KnowItAll® Informatics Training

NMR Analysis Tools

WILEY

NMR

Analyze NMR Multiplets and Store in a Database

Purpose

This exercise demonstrates how to label multiplets and coupling constants for NMR spectra, and how to assign the assessed multiplets when the structure associated with the spectrum is known. The NMR Tools in ProcessIt can be applied to ^{1}H-NMR, ^{13}C-NMR and X-NMR.

Objectives

This exercise will teach you:

- How to define multiplets for a processed NMR spectrum in MineIt
- How to edit multiplet assignments using the NMR Tools available in MineIt
- How to automatically generate an NMR Report

Background

Storing processed NMR spectra in a database is valuable for R&D, quality control, and quality assurance laboratories, and for verification of unknown chemical compounds. Adding assignments enhances the merit of the archived reference material.

Training Files Used in This Lesson

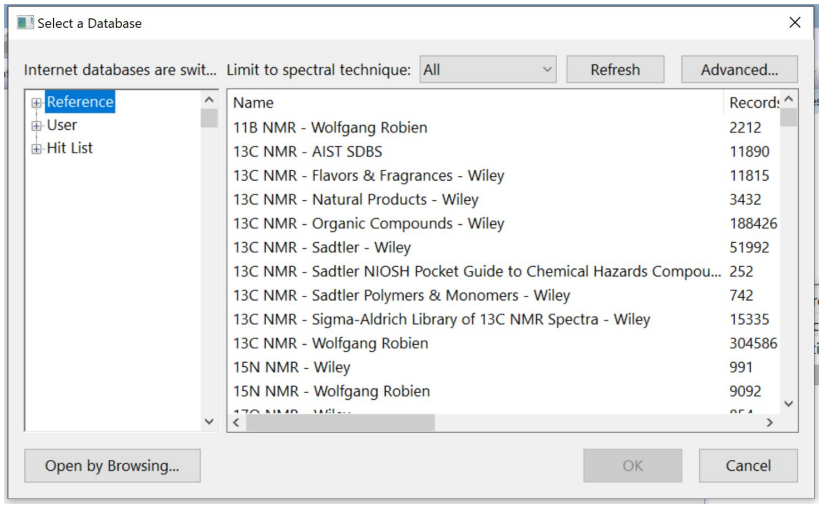
- C14H10ClNO3 H1/fid
- C14H10ClNO3 H1.dsf
- C14H10ClNO3 H1.sdbx

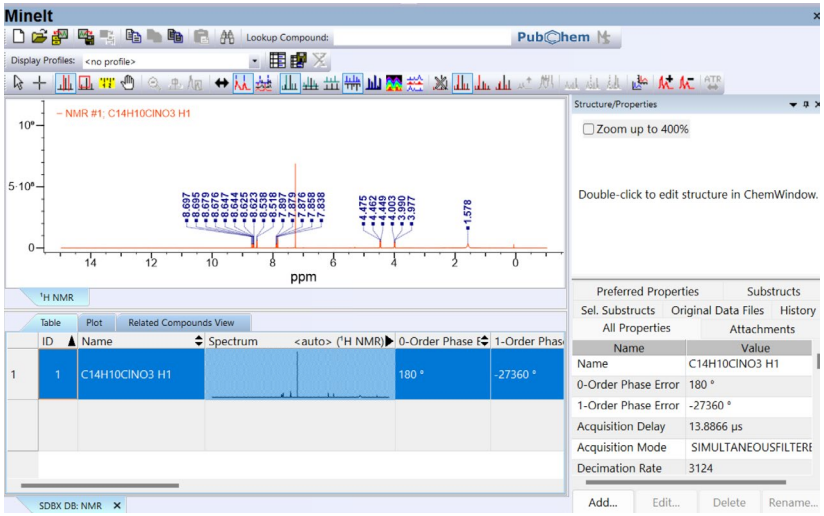
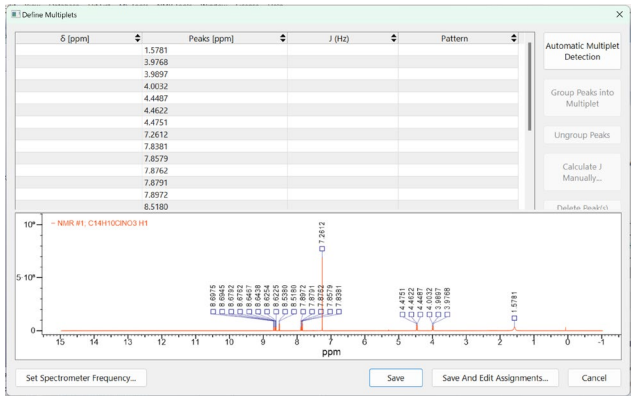
KnowItAll Applications Used

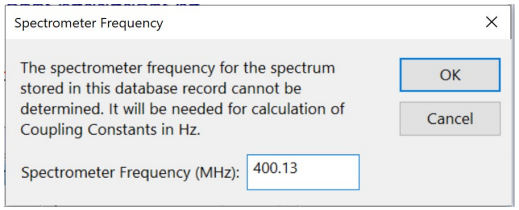
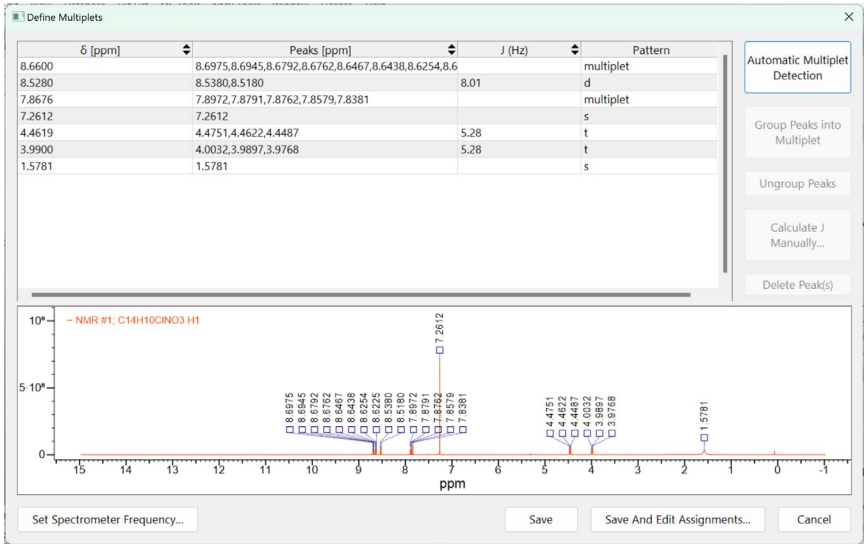
- MineIt
- ProcessIt

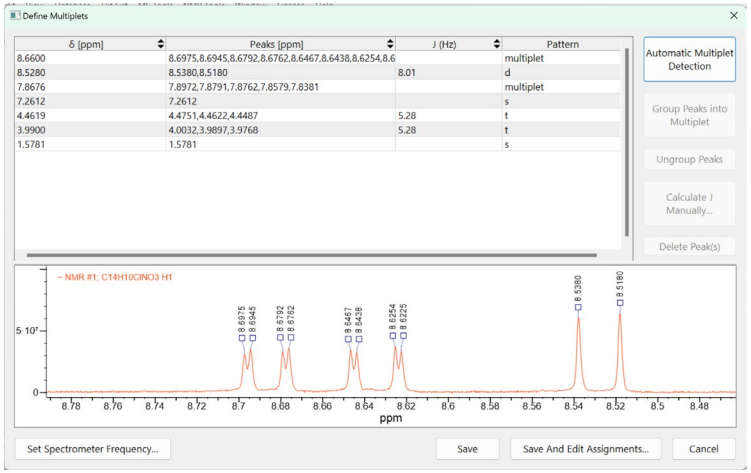
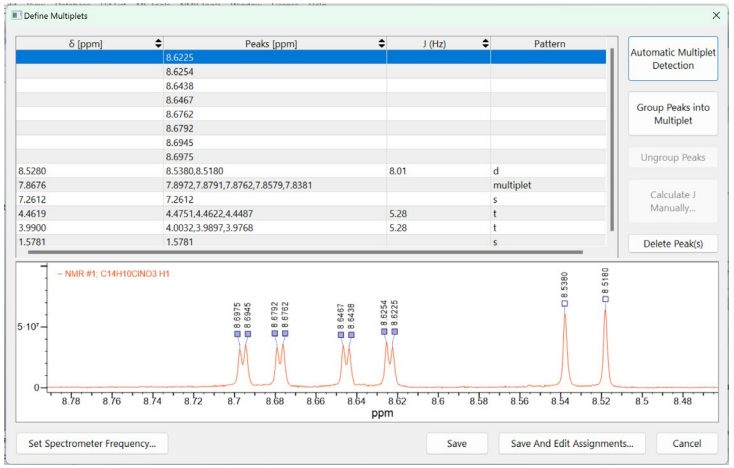
Calculate Spectrum Multiplets using NMR Tools

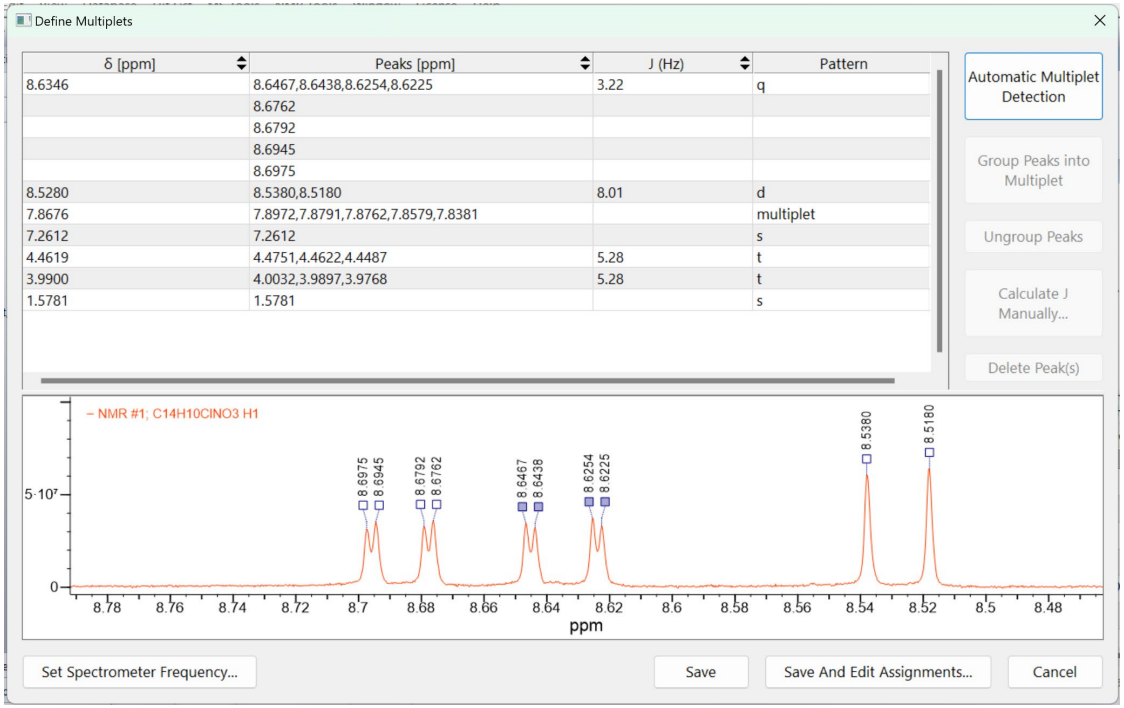
The Define Multiplets dialog in MineIt NMR Tools is used to calculate J-values and transition peak lists into defined multiplets with splitting patterns. The tool is available for ^{1}H, ^{13}C and X-NMR spectra.

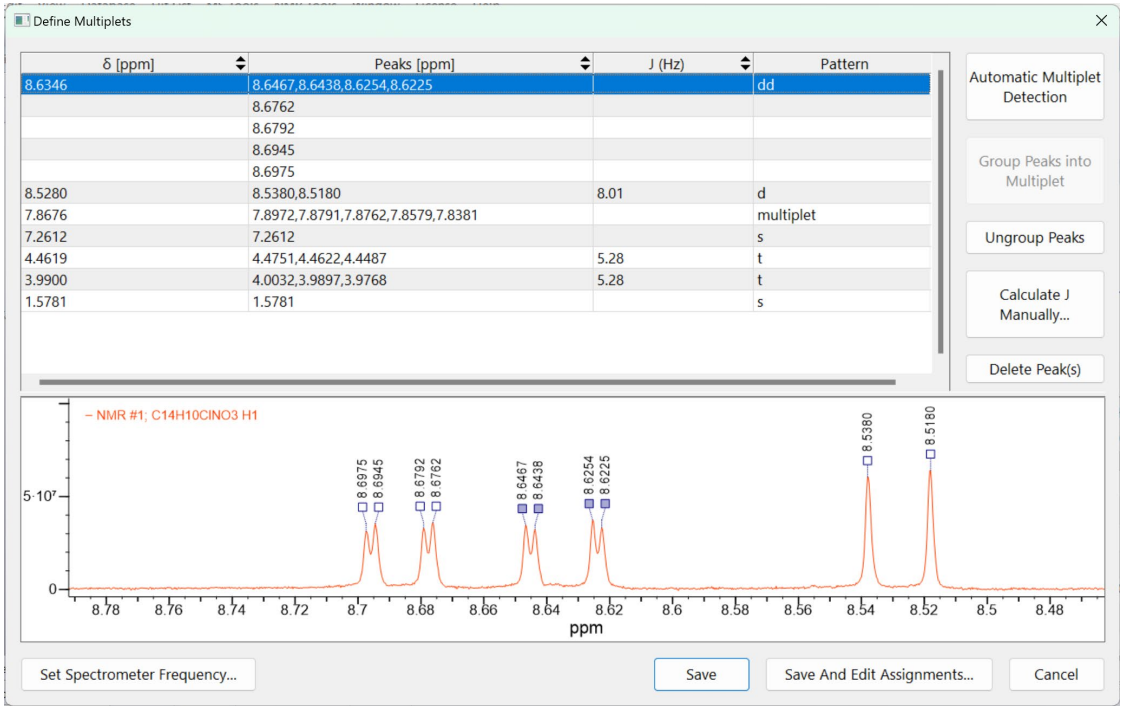
	Action	Result
1	**Note**: For this section, you will need a fully processed NMR spectrum. This training will apply the processed file from Chapter 13 stored in a **MineIt** user database.	
2	Open the **MineIt** application by clicking its icon, typically found in the **Data** toolbox. 	
3	Click the **Open Database** icon (), and then click **Open by Browsing** on the **Select a Database** dialog.	Clicking the **Open Database** launches the **Select a Database dialog**. Clicking **Open by Browsing** launches a file explorer to select a file: 

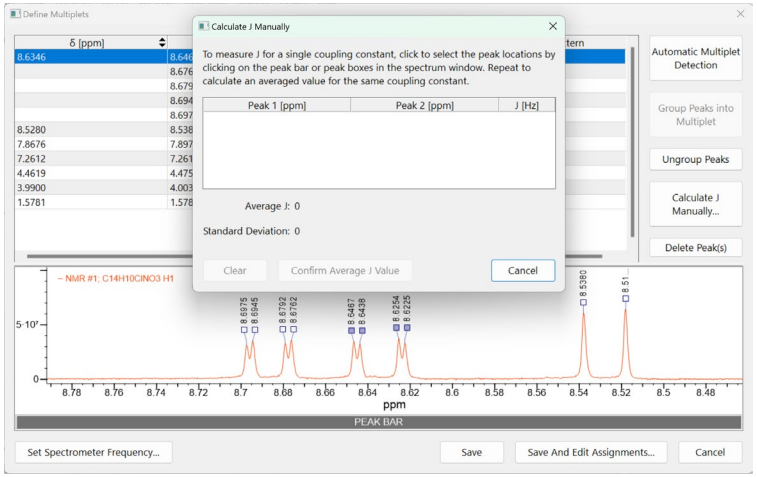
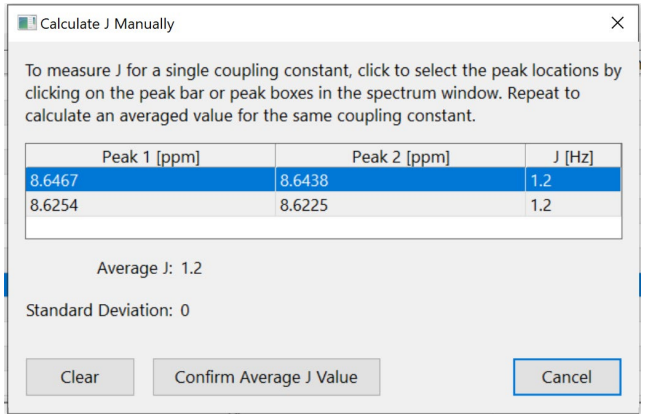
	Action	Result
4	Navigate to "**C:\Users\Public\Public Documents\Wiley\KnowItAll\ Samples\NMR\Bruker TopSpin\ C14H10ClNO3\ C14H10ClNO3 H1.sdbx**". Double click to open the file.	Upon opening the database, a processed NMR spectrum is displayed in **MineIt**: 
5	Choose **NMR Tools > Define Multiplets**.	The **Define Multiplets** dialog is launched:  The **Define Multiplets** dialog is used to group peaks into multiplets with assigned splitting patterns and coupling constant information.

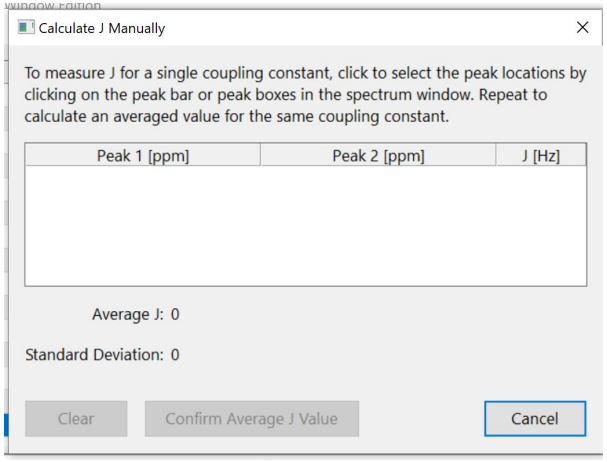
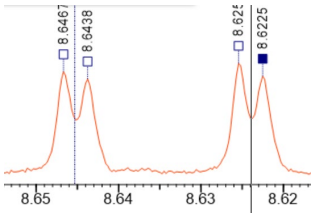
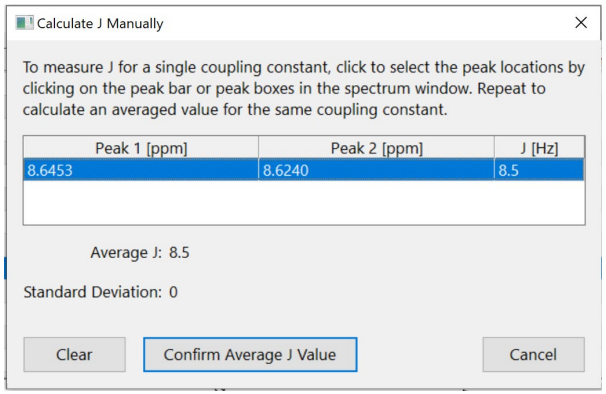
	Action	Result
6	**Note**: If the record does not contain a property value for **NMR Spectrometer Frequency**, the **Spectrometer Frequency** dialog will appear before the **Define Multiplets** dialog is launched.	In this example, the **Spectrometer Frequency** dialog is bypassed because the record contains a property value for **NMR Spectrometry Frequency**. It can be relaunched directly from the **Define Multiplets** dialog by clicking **Set Spectrometer Frequency**: 
7	On the **Define Multiplets** dialog, select the button for **Automatic Multiplet Detection**. **Note:** The button for **Automatic Multiplet Detection** is only available for ^{1}H-NMR.	The peaks have been grouped into multiplets using an automatic algorithm. Note that the spectrum has 2 multiplets, 2 triplets (t), 1 doublet (d), and 2 singlets (s). Any incorrect assignments will be updated in the proceeding steps. For each multiplet: • There is a shift value in the δ column • The peaks were assigned the default simple splitting pattern • The J-value for the simple splitting patterns were automatically calculated 

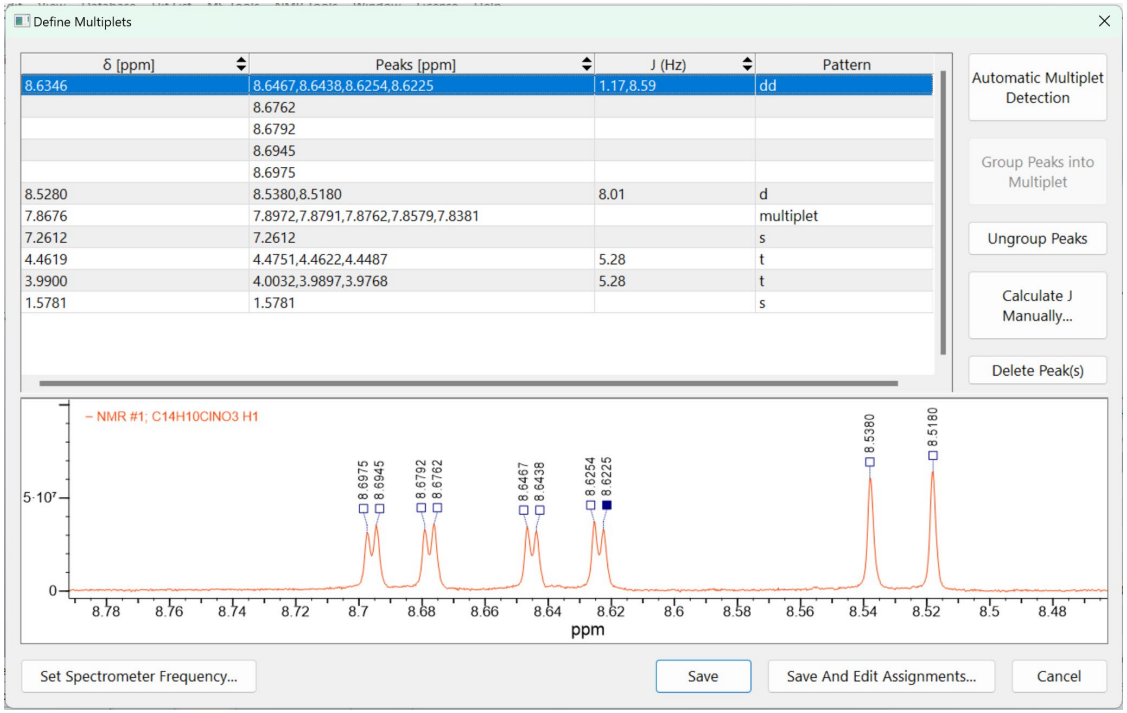
	Action	Result
8	Click and hold the left mouse button on the spectrum at ~ 8.5 ppm. Drag the mouse across the region on the spectrum from ~ 8.5 ppm to ~ 8.8 ppm. Release the mouse button. **Note**: The zoom cursor should still be active. If not, you can activate it by right clicking on the spectrum and selecting **Horizontal Zoom Mode**.	Three groups of peaks are visible. The set of peaks near 8.5 ppm are correcrtly identified as a doublet (d), and the set of peaks near 8.6 ppm will become divided into two sets of doublet of doublets (dd). 
9	In the **Define Multiplets** dialog, click to select the row assigned as **multiplet** at **8.6600 ppm**. Then click **Ungroup Peaks** button on the same dialog.	The set of peaks near 8.6 ppm have been ungrouped to enable further analysis. 

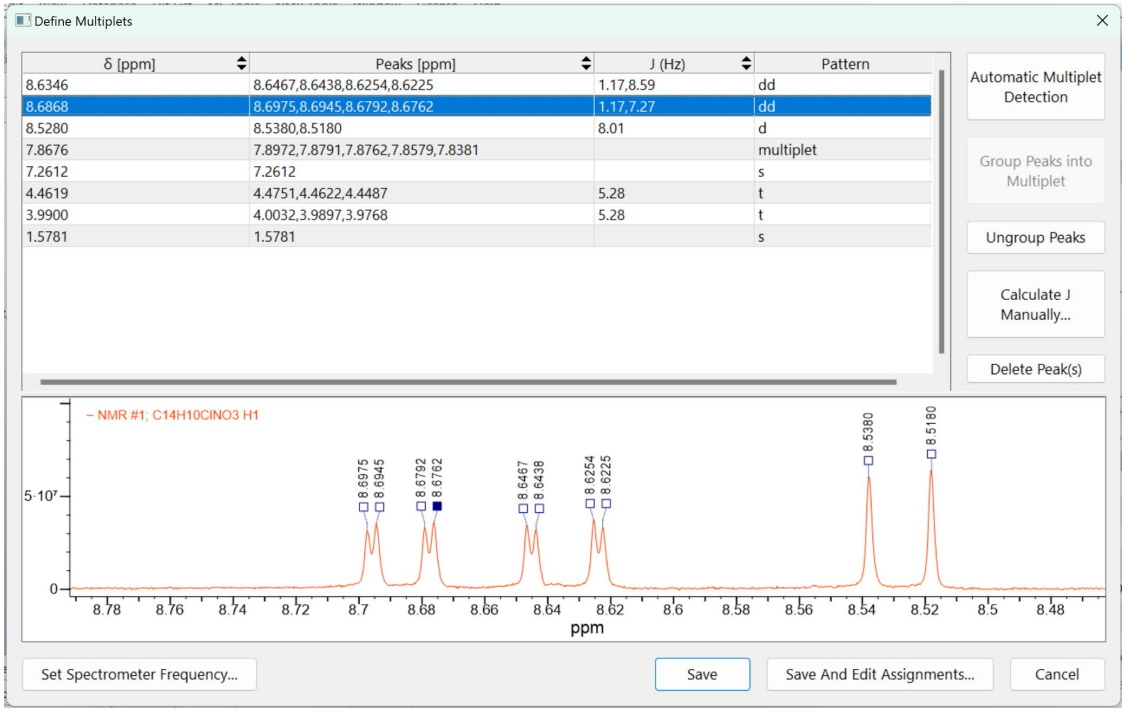
	Action	Result
10	Press and hold **CTRL** button on the keyboard. In the **Multiplets Table**, click on the four peaks near ~ 8.62 – 8.64 ppm (8.6225, 8.6254, 8.6438 and 8.6467). Click **Group Peaks into Multiplet** button. **Note**: Coupling constants (J) will automatically calculate for the simple splitting patterns: doublet (d), triplet (t), and quartet (q). Groups of 5 or more peaks will be labelled as "multiplet" for the splitting pattern. They can be reassigned if needed using the dropdown menu in the related cell.	In the **Multiplets Table**, the two peaks at 8.6346 ppm have been grouped together: • There is now a shift value in the δ column • The peaks were assigned the default simple splitting pattern (q for quartet, which will be adjusted in a proceeding step) • the J-value for the simple splitting pattern automatically calculated 

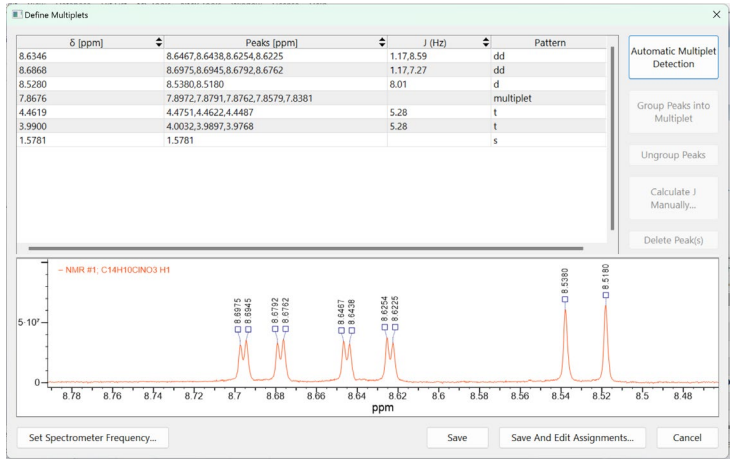
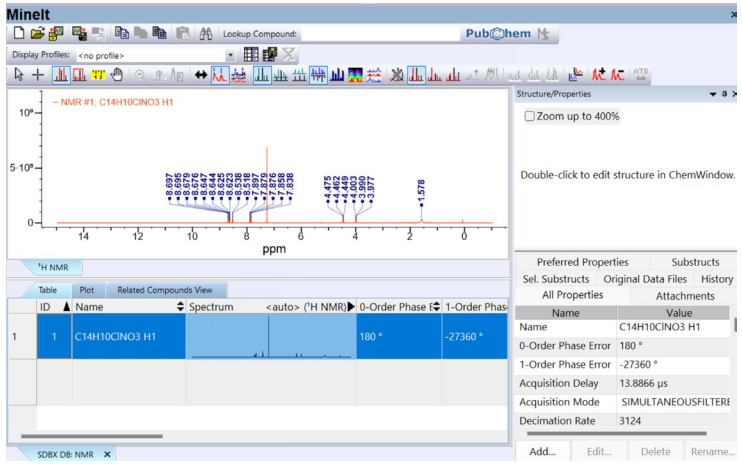
	Action	Result
11	In the **Multiplets Table**, click on the **Pattern** cell for the multiplet at 8.6346 ppm to change it from a “q” to a “dd” using the dropdown menu.	The pattern in the **Multiplets Table** for the multiplet at 8.6346 ppm now displays as dd. The cell for the J-value is blank. 

	Action	Result
12	Click **Calculate J Manually** in the **Define Multiplets** dialog. **Note**: The coupling constants (J) for complex splitting patterns (*e.g.*, dd, td, dt, ddd, etc.) have to be manually calculated using **the Calculate J Manually** tool.	The **Calculate J Manually** dialog is launched:  This dialog will be used two times for this multiplet, to calculate two separate J-values for the dd.
13	Begin by calculating the smaller J-value: click on the peak boxes on the spectrum in the **Define Multiplets** dialog from left to right for the peaks at 8.6467, 8.6438, 8.6254 and 8.6225 ppm.	When the peak box is selected, its shift value adds to the Calculate J Manually table in the order that they are clicked. The J-value is calculated for the first two selected peaks (8.6467 and 8.6438) and then the second two selected peaks (8.6254 and 8.6225). The average J-value for all of the rows in the table is displayed as Average J: 

	Action	Result
14	Click **Confirm Average J Value** to save the small J-value. Do not close the dialog.	The J-value is commited to the record and the **Calculate J Manually** dialog is cleared: 
15	To calculate the larger J-value, use the **Peak Bar** to click on the centroid of the peaks for each of the two groups of peaks: once between 8.6467 and 8.6438 ppm, then again between 8.6254 and 8.6225 ppm. e.g., as shown below with lines: 	When the **Peak Bar** is clicked, the shift values adds to the **Calculate J Manually** table. The J-value is calculated as the central value for each of the two groups of peaks: 

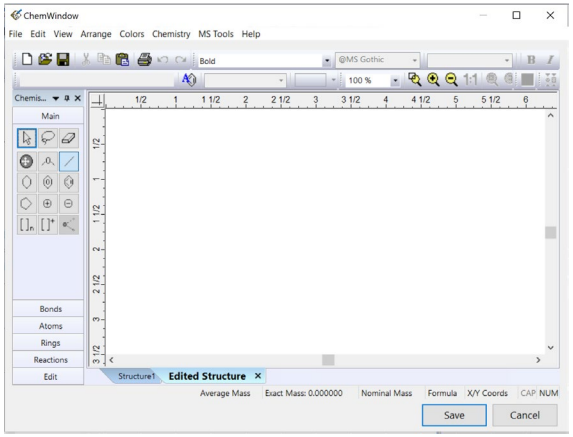
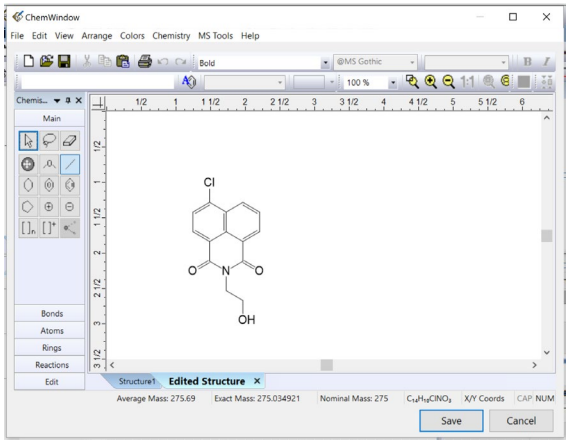
	Action	Result
16	Click **Confirm Average J Value** to save the large J-value. Next, click **Cancel** to close the **Calculate J Manually** dialog.	Two J-values are displayed in the **Define Multiplets** table for the multiplet at 8.6346 ppm: 

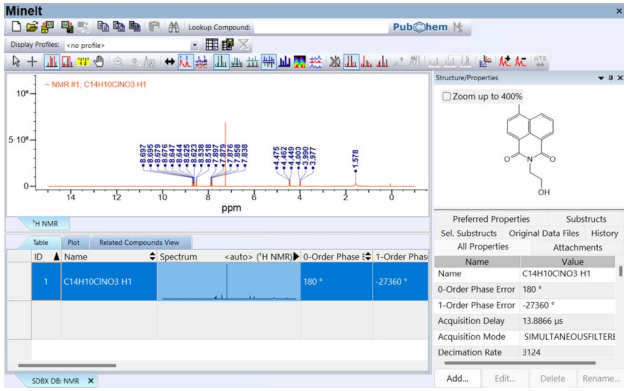
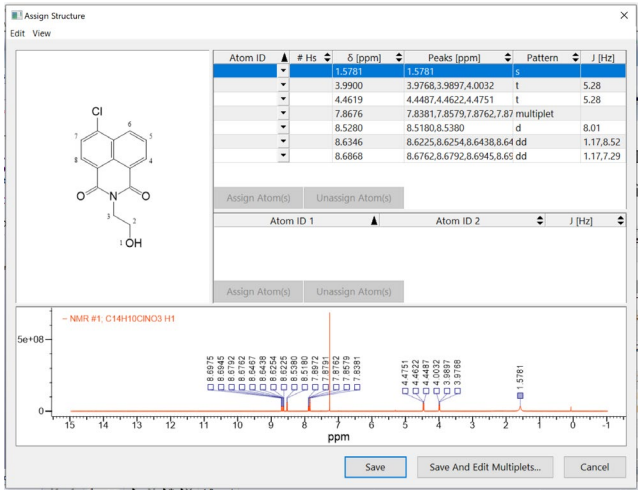
	Action	Result
17	Repeat steps 10 to 16 to group the 4 peaks at ~ 8.67 – 8.70 ppm (8.6762, 8.6792, 8.6945 and 8.6975) into a dd with two coupling constants.	The peaks are grouped into a multiplet at ~ 8.6868 ppm with dd as the splitting pattern. Two J-values for the multiplet are added to the table: 

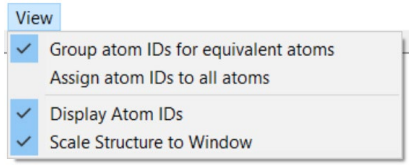
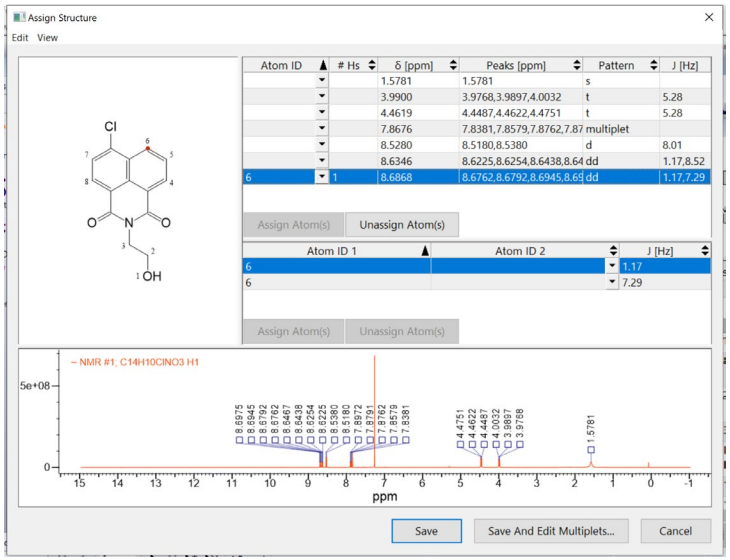
	Action	Result
18	Click to select the row at **7.2612 ppm** which represents the solvent peak. Click **Delete Peak(s).**	The solvent peak (7.2612 ppm) is removed from the table: 
19	Click **Save** to save the multiplets to the record and exit the **Define Multiplets** dialog.	The dialog is closed and the **MineIt** record is displayed: 

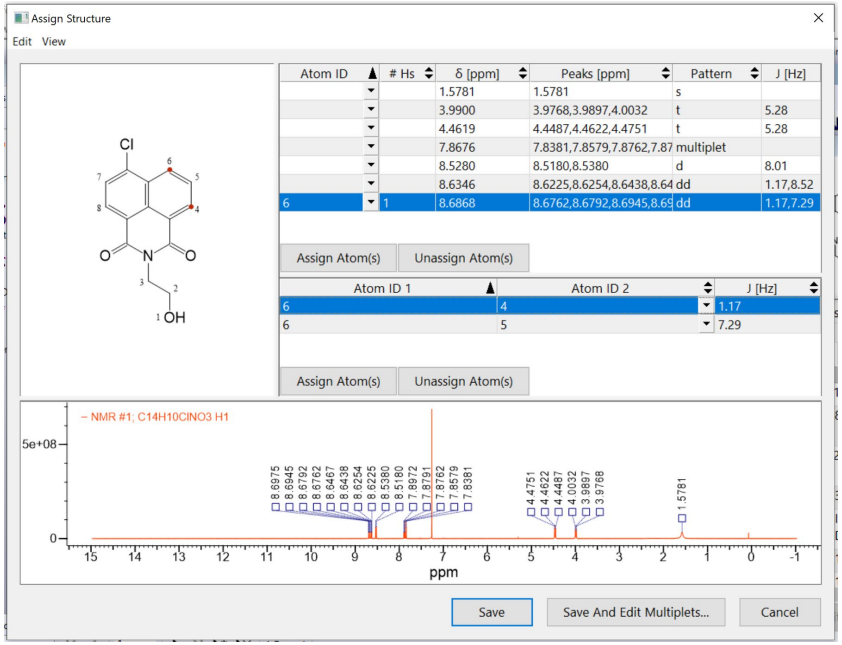
Assign Multiplets to a Structure using NMR Tools

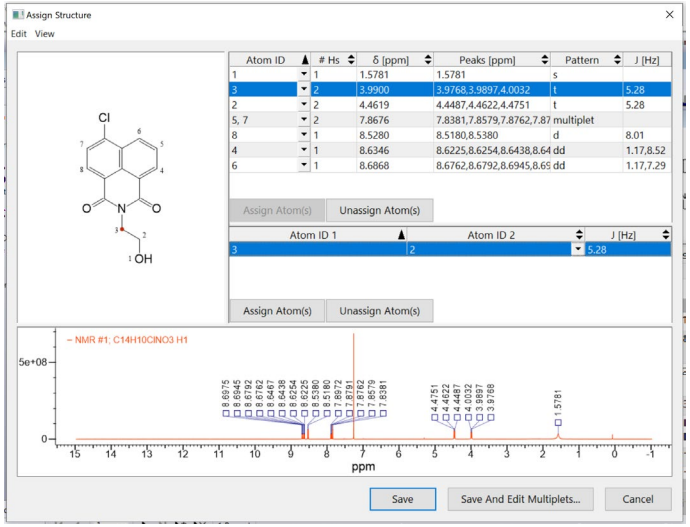
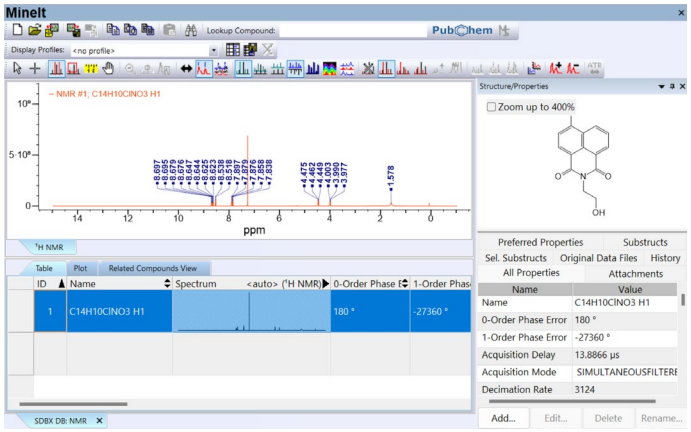
The Assign Multiplets dialog in MineIt NMR Tools allows for the assignment of peaks and multiplets to a structure in MineIt, for ^{1}H, ^{13}C and X-NMR.

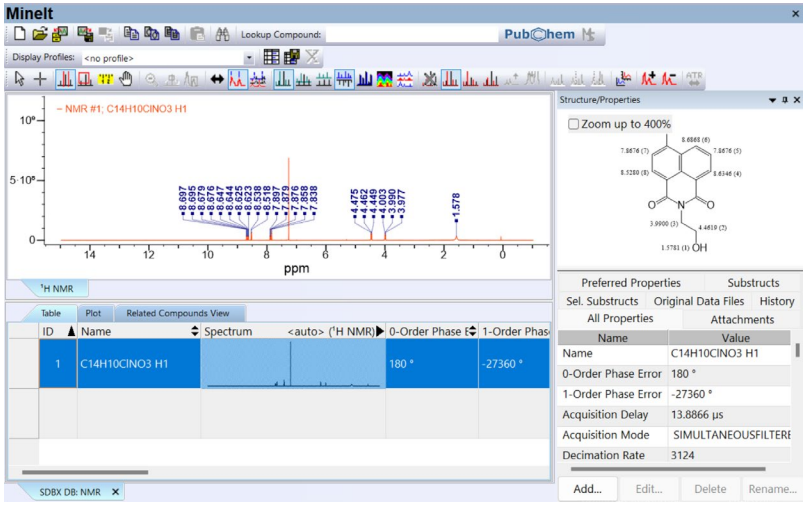
	Action	Result
1	Select the **MineIt** record for the previous section. Click in the **Structure/Properties** window on the text "Double-click to edit structure in ChemWindow." **Note**: To assign atoms to a structure, a structure must be attached to the **MineIt** Record.	**ChemWindow** is launched: 
2	Choose **File > Open** and open the structure for **"C14H10ClNO3.dsf"** located in "**C:\Users\Public\Public Documents\Wiley\KnowItAll\ Samples\NMR\Bruker TopSpin\ C14H10ClNO3.dsf**".	The structure C14H10ClNO3.dsf opens in **ChemWindow**: 

	Action	Result
3	Click **Save** to add the structure to the **MineIt** record.	The structure is attached to the **MineIt** record: 
4	Choose **NMR Tools > Assign Structure**.	The **Assign Structure** dialog is launched, and the multiplet information from the **Define Multiplets** dialog is prepopulated:  The **Assign Structure** dialog is used to assign peaks and multiplets to atoms in the structure.

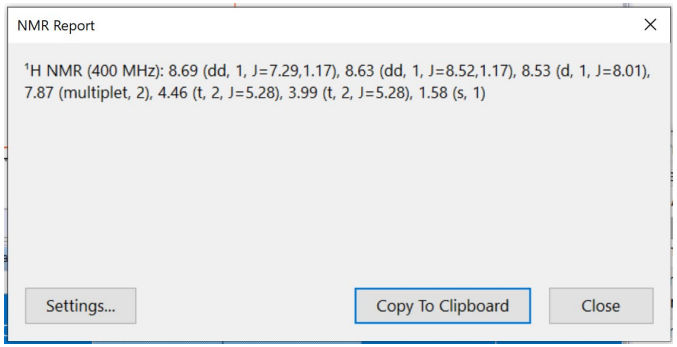
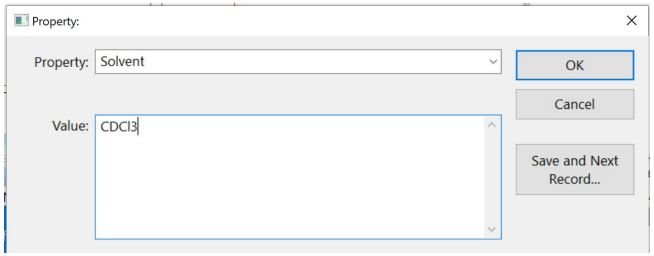
	Action	Result
5	Verify the **Assign Structure** dialog settings under **View** tab: • **Group atom IDs for equivalent atoms** should be selected with a checkmark • **Assign atom IDs to all atoms** should be deselected without a checkmark	 **Group atom IDs for equivalent atoms** is used to add/remove equivalent numeration for symmetrical structures. **Assign atom IDs to all atoms** is used to add/remove numeration for heteroatoms, which may be necessary to label cross-coupling in the spectrum (*e.g.,* H-P).
6	Click on the row with **δ** value 8.6868 ppm. Use the dropdown menu under **Atom ID** to select proton 6 for assignment to the multiplet. Click on the white space below the table to commit the change. **Note**: More than one proton can be selected for assignment using this menu. Atom IDs can also be assigned to the cells using the numbers on a keyboard or using the **Assign Atom(s)** button and selecting an atom in the structure. Protons can be unassigned at any time by clicking **Unassign Atom(s)**.	The **Atom ID** for the dd at 8.6868 is proton 6. **# Hs** is populated with the number of assigned protons: 

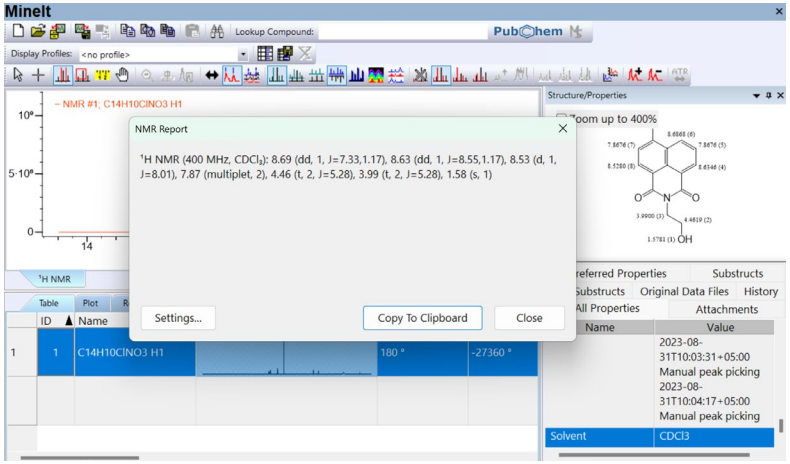
	Action	Result
7	In the lower table within the **Assign Structure** dialog, use the **Atom ID 2** column and the dropdown menus within the cells to assign the small J-value (~1.17 Hz) to proton #4 and the large J-value (~7.29 Hz) to proton #5.	The **Atom ID 2** column in the lower table becomes populated with atoms #4 and #5:  The lower table is used to assign cross-coupling.

<table>
<tr><th></th><th>Action</th><th>Result</th></tr>
<tr><td>8</td><td>Repeat steps 6 and 7 for each proton in the structure. Assign the following pairs:
<table>
<tr><th>δ</th><th>Atom ID</th><th>Atom ID 2</th></tr>
<tr><td>1.5781</td><td>1</td><td>N/A</td></tr>
<tr><td>3.9900</td><td>3</td><td>2</td></tr>
<tr><td>4.4619</td><td>2</td><td>3</td></tr>
<tr><td>7.8676</td><td>5, 7</td><td>N/A</td></tr>
<tr><td>8.5280</td><td>8</td><td>7</td></tr>
<tr><td>8.6346</td><td>4</td><td>6 (1.17)
5 (8.52)</td></tr>
</table>
N/A means no value can be added in the lower table.</td><td>The Atom ID column for the Assign Structure dialog is filled:
 
</td></tr>
<tr><td>9</td><td>Click Save to commit the changes to the record.</td><td>Upon clicking Save, the dialog is closed and the MineIt record is displayed.
 
</td></tr>
</table>

	Action	Result
10	To view the assignments on the structure, choose **View > Assignment Information > Both**.	The **atom IDs** are displayed on the structure in the **Structure/Properties** window: 
11	To view the cross-coupling information, choose **View > Windows/Tables > Coupling Data Table**.	**Coupling Data Table** Pos (ppm) | Multiplicity | Atom # | Atom # | J (Hz) 8.6346 | dd | 4 | 6 | 1.17 8.6346 | dd | | | 8.55 8.6868 | dd | | | 7.33 8.5280 | d | 8 | 7 | 8.01 7.8676 | m | | | 4.4619 | t | 2 | 3 | 5.28 3.9900 | t | 3 | 2 | 5.28 1.5781 | s | | |

Viewing the NMR Multiplet Report

	Action	Result
1	In **MineIt**, choose **NMR Tools > Multiplet Report**. **Note:** Clicking **Copy to Clipboard** will copy the report information in the dialog to the clipboard.	The **Multiplet Report** is prefilled with the information saved to the record using the **Define Multiplets** dialog. The integral information is attached from the **Assign Structure** dialog:  The NMR Report will automatically generate for all NMR spectra (^{1}H, ^{13}C and X-NMR). The specific settings for the **NMR Report** for these can be adjusted by clicking **Settings**.
2	Click **Close** on the dialog. In the **Structure/Properties** window, click **Add**. Choose “Solvent” in the dropdown list. Enter “CDCl3” as the value.	The **Property** dialog is launched: 

	Action	Result
3	Click **OK** on the **Property** dialog to add the Solvent to the **MineIt** record. Relaunch the **NMR Report** dialog (**NMR Tools > Multiplet Report**).	The **NMR Report** now displays the NMR solvent for the specific record: 

NMR

Generate an NMR Spectrum

Purpose

This exercise demonstrates how to generate an NMR spectrum using peak lists or an NMR report for a decoupled spectrum.

Objectives

This exercise will teach you:

- How to import peak lists to MineIt

Background

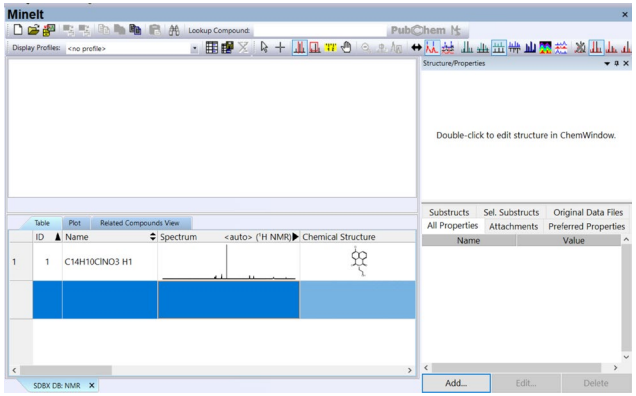
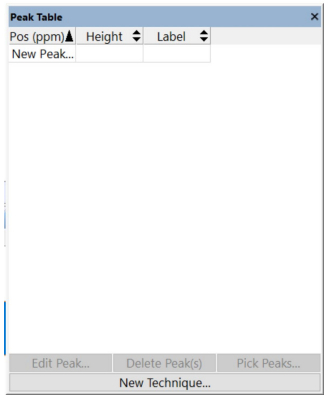
Being able to overlay reference material to experimental spectra is important for confirmation of compounds and identification of impurities. Through importing tabulated peak lists from reference material such as NMR reports into MineIt user databases, the spectra for these compounds can be directly overlayed, subtracted and searched against experimental data.

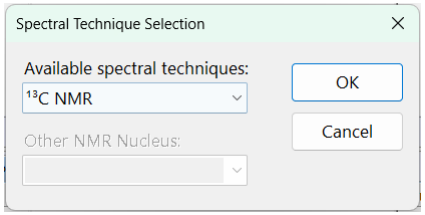
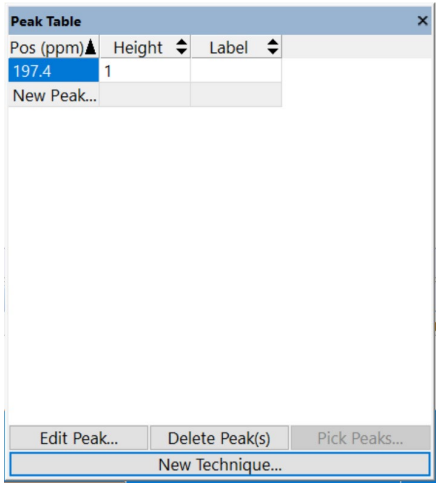
KnowItAll Applications Used

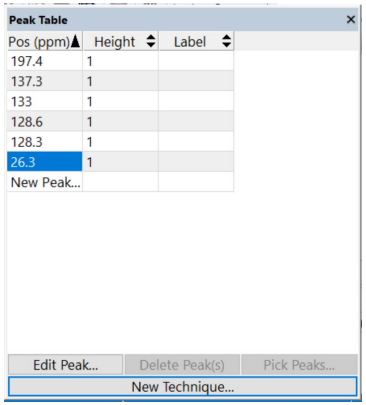
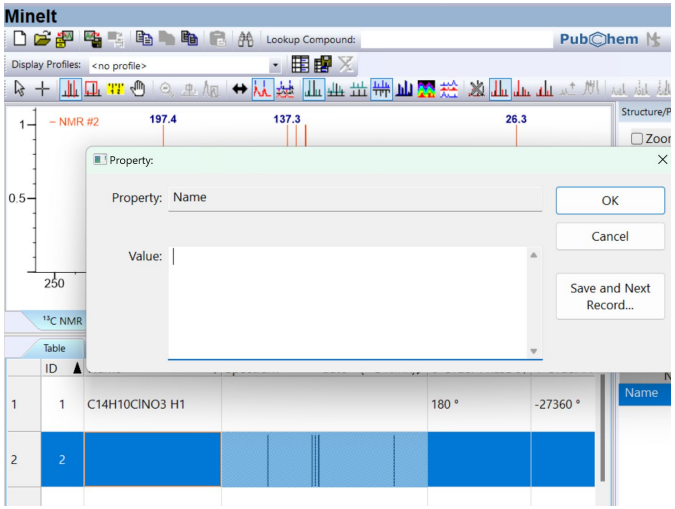
- MineIt

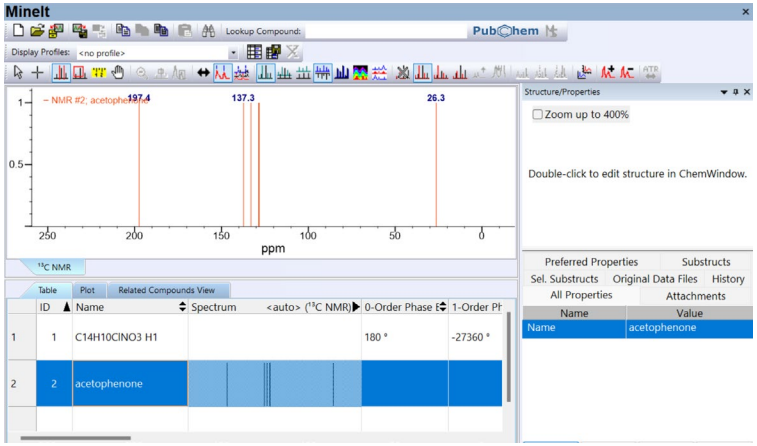
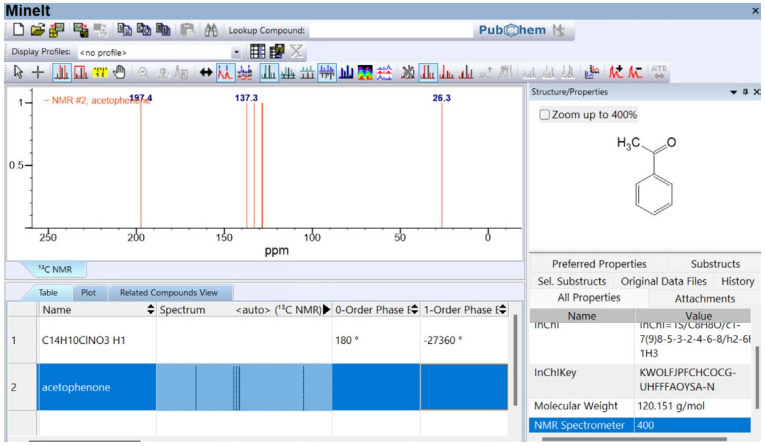
Generating a Database Record from NMR Report or Peak List

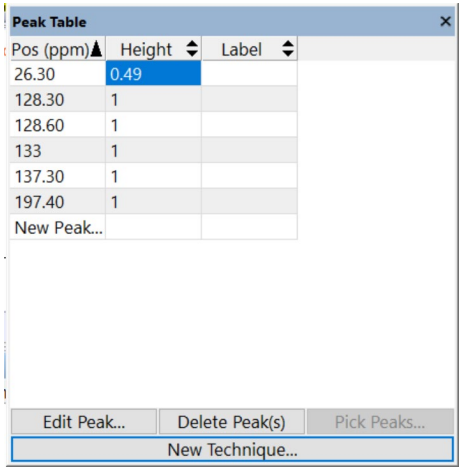
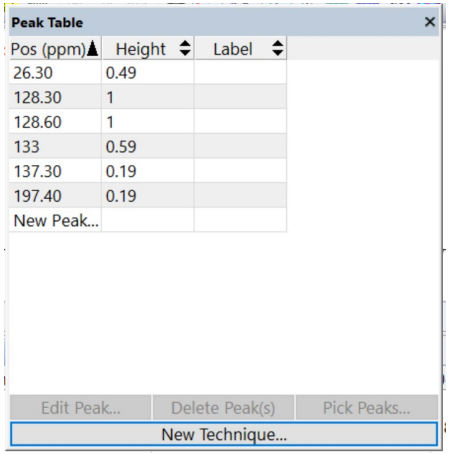
This section shows how an NMR peak spectrum can be generated from peak list information.

	Action	Result
1	Using the user database from the previous section, click on the blank row in the **Table** section. This is currently the second row for the opened database.	A blank record is displayed: 
2	Choose **View > Windows/Tables > Peak Table**	A blank **Peak Table** dialog opens: 

	Action	Result
3	Click **New Technique** to choose the spectrum type on the **Peak Table** dialog.	The **Spectral Technique Selection** dialog opens: 
4	Use the **Available spectral techniques** dropdown menu to choose ^{13}C NMR, then click **OK**.	The **Spectral Technique Selection** dialog is closed and the blank **Peak Table** remains visible.
5	Double click on the cell that reads "**New Peak**" in the **Peak Table** and enter the value 197.4. Click the down arrow to begin a new row.	The **Peak Table** displays 197.4 as a peak in the first cell, with a default peak height of 1: 

	Action	Result
6	Repeat step 5 for each of the following peaks: 137.3, 133, 128.6, 128.3, 26.3. **Note**: This simulates the spectrum for the NMR Report: "^{13}C NMR (80 MHz): 197.4, 137.3, 133.0, 128.6, 128.3, 26.3".	The **Peak Table** is filled with the peaks: 
7	Click the **X** button to close the **Peak Table** dialog, then double click on the **Name** cell for the active record.	The Peak Table closes. Upon clicking the **Name** cell, **MineIt** refreshes and the generated spectrum displays. The **Property** dialog appears: 

	Action	Result
8	Enter “acetophenone” as in the **Value** box and click **OK**.	The simulated spectrum is displayed with name of record “acetophenone”: 
9	**Note**: The **chemical structure** and **NMR Spectrometer Frequency** can be attached to the record by applying skills previously reviewed in this document.	The chemical structure and NMR spectrometer frequency information have been attached to the simulated spectrum: 

	Action	Result
10	Peak Height information can also be included in the simulation. Choose **View > Windows/Tables > Peak Table**. Double click on the cell for **Height** in the row next to the peak 26.30 ppm. Enter 0.49 and press **Enter** on the keyboard. **Note:** Clicking enter jumps to the cell below.	The peak height value is displayed in the **Peak Table**: 
11	Repeat step 10 to enter the following values: 0.59 (133 ppm), 0.19 (137.30 ppm), 0.19 (197.40 ppm).	The peak height values are displayed in the **Peak Table**: 

	Action	Result
12	Click the **X** button to close the **Peak Table** dialog. **Note:** Refresh to save the changes, such as clicking on another record then returning to record #2.	The simultated spectrum is updated according to the peak height values: