

The JEOL logo is displayed in a bold, blue, sans-serif font. It is positioned in the upper left quadrant of the slide, to the right of a vertical blue decorative bar. The bar contains a stylized globe at the bottom and binary code (0s and 1s) above it. A large, faint, white graphic of a stylized 'J' or a similar shape is overlaid on the background, extending from the top right towards the center.

JEOL



Delta V5 operation

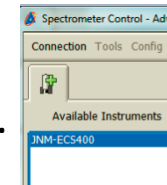
**Widetron Technologies Corp.
Wu, Chung-Ying**

Progress through Synergy

Connect to spectrometer



1. Start Delta V5 (double click ).
2. Open Spectrometer Control (click ).
3. Select spectrometer on Available Instruments.





4. Click  and login with delta account (click ).

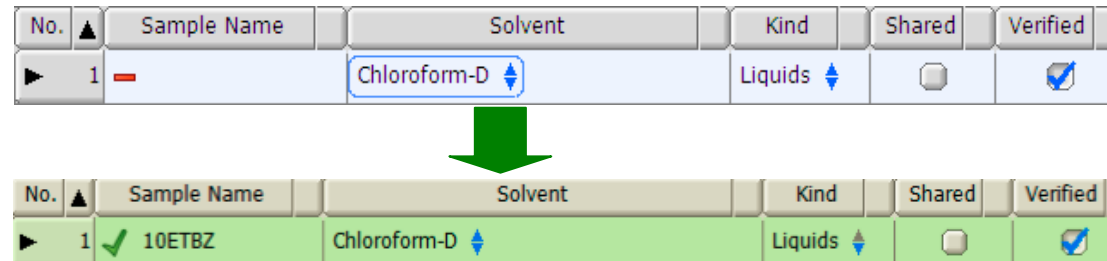


Name	Password	remarks
delta	delta	For installation account

Sample preparation



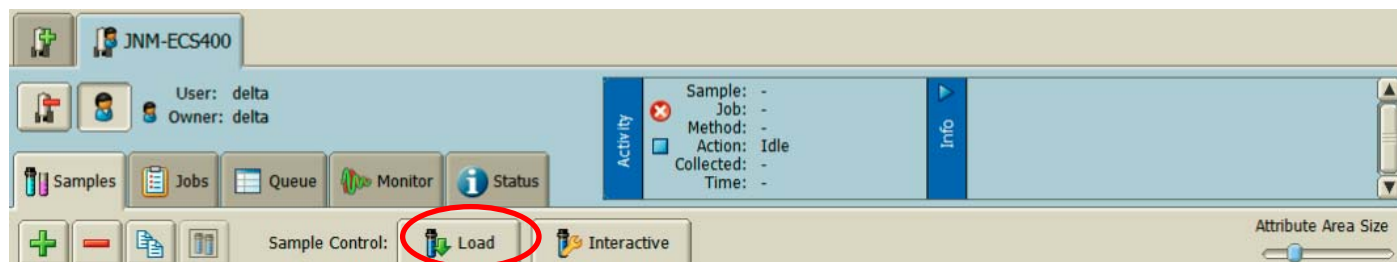
1. Set sample tube on SCM .
2. On Samples tab  , you must defined your sample information.
3. On Samples tab, click  . You can see new sample definition space on sample list.
4. Input sample name.
5. Select solvent.
6. Click Verified.
7. Click sample number. Clicked sample box becomes green color.



The screenshot shows a table with columns: No., Sample Name, Solvent, Kind, Shared, and Verified. In the first row, the 'No.' is 1, 'Sample Name' is empty, 'Solvent' is 'Chloroform-D', 'Kind' is 'Liquids', 'Shared' is unchecked, and 'Verified' is checked. A green arrow points down to a second row where the 'No.' is 1, 'Sample Name' is '10ETBZ', 'Solvent' is 'Chloroform-D', 'Kind' is 'Liquids', 'Shared' is unchecked, and 'Verified' is checked. The entire row is highlighted in green.

No.	Sample Name	Solvent	Kind	Shared	Verified
1		Chloroform-D	Liquids	<input type="checkbox"/>	<input checked="" type="checkbox"/>
1	10ETBZ	Chloroform-D	Liquids	<input type="checkbox"/>	<input checked="" type="checkbox"/>

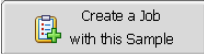

8. Click  Load for sample loading.

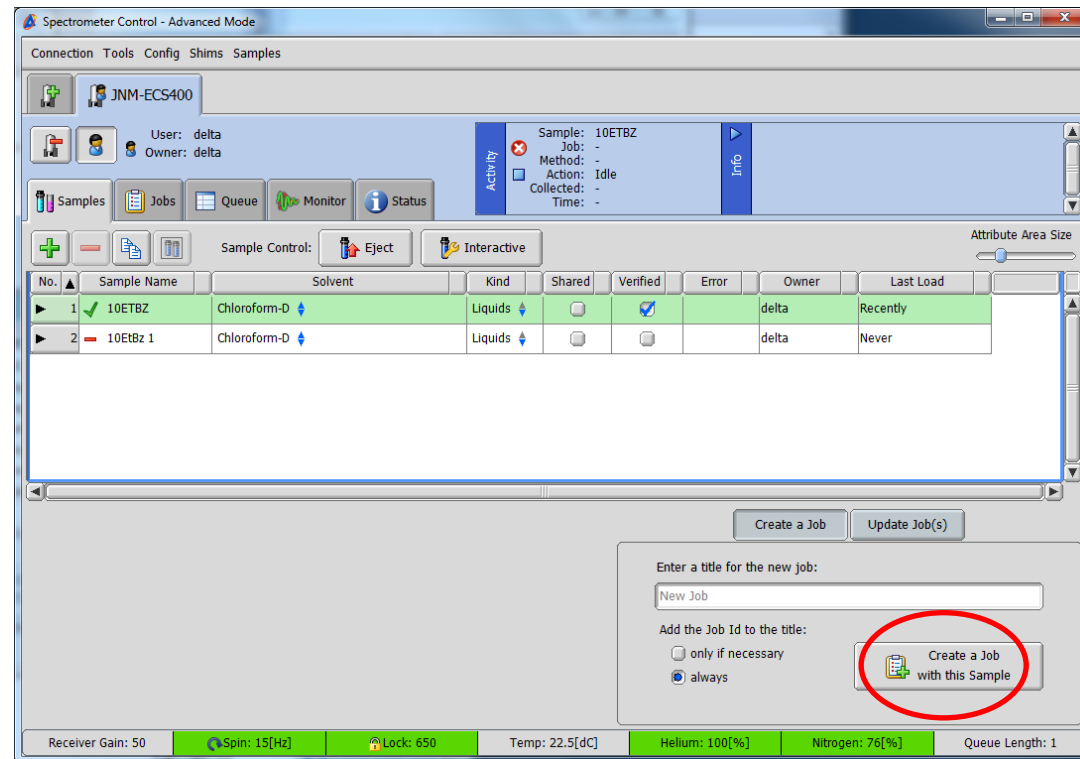


Progress through Synergy

Set up experiment (automation)




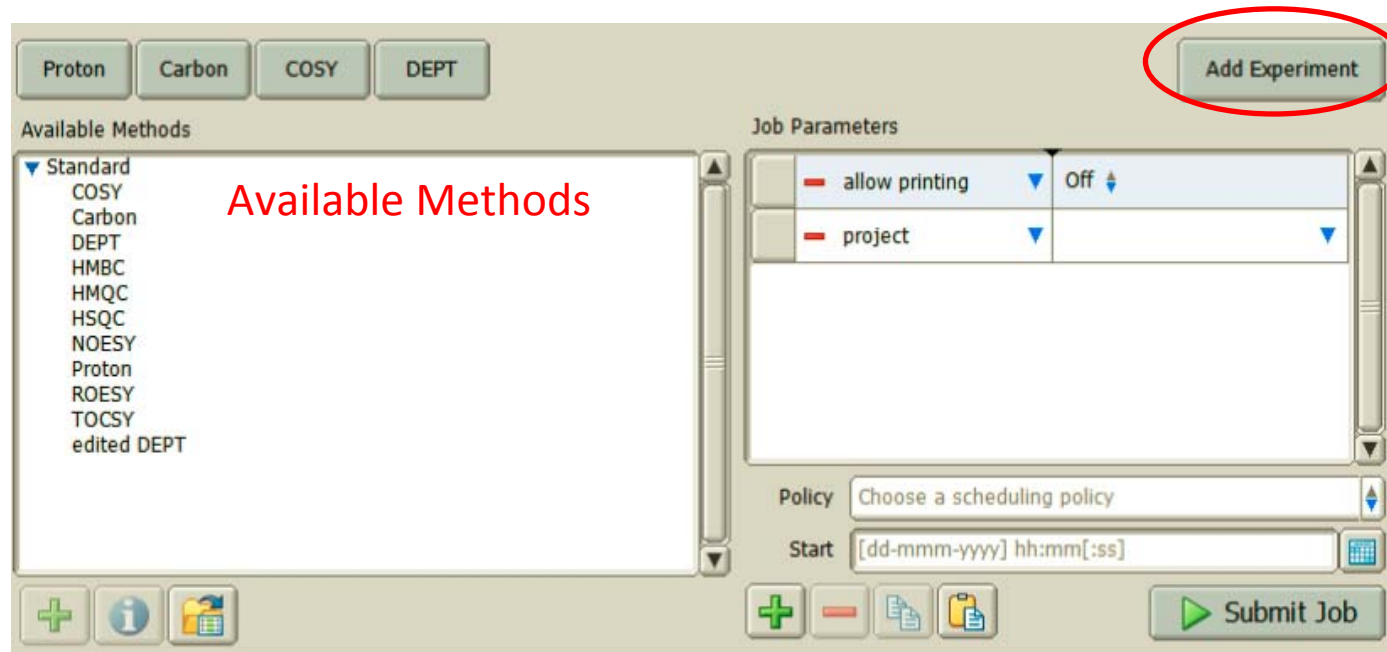
1. Click  on Samples tab or key in the job name which you want to define your job. You can see the next tab  (Jobs tab).



Set up experiment (automation)



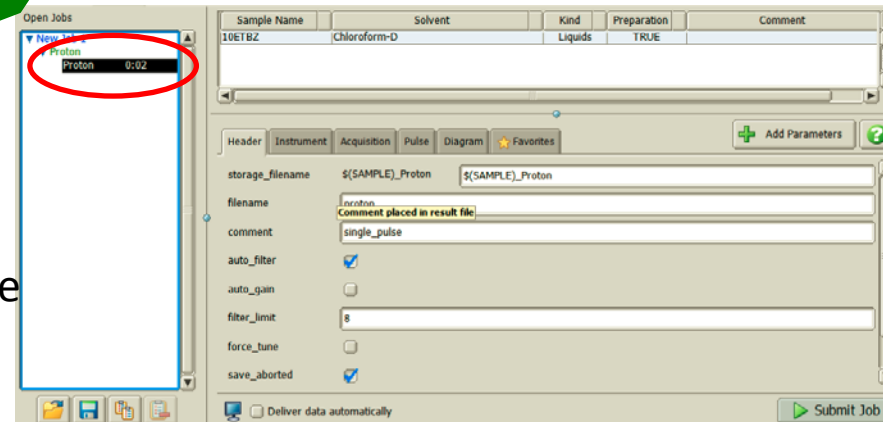
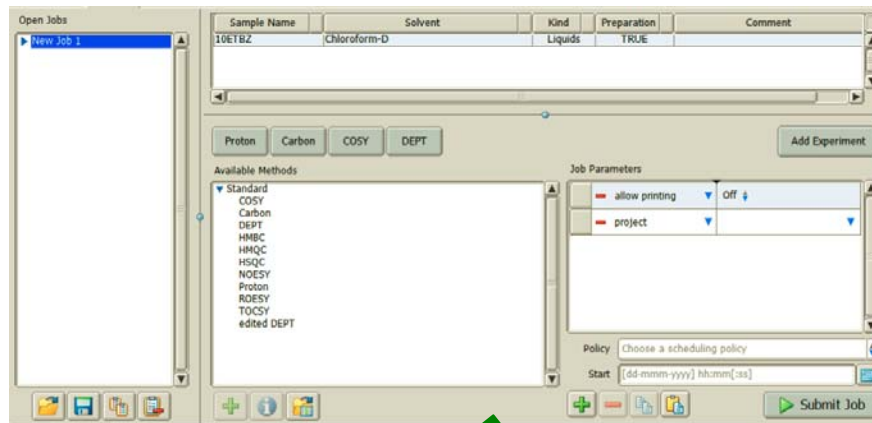
2. We can choose some experiments which user want to do on Job Parameters box.
3. If user want to do another experiment which is not save in available methods, click  for another experiments.



Set up experiment (automation)



4. If you want to change the more detail parameters, select experiment name on Open Jobs list.



- ▼ Job Name
- ▼ Method Name
- ▼ Experiment Name

Progress through Synergy

Set up experiment (automation)



5. We can change some experiments parameters on Job Parameters box.

The screenshot shows the 'Job Parameters' box in a software interface. The 'Header' tab is selected and circled in red. The 'comment' field contains the text 'single_pulse'. Other parameters visible include 'storage_filename', 'filename', 'auto_filter', 'auto_gain', 'filter_limit', 'force_tune', and 'save_aborted'. The 'Submit Job' button is located at the bottom right.

Sample Name	Solvent	Kind	Preparation	Comment
10ETBZ	Chloroform-D	Liquids	TRUE	

Header Instrument Acquisition Pulse Diagram Favorites

storage_filename \$(SAMPLE)_Proton \$(SAMPLE)_Proton

filename proton
Comment placed in result file

comment single_pulse

auto_filter

auto_gain

filter_limit 8

force_tune

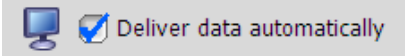
save_aborted

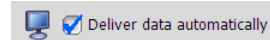
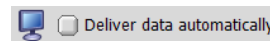
Deliver data automatically

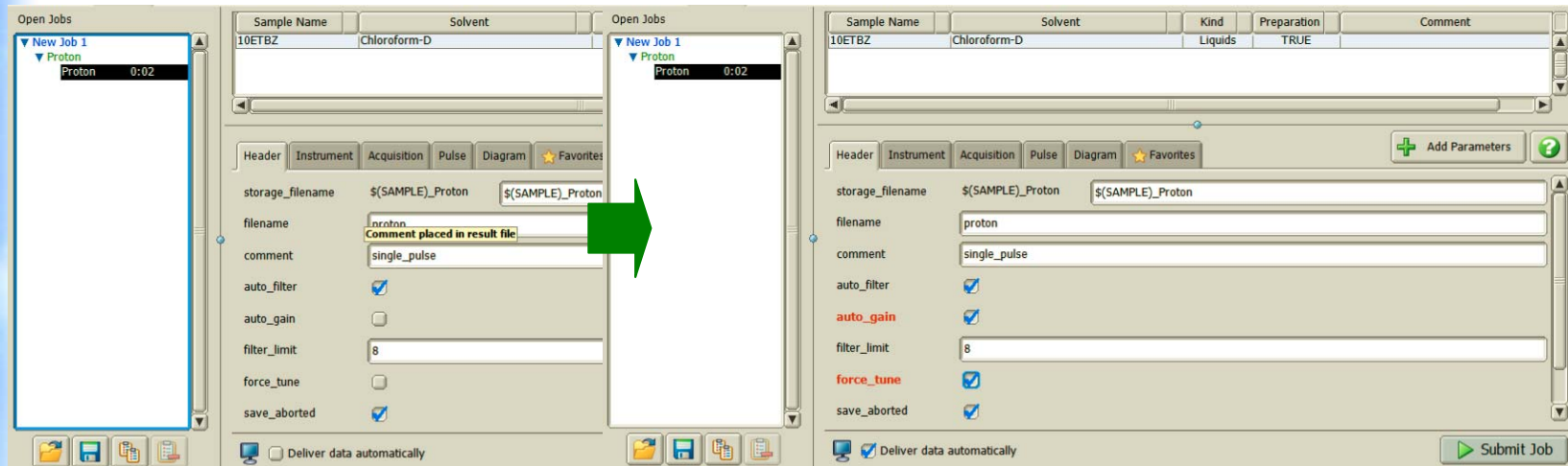
Submit Job

Set up experiment (automation)



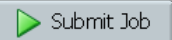
- If you first time do this sample, click **“Force tune”** and **“Auto_gain”**.
- If you tick **“Deliver data automatically”**  , you can see the results on your display.
- The parameters became red word when changed.

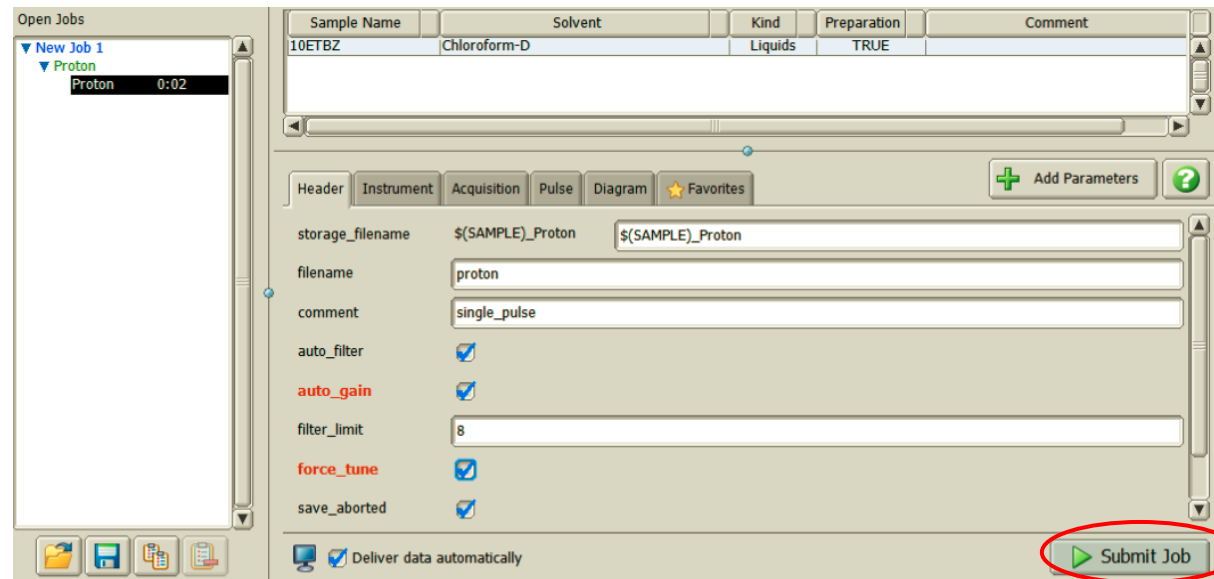
Deliver data automatically	results	Data is saved to ...
	You can see results on your display.	Data Servers (spectrometer) and your workstation
	You can't see results on your display.	Data Servers (spectrometer) only



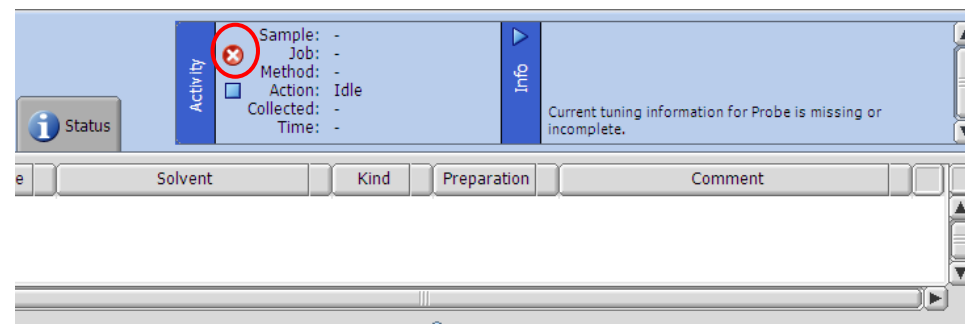
Submit experiment (automation)



9. Click . The experiments are started.



10. If you want to stop experiment, Click  .



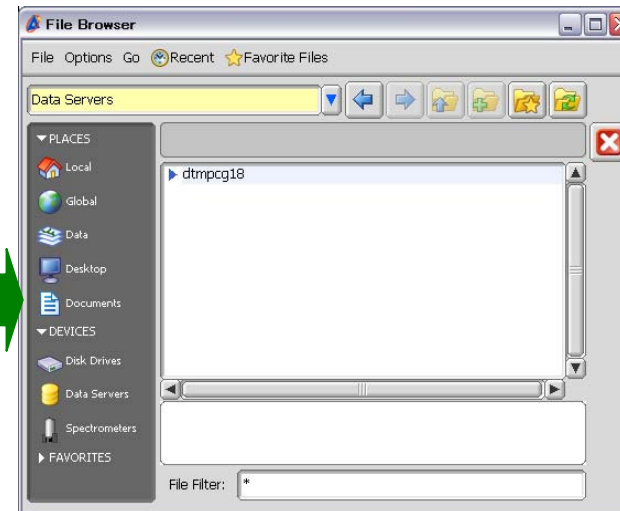
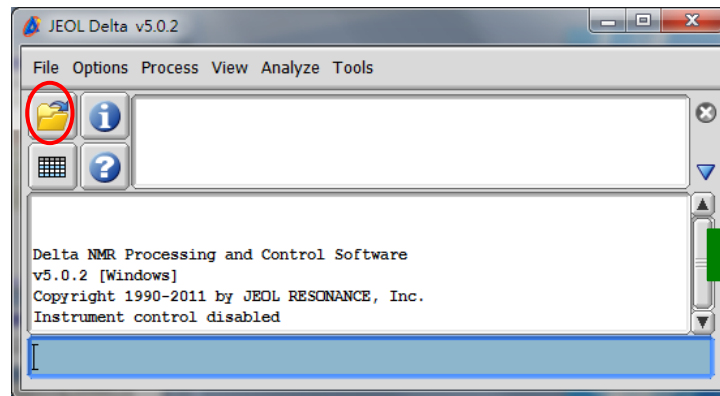
Progress through Synergy

Open data (1)

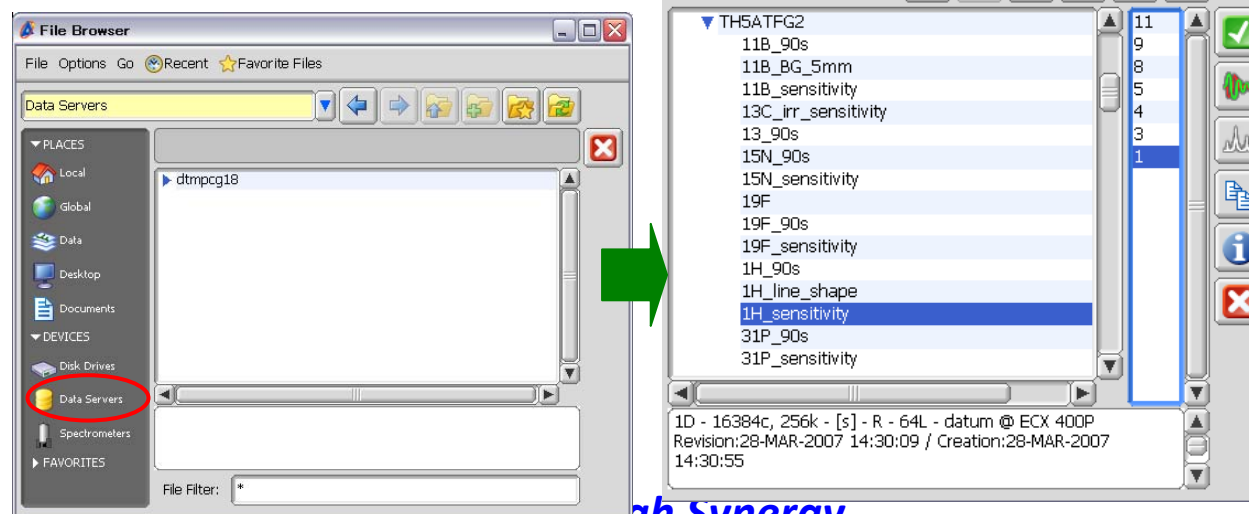


Case A: You have already connected to spectrometer.

1. Click  on Delta Console window.



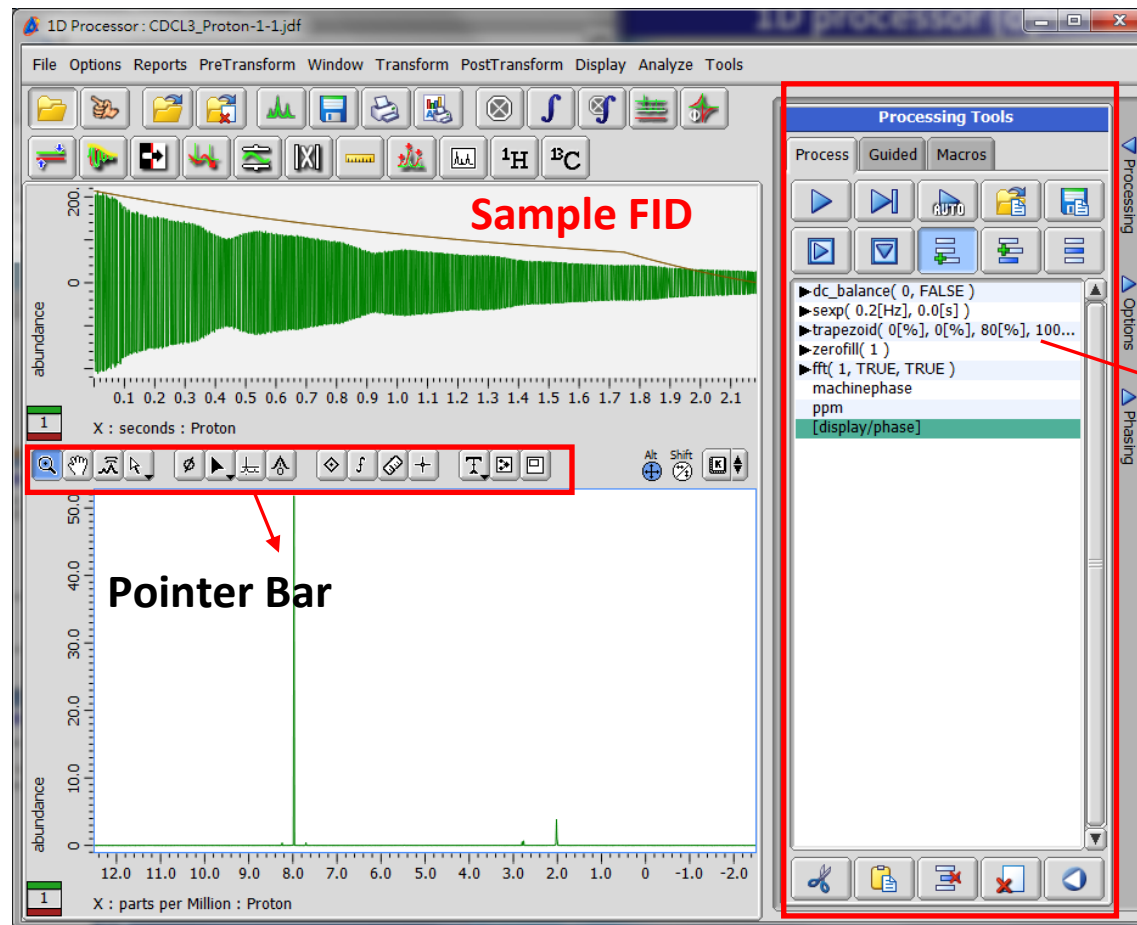
2. Click  Data Servers for downloading from spectrometer. You can select and download data.



1D processor (open data file)



1. When you open 1D NMR data, you can see 1D processor window.



Processing
















Pointer Bar

1D processor (Pointer Bar)



1. When you open 1D NMR data, you can see “Pointer Bar” .

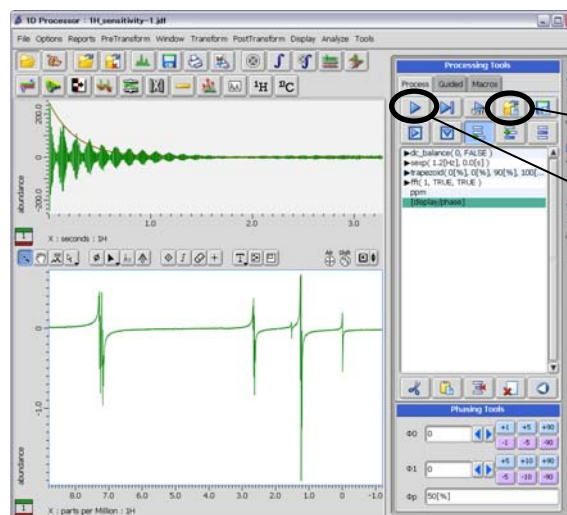


-  : Zoom (Zoom view of data)
-  : Pan View (Pan view of data or slide view)
-  : Amplitude gain (apply amplitude gain)
-  : Select (To select data of geometry)
-  : Phase correct (To adjust the phase of spectra)
-  : Copy position (Copy position to paste buffer)
-  : Peak threshold (Adjust the peak threshold)
-  : Reference (To set a chemical shift reference axis marker)
-  : Peak (Peak picking tool)
-  : Integral (Integral tool)
-  : Measure (To measure distance between peaks)
-  : Cursor (make the horizontal and vertical line)
-  : Annotation (edit annotation in the geometry)
-  : Molecule (To display a structural formula and molecular formula in the geometry)
-  : PiP (Picture in Picture)

1D processor (open process list)







1. When you open 1D NMR data, you can see 1D processor window.



Open processing list

Apply process_list

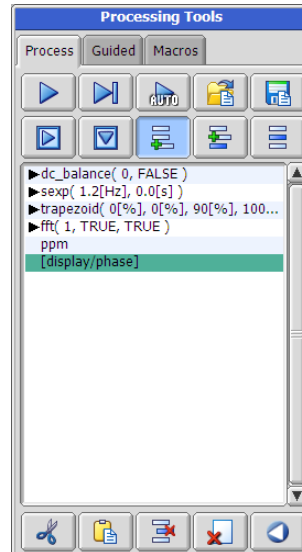
2. If you want to open process_list, click  .
3. When you apply process_list, click  .

*  : for 1H process_list,  : for 13C process_list

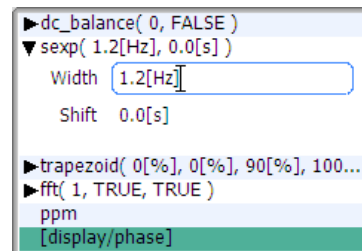
1D processor (edit process list)



1. When you want to edit process, you can edit on Processing tool.




2. If you click ▶, you can see detail parameters for processing command.

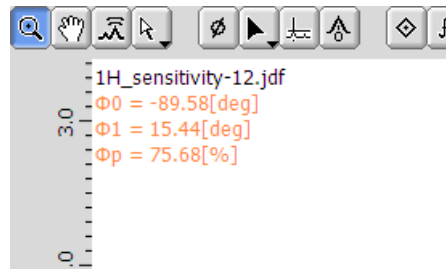


3. When you apply process, click ▶.
4. If you click ◀, you can undo your process list.

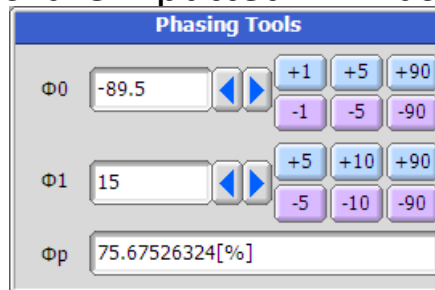
1D processor (phase correction 1)


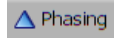


1. When you click  (auto phase), the phase of spectrum is adjusted.
2. You can see phase correction values on the left upper in spectrum.





3. Those values are inputted in Phasing Tool.

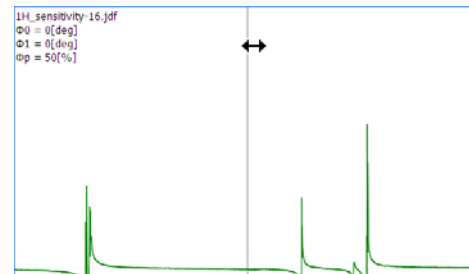


4. If you want to adjust those, you can manipulate with Phasing Tool.
5. When you finish to adjust, click  .
(If you can't see Phasing Tool, please click  on the left.)

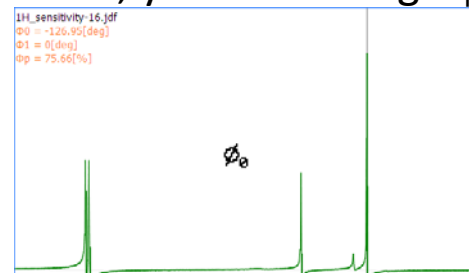
1D processor (phase correction 2)



1. Click  at "Pointer Bar". (Pointer bar is  on processor window.)
2. You can see the vertical line on you spectrum.





3. When your mouse cursor moves to that line, mouse cursor is changed to \leftrightarrow .
4. In that situation, you can change ϕ_p with dragging.

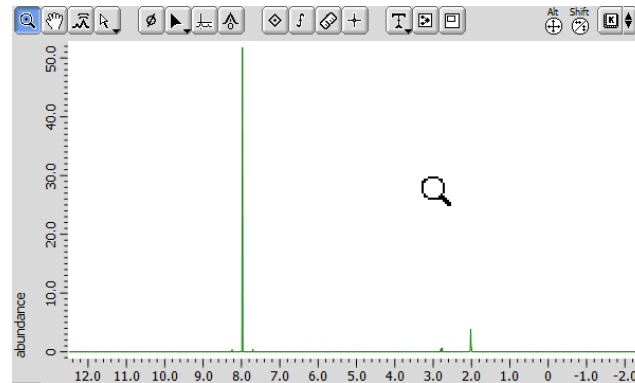


5. If you want to adjust ϕ_0 and ϕ_1 , you can manipulate with Phasing Tool.

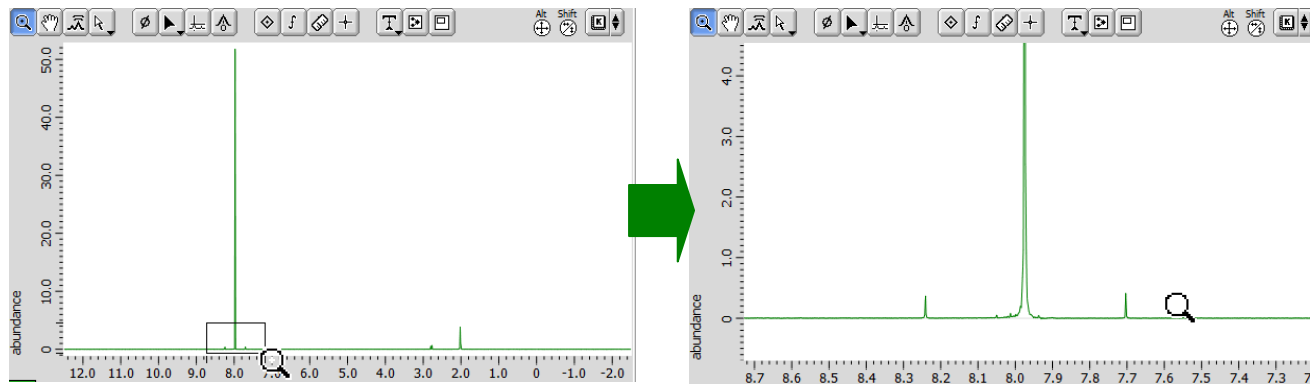
1D processor (Zoom process)



1. Click  at "Pointer Bar". (Pointer bar is  on processor window.)
2. You can see your mouse cursor became magnifier.





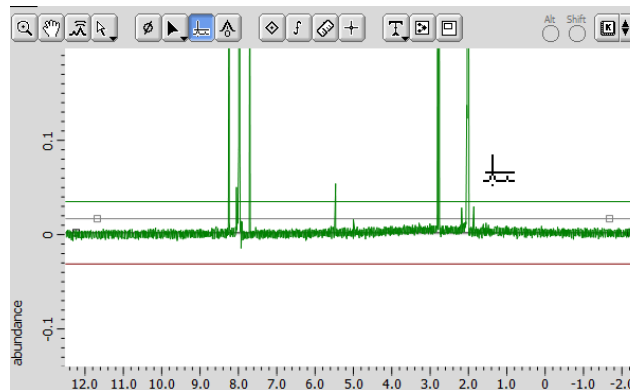
3. When you drag any region or the border, the process window zoom will be changed.



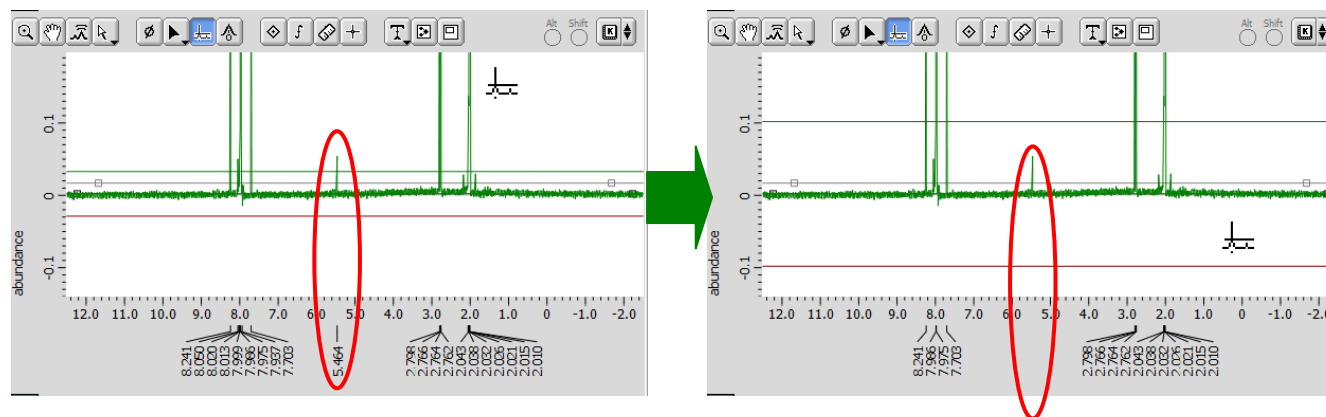
1D processor (Peak threshold)



1. Click  at "Pointer Bar". (Pointer bar is  on processor window.)
2. You can see your mouse cursor became peak threshold.



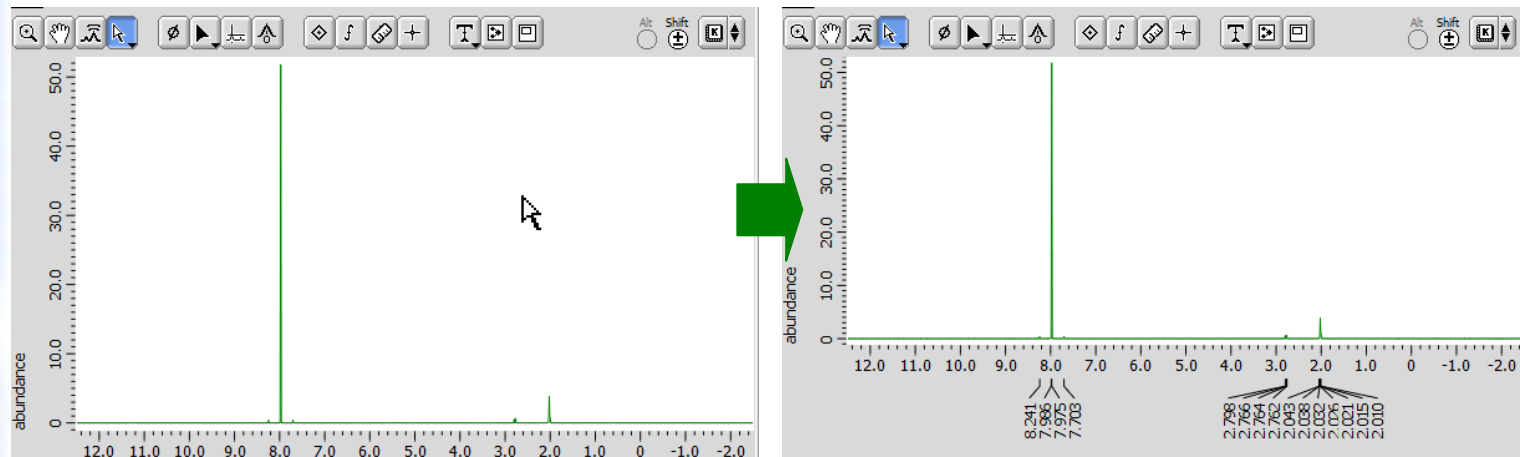
3. You could drag the green line or red line, this process influence peak picking and integral.



1D processor (Peak picking 1)








1. When user decide their peak threshold, click  for auto peak picking

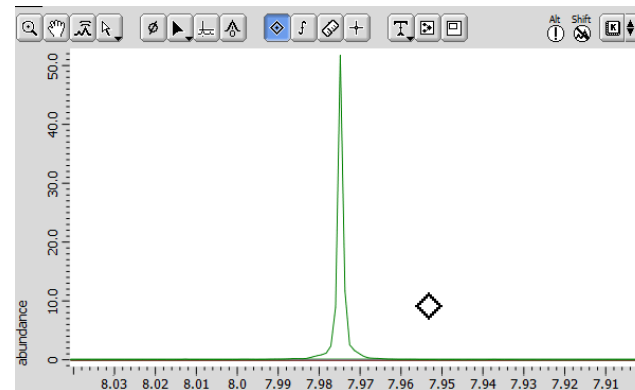


Progress through Synergy

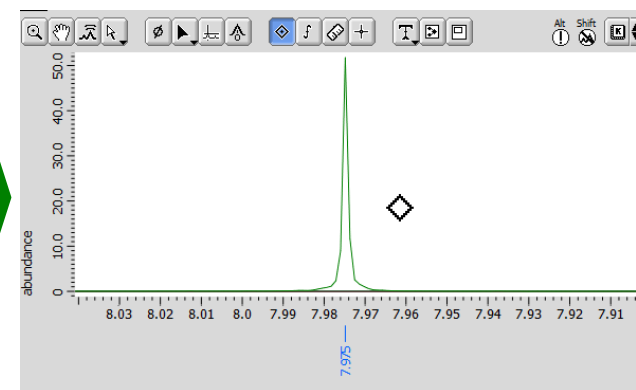
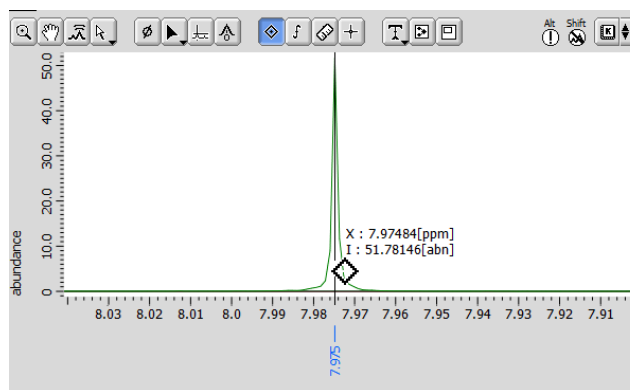
1D processor (Peak picking 2)



1. Click  at "Pointer Bar". (Pointer bar is     on processor window.)
2. You can see your mouse cursor became peak picking.



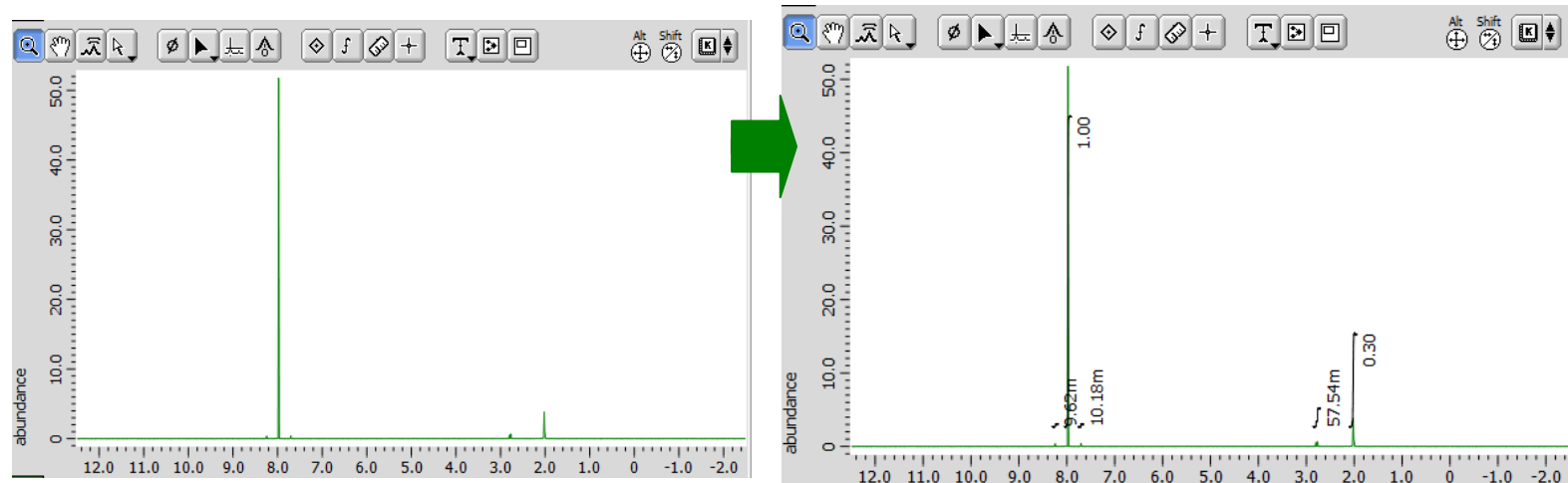
3. Which peak you want to pick, move the mouse cursor to peak and click left mouse button.



1D processor (Peak integral 1)








1. When user decide their peak threshold, click  for auto peak integral.

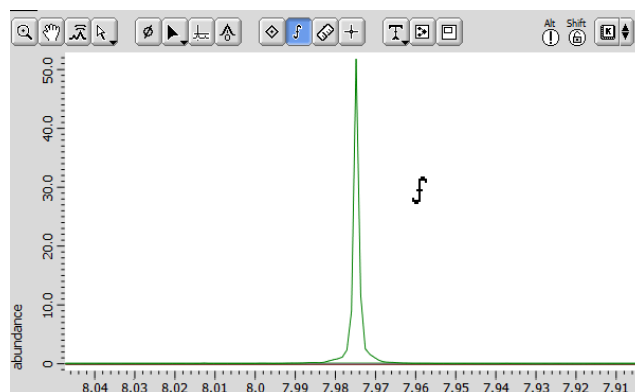


Progress through Synergy

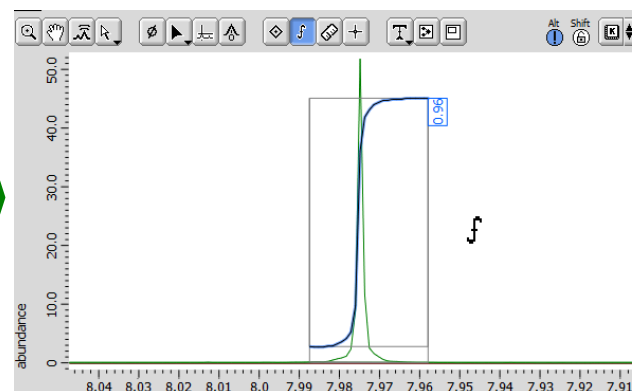
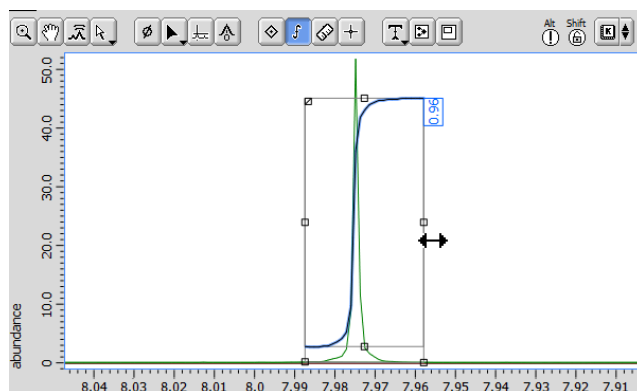
1D processor (Peak integral 2)



1. Click  at "Pointer Bar". (Pointer bar is     on processor window.)
2. You can see your mouse cursor became peak picking.




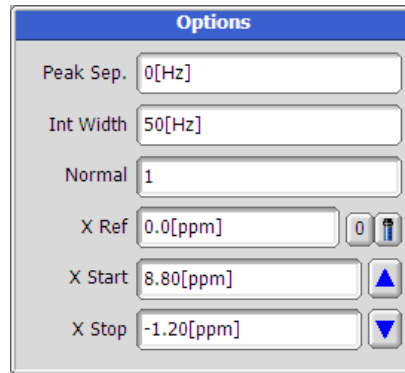
3. Which peak you want to integral, move the mouse cursor to peak and drag the region by left mouse button.



1D processor (options)



If you can't see "Options" panel, please click  Options on the left.



Options	
Peak Sep.	0[Hz]
Int Width	50[Hz]
Normal	1
X Ref	0.0[ppm] 0
X Start	8.80[ppm] ▲
X Stop	-1.20[ppm] ▼

Peak Sep. : The minimum value between peak and peak for peak picking.

Int Width : The range of integral.

Normal : Normalize value for integral.



X Ref : the value for calibrating chemical shift.

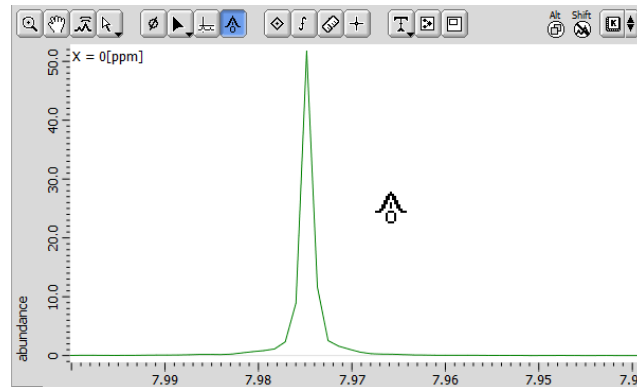
X start : the right edge of the spectrum.

X Stop : the left edge of the spectrum.

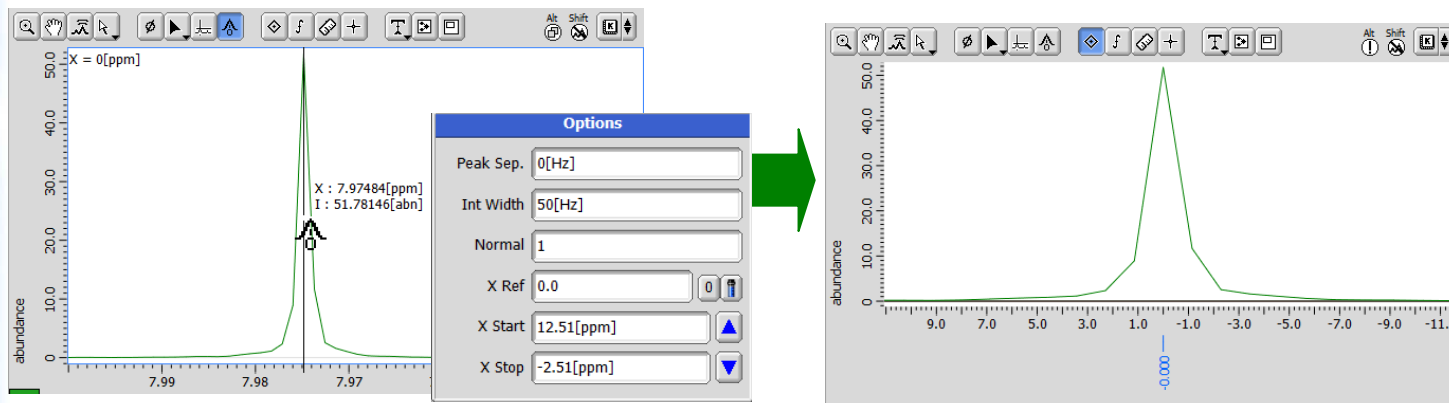
1D processor (Peak reference)



1. Click  at "Pointer Bar". (Pointer bar is  on processor window.)
2. You can see your mouse cursor became reference.



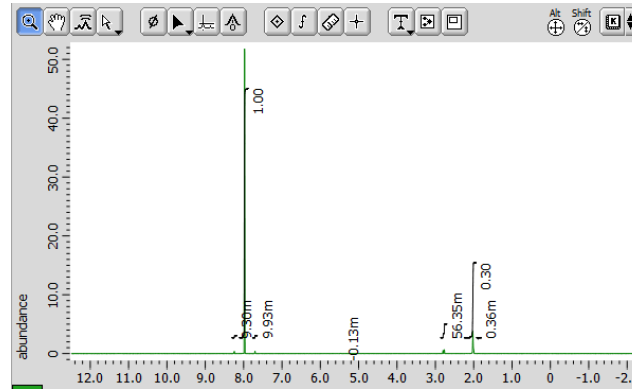
3. Which peak you want to decide reference peak, set the value in X ref on option bar and move the mouse cursor to peak and click by left mouse button.








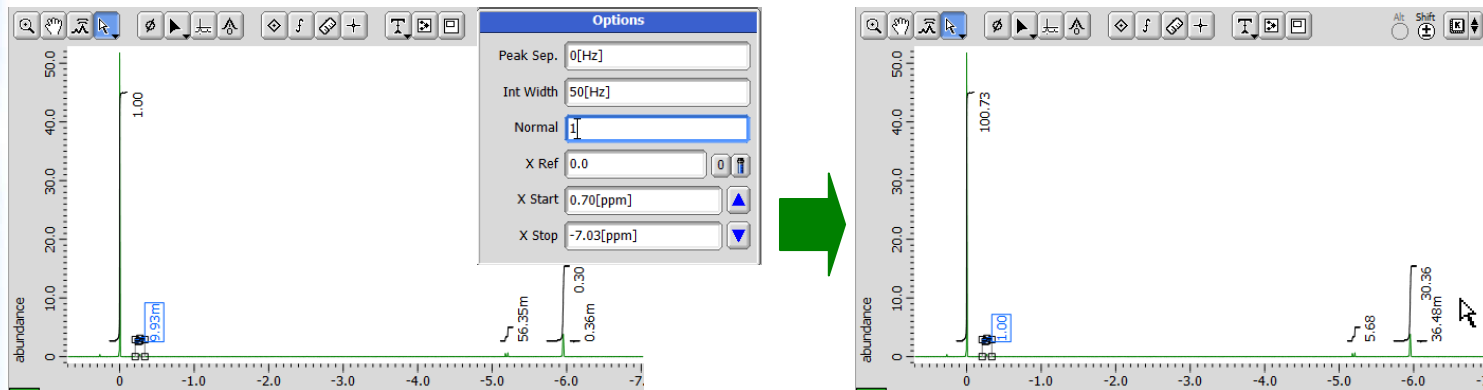
1D processor (Peak integral normalized)



1. After auto integral, user could see the result about integral.



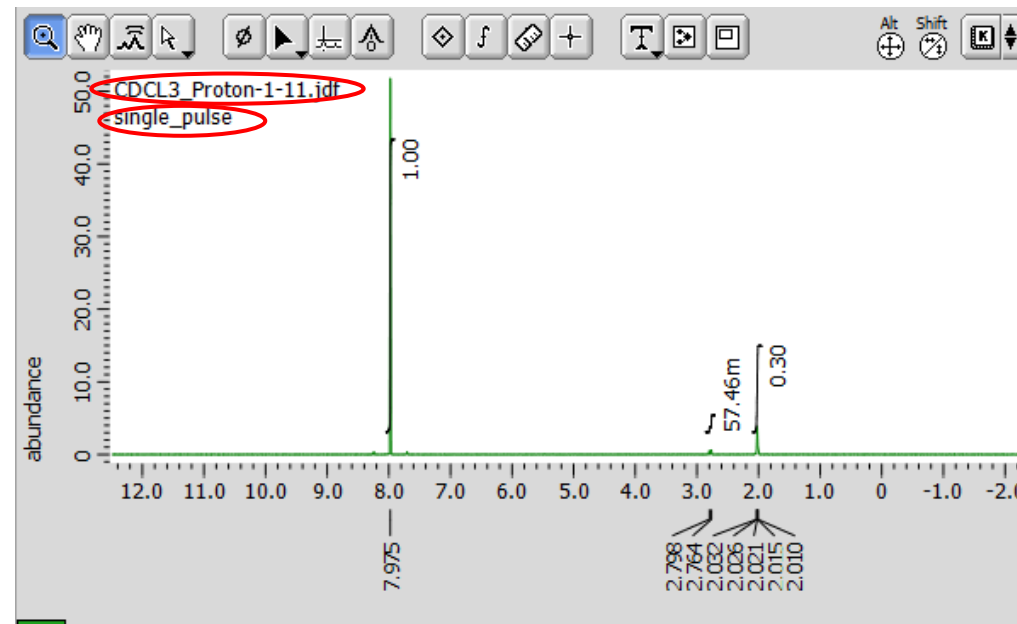
2. Click  at "Pointer Bar". (Pointer bar is     on processor window.) , select the integral and key in the value which user want to normalized on option bar



1D processor (prepare print)



1. After data process, click alt+f for data file name and alt+shift+c for method.



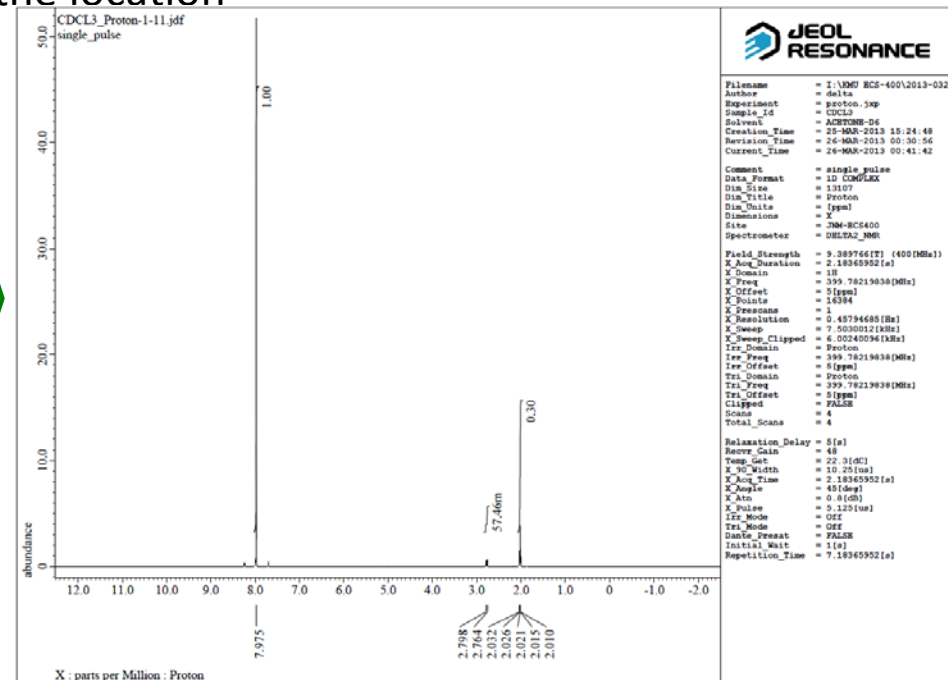
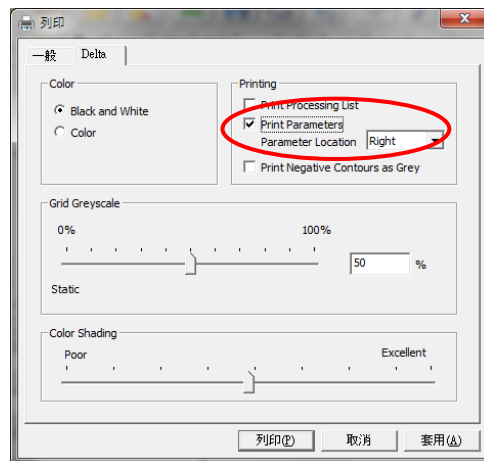
1D processor (prepare print)



1. Click  For print data file.



2. If user want to print shim parameters, click delta and tick the print parameters and choose the location

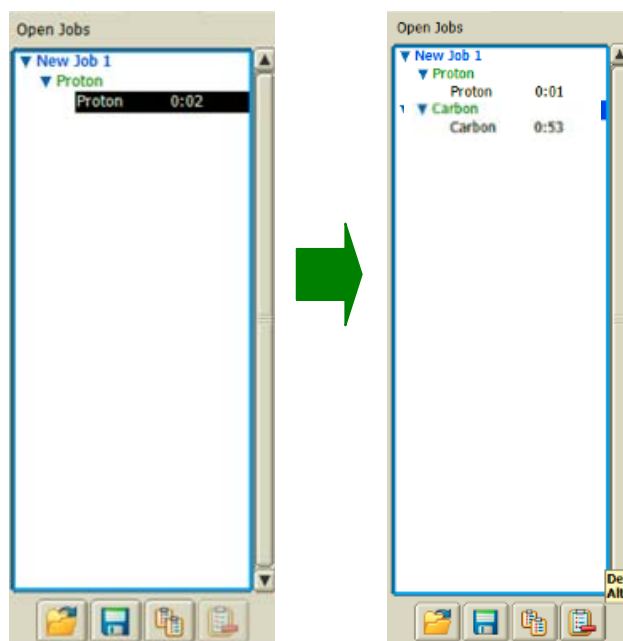
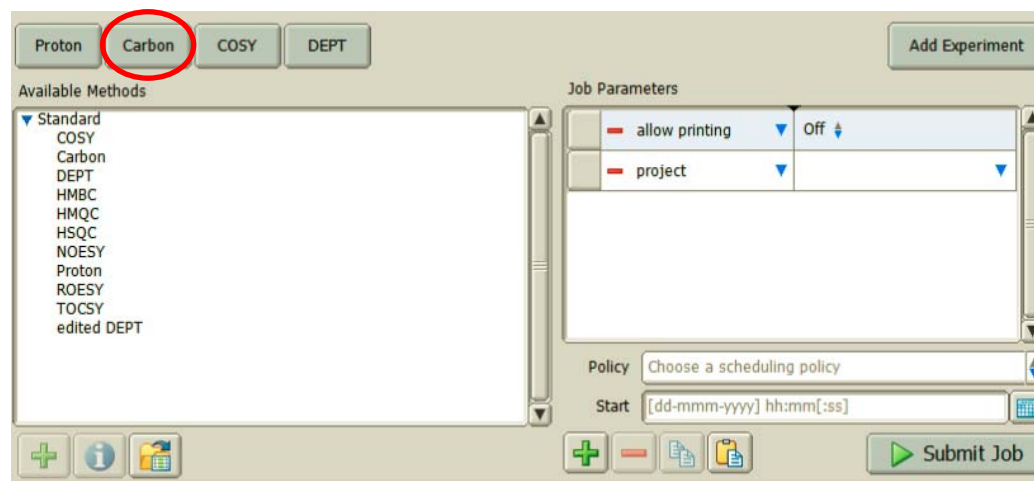


Progress through Synergy

Set up experiment (^{13}C automation)



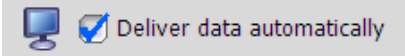
1. We can click the carbon experiment icon on Job tab.

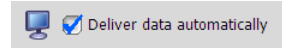



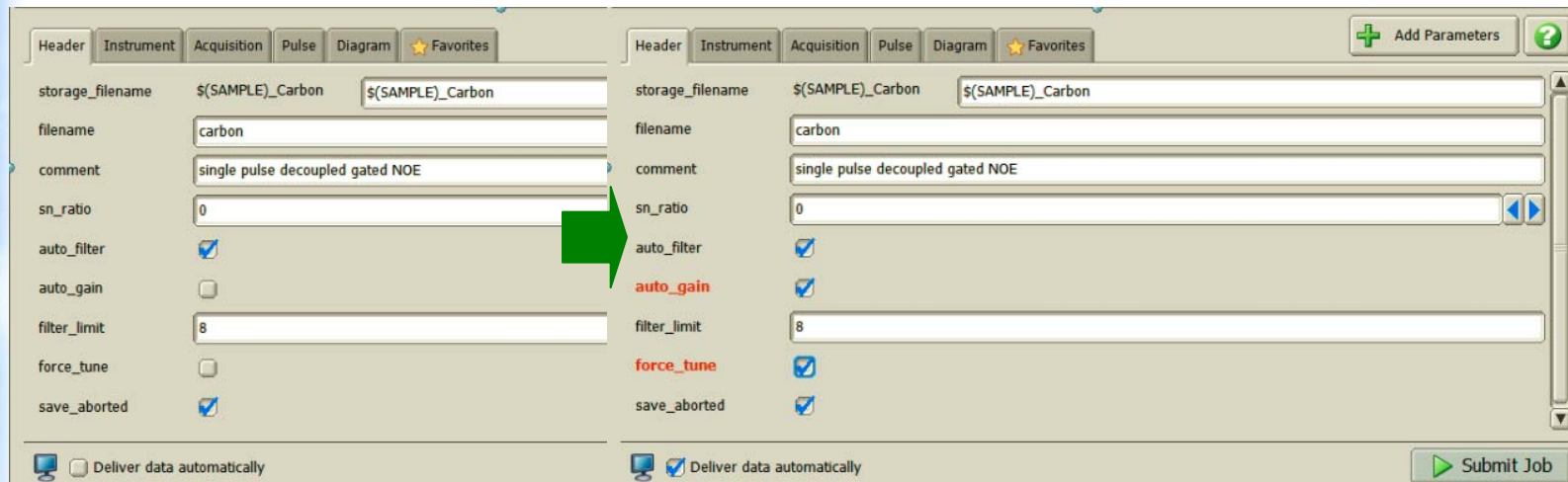
Progress through Synergy

Set up experiment (^{13}C automation)



1. If you first time do this sample, click “Force tune” and “Auto_gain”.
2. If you tick “Deliver data automatically”  , you can see the results on your display.
3. The parameters became red word when changed.

Deliver data automatically	results	Data is saved to ...
	You can see results on your display.	Data Servers (spectrometer) and your workstation
	You can't see results on your display.	Data Servers (spectrometer) only




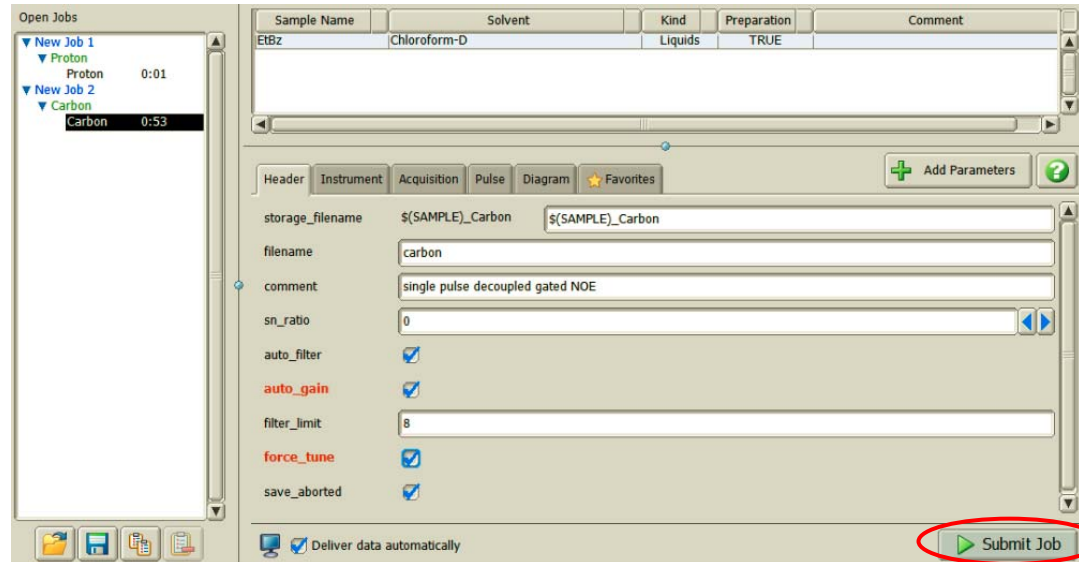
The screenshot displays two side-by-side views of the experiment setup interface. The left view shows the 'auto_gain' parameter as a standard checkbox. The right view shows 'auto_gain' and 'force_tune' in red text, indicating they have been modified. A green arrow points from the 'auto_gain' parameter in the left view to the 'auto_gain' parameter in the right view. The interface includes tabs for Header, Instrument, Acquisition, Pulse, Diagram, and Favorites, and a 'Submit Job' button at the bottom right.

Progress through Synergy

Set up experiment (^{13}C automation)



1. Click  The experiments are started.



Sample Name	Solvent	Kind	Preparation	Comment
EtBz	Chloroform-D	Liquids	TRUE	

Header Instrument Acquisition Pulse Diagram Favorites

storage_filename \$(SAMPLE)_Carbon \$(SAMPLE)_Carbon

filename carbon

comment single pulse decoupled gated NOE

sn_ratio 0

auto_filter

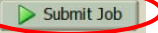
auto_gain

filter_limit 8

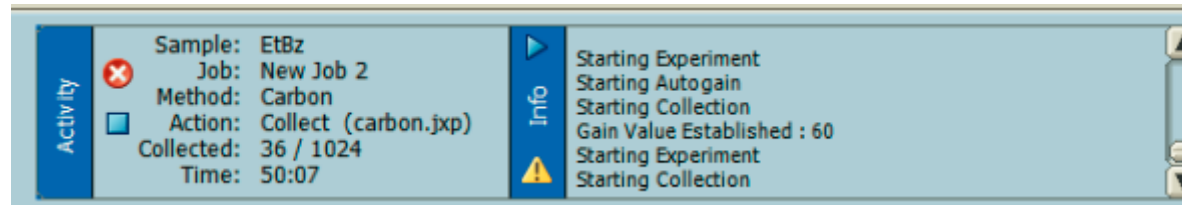
force_tune


save_aborted


Deliver data automatically



2. Wait to collect data.



Activity  Sample: EtBz
Job: New Job 2
Method: Carbon
Action: Collect (carbon.jxp)
Collected: 36 / 1024
Time: 50:07

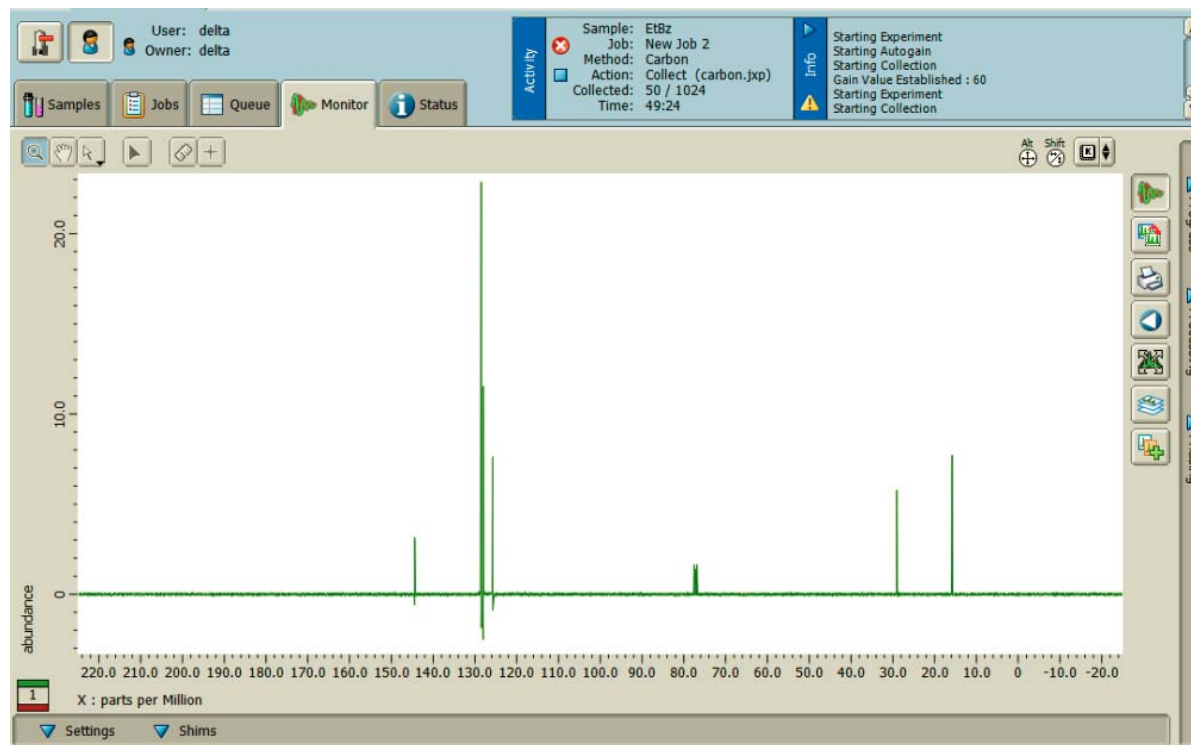
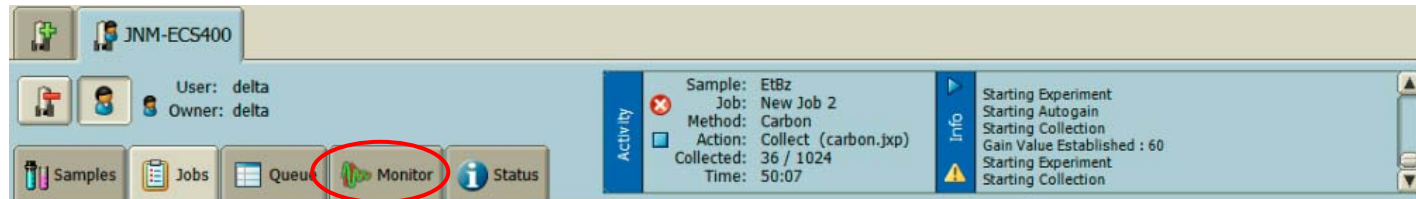
Info  Starting Experiment
Starting Autogain
Starting Collection
Gain Value Established : 60
Starting Experiment
Starting Collection

Progress through Synergy

Set up experiment (^{13}C automation)



1. Click , and observed the real time spectrometer.

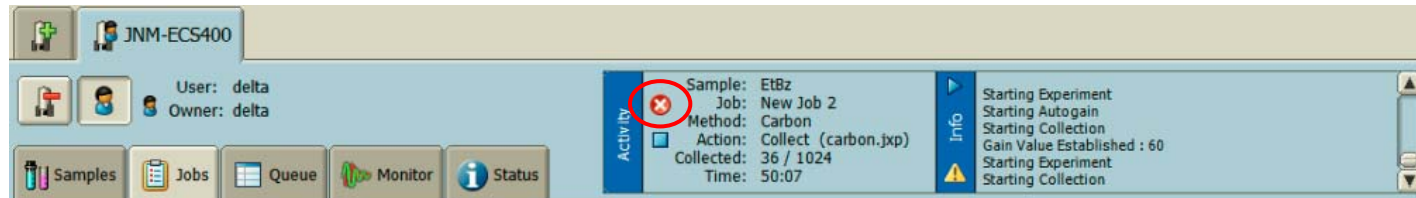


Progress through Synergy

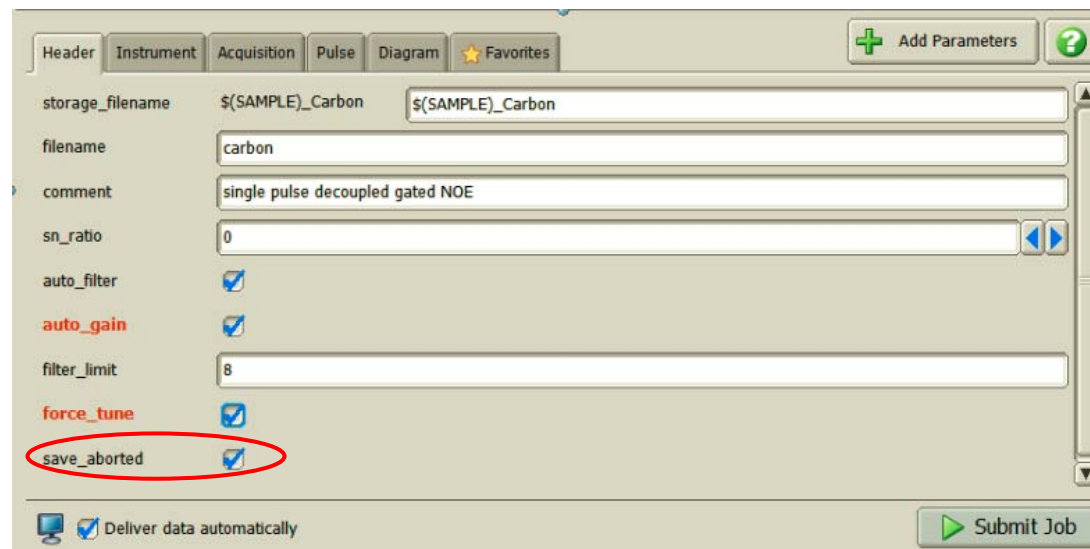
Set up experiment (^{13}C automation)



1. If you want to stop experiment, Click  .



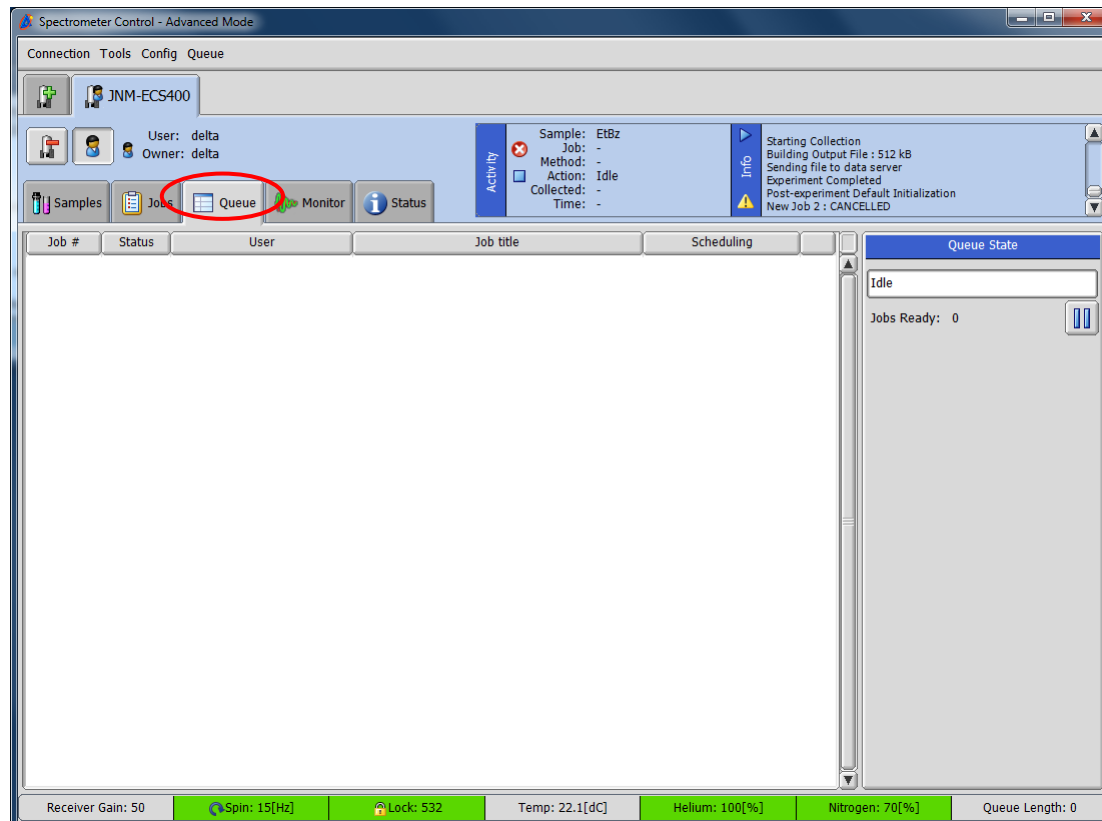
2. If tick save_aborted (default parameters), stop experiment, the data file will be saved in console



Finish experiment





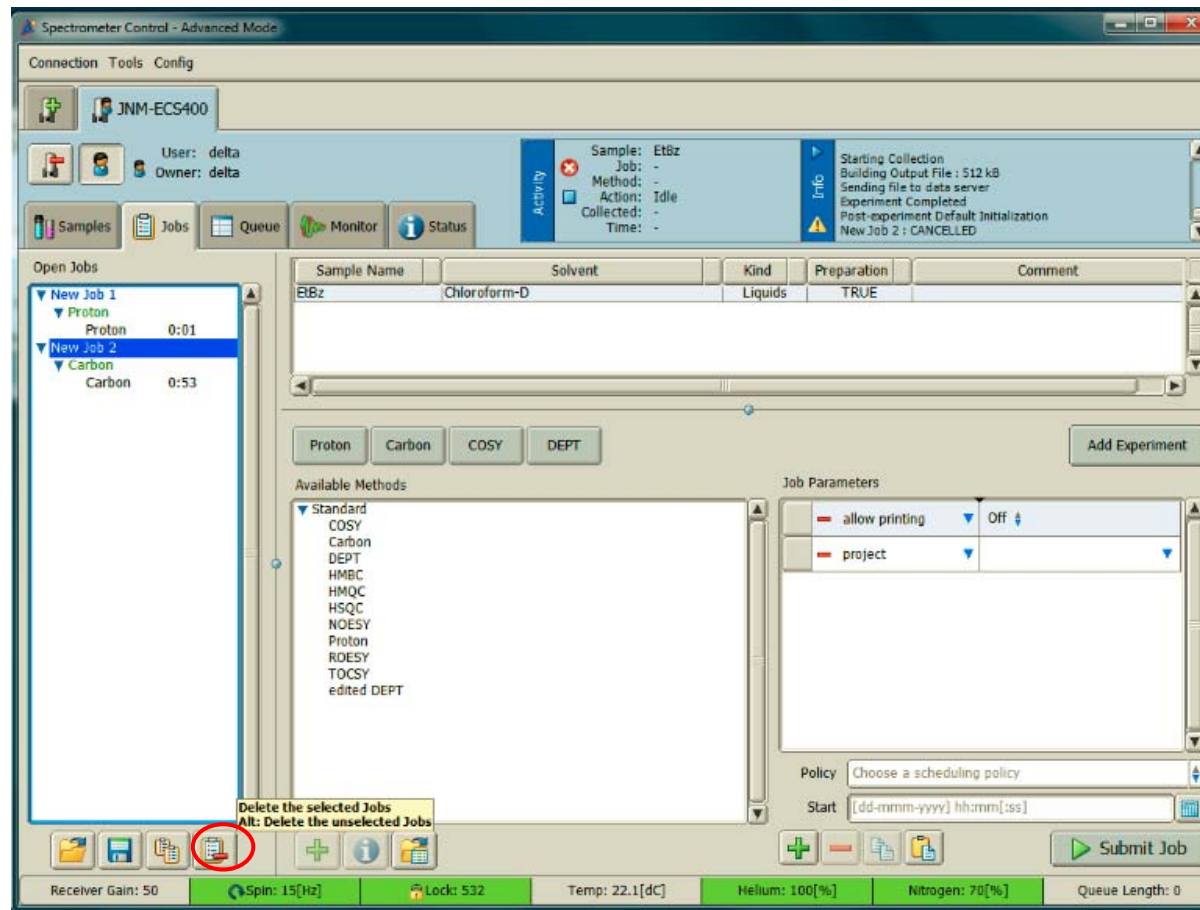
1. When finish your experiment, click  and check the Queue tab which is empty.



Finish experiment

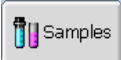


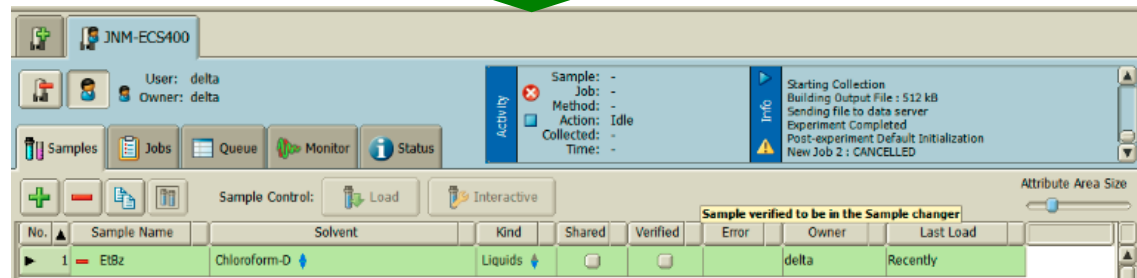
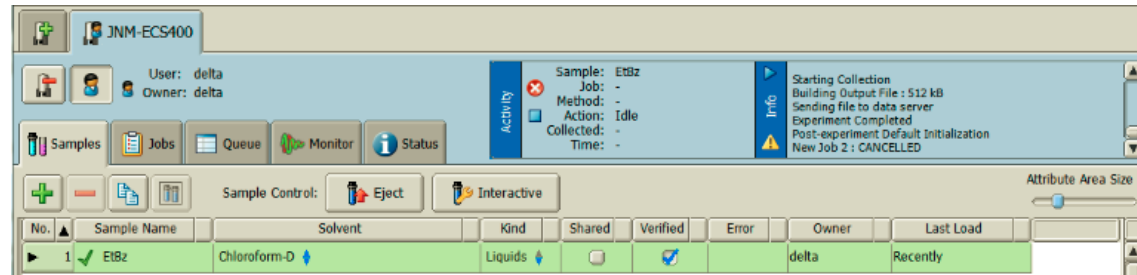
1. Click  and check the Job tab which is empty.
2. If not empty, click the Job and click  to delete Job.




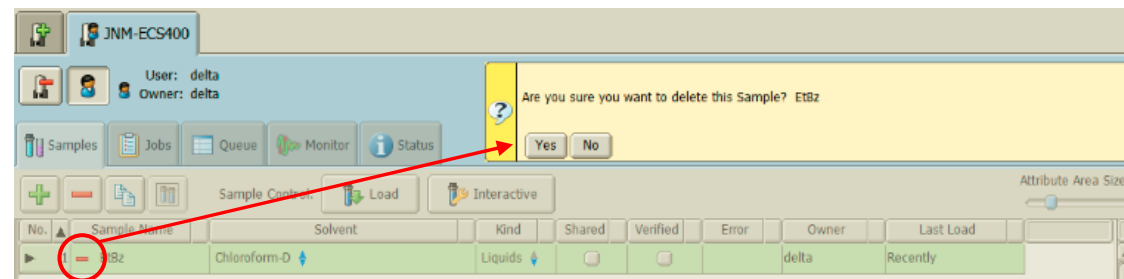
Finish experiment



1. Click  Samples and click verified.
2. Sample will eject



3. Click  to delete sample for next user to use software.

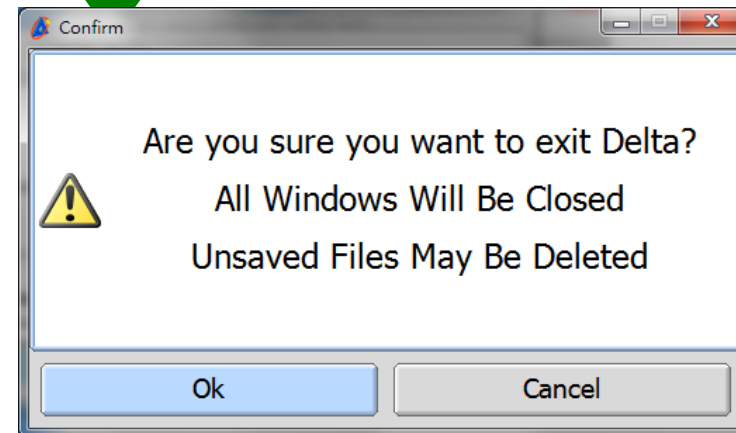
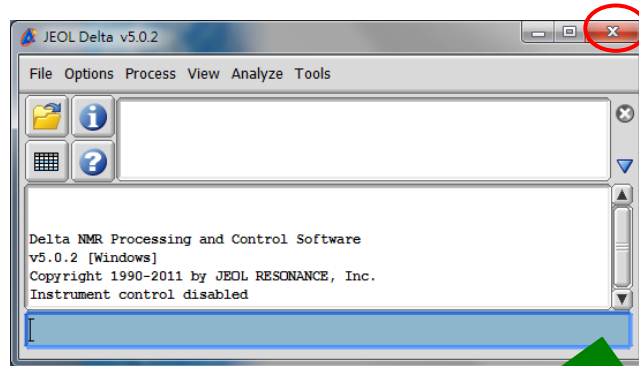


Progress through Synergy

Finish experiment



1. Check all your file will be save and click  to close delta software.



Progress through Synergy