2D Step-by-Step - Basic Manual.

2.3.2 How To Create a Calibration File

- After the acquisition is finished, process the data by entering **xaup** on the command line.
- Change to integration menu.
- If there are integrals already defined delete them (~~X~~), then manually integrate () one or more well defined signals that are easily assigned to a certain number of protons.
- Define this integral as the concentration reference.
 - Right-click on one of the integrals
 - Select **Eretic - Define as Eretic Reference**

Number of atoms	Region start [ppm]	Region end [ppm]	Molecule name	Molar mass [g/mol]
2	7.587774	7.443568	Phenazone	188.2260
3	7.383925	7.186068	Phenazone	188.2260
3	6.442705	6.136345	Phenazone	188.2260
1	5.360341	5.292385	Phenazone	188.2260
3	3.208429	2.957688	Phenazone	188.2260
3	2.353371	2.106603	Phenazone	188.226

- In the **Define Integrals as Eretic Reference** window
 - Type the known concentration (mmol/l) in the **Concentration** field.
 - Enter the volume (ml) in the **Sample volume** field.
 - Fill in the number of protons corresponding to the signals in the **Number of atoms** field for each signal you want to use. For example, if the signal comes from a methyl group, enter 3.
- This experiment can now be used as a calibration file in CMC-q for any verification types using this 1D proton parameter set.

- This procedure must be repeated for each verification type that uses a different 1D proton parameter set.
- In the **NMR Tab** Menu in CMC-q, this calibration file can be assigned to a particular verification type. See section [Path for Calibration Files \[20\]](#) for more details on assigning a calibration file.

2.4 Launching CMC-q

CMC-q is easily accessed through either Topspin or CMC-assist. To launch the main CMC-q **Setup** window from Topspin or CMC-assist, enter **cmcq** in the command line.

3 The CMC-q Interface

The **CMC-q Setup** window is the control center for batch automation. From this window the user defines all required parameters to set up a batch acquisition. This chapter will explain each of the tabs of the **CMC-q Setup** window.

The screenshot shows the 'CMC-q Batch Automation Settings' window with the 'General' tab selected. The window contains several configuration fields:

- Verification Type:** STANDARD_USUP
- IconNMR User:** CMCQ
- Solvent:** DMSO
- Path for SD File:** C:\Bruker\CMCQ\data\GUI_EXAMPLE.sdf (with 'New...', 'Merge...', and 'View' buttons)
- Molecule ID (Mol-ID):** IDNUMBER
- Sample Position (SPos):** WELL
- Rack Number:** 3

At the bottom of the window are 'Save', 'Start', and 'Cancel' buttons.

3.1 General Tab

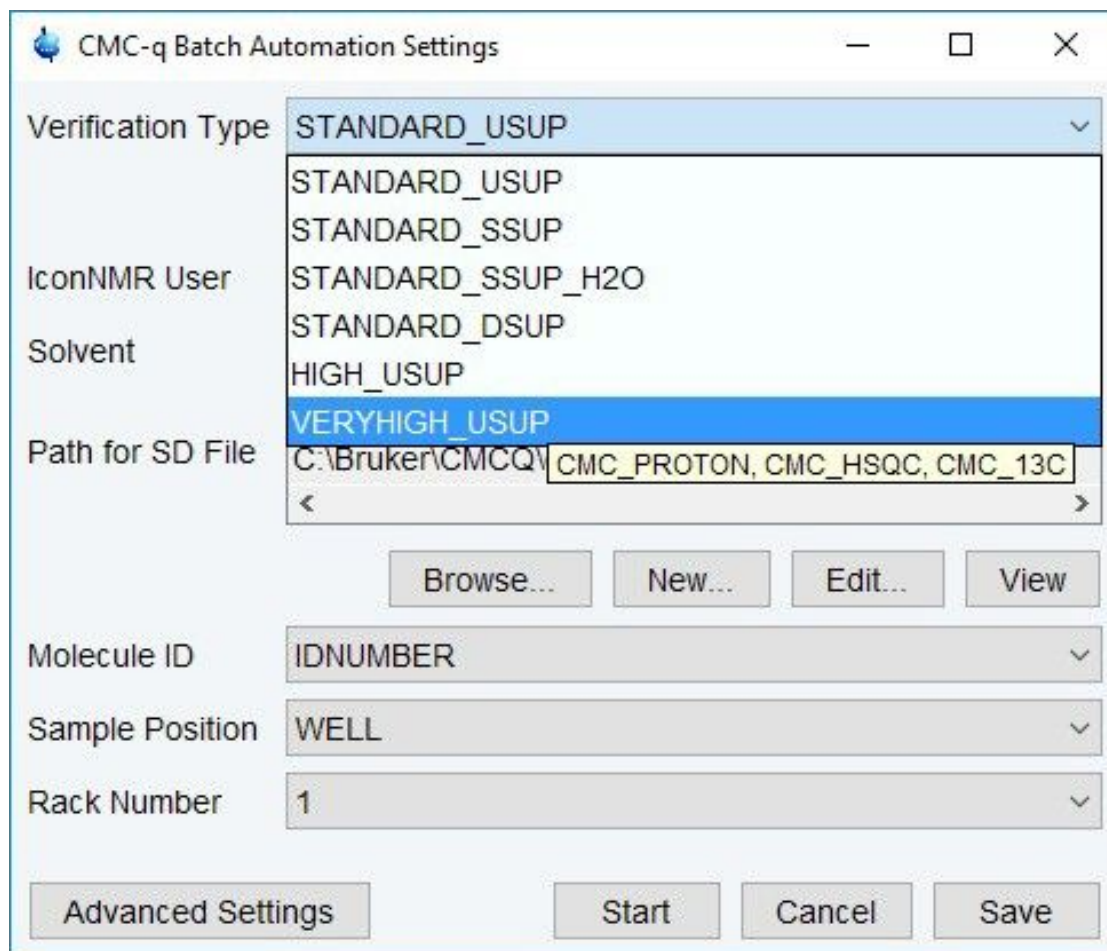
3.1.1 Verification Type

A verification type defines which experiments will be performed during the batch acquisition. For every sample, a structure verification project is created that links the spectra in the verification type. Any ¹H, HSQC, HMBC, or ¹³C experiment will be added to the project to prepare for a joint automated analysis.

3.1.1.1 Choosing a Verification Type

Click on the **Verification Type** pull-down menu to select the verification type

- Let the mouse hover over a verification type in the pull-down menu to display the corresponding experiments, or in the case of user defined verification types, the comments entered in the **Verifications Tab** window.



3.1.1.2 Predefined Verification Types

There are several predefined verification types provided with CMC-q.

- **STANDARD_USUP** - USUP stands for unsuppressed, and this verification type acquires a 1D proton spectrum using CMC_PROTON, without solvent suppression.
- **STANDARD_SSUP** - SSUP stands for single suppressed. This verification type acquires a 1D proton spectrum with single solvent suppression using the experiment CMC_SINGLE; optimized for water in DMSO-d6.
- **STANDARD_SSUP_H2O** - This verification type acquires a 1D proton spectrum with single solvent suppression using the experiment CMC_SINGLE_H2O; optimized for aqueous solutions.
- **STANDARD_DSUP** - This verification type acquires a 1D proton spectrum with double solvent suppression using the experiment CMC_WET. This verification type is ideal for use with samples in non-deuterated DMSO (HDMSO).
- **HIGH_USUP** - This verification type acquires a 1D proton spectrum and an HSQC spectrum using the experiments CMC_PROTON and CMC_HSQC.

- **VERYHIGH_USUP** - This verification type acquires a 1D proton spectrum, an HSQC spectrum, and a 1D ¹³C spectrum with the experiments CMC_PROTON, CMC_HSQC, and CMC_13C.

3.1.2 IconNMR User

CMC-q operates through IconNMR and therefore must be set with the correct IconNMR user settings. This user must have access to the parameter sets used in the verification type and be allowed to manually set the parameters ns and ds. The user must also be able to set the dataset names individually and be able to edit parameter sets. If no user exists with these privileges, create one in the IconNMR configuration menu. For more information about creating IconNMR users and changing user privileges, see section [Use \[8 \]r](#) or the IconNMR User Manual.

To set the IconNMR user in CMC-q:

- Click on the **IconNMR User** pull-down menu
- Select the desired user from the list

3.1.3 Solvent

In the **Solvent** pull-down menu, the user defines the solvent used for the samples. Information in the SD file under <SOLVENT> will not be taken into account. Only one solvent can be defined per rack of samples. If more than one solvent is used in a rack, this can be altered within IconNMR or jobs can be set up using different SD files.

To set the solvent:

- Click on the **Solvent** pull-down menu
- Select the solvent from the list

NOTE: When HDMSO is the solvent, the DMSO fraction is assumed to be approximately 10% DMSO-d₆/ 90% DMSO-H₆. Based on this assumption, the water content is automatically determined during the analysis.

3.1.4 Path for SD File

In the **Path for SD File** field, choose the SD file that defines the properties of the current batch of samples.

3.1.4.1 What is an SD File?

An SD file is a user-supplied text file, of a certain format, that describes the samples to be measured and analyzed. To use the SD file in CMC-q, it must contain one entry for each sample with the following information:

- an individual compound identifier
- the molecular structure in .mol file format (V2000 or V3000 mol file convention)
- the sample position

The SD file may contain other information under identifiers in the format <IDENTIFIER> to describe other attributes of the batch of samples.

Following is an example of one entry in an SD file representing all of the input information describing one sample.

```

16 16 0 0 0 0 0 0 0 0999 V2000
  0.5893   0.7192   0.0000 C   0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
  3.4166   1.7032   0.0000 C   0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
  2.4575   1.3687   0.0000 C   0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
 -1.5186  -0.9092   0.0000 C   0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
 -2.8171  -1.8684   0.0000 C   0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
  1.3337   0.0699   0.0000 C   0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
 -0.3696   0.4096   0.0000 C   0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
  0.7791   1.7032   0.0000 C   0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
 -2.3577  -0.3349   0.0000 C   0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
 -3.4166  -2.6872   0.0000 C   0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
 -0.5594  -0.5745   0.0000 N   0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
  1.1390  -0.9092   0.0000 O   0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
  2.2677   0.3847   0.0000 O   0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
  0.9989   2.6872   0.0000 N   0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
 -1.8331  -1.8481   0.0000 O   0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
 -3.1270  -0.9092   0.0000 N   0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
16  9  1  0  0  0  0  0
15  4  1  0  0  0  0  0
 4 11  1  0  0  0  0  0
 5 15  1  0  0  0  0  0
 6  1  1  0  0  0  0  0
 7  1  2  0  0  0  0  0
 8  1  1  0  0  0  0  0
 9  4  2  0  0  0  0  0
14  8  3  0  0  0  0  0
11  7  1  0  0  0  0  0
12  6  2  0  0  0  0  0
13  6  1  0  0  0  0  0
10  5  1  0  0  0  0  0
 3 13  1  0  0  0  0  0
 2  3  1  0  0  0  0  0
16  5  2  0  0  0  0  0
M  END
> <IDNUMBER> (BB012345)
BB012345

> <PLATE> (BB012345)
2

> <WELL> (BB012345)
B04

> <AMOUNT> (BB012345)
0.11

> <SALTDATA> (BB012345)
0.5 C2H5OH

> <H_ACCEPTORS> (BB012345)
7

> <H_DONORS> (BB012345)
1

$$$
-- StrEd --

```

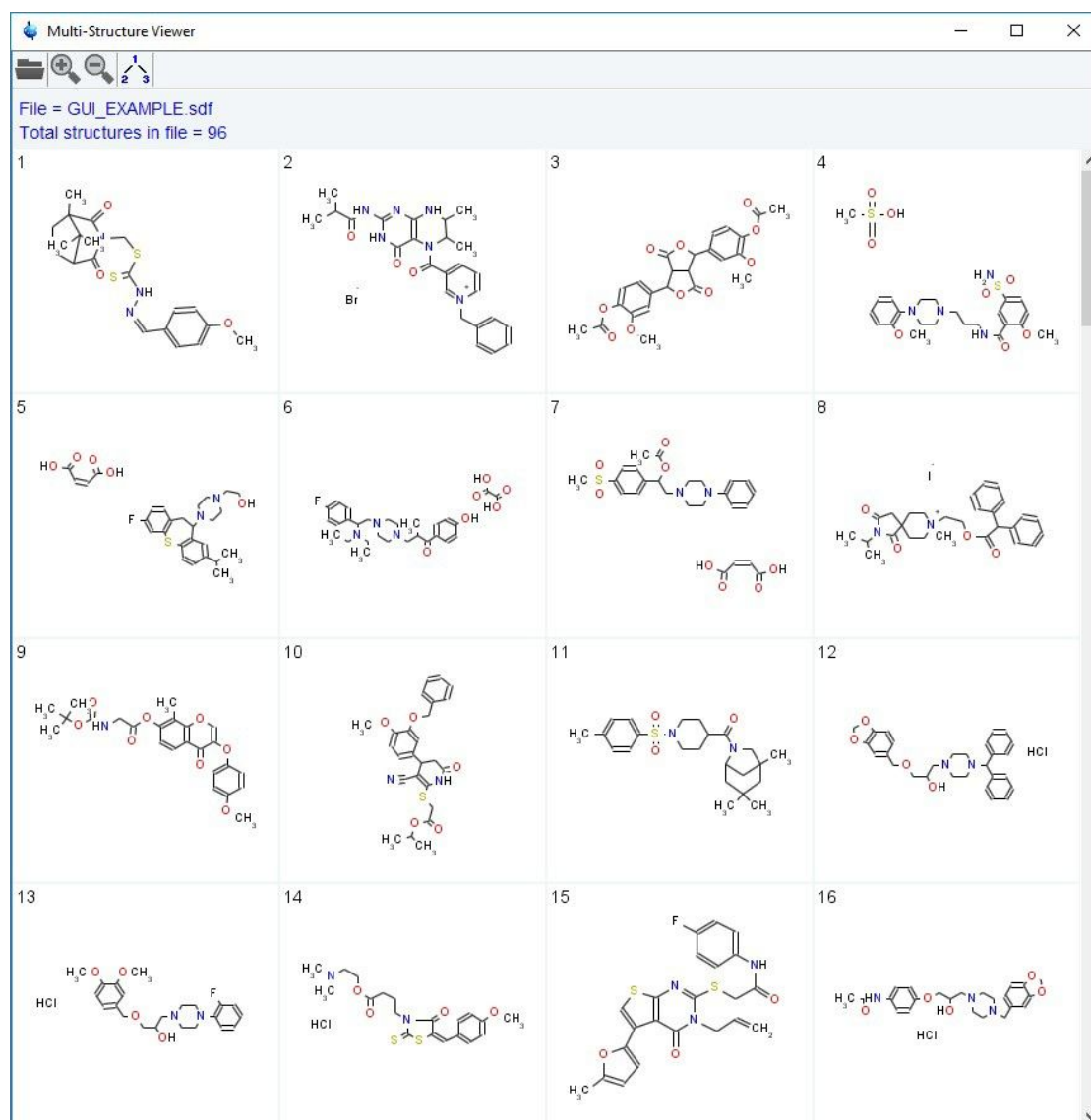
This example SD file entry contains the sample structure in .mol file format, a unique sample identifier (<IDNUMBER>), sample position (<WELL>), and further parameters with their identifiers in the format <IDENTIFIER> (e.g <SALTDATA>).

3.1.4.2 Defining the Batch of Samples with an SD File

To instruct CMC-q which SD file to choose, the file's data path must be defined in the **Path for SD File** field. To do this click **Browse**. This will launch the **Select SD File** window where the user can browse for the SD file. Once the SD file is selected, click **Open** to define the data path for this file.

3.1.4.3 Multi-Structure Viewer

After an SD file is defined for a batch of samples, it may be viewed from within the Multi-Structure Viewer of CMC-q. This viewer displays each molecule of the SD file.



- To open the Multi-Structure Viewer, click the **View** button below the SD file field.

3.1.5 Molecule ID

This parameter assigns certain information in the SD file as an individual compound identifier for each sample.

- To assign an SD file identifier, click the **Molecule ID** pull-down menu.
- Select an SD file identifier that assigns a unique identifier for each sample.

In the example SD file entry from section [What is an SD File?](#) [13], the identifier is IDNUMBER.

3.1.6 Sample Position

This parameter determines the SD file identifier that should be used to define where each sample is located within the sample changer.

- To assign an SD file identifier, click the **Sample Position** pull-down menu.
- Select an SD file identifier that defines the position of the sample appropriately for the type of sample changer.
 - If using a 96-well plate in a SampleJet, the format for this identifier must be a capital letter between A and H followed by a two digit number between 01 and 12 (e.g. B02 or E11).
 - If using any other sample changer, or the SampleJet open shop ring, this identifier must be a number corresponding to the sample's position in the sample changer.

In the example SD file entry from section [What is an SD File?](#), [13] the identifier is <WELL> and the information carried under this identifier for this sample is B04.

3.1.7 Rack Number

In the case of a SampleJet, the rack number defines where the samples are located within the sample changer.

- If using a 96-well plate in a SampleJet, choose 1-5 corresponding to the location of the sample rack within the sample changer.
- If using SampleJet open shop ring or any other sample changer, choose 0.

To set the rack number:

- Click on the **Rack Number** pull-down menu
- Select the appropriate rack number from the list

3.2 Naming Tab

From the **Naming Tab**, the naming of the data sets can be configured, as well as a title that will be displayed in the data sets after acquisition. A variety of options is available to suit individual requirements. This section will give a description of each option and how to change it.

CMC-q Batch Automation Settings

General Naming NMR Impurities Verifications

Data Set Name

Mol-ID Example: AA-504_32628011

Plate ID (Plate-ID)

SDF Identifier Select

Text PlateName

Title

SDF Identifier IDNUMBER

Pattern

\$NAMES\$ \$PLATES\$ \$WELLS\$

NAME
ID
WELL
PLATE
EXPNO

Save Start Cancel

3.2.1 Data Set Name

The **Data Set Name** defines the format for naming each data set in the batch. The available options for **Data Set Name** format are Mol-ID, Mol-ID_SPos, SPos_Mol-ID, Mol-ID_Plate-ID_SPos, Mol-ID_Date

- The variable Mol-ID takes the information stored in the SD file identifier assigned to Molecule ID in the **General Tab**.
- The variable PLATE-ID takes the information stored in Plate ID defined below in the **Naming Tab** menu.
- The variable SPos takes the information stored in the SD file identifier assigned to Sample Position, defined in the **General Tab**.
- Date is defined as the setup date.
- Click the **Data Set Name** pull-down menu to choose how to define the name of the data set. An example name will be shown to the right of the pull-down menu, based on the current selection of the SD file.

3.2.2 Plate ID

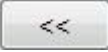
This parameter assigns information to the parameter PLATE which can be used in defining the **Data Set Name** and the **Title**.

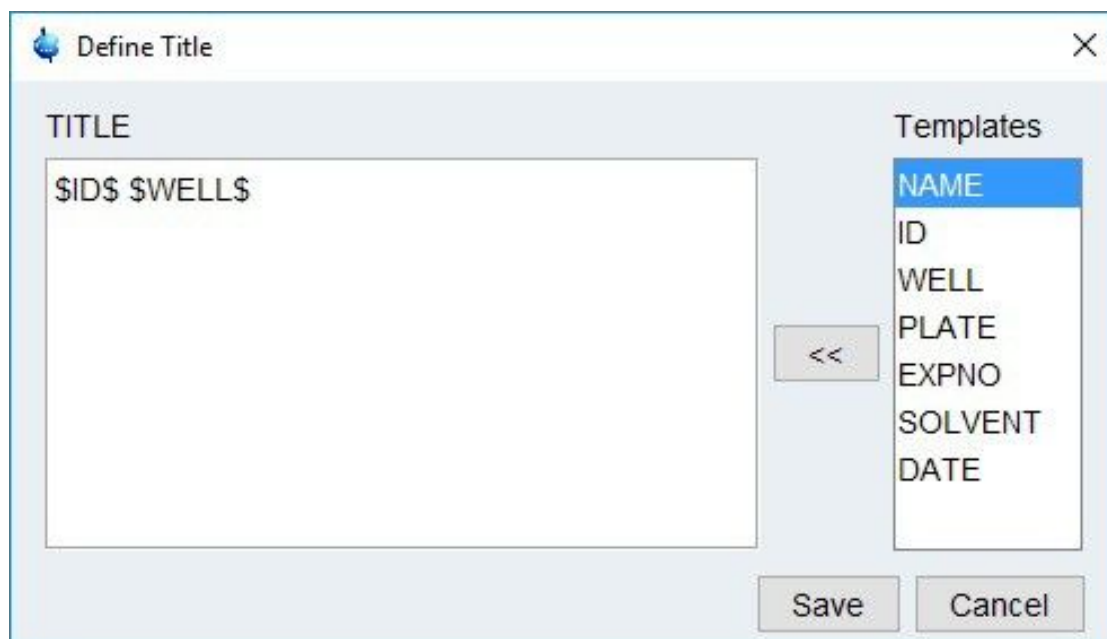
- With the **SDF identifier** radio button selected the title is defined by an SD file identifier
 - Click the **Plate ID** pull-down menu to select an SD file identifier to be used as the plate identifier.

- In the example SD file from section [What is an SD File? \[13\]](#) the identifier is `<PLATE>` and the information carried under this identifier is 2.
- With the **Text** radio button selected the Plate ID can be defined manually.
 - Type the desired plate identifier in the Plate ID field

3.2.3 Title

This parameter defines the title of each experiment within the data set

- With the **SDF Identifier** radio button selected, the title is defined by an SD file identifier.
 - Click the pull-down menu to select an SD file identifier to be used as the title
- With the **Pattern** radio button selected the title can be defined by a combination of other variables. These variables include ID, PLATE, WELL, and DATE. Other variables available for use in defining the title are NAME, EXPNO, and SOLVENT. Additionally, custom text may be typed in this field.
 - Click the **Edit** button to bring up the **Define Title** menu
 - In the template field are the available parameters to be used in defining the title
 - Click on a parameter in the **Templates** field to select it
 - To use this parameter in the **Title** click the  button
 - To remove a parameter from the title, select it in the **Title** field and use the delete button on the keyboard.



3.3 NMR Tab

The **NMR Tab** offers a variety of parameters to customize the batch acquisition. Each individual parameter will be described in this section to allow a tailored acquisition for your needs.

The screenshot shows the 'CMC-q Batch Automation Settings' dialog box with the 'NMR' tab selected. The 'Verification parameters for STANDARD_USUP' section contains the following controls:

- Skip Locking
- Skip Shimming
- Number of Scans:**
 - PROTON: 16 (with up/down arrows)
- EXPNO:**
 - PROTON: 1 (with up/down arrows)
 - Auto
- Calibration File:**
 - Text input field
 - Edit... button

At the bottom of the dialog are three buttons: Save, Start, and Cancel.

3.3.1 Locking, Shimming

In some scenarios it might be useful to measure without locking and/or shimming. With the check boxes **Skip Locking** and **Skip Shimming** this can be turned off. Please note that this setting, as well all other settings will be saved along with the verification type and will be reused for later acquisitions of this specific verification type. We strongly recommend not to turn off locking and shimming as long as a proper lock solvent is available to enhance the spectral quality.

3.3.2 Scan Number

The number of scans can be set for each experiment of the verification types from the **NMR Tab**.

- The number of scans for each experiment of the verification type are automatically set to the standard defined values.
- To change the number of scans, type the desired number in the field next to the experiment type or increment the number of scans by one using the click arrows.

3.3.3 Experiment Number

The experiment number can be set for each experiment of the verification type individually or tick the **Auto** check box to allow IconNMR to select the next free experiment number.

- To change the experiment number, type the desired number in the field next to the experiment or increment the number of scans by one using the click arrows

3.3.4 Calibration File

To use the quantification features in CMC-q, a calibration file must be assigned to the verification type being used. A calibration file can be assigned to more than one verification type if they use the same 1D proton parameter set for the quantification analysis. For detailed information on what a calibration file is and how to create one, see section [Calibrate the Spectrometer. \[▶ 8\]](#)

- Click **Edit** next to the **Calibration File** field to bring up the **Calibration** window
- Click the verification type chosen for the current acquisition
- When the verification type is highlighted, click **Edit**
- In the **Select Calibration Directory** browse for the directory containing the calibration file created for the verification type
- When the corresponding directory is selected, click **Select Calibration Directory**
- To accept the changes made in the **Calibration** window, click **OK**

3.4 Impurities Tab

For accurate structure verification and consistency determination, impurities in the sample must be defined in the **Impurities Tab** before acquisition. Impurities may be defined after acquisition in CMC-assist, but this can lead to inaccurate consistency decisions when using CMC-q.

There are three types of impurities that can be defined in the **Impurities** menu: Known Impurities, Custom Impurities and Shift References.

The screenshot shows the 'CMC-q Batch Automation Settings' dialog box with the 'Impurities' tab selected. The 'Shift Reference' section has radio buttons for TMS (selected), TSP, DSS, and Not specified. The 'Known Impurities' section contains a grid of checkboxes for various solvents: H2O, MeOH, DMSO_D5, DMSO_H6, Dimethylsulfon, EtOH, iPrOH, C6H6, Acetone, CH3CN, CHD2CN, Ethylacetate, DMF, NH4, CYCLOHEXANE, and ACETIC_ACID. Below this is a table of active impurities with columns for Active, Identifier, H Shift [ppm], Multiplicity, Coupling [Hz], Proto..., C Shift [ppm], and Carb... The table contains one entry: Dioxan with H Shift [3.6,3.5], Multiplicity s, Coupling -, Proto 8, C Shift -, and Carb ?. To the right of the table are buttons for New..., Edit..., and Remove. At the bottom of the dialog are Save, Start, and Cancel buttons.

3.4.1 Shift References

These are common impurities in typical NMR samples whose chemical shift, multiplicity, and coupling information are known in a variety of solvents. In addition, these impurities are used as a chemical shift reference to calibrate the chemical shifts within the sample, by setting their shift to 0 ppm. If one of these shift references is used click the radio button next to the name.

3.4.2 Known Impurities

These are common impurities in typical NMR samples whose chemical shift, multiplicity, and coupling information are known in a variety of solvents. To alert CMC-q to this type of impurity click the tick boxes next to their names.

3.4.3 Custom Impurities

These are impurities known to the user but not defined in the Known Impurities list. To define a custom impurity:

- Click **New** to open the **Edit Impurities** dialog

The screenshot shows the 'Edit Impurity' dialog box with the following fields and values:

- Identifier:** NITROMETHANE
- Protons (checked):**
 - Shift [ppm]: from 4.5 to 4.3
 - Multiplicity: s
 - Coupling [Hz]: (empty)
 - Number of protons: 3
- Carbons (checked):**
 - Shift [ppm]: from 64.0 to 62.5
 - Number of carbons: 1

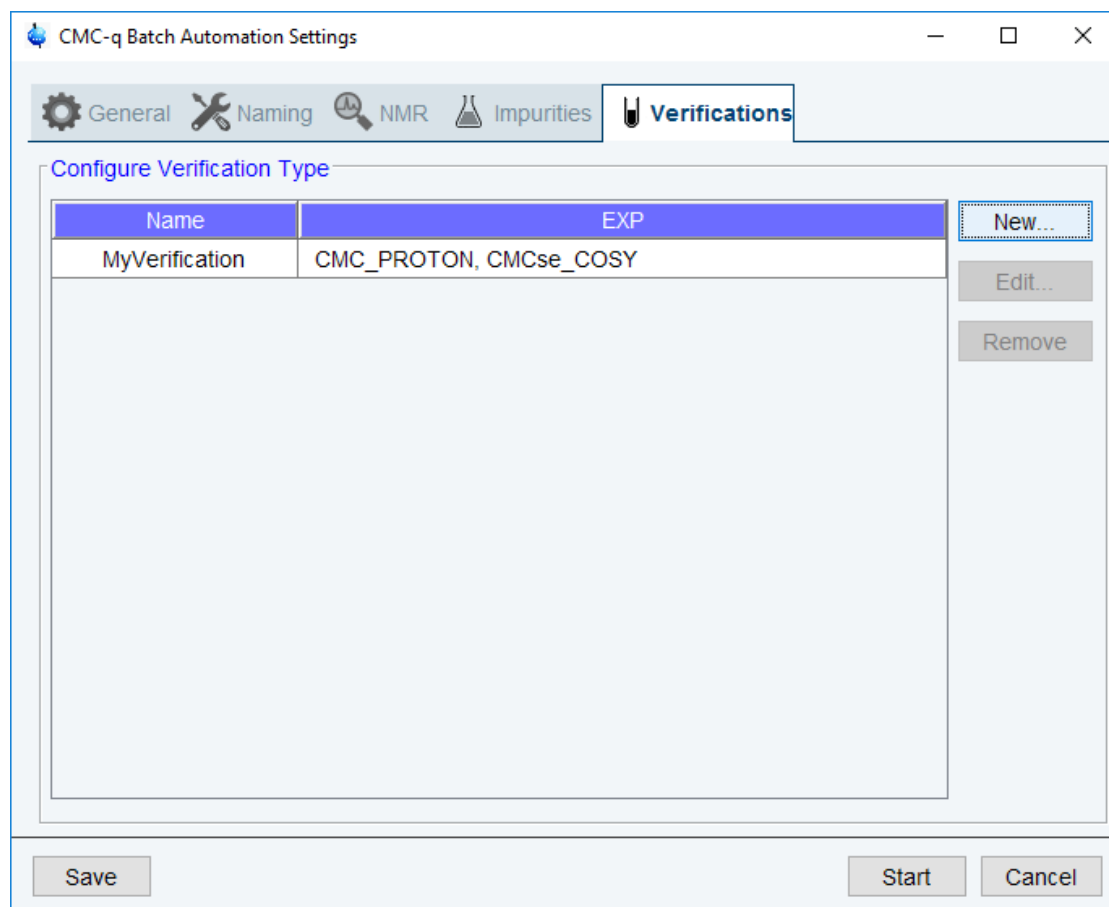
Buttons: OK, Cancel

- Enter the name of the impurity in the **Identifier** field
- Tick the box next to **Protons** if the impurity will cause a signal in the 1D proton spectrum
 - Define the chemical shift region where the signal will appear. This region must be greater than 0.01 ppm.
 - Define the multiplicity of the signal in the **Multiplicity** pull-down menu. The options are s - singlet, d - doublet, t - triplet, and other. Choose other if the multiplicity is unknown or not an option in the pull-down menu.
 - Enter the coupling for the signal in Hz in the **Coupling** field. If the multiplicity is chosen as 'd' or 't' this information must be given. If the multiplicity is chosen as 's' or 'other' this information cannot be given. If a signal is known to be a doublet or triplet but the coupling information is unknown, choose other in the **Multiplicity** pull-down menu.
 - If known, the number of protons giving rise to this signal can be entered in the **Number of protons** pull-down menu. If the information is unknown or unavailable in the pull-down menu, choose '?'.
- Tick the box next to **Carbons** if the impurity will cause a signal in the Carbon spectrum
 - Define the chemical shift region where the signal will appear. This region must be greater than 0.1 ppm.
 - If known, the number of carbons that will give rise to this signal can be entered in the **Number of carbons** pull-down menu. If the information is unknown or unavailable in the pull-down menu, choose ?.
- Click **OK** to save the custom impurity.
- After a Custom Impurity is defined, it must be checked in the **Active** column of the **Impurities** Menu to be used for the automatic analysis.
- For a single impurity in the sample, each signal derived from the impurity must be defined separately. For example, if defining ethanol as a custom impurity; the proton and carbon signals from the CH₃ group would be defined as one custom impurity and the proton and carbon signals from the CH₂ group would be defined as another custom impurity.

3.5 Verifications Tab

New verification types can be created using any combination of available parameter sets. These parameter sets are not limited to the CMC parameter sets. The data from any proton, HSQC, HMBC, or ¹³C experiment will be grouped into a project for streamlined analysis in CMC-assist.



User defined verification types are created, edited, and deleted from the **Verifications Tab**. Click the **Configure** button next to the **Verification Type** pull-down menu in the **CMC-q Setup** window to launch the **User Verification** window seen below.



3.5.1 Create a Verification Type

To create a new Verification Type:

- Click **New** in the **Verification Tab** to bring up the **User Verification** window seen below.

- Enter the name of the new verification type in the **Name** field
- If desired, enter a comment in the **Comment** field. To view this comment let the mouse hover over the verification type in the **Verification Type** pull-down menu.
- Select the desired parameter set from the **Parameter Set** pull-down menu
 - Use at least one 1D 1H parameter set
 - Every parameter set must have a defined SPECTYP in the parameter set proc file.
 - Any PROTON, HSQC, HMBC, or 13C parameter set (including non-CMC parameter sets) will be added to the verification project in CMC-assist. This allows for streamlined joint analysis.
 - All other experiment types will be acquired but will not be added to the project in CMC-assist.
- If a parameter set is not available in the **Parameter Set** pull-down menu:
 - Click **Possible Parameter Sets**
 - The Possible Parameter Sets pool lists all of the available parameter sets with a defined SPECTYP and the Active Parameter Sets pool lists all of the parameter sets that will be available in the **Parameter Set** pull-down menu
 - To move a parameter set between the pools select the parameter set and click either  or .
- If the desired parameter set does not have the SPECTYP defined this can be added in the parameter set proc file.
 - To access this file go to `<TopspinHome>\exp\stan\nmr\par\user\<ParameterSetName>\proc`

- Open the proc file with a text editor and scroll to the parameter SPECTYP. Between the brackets < > enter the spectrum type that will be acquired. e.g. PROTON, HSQC, COSY etc.
- Click **Add** to add another experiment to the verification type. Any number of experiments can be defined in the verification type and any type of experiment can be chosen as long as the SPECTYP is defined.
- Click **OK** to save the verification type. The new verification type will be displayed in the **Verification Type** pull-down menu of the **General Tab**.

3.5.2 Assign a Calibration File

A calibration file must be assigned to a verification type to use the quantification features of the CMC-assist analysis. The data path to this reference spectrum has to be specified in order to calculate the concentration of the compound of interest. For more information about calibration files and calibration experiments see section 2.3 Calibrate the Spectrometer. To assign a calibration file to a verification type:

- Click **Browse** in the User Verification Window
- In the **Select Calibration Directory** browse for the directory with the calibration experiment created for the verification type.
- When the calibration directory is selected, click **Select Calibration Directory**

3.5.3 Modify a Verification Type

To edit a previously defined verification type:

- Select the verification type in the **Verification Tab**
- Click **Edit** to access the various settings in the **User Verification** window
- Click **OK** to save the changes to the verification type

To delete a previously defined verification type:

- Select the verification type in the **Verification Tab**
- Click **Remove** to delete the verification type

3.5.4 Analysis of Spectra from User Defined Verification Types

From user defined verification types, spectra of type PROTON, HSQC, HMBC, and ¹³C can be automatically analyzed after acquisition. For this to work, the 1D proton spectrum must be processed using a cmc processing program. The automatic processing program used in a parameter set is defined in the parameter sets proc file. To access this file, go to <TopspinHome>\exp\stan\nmr\par\user\<ParameterSet Name>\proc. From the proc file, the processing program is set by filling in the < > brackets after the header AUNMP.

- For unsuppressed spectra use cmc_proc1h_usup
- For spectra acquired using single solvent suppression, use cmc_proc1h_ssup
- For spectra acquired with double solvent suppression, use cmc_proc1h_dsup

Alternatively, a user defined processing program may be altered to include the following CMC-specific line:

- For unsuppressed spectra: XAU("rwcmaq", "dec yes eretic no supno 0");

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- For spectra acquired using single solvent suppression: XAU("rwcmaq", "dec yes eretic no suppno 1 suppsrc SOLVENT_FILE " "suppfile solvents.f1list rem 80 in 160 out 400");
- For spectra acquired with double solvent suppression: XAU("rwcmaq", "dec yes eretic no suppno 2 suppsrc SOLVENT_FILE " "suppfile solvents.f1list rem 80 in 160 out 400");

If the spectra were acquired without decoupling, use "dec no" instead of "dec yes".

For spectra acquired using solvent suppression, the suppression frequencies must be recorded in a file named "solvents.f1list". Examples of a solvents.f1list for spectra acquired with single and double solvent suppression are seen below.

solvents.f1list - single solvent suppression

```
O 400.140  
1393.528
```

solvents.f1list - double solvent suppression

```
O 600.130  
1525.170  
2289.616
```

4 Quick Start: Set Up a Standard Batch Acquisition

This section is designed as a step-by-step guide for setting up batch acquisition projects using CMC-q. Following these steps will create a verification project for a batch of samples dissolved in DMSO-d₆, in a 96-well plate, using the predefined verification type STANDARD_USUP. The example workflow outlined here can be used as a template for all batch acquisition projects set up with CMC-q. For detailed information on each setting, see [The CMC-q Interface \[11 \]](#).

4.1 System Preparation

Before starting a batch acquisition with CMC-q, ensure that the spectrometer and Icon-NMR are properly configured. Follow the steps below to ensure the system is prepared for use with CMC-q.

- IconNMR Configuration
 - Create an IconNMR user called CMCQ. This user should be configured with access to the CMC parameter sets as well as the parameters ns and ds. For detailed information on creating an IconNMR user see section [User \[8 \]](#).
 - In the IconNMR configuration menu turn on FastLaneNMR and set the sample changer to the Sample Jet.
- Spectrometer Configuration
 - Ensure the 90 degree pulse is properly calibrated and saved in the Topspin prosol table.
 - Calibrate the spectrometer for quantification analysis using CMC_PROTON. See section [Calibrate the Spectrometer \[8 \]](#) for detailed instructions.
- Place the sample rack in holder number one in the Sample Jet.

4.2 Define the Samples

CMC-q requires at least three pieces of information for every sample in a batch; its proposed chemical structure, a unique identifier, and its position in the sample changer. An SD file defines this information for every sample in a batch. To pass the information from the SD file to CMC-q, the data path for this file must be defined. To choose the data path for the SD file defining the batch of samples, click **Browse** in the **CMC-q Setup** window. Click **Open** when the file, which must end in .sd or .sdf, is selected.

4.3 Basic Acquisition Settings

The following settings define the basic parameters of the experiment as well as how to coordinate with IconNMR for acquisition management. They are set from the main **CMC- q Setup** window.

- **Verification Type** - Set the Verification Type to STANDARD_USUP. This will run a standard 1D proton experiment without solvent suppression using the parameter set CMC_PROTON.

Quick Start: Set Up a Standard Batch Acquisition

- **IconNMR User** - Choose the cmcq IconNMR user with access to each CMC parameter set. In the example below this is set to CMCQ
- **Solvent** - Pick DMSO in the **Solvent** pull-down menu
- **Path for SD File** - Choose the SD file that contains the structures of the samples of your batch, along with an identifier for each structure and the position of the sample in the sample changer.
- **Molecule ID** - assign an SD file identifier that defines a unique identifier for each compound. In the example below, this is set to IDNUMBER.
- **Sample Position** - assign an SD file identifier that indicates a unique location for each sample in the sample changer. In the example below this is set to WELL.
- **Rack** - Select Rack 1 from the **Rack** pull-down menu.

At this point the **CMC-q Setup** window should look similar to the one pictured below.

CMC-q Batch Automation Settings

General Naming NMR Impurities Verifications

Verification Type STANDARD_USUP

IconNMR User CMCQ

Solvent DMSO

Path for SD File
C:\Bruker\CMCQ\data\GUI_EXAMPLE.sdf

New... Merge... View

Molecule ID (Mo-ID) IDNUMBER

Sample Position (SPos) WELL

Rack Number 3

Save Start Cancel

4.4 Data Set Naming

Select the **Naming Tab** to adjust the names of the created data sets according to your needs.

- Choose Mol-ID_SPos for the Data Set Name. This will create data set names like: BB012345_B04.

- Toggle the Plate ID switch to Text. This allows the option to type a Plate ID as desired.
- Leave the default title structure provided by CMC-q.

4.5 Advanced Acquisition Settings

Open the **NMR Tab** to tailor the acquisition parameters to the needs of the specific project.

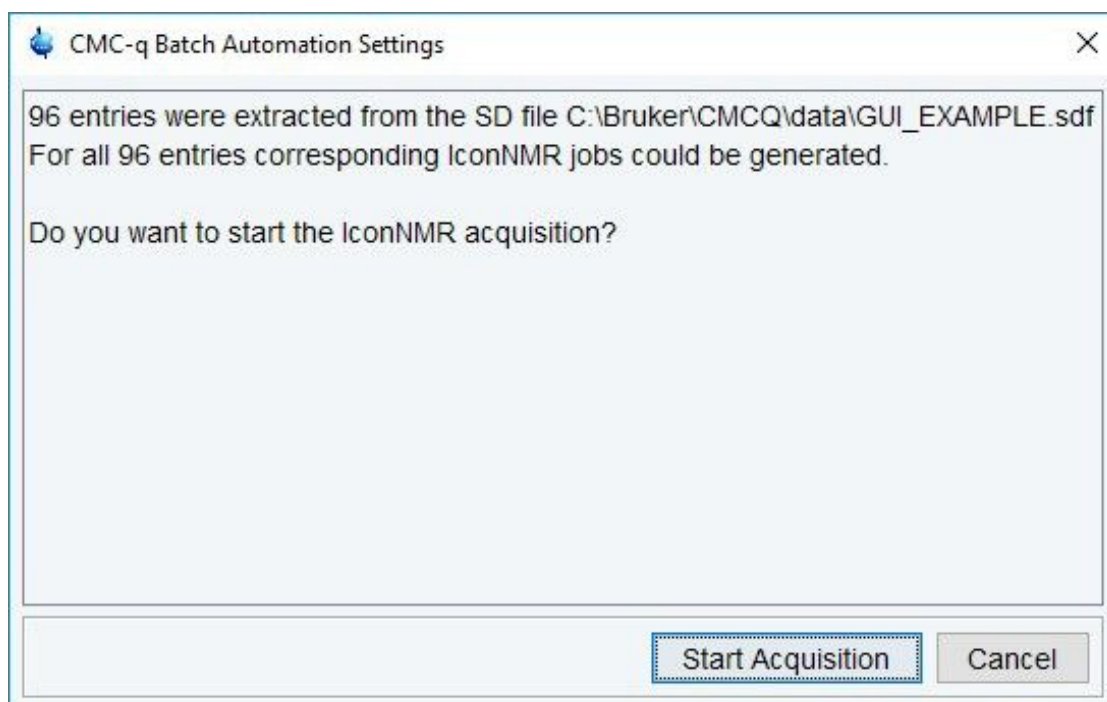
- Leave the default values for **Scan Number** and **Experiment Number**. The default number of scans is 16 and the default experiment number is 1. If required for these samples, the number of scans can be changed by clicking on the upwards or downwards facing arrows.
- Assign the calibration file created in section [System Preparation \[27\]](#), to the STANDARD_USUP verification type.
- For samples believed to be fairly pure, no impurities need to be defined in the Impurities tab. When using the solvent DMSO, the automatic analysis already takes water and the residual protonated solvent into account as an impurity.

4.6 Start the Acquisition

To save the current CMC-q setup without starting the acquisition click **Save**

To begin the acquisition with the current settings click **Start**.

This will bring up a window that displays how many entries were generated from the SD file and ask for confirmation to start the acquisition. Click **Start Acquisition**.




After clicking **Start Acquisition**, the experiments will be set up in an IconNMR run. If the run is not started automatically, click **Start** in the upper left corner of the **IconNMR: Automation** window.

5 How To: View the Results

When using CMC-q to facilitate batch acquisition, data processing and analysis is automatically handled by CMC-assist. The structure vs. spectrum consistency decision can be viewed directly in IconNMR, even while the IconNMR run is still in progress. A more detailed analysis of the batch as well as each individual sample can be viewed in CMC-assist.

5.1 Viewing Detailed Results in CMC-assist

From CMC-assist there are two ways to view the analysis results. An overview of the results for the entire batch can be seen in **Batch View** or the analysis can be viewed for each sample individually.

To launch CMC-assist, double click the CMC-assist icon on the desktop  or enter **cmca** on the command line in Topspin.

5.1.1 Batch View

Batch view is a comprehensive viewing tool that collectively displays the results of the automated analysis for each sample in the batch.

5.1.1.1 Launching Batch View

A serial processing list is required to see the results of a batch acquisition and analysis in **Batch View**. A serial processing list defines the data that should be viewed together as a batch. To create a serial processing list:

- Ensure that the data directory is displayed in the browser in CMC-assist. To add a directory to the CMC-assist browser, right click in the browser area and select **Add New Data Dir**.
- Enter **serial** on the command line in CMC-assist to open a new submenu with the tabs **Define List**, **Define Command**, and **Execute**.
- Click the down arrow on the right side of the **Define List** button and choose the option **Build data-set list using "find"**, which opens the following dialog.

How To: View the Results

Find data

Searching will be performed in all data directories marked in the data directories list below!
The checkboxes at the right will enforce exact matching if enabled.

NAME	<input type="text"/>	<input type="checkbox"/>
EXPNO	<input type="text"/>	<input checked="" type="checkbox"/>
PROCNO	<input type="text"/>	<input checked="" type="checkbox"/>
Title	<input type="text"/>	<input type="checkbox"/>
Pulse Prog.	<input type="text"/>	<input type="checkbox"/>
Dimension	Any	<input type="checkbox"/>
Data type	Any	<input type="checkbox"/>
Date, from: mm/dd/yy	<input type="text"/>	
Date, till: mm/dd/yy	<input type="text"/>	

Data directories

- C:\Bruker\CMCQ=alias=CMCQ
- D:\expdat\BrukerChemicals=alias=BrukerChemicals
- D:\expdat\CrossCheck=alias=CROSS
- D:\expdat\HMDB=alias=HMDB
- D:\expdat\Impurities=alias=IMPURITIES
- D:\expdat\Misc=alias=MISC
- D:\expdat\Parallelsynthesis=alias=PARALLEL
- D:\expdat\QNMR=alias=QNMR

OK Reset mask Cancel Help

- A search will be performed through the data directory, or directories, highlighted in the **Data directories** table.
 - This table shows all of the data directories displayed in the browser in CMC-assist.
- Select the data directories to be searched through in the lower part of the dialog (if no directories are selected, all directories will be used for search). The search can be further modified to select data sets based on the NAME, EXPNO, PROCNO, title, dimension etc.
- For more details on creating a serial processing list, see chapter 5.4 in the CMC-assist manual.
- **OK** starts the search and the results will be displayed within a new dialog.

Search result

Found: 96 Data Sets.
Please right-click in a list for more options!

AA-504_32628011	1	1	C:\Bruker\CMCQ\data\EXAMPLE\nmr	1	zg30	2013-07-19 07:42:30
AB-323_25048479	1	1	C:\Bruker\CMCQ\data\EXAMPLE\nmr	1	zg30	2013-07-17 15:42:47
AC-776_15493123	1	1	C:\Bruker\CMCQ\data\EXAMPLE\nmr	1	zg30	2013-07-18 17:48:34
AE-641_00358061	1	1	C:\Bruker\CMCQ\data\EXAMPLE\nmr	1	zg30	2013-07-17 16:16:25
AE-641_00600032	1	1	C:\Bruker\CMCQ\data\EXAMPLE\nmr	1	zg30	2013-07-18 19:09:06
AE-641_30108063	1	1	C:\Bruker\CMCQ\data\EXAMPLE\nmr	1	zg30	2013-07-18 18:15:39
AE-641_30118027	1	1	C:\Bruker\CMCQ\data\EXAMPLE\nmr	1	zg30	2013-07-17 18:03:59
AE-641_30156032	1	1	C:\Bruker\CMCQ\data\EXAMPLE\nmr	1	zg30	2013-07-17 18:30:49
AE-848_08645021	1	1	C:\Bruker\CMCQ\data\EXAMPLE\nmr	1	zg30	2013-07-19 02:19:32
AE-848_11829293	1	1	C:\Bruker\CMCQ\data\EXAMPLE\nmr	1	zg30	2013-07-18 17:20:54
AF-399_13200030	1	1	C:\Bruker\CMCQ\data\EXAMPLE\nmr	1	zg30	2013-07-17 19:24:21
AF-399_14739190	1	1	C:\Bruker\CMCQ\data\EXAMPLE\nmr	1	zg30	2013-07-18 14:36:03
AF-399_15128628	1	1	C:\Bruker\CMCQ\data\EXAMPLE\nmr	1	zg30	2013-07-18 14:09:17
AF-399_36013017	1	1	C:\Bruker\CMCQ\data\EXAMPLE\nmr	1	zg30	2013-07-19 03:40:03
AF-399_40756763	1	1	C:\Bruker\CMCQ\data\EXAMPLE\nmr	1	zg30	2013-07-18 11:54:58

Display Close

- To save this list as a serial processing list, highlight all the entries in the list using **[ctrl+a]**. Right-click on the list and select **Save Selection In File**.
- For acquisitions using verification types consisting of more than one experiment, only the 1D proton spectrum should be used to create the serial processing list.
- From the **Data** tab select **Open Batch**
- Browse for the desired serial processing list and click **OK**
- This will launch two windows, the **Table Display** window and the **Samples View** window.

5.1.1.2 The Table Display Window



This window displays the consistency decision, concentration, and water content (if applicable) for each sample along with its proposed structure and sum formula. The table also displays the chemical shift of the signal used for the concentration analysis as well as the number of protons assigned to that signal. Besides this a column containing the SMILES code of the structures can be displayed as well as the sample position. By default, the table view will only display the main proton experiment. The **Expand** button of the table allows you to also view all other experiments that are part of the verification type chosen and were acquired along with the main proton experiment.

Table view of batch: C:\Bruker\CMCQ\data\ExampleList.txt

Status	Structure	Sum Formula	Mass	Structure used	Spectrum	Conc (mM)	Proton	Shift (ppm)	Purity	Conc. Error (mM)	SMILES Formula	Spectrum Type
Inconsistent Auto		C ₂₂ H ₂₄ ClFN ₂ O ₃ S	450.12	yes	AN-153_42837211 1 1	20.49	2H	7.787	very high purity	0.008	ClO=S(=O)(N)C1...	PROTON
Consistent Auto		C ₂₀ H ₂₈ N ₂ O ₅ S	408.17	yes	AN-038_41894853 1 1	21.58	1H	5.124	high purity	0.015	O=C1OC(COCC...	PROTON
Unknown		C ₂₄ H ₂₂ O ₁₀	470.12	no	AC-776_15493123 1 1	36.76	1H	7.148	very high purity	0.015	O=C1OC1=CC=C...	PROTON
Consistent Auto		C ₂₀ H ₂₅ N ₃ O ₃ S ₂	419.13	yes	AA-504_32628011 1 1	20.98	3H	1.123	very high purity	0.013	O=C1N(C(=O)C2[...	PROTON

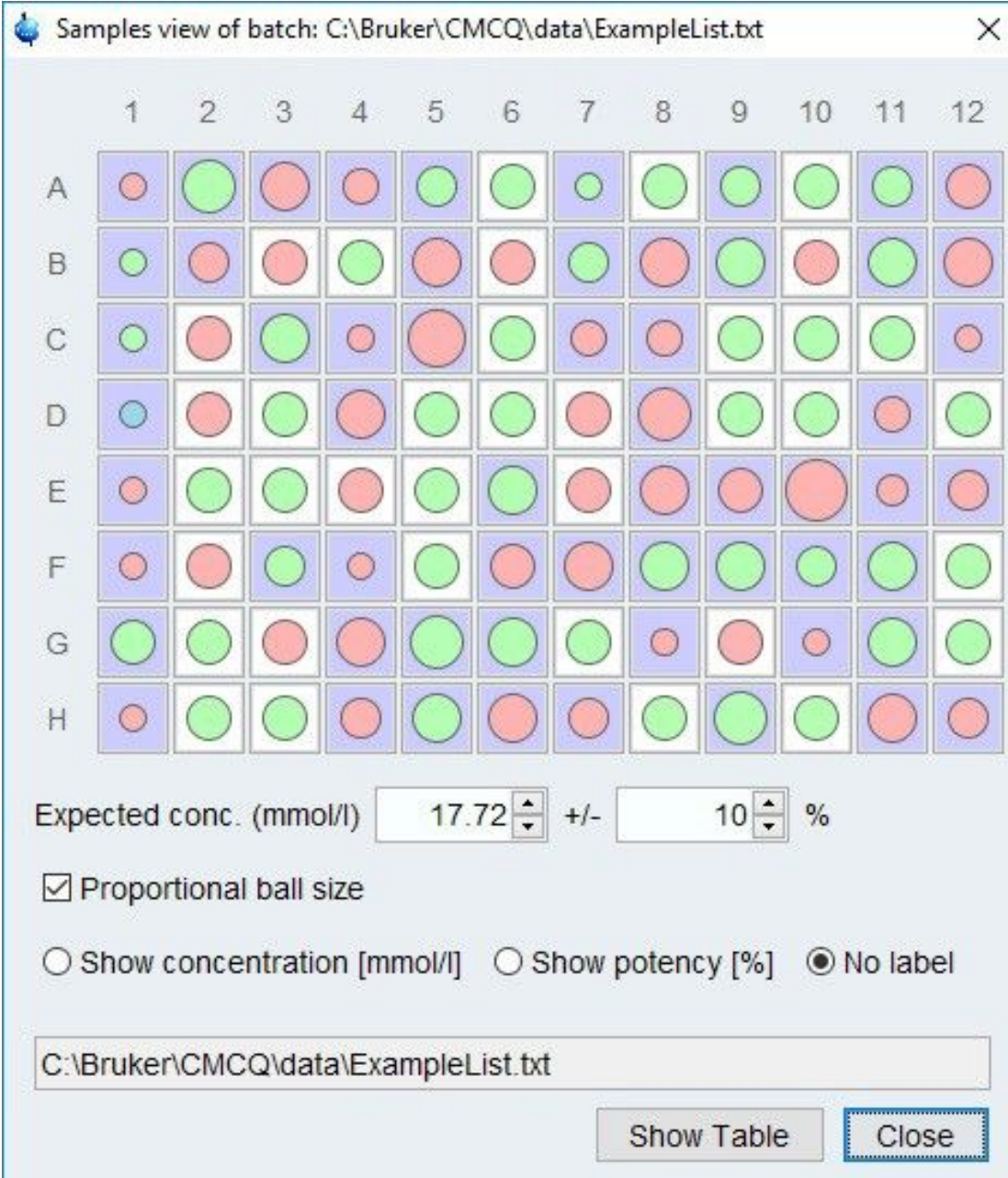
Expand Samples Show Samples Close

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This table can be exported to spreadsheet format (.csv or .xls) or document format (.pdf or .html) by clicking the save  button. This table can be printed by clicking the print  button.

5.1.1.3 The Samples View Window

This window is a graphical display of concentration and consistency decision for each sample in a batch. Each sample is represented by a circle whose size and color correspond to the calculated concentration and consistency decision



The screenshot shows a window titled "Samples view of batch: C:\Bruker\CMCQ\data\ExampleList.txt". The window displays a grid of 96 circles (8 rows by 12 columns). The columns are numbered 1 to 12, and the rows are labeled A to H. Each circle's size and color represent a sample's concentration and consistency decision. The colors are green, red, or blue. Below the grid, there are controls for "Expected conc. (mmol/l)" set to 17.72, a tolerance of +/- 10%, and a checked "Proportional ball size" option. There are also radio buttons for "Show concentration [mmol/l]", "Show potency [%]", and "No label" (selected). At the bottom, there is a text box containing the file path "C:\Bruker\CMCQ\data\ExampleList.txt" and two buttons: "Show Table" and "Close".

	1	2	3	4	5	6	7	8	9	10	11	12
A	Small Red	Large Green	Medium Red	Small Red	Medium Green	Large Green	Very Small Green	Medium Green	Medium Green	Large Green	Medium Green	Medium Red
B	Small Green	Medium Red	Medium Red	Medium Green	Medium Red	Medium Red	Medium Green	Medium Red	Large Green	Medium Red	Large Green	Medium Red
C	Small Green	Medium Red	Large Green	Very Small Red	Large Red	Medium Green	Small Red	Small Red	Large Green	Large Green	Large Green	Very Small Red
D	Very Small Blue	Medium Red	Large Green	Medium Red	Medium Green	Large Green	Medium Red	Large Red	Large Green	Large Green	Small Red	Large Green
E	Small Red	Large Green	Large Green	Medium Red	Medium Green	Large Green	Medium Red	Large Red	Large Red	Very Large Red	Very Small Red	Medium Red
F	Small Red	Medium Red	Medium Green	Very Small Red	Medium Green	Medium Red	Medium Red	Large Green	Large Green	Medium Green	Large Green	Large Green
G	Large Green	Large Green	Medium Red	Medium Red	Large Green	Large Green	Medium Green	Very Small Red	Medium Red	Very Small Red	Large Green	Large Green
H	Small Red	Large Green	Large Green	Medium Red	Medium Green	Medium Red	Medium Red	Medium Green	Large Green	Large Green	Medium Red	Medium Red

Expected conc. (mmol/l) +/- %

Proportional ball size

Show concentration [mmol/l] Show potency [%] No label

- The color of the circle will be either green, red, or blue; indicating if the spectrum and proposed structure are consistent, inconsistent, or undetermined respectively.

- The size of the circle will be proportional to the concentration

The **Expected Concentration** and **Expected Range** fields below the simulated well plate can be adjusted by using the spinners right to the fields, or alternatively, by typing the desired value into the corresponding field. When these values are adjusted, samples whose concentration falls within the specified range of the expected concentration are displayed on a white background. Those samples whose concentration does not fall within the expected range are displayed on a blue background.

Further options can be adjusted at the bottom of the **Samples View** window

- Select the **Show concentration** radio button to view the calculated concentration of each sample on top of its representative circle. If your batch used an internal standard and the potency was calculated for each sample you may want to select the **Show potency** radio button. In case no label is desired select the **No label** button.
- The **Proportional ball size** option will automatically be chosen when the **Samples View** window is opened. This option is a visual display of the relative concentrations of each sample. By unticking the **Proportional ball size** box, all of the sample balls will appear the same size.

Clicking on a sample in the **Well Plate** view selects that sample in the **Table View** and vice versa. Double clicking on a sample in either the **Well Plate** or **Table View** will open the corresponding data set in CMC-assist.

5.1.2 Viewing Spectra in CMC-assist

The automatic analysis of each spectrum produces a variety of information that can be viewed in CMC-assist. Along with the consistency decision and concentration, CMC-assist displays a structure verification analysis. If the batch was acquired using a verification type that included more than one experiment, each spectrum (and automatic analysis if applicable) can be viewed from CMC-assist.

5.1.2.1 Opening Spectra in CMC-assist

There are various ways to open a single spectrum in CMC-assist. Listed below are three of the main ways to do so.

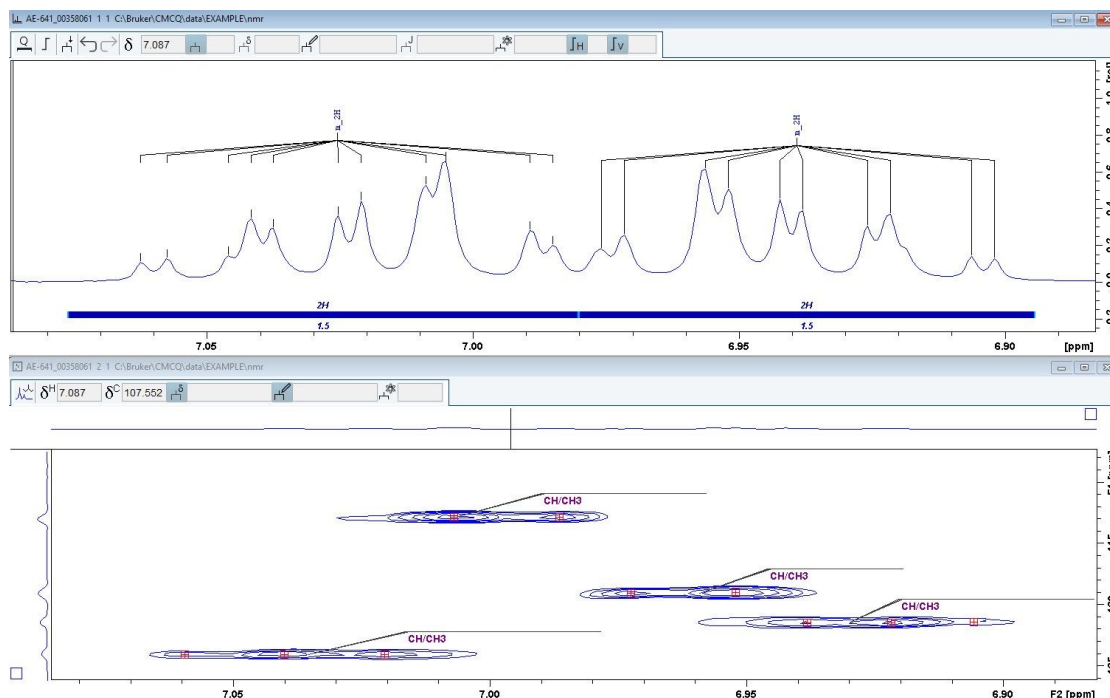
- Double-click on the data set in the CMC-assist browser.
- From the **Table View** or **Samples View** window, click on the desired sample entry to open its spectrum in CMC-assist.
- From IconNMR, right-click on the desired entry in the **Preceding Experiments** panel and select **Open in CMC-assist**.

5.1.2.2 Opening a Project in CMC-assist

A CMC-assist project is created for each sample in a batch acquisition setup with CMC-q. Any 1D proton, HSQC, HMBC, or 13C spectrum, whose acquisition was set up through CMC-q, will be added to the project and automatically analyzed after acquisition. The consistency decision will be based on the automatic analysis of each spectrum in the project. To open a project:

- Open the 1D proton spectrum by double-clicking on the data set in the CMC-assist browser.
- Click **Open Project** to open each spectrum defined in the project.
- This will open each spectrum of the project in stacked view.

How To: View the Results



5.1.2.3 The 1D Proton Spectrum Analysis

The automatic structure verification analysis of proton spectra produces the following results:

- Structure Consistency Decision - The consistency decision displays whether the structure and the spectrum are consistent with each other. The consistency decision is displayed in the lower left part of the CMC-assist window. It displays the consistency decision for the entire project, even while viewing only one of the spectra.

 **Status: Consistent**

- The consistency status may be consistent, inconsistent, or undetermined.
- To view a more detailed description of the consistency decision click on the **Consistency** button to bring up the **Project Status / Description** window.

Project Status / Description

Consistency:

Consistent (by automatic analysis) Consistent Inconsistent UNCLEAR

Purity:

Very High (by automatic analysis) Very High High Medium Low Unknown

Result Source:

Automatic analysis generated by Bruker CMC (b:188).

Result Summary


Automatic evaluation: Spectrum and structure are in agreement.

Result Details

All major signals in the spectrum could be assigned. All elements of the structure could be assigned to regions in the spectrum. All given impurities could be assigned to regions in the spectrum.

Quantification Details

OK Cancel

- Sample Concentration - The sample concentration is determined using the calibration file provided during experimental setup. It is displayed in green on the spectrum above the signal used for quantification. The concentration unit is displayed on the top right corner of the spectrum.
 - If desired, each spectrum can be opened zoomed into the signal used for quantification. To do this click the  button located at the top left side of the CMC-assist window.
- Integration Regions - an integration region is defined for each signal as well as the number of protons assigned to this signal.
- Purity - The sample purity is determined and displayed in the **Project Status** window.
- Multiplet Analysis and Assignment - Each signal in the spectrum is analyzed and given a multiplet identifier. If the structure and spectrum are deemed consistent, each proton in the structure is assigned to a signal in the spectrum.
 - When the cursor is hovering over a multiplet, its multiplet identifier is displayed in the bar above the spectrum. It is given in the format 'multiplicity_number of protons'. An example of a multiplet identifier would be q_2H, indicating a quartet worth two protons.
 - The multiplicity information uses the following conventions
 - s - singlet
 - d - doublet

How To: View the Results

dd - doublet of a doublet

t - triplet

q - quartet

quint - quintet

sept - septet

m - other multiplet pattern

- To view the multiplet assignment, move the cursor over any atom of the structure to highlight this atom as well as the corresponding multiplet. Also, moving the cursor over any multiplet will highlight the atom(s) of the molecule assigned to this multiplet.
- The solvent, defined impurities, and any suppression regions will also be labelled with a multiplet identifier. For example, 'SUP' for a suppression region.

Part of an automatically analyzed spectrum viewed in CMC-assist is seen below.

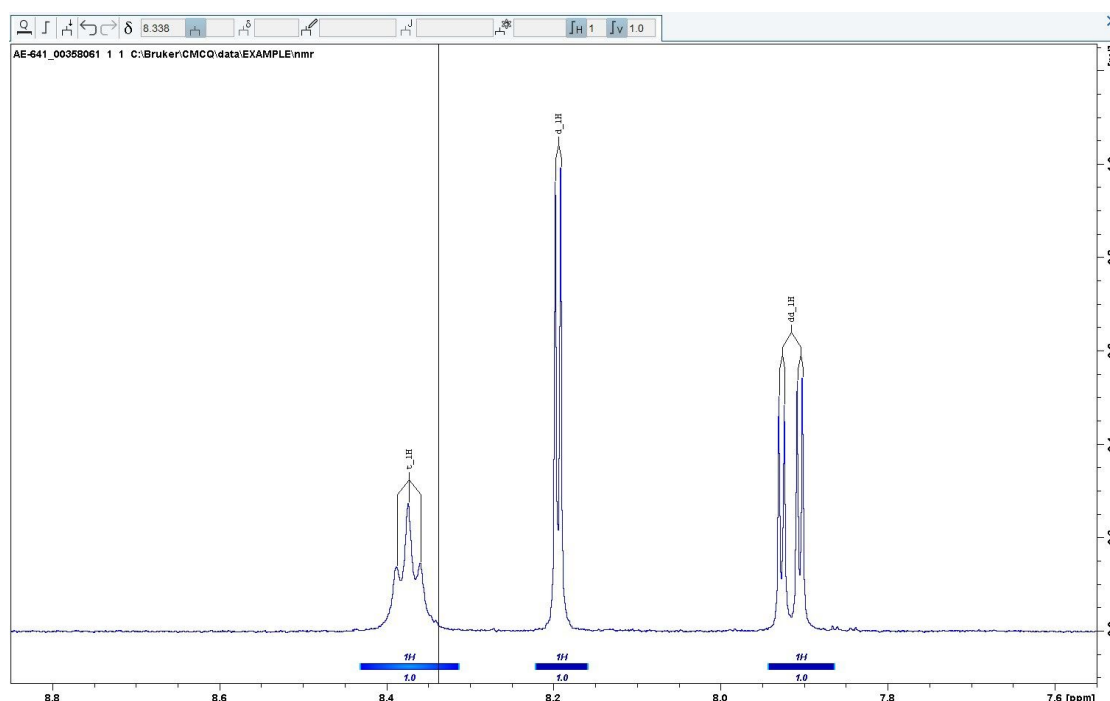


Figure 5.1:

For instructions on editing the automatic analysis see the CMC-assist user manual.

5.1.2.4 The HSQC, HMBC, and ¹³C Analysis

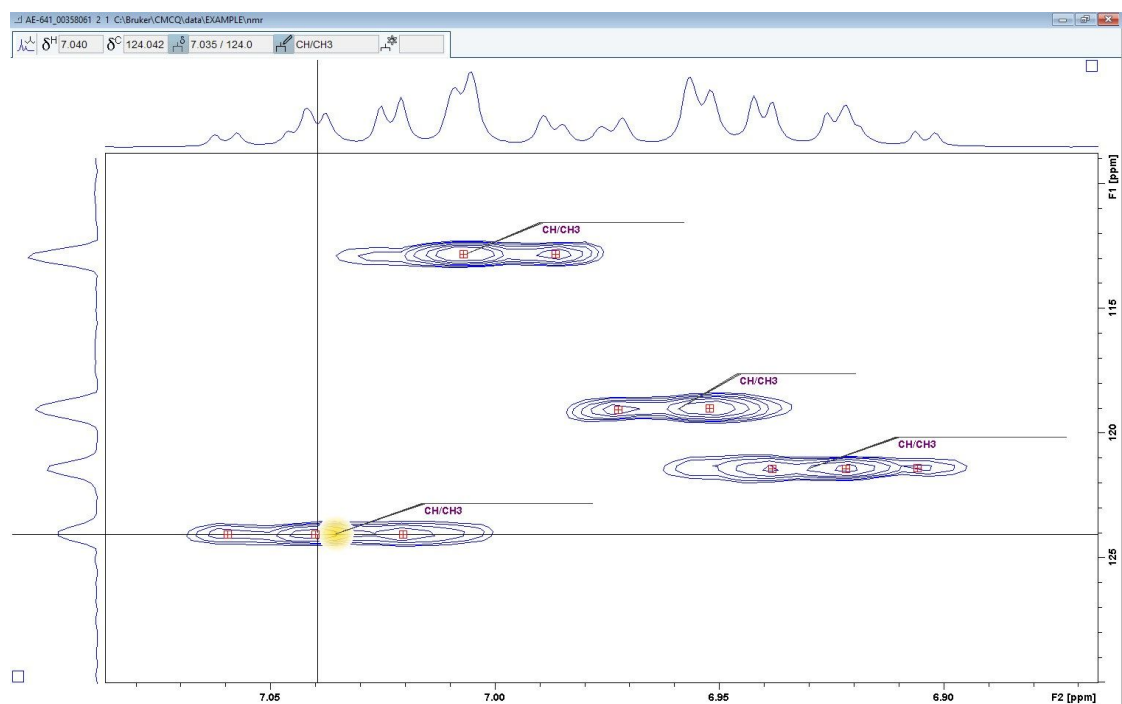
If a consistency project includes additional spectra like HSQC, HMBC, and/or ¹³C spectra, these types of spectra will be analyzed together. The consistency decision will be based on this joint analysis. If the project is consistent, an analysis and assignment is displayed for each signal in the corresponding spectrum, except the HMBC spectrum.

Each signal in the spectrum is marked and given an identifier. The HSQC identifiers are given in the following format 'type of CH group number of protons'. For example, CH₂_4H indicates the signal arises from two equivalent CH₂ groups. The 'type of CH group' can be listed as CH, CH₂, or CH₃ indicating a carbon bonded to one, two, or three protons respectively.

The identifier in the ^{13}C spectrum indicates the number of the assigned carbons and the 'type of carbon' giving rise to the signal, e.g., C_2C or CH3_3C. Impurities and the residual solvent are marked with the corresponding name.

Every proton in the molecule is assigned to a signal in the spectrum. To view the assignment, move the cursor over a signal in the spectrum to highlight the signal and the atom(s) in the structure it is assigned to. This also works by moving the mouse over an atom in the structure to highlight the atom and the corresponding signal(s) in the spectrum.

Below is an example of an automatically analyzed HSQC spectrum in CMC-assist.



6 Contact

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WEEE DE43181702

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Contact our NMR service centers.

Bruker BioSpin NMR provides dedicated hotlines and service centers, so that our specialists can respond as quickly as possible to all your service requests, applications questions, software or technical needs.

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