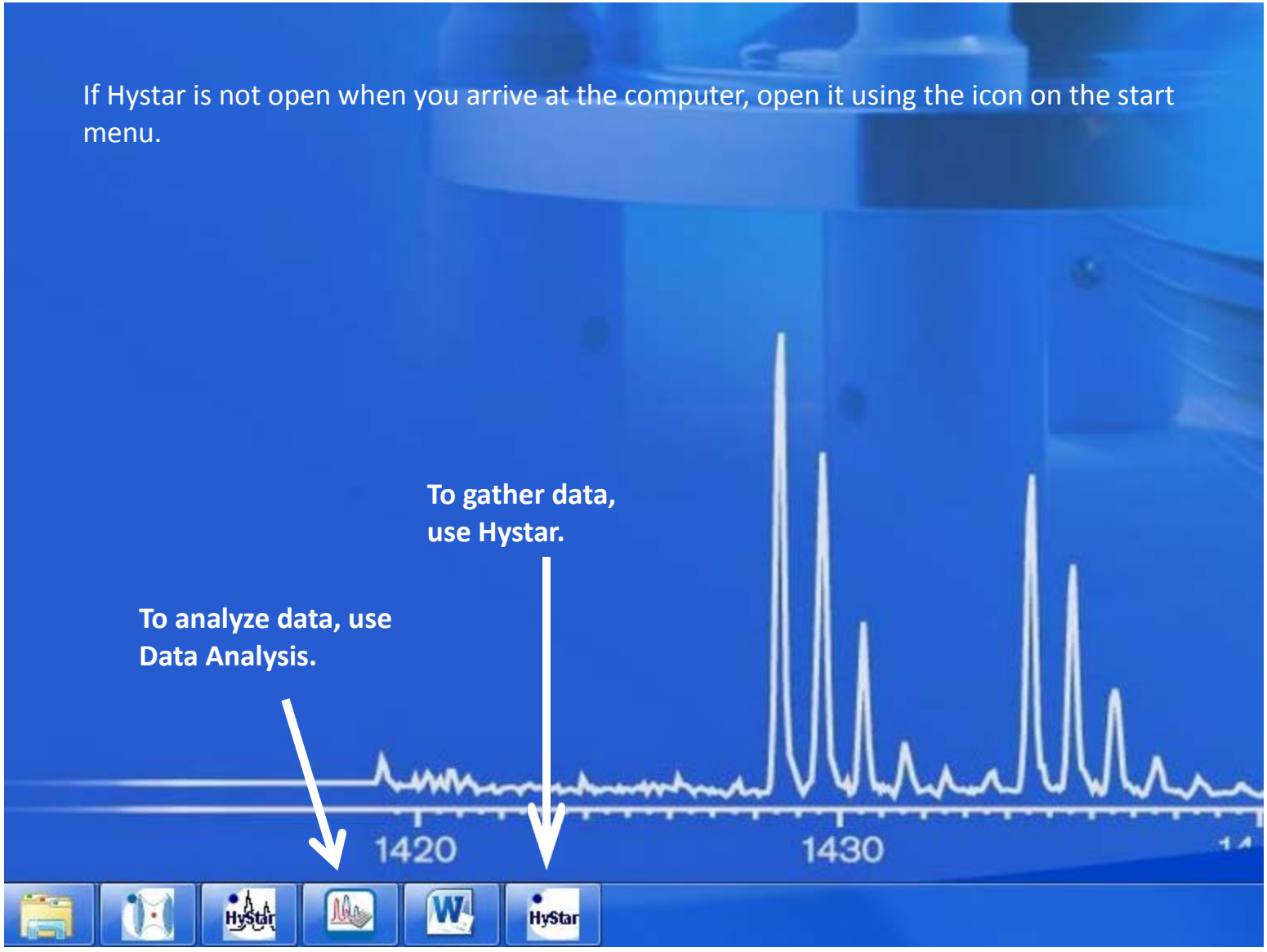
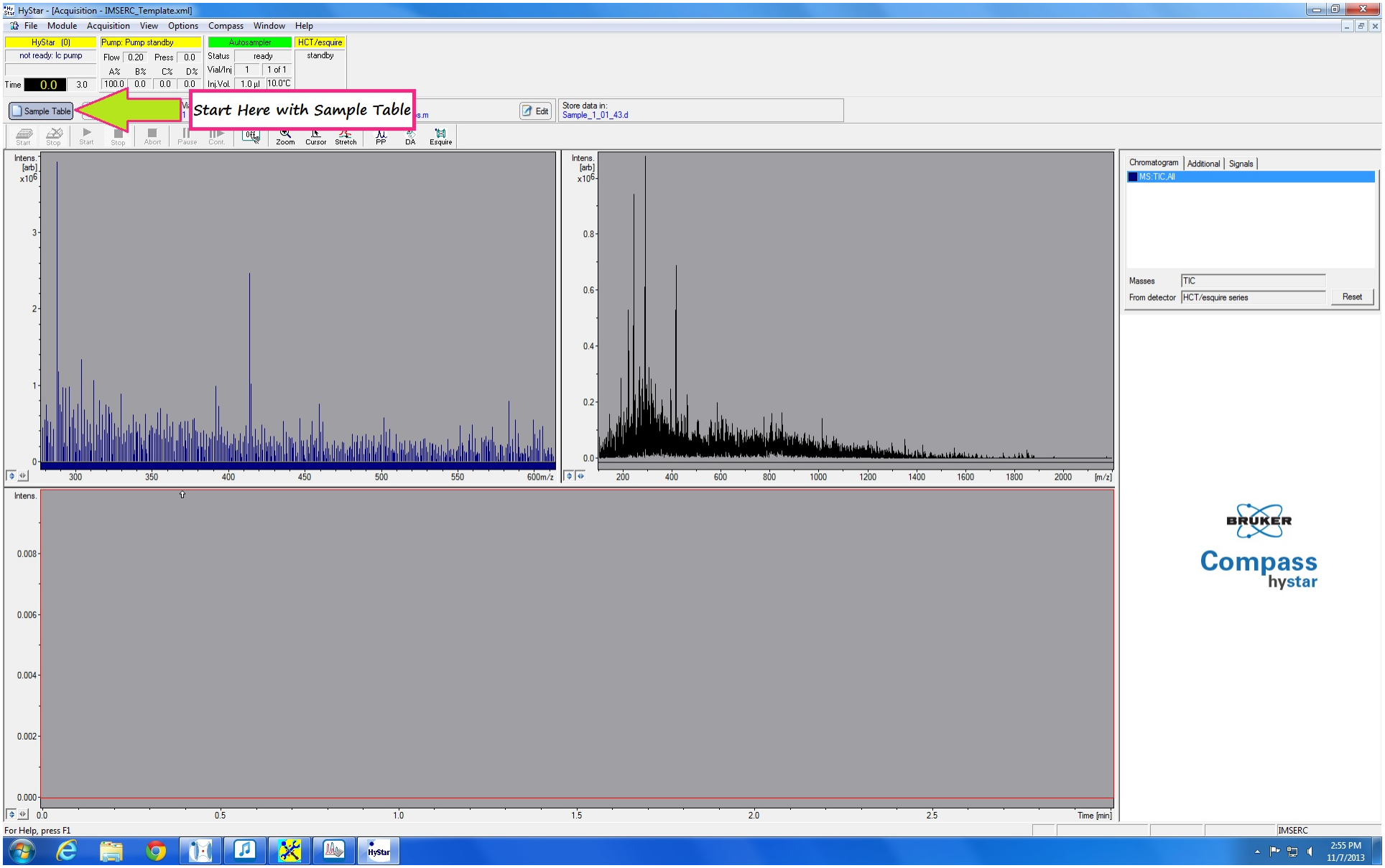
Bruker Amazon X

ESI-Ion Trap Mass Spectrometer

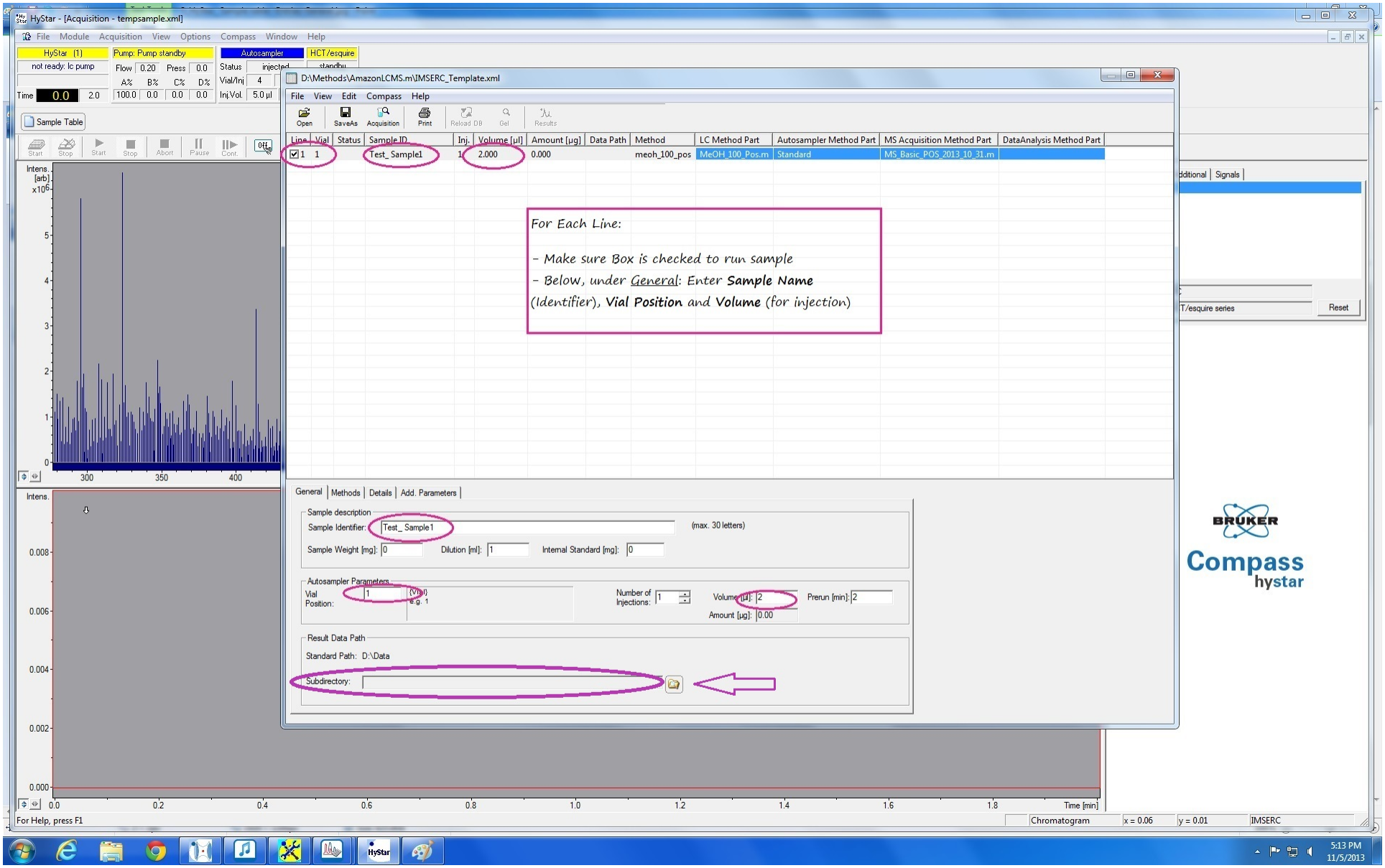
Direct Injection

If Hystar is not open when you arrive at the computer, open it using the icon on the start menu.

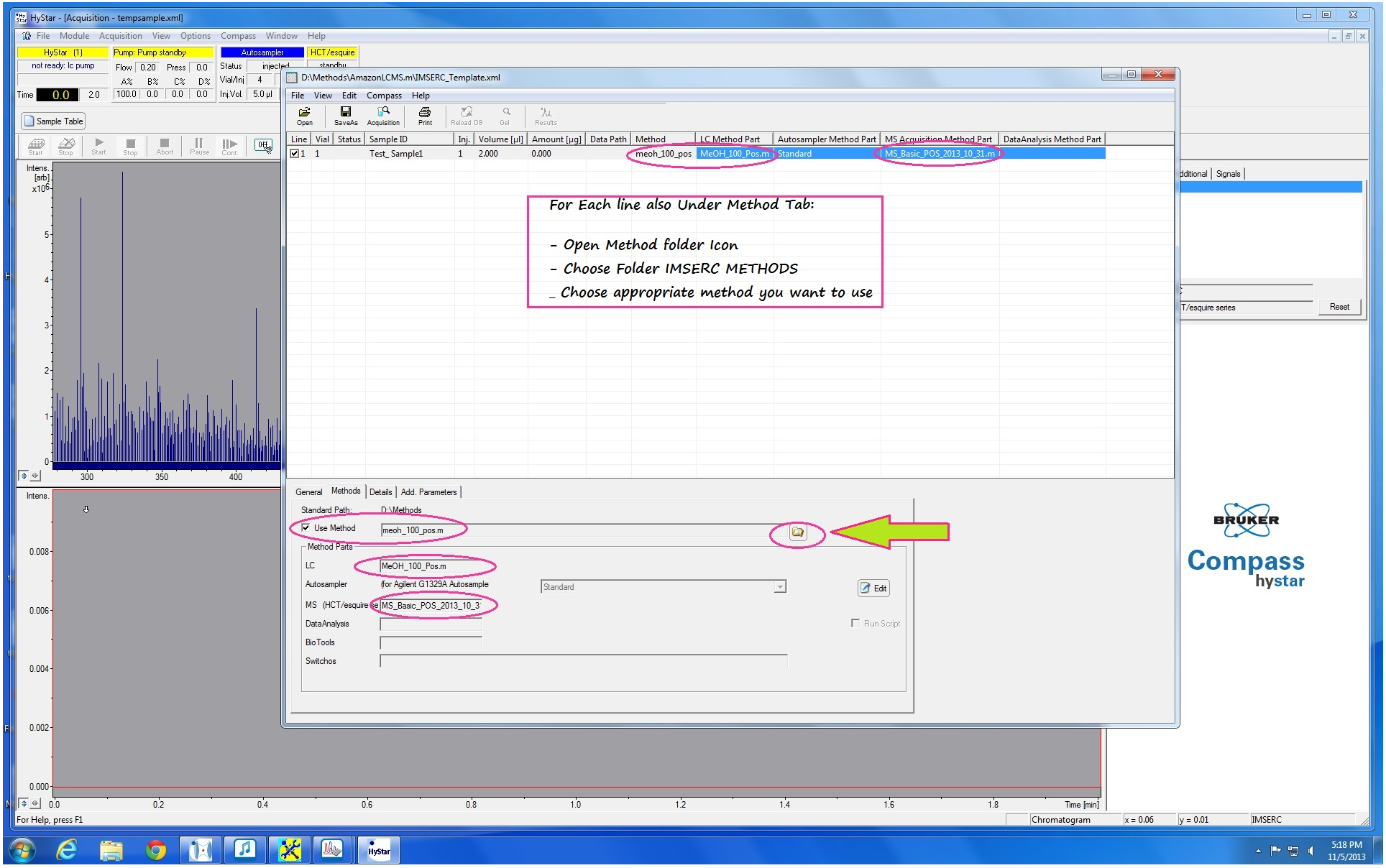




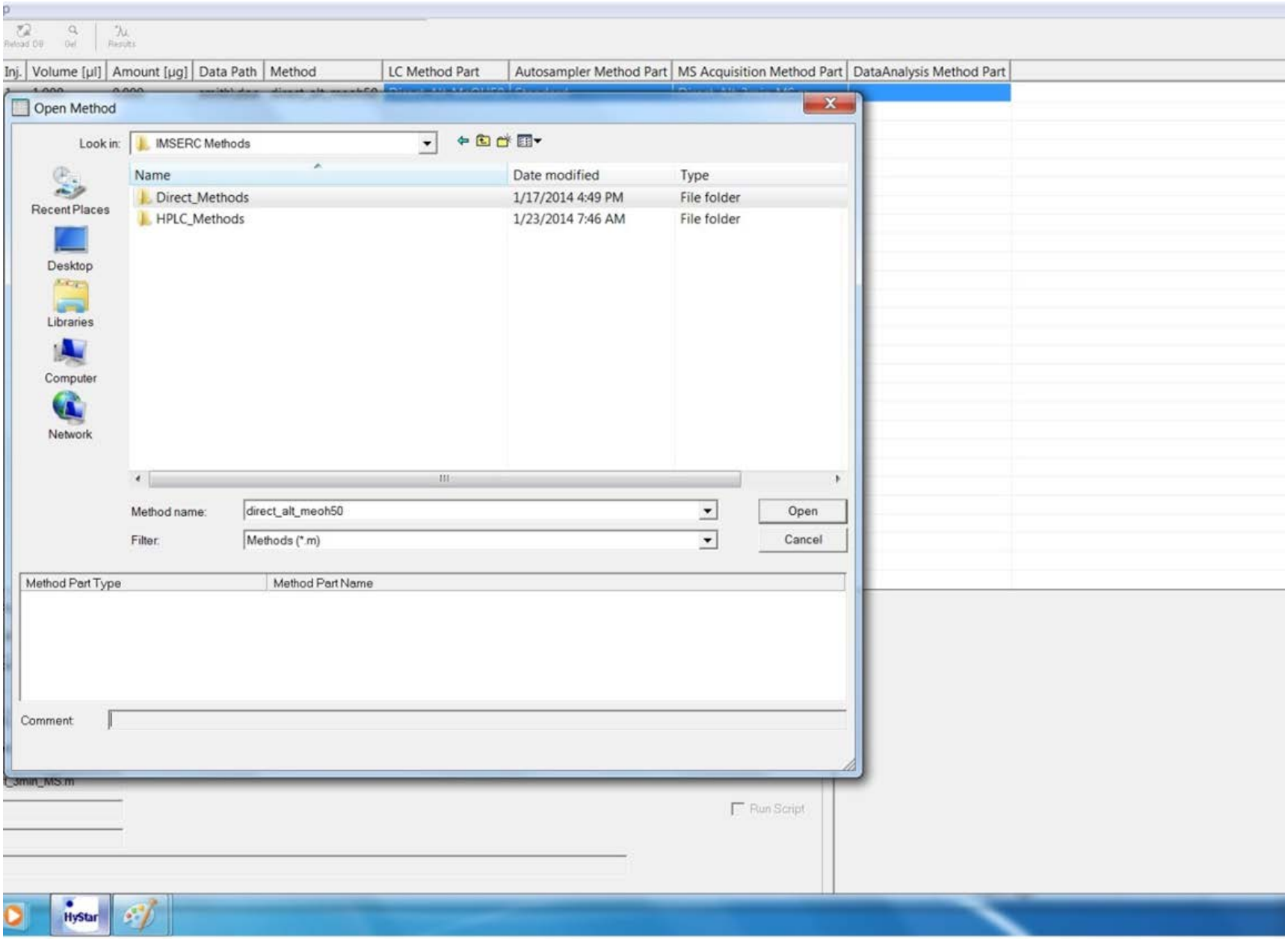
Open your sample table by selecting the sample table icon and navigating to your sample table. (If this is the first time you are using the instrument, go to your PI group folder and open the IMSERC Sample Table Template.)



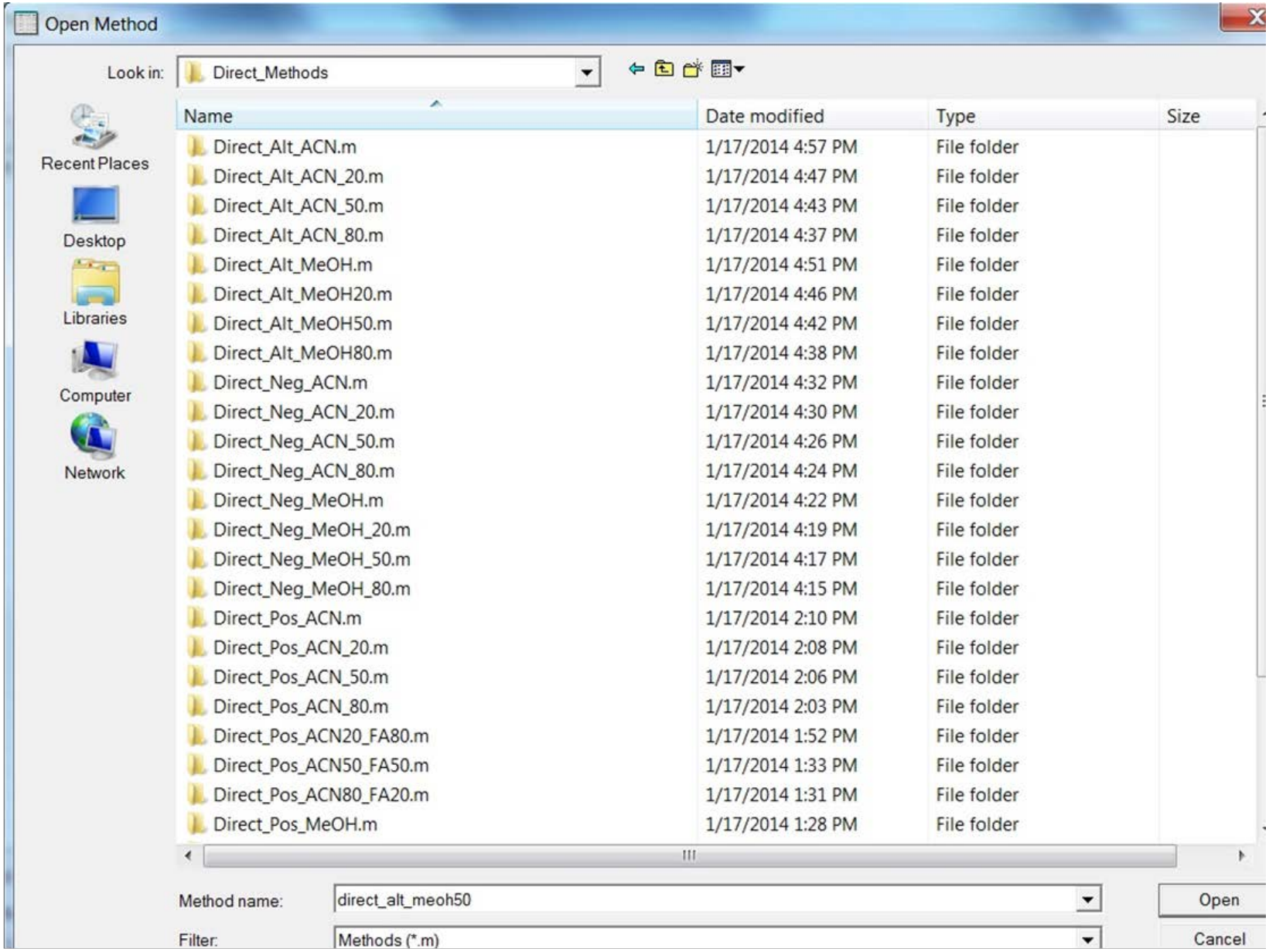
Under the “General” tab you can name your sample, change the vial position, and change the volume of the sample that you would like to inject. You also must make sure that your data is being saved to the appropriate folder, which can be changed in the “Subdirectory” field.



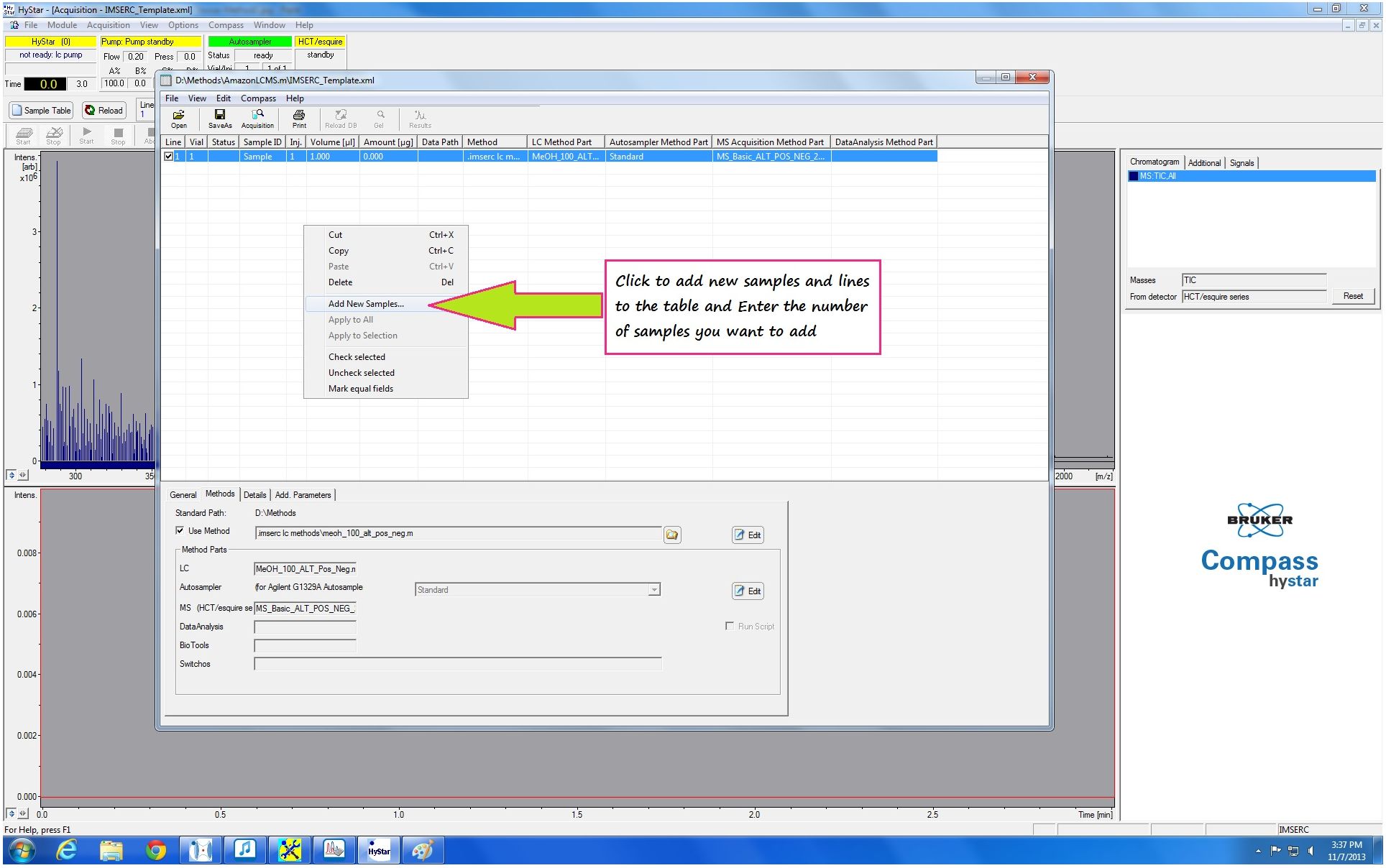
Under the “Methods” tab it is possible to change the method that your sample will be run using by navigating through the IMSERC METHODS folder and selecting the appropriate method.



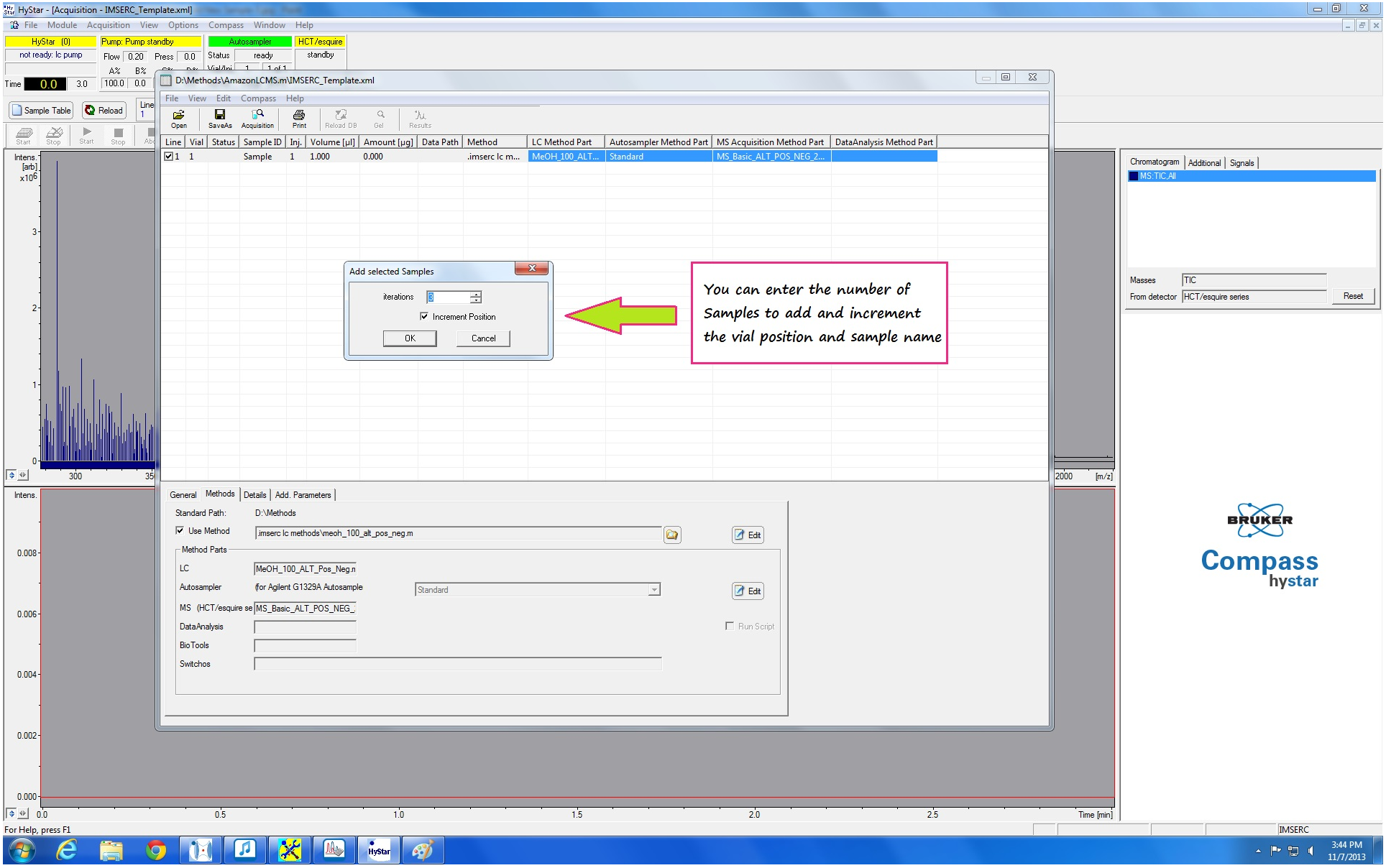
Choose the Direct Method Folder



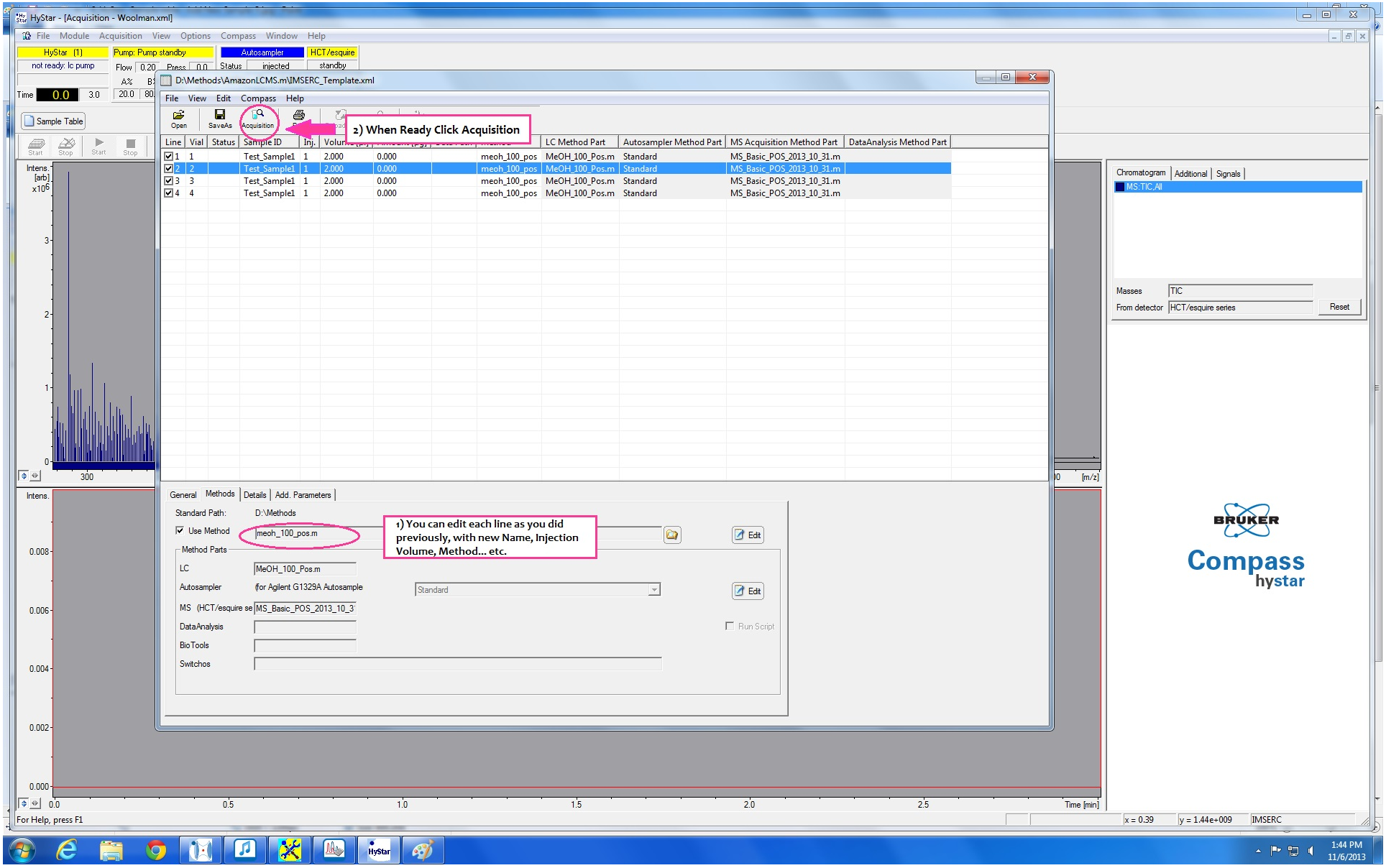
Choose the direct method that you would like to use for your sample.



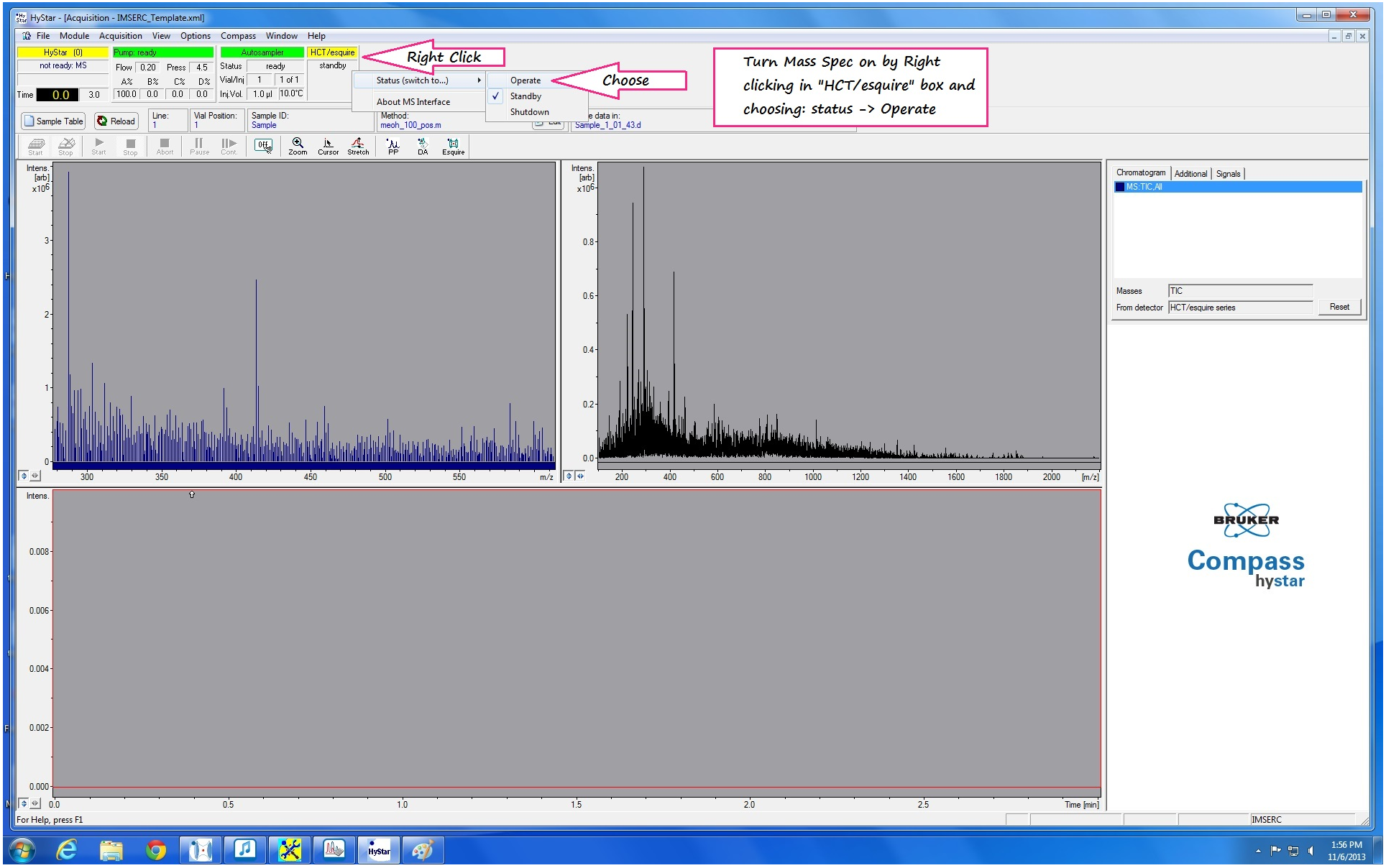
To add new samples, right click anywhere in the sample table and select “Add New Samples”



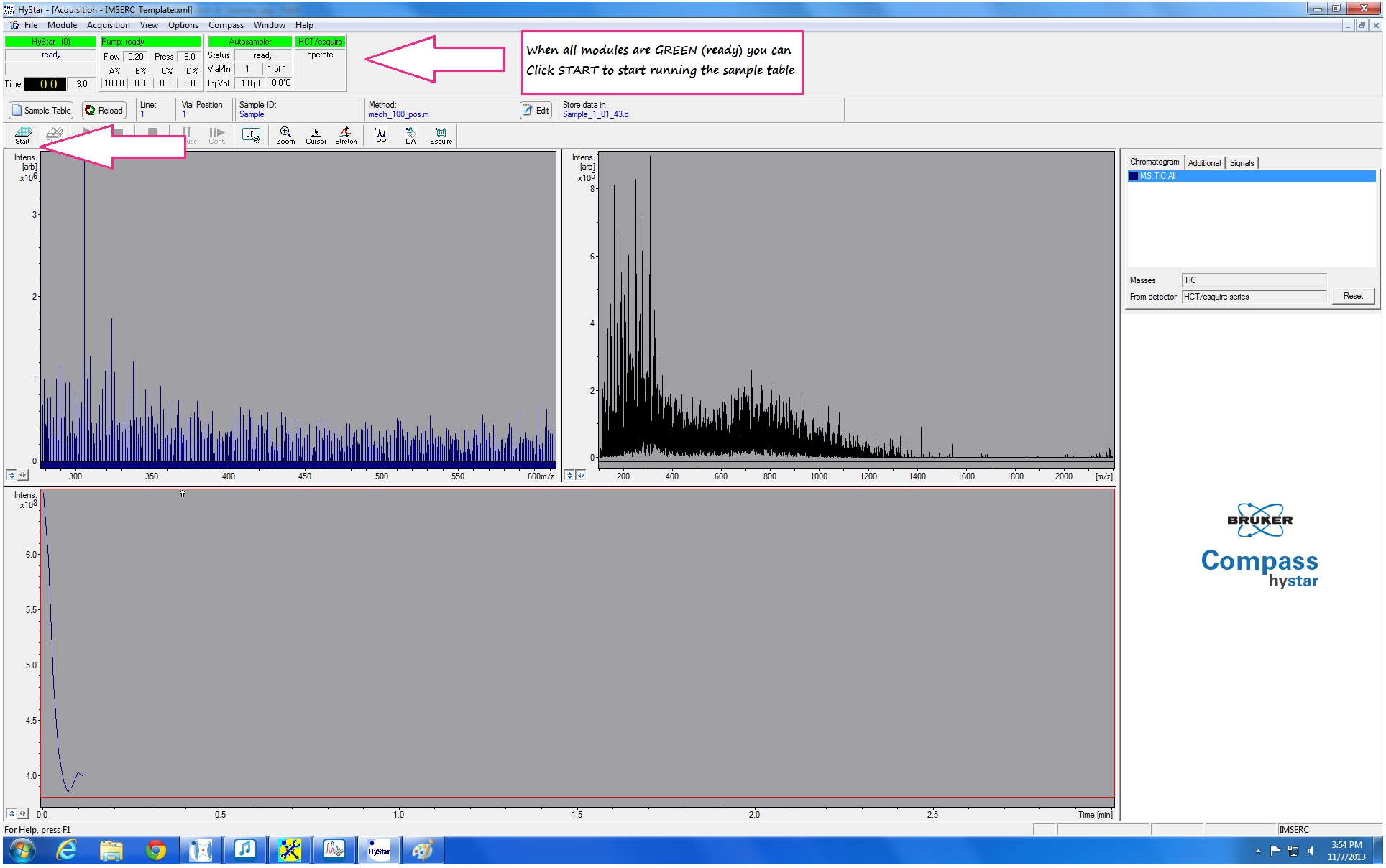
Enter the number of samples you would like to add and check the “Increment Position” box if you would like the program to place the samples in sequential vial positions



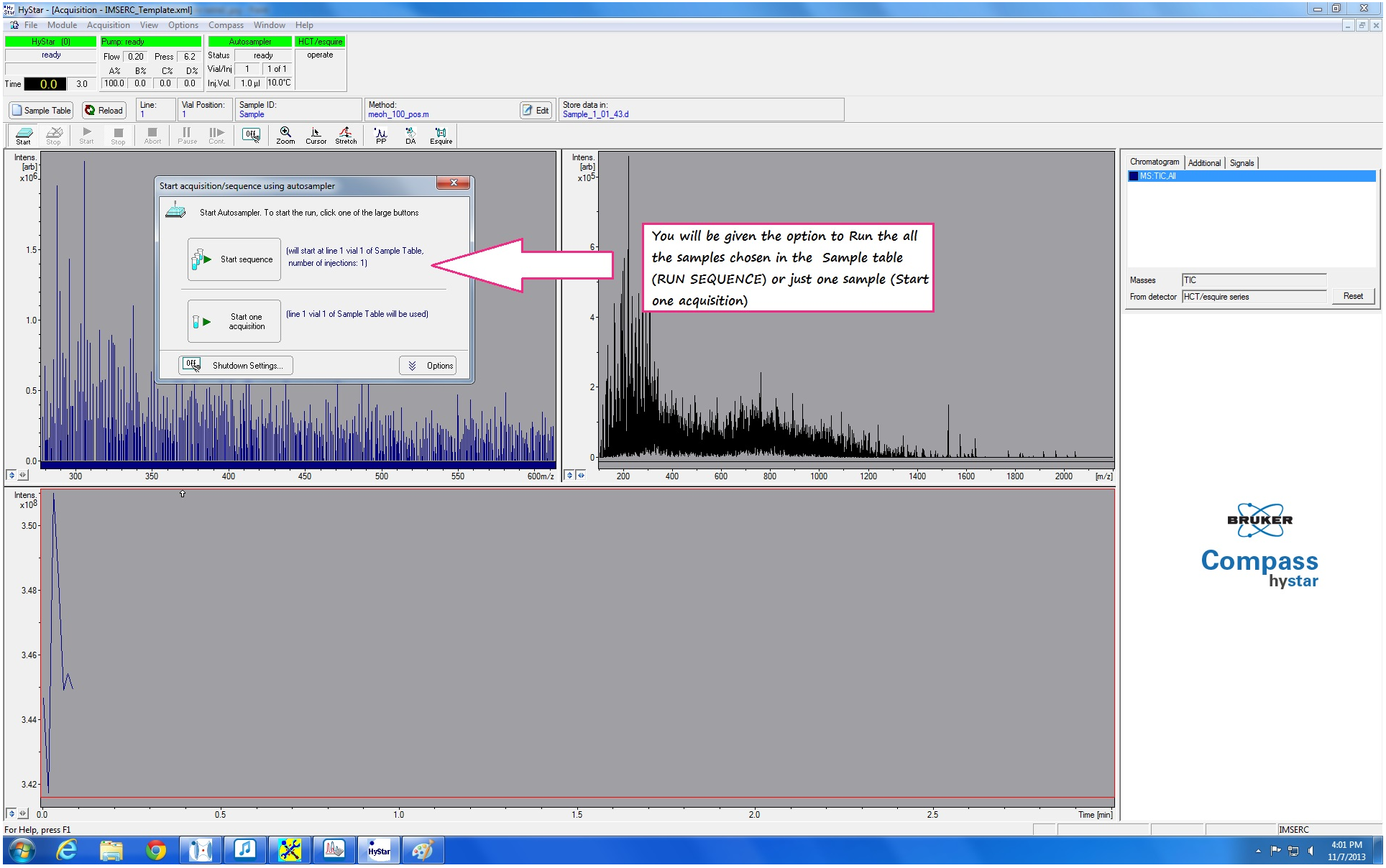
Once the samples are all completely ready (names, vial positions, methods, etc.) highlight the top sample you would like to run and click the “Acquisition” button above. If you have a sample below the top one highlighted, it will run through the samples after the highlighted one without running the ones above.



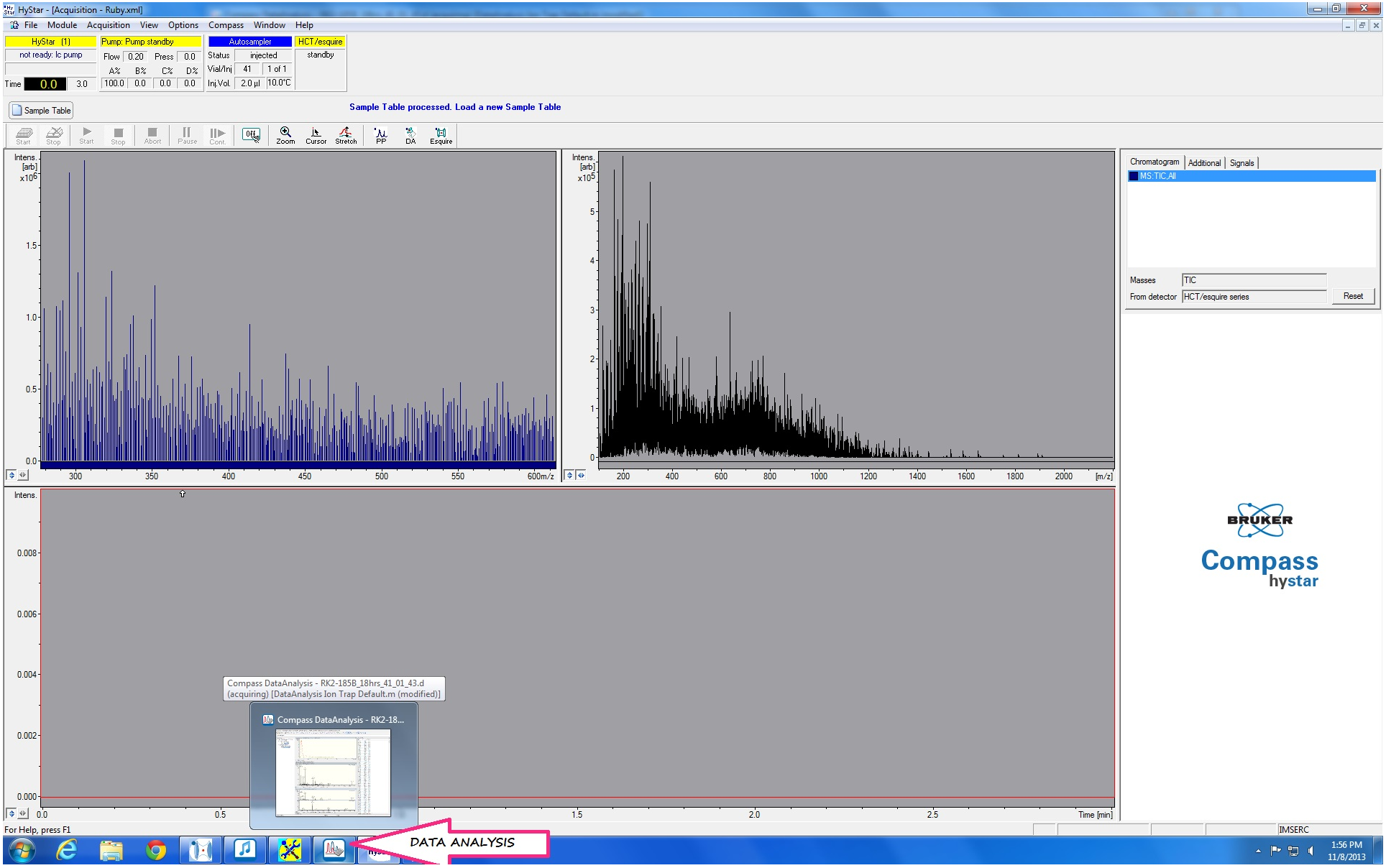
To turn on the mass spec, right click on the “HCT/esquire” box and select “Operate” under the “Status” menu. (If the Pump ready light stays yellow, you may have to right click that also and turn the pump on.)



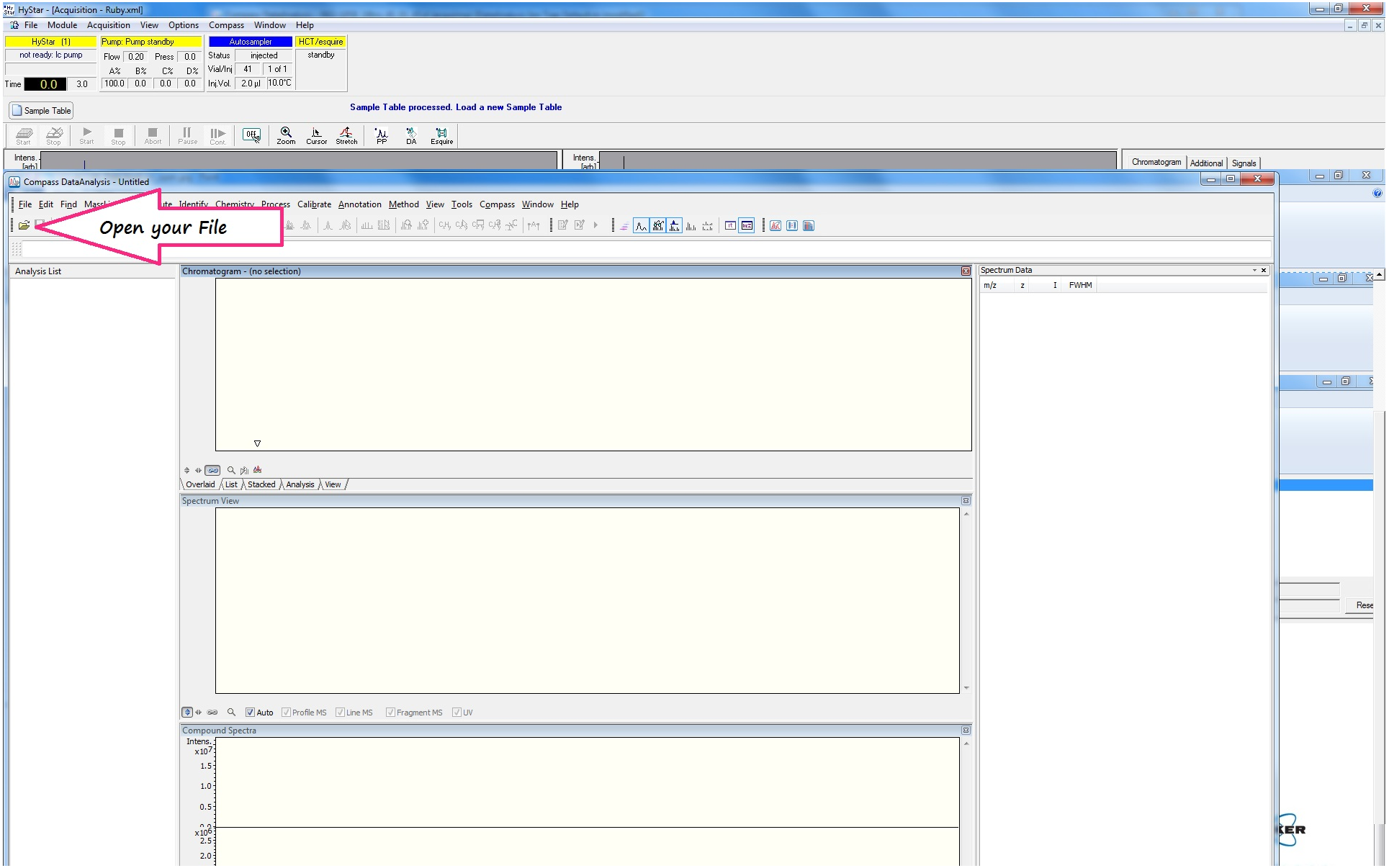
Once the instrument is ready and all of the boxes above are green, the Start icon will turn light blue in color. Click “Start” under the “Sample Table” button

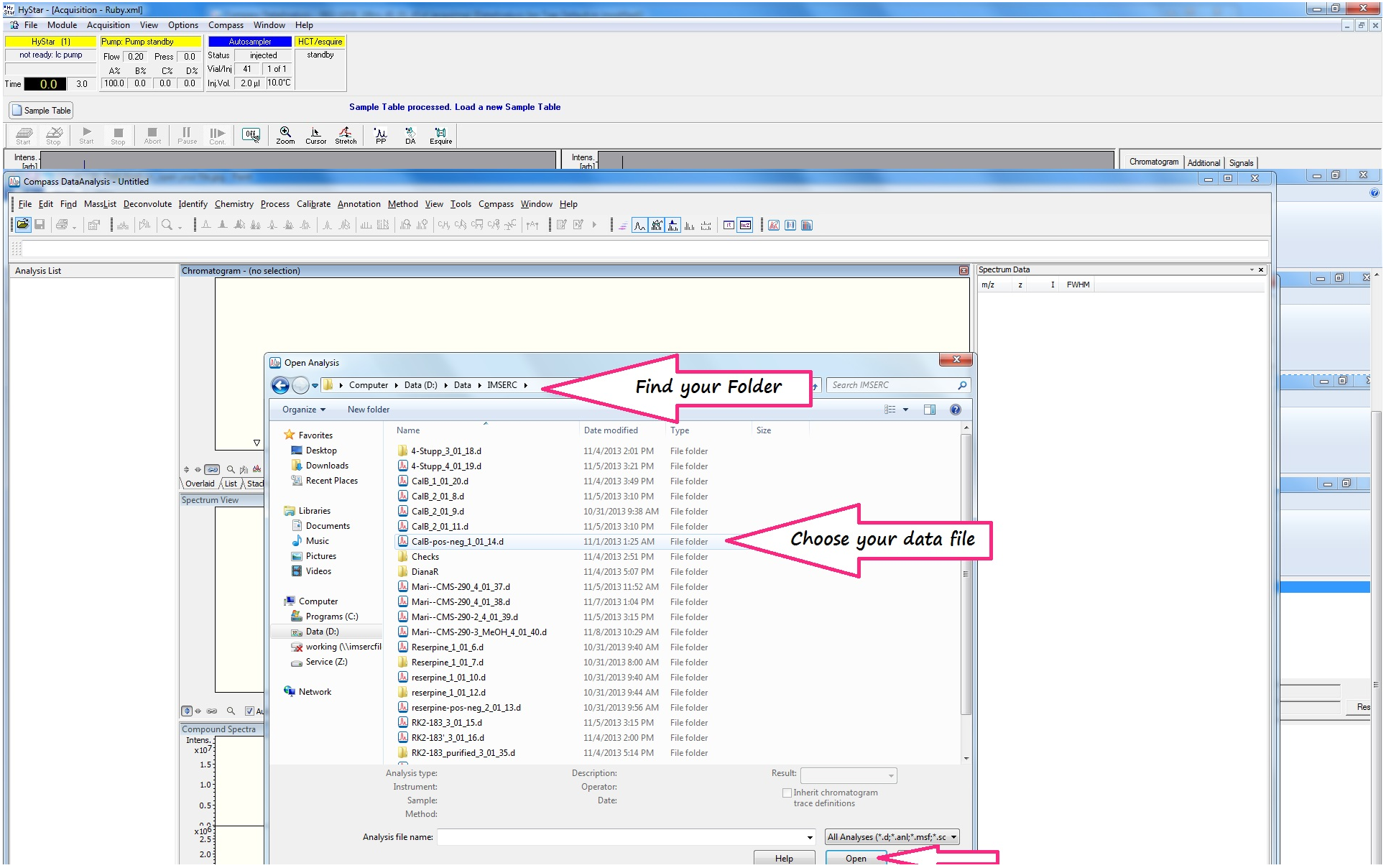


If you only want to run one sample, select “Start One Acquisition.” For multiple samples, select “Start Sequence”

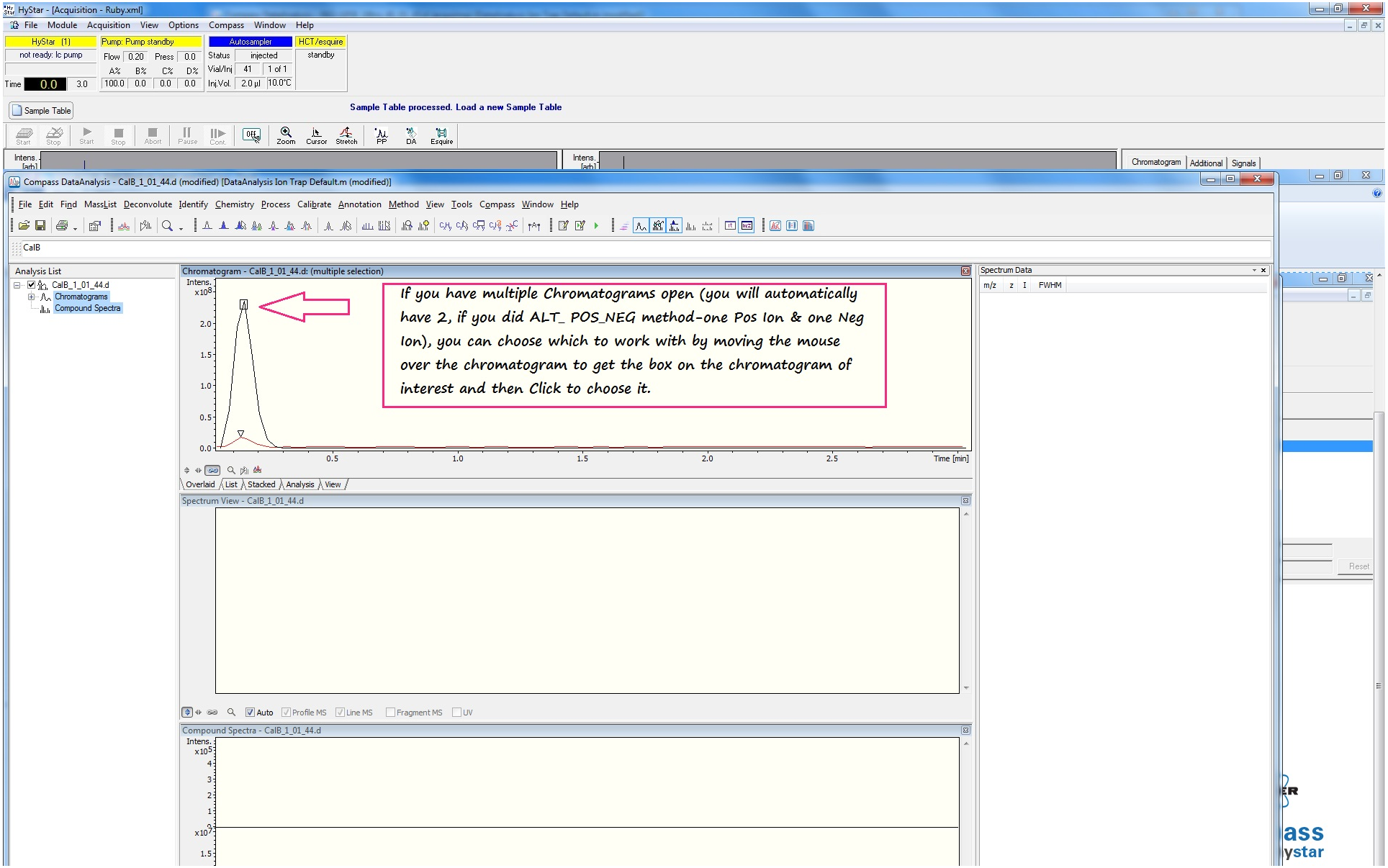


To analyze your data, open “Data Analysis” below (The icon with the two spectra on a white field)

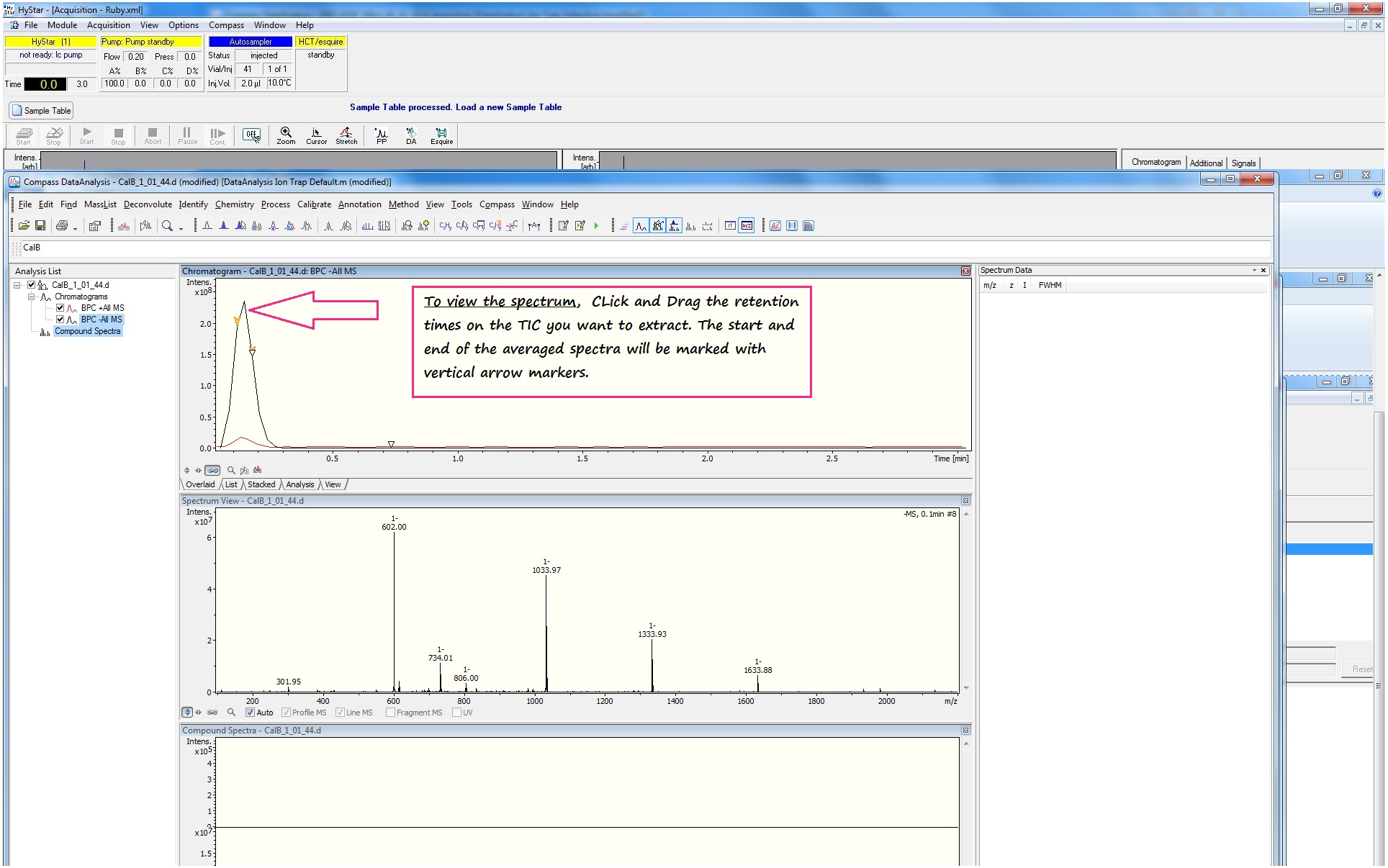

HyStar - [Acquisition - Ruby.xml]
File Module Acquisition View Options Compass Window Help
Sample Table processed. Load a new Sample Table
Compass DataAnalysis - Untitled
File Edit Find
Identify Chemistry Process Calibrate Annotation Method View Tools Compass Window Help
Open your File
Analysis List
Chromatogram - (no selection)
Spectrum Data
m/z z I FWHM
Overlaid List Stacked Analysis View
Spectrum View
Auto Profile MS Line MS Fragment MS UV
Compound Spectra
Intens.
Chromatogram Additional Signals



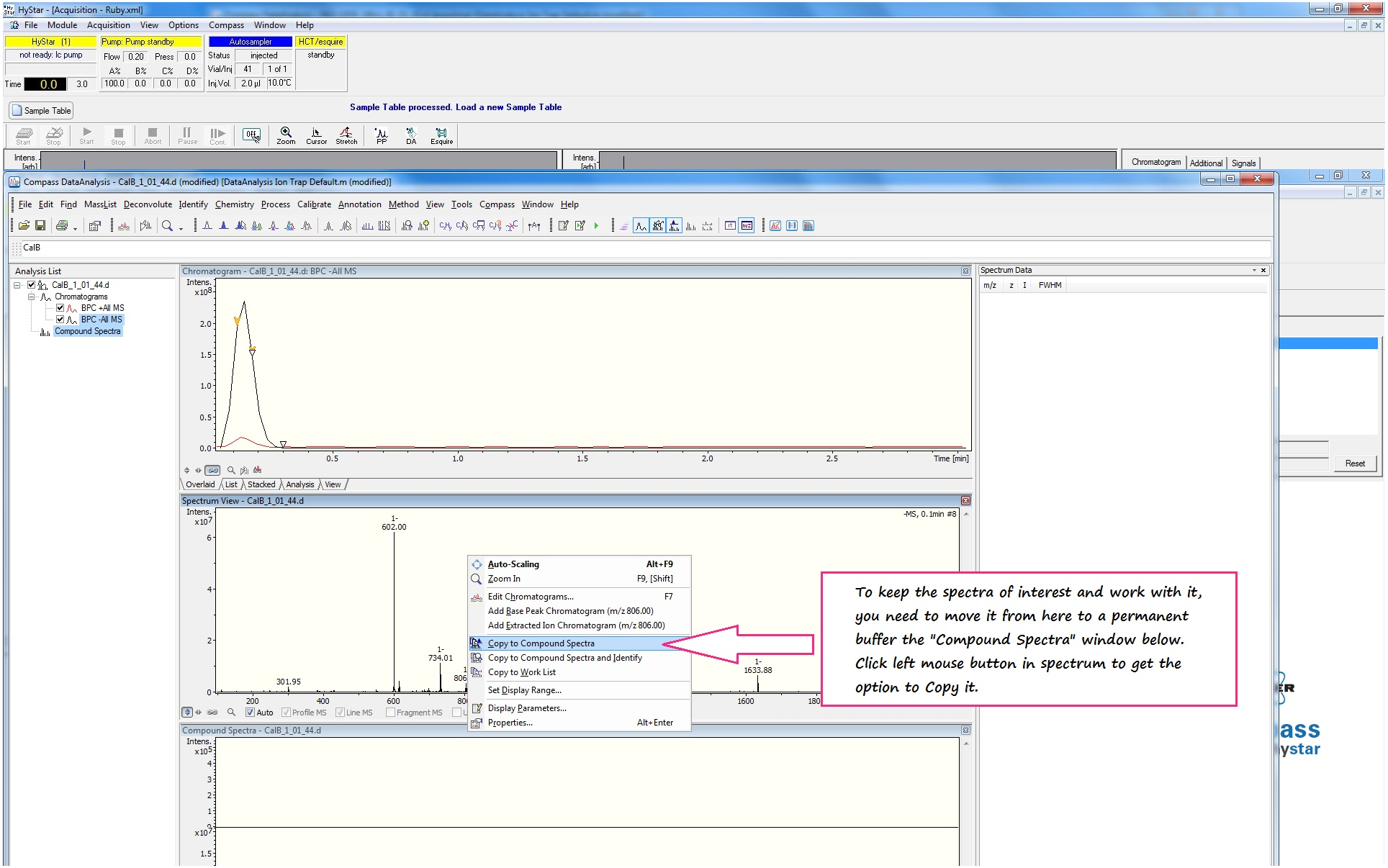
Find your group's folder and the folder you saved your samples to. Choose your sample's file.



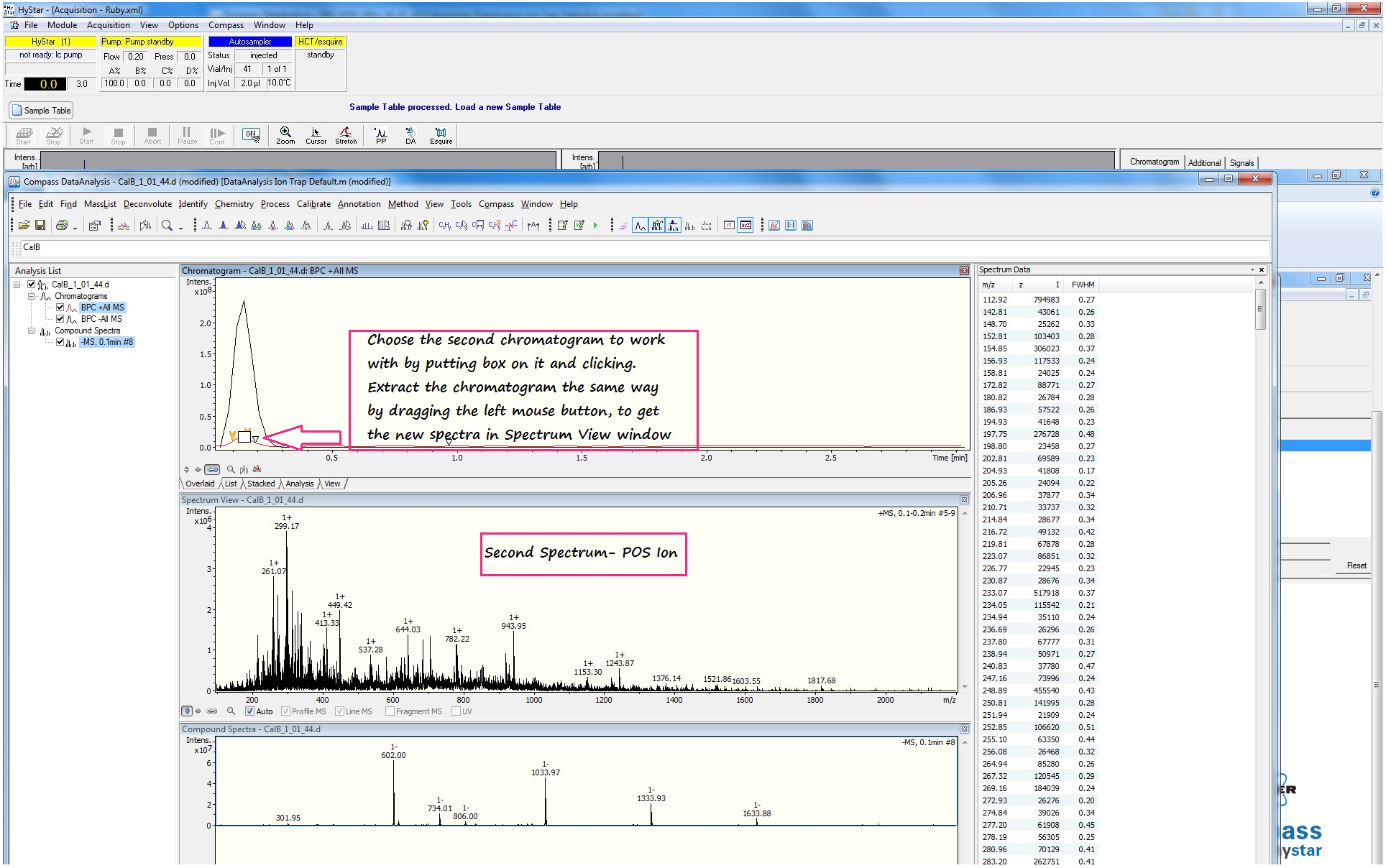
A square on a chromatogram shows which chromatogram you are working with



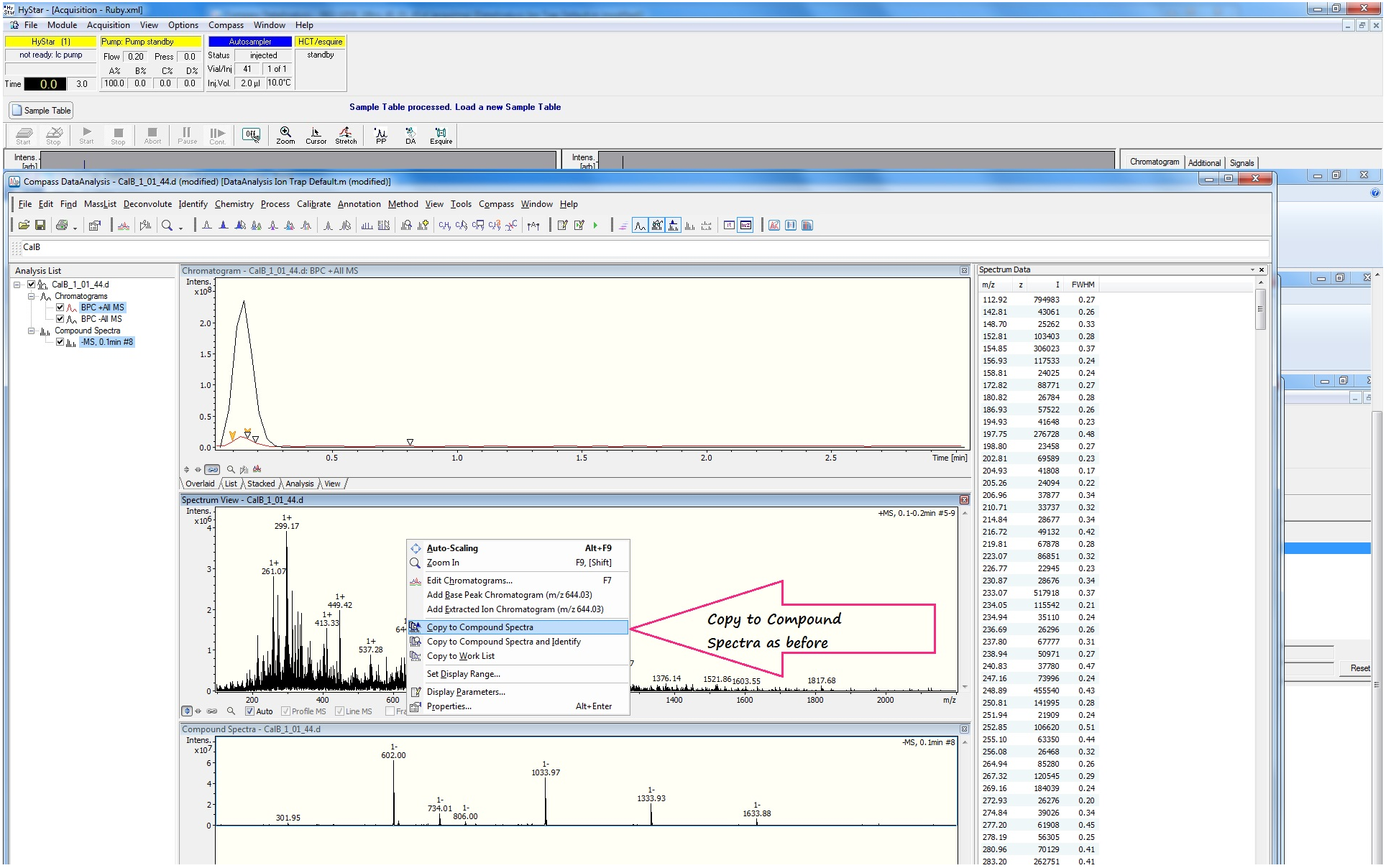
By clicking and dragging over the chromatogram you can view the averaged spectra for that range.

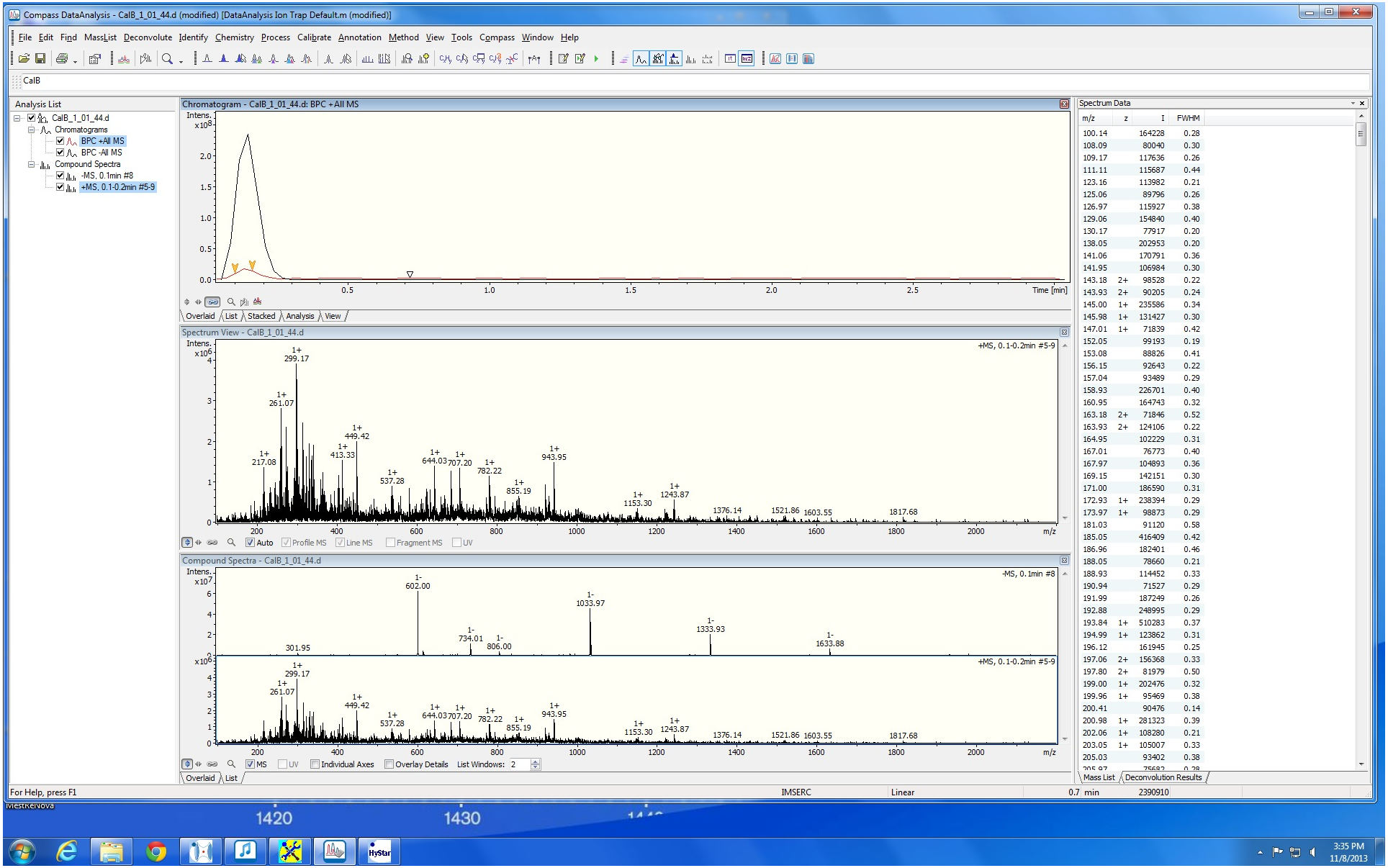


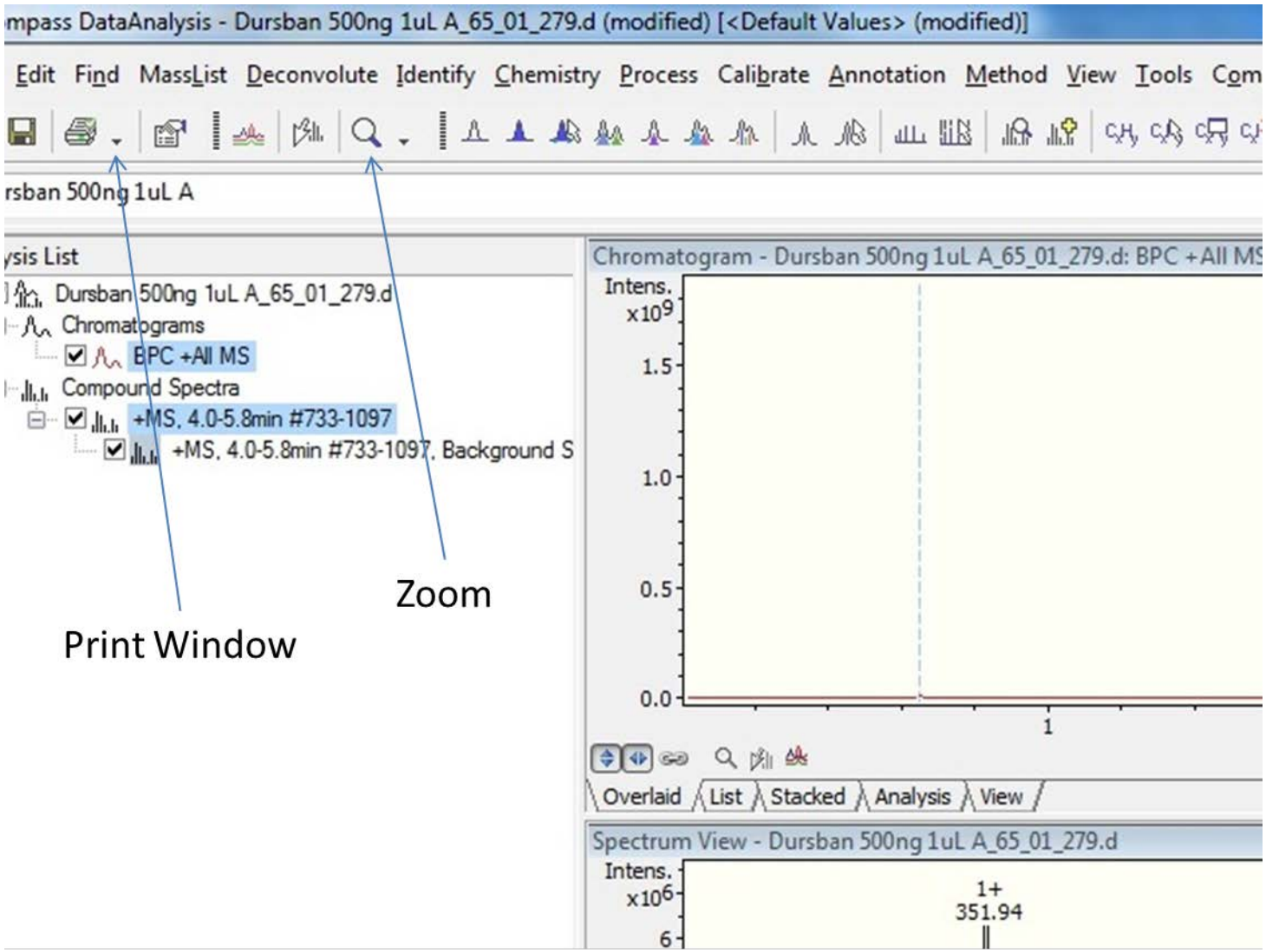
To work with this spectra you must *right* click on it, and select “Copy to Compound Spectra”



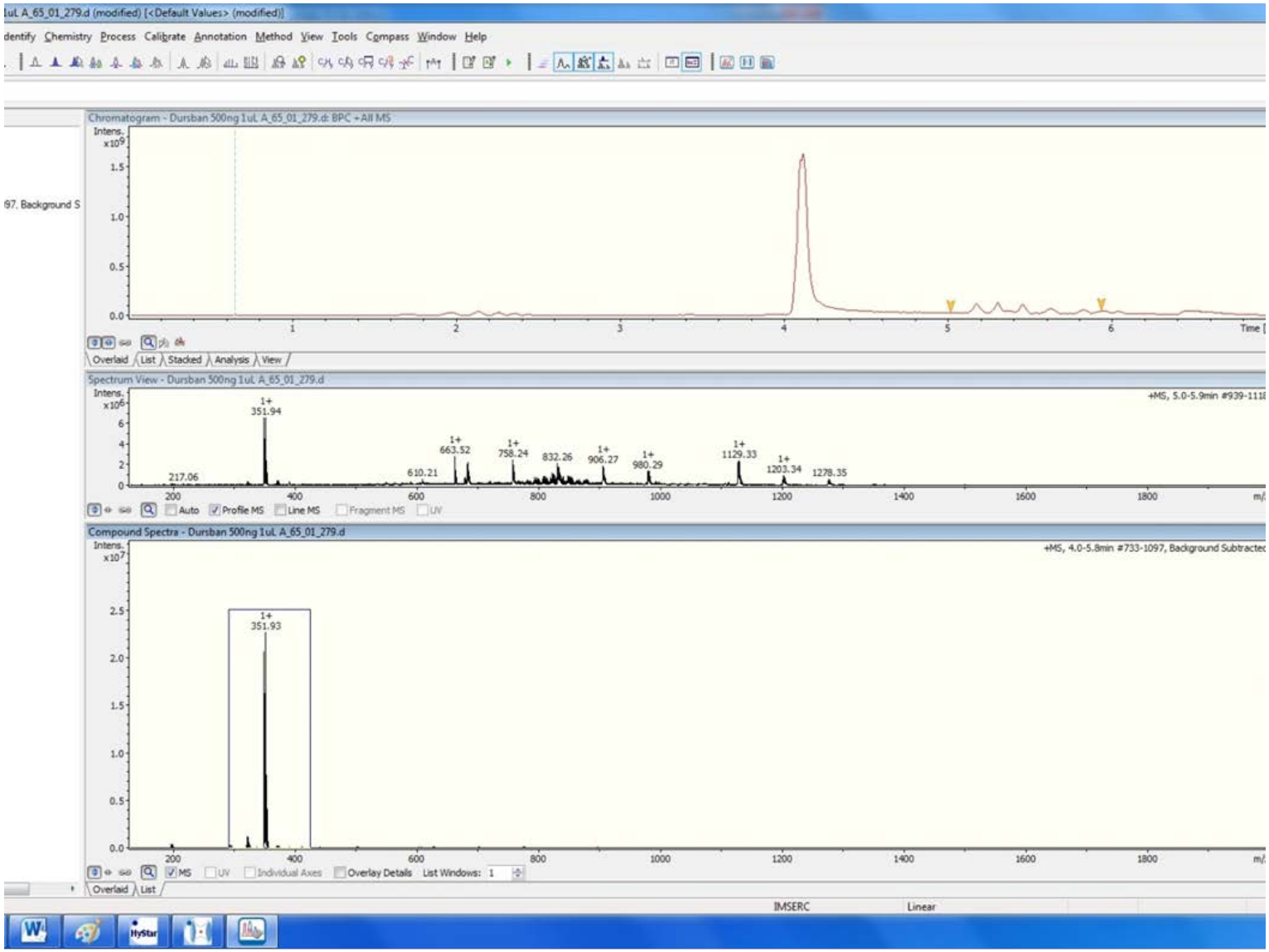
Repeat above with second chromatogram (if you ran Alt Pos/Neg)


HyStar - [Acquisition - Ruby.xml]
Sample Table processed. Load a new Sample Table
Compass DataAnalysis - CalB_1_01_44.d (modified) [DataAnalysis Ion Trap Default.m (modified)]
Analysis List
CalB_1_01_44.d
Chromatograms
BPC +All MS
BPC -All MS
Compound Spectra
-MS, 0.1min #8
Chromatogram - CalB_1_01_44.d: BPC +All MS
Time [min]
Spectrum View - CalB_1_01_44.d
+MS, 0.1-0.2min #5-9
Auto-Scaling Alt+F9
Zoom In F9, [Shift]
Edit Chromatograms... F7
Add Base Peak Chromatogram (m/z 644.03)
Add Extracted Ion Chromatogram (m/z 644.03)
Copy to Compound Spectra
Copy to Compound Spectra and Identify
Copy to Work List
Set Display Range...
Display Parameters...
Properties... Alt+Enter
Copy to Compound Spectra as before
Compound Spectra - CalB_1_01_44.d
-MS, 0.1min #8
Spectrum Data
m/z z I FWHM

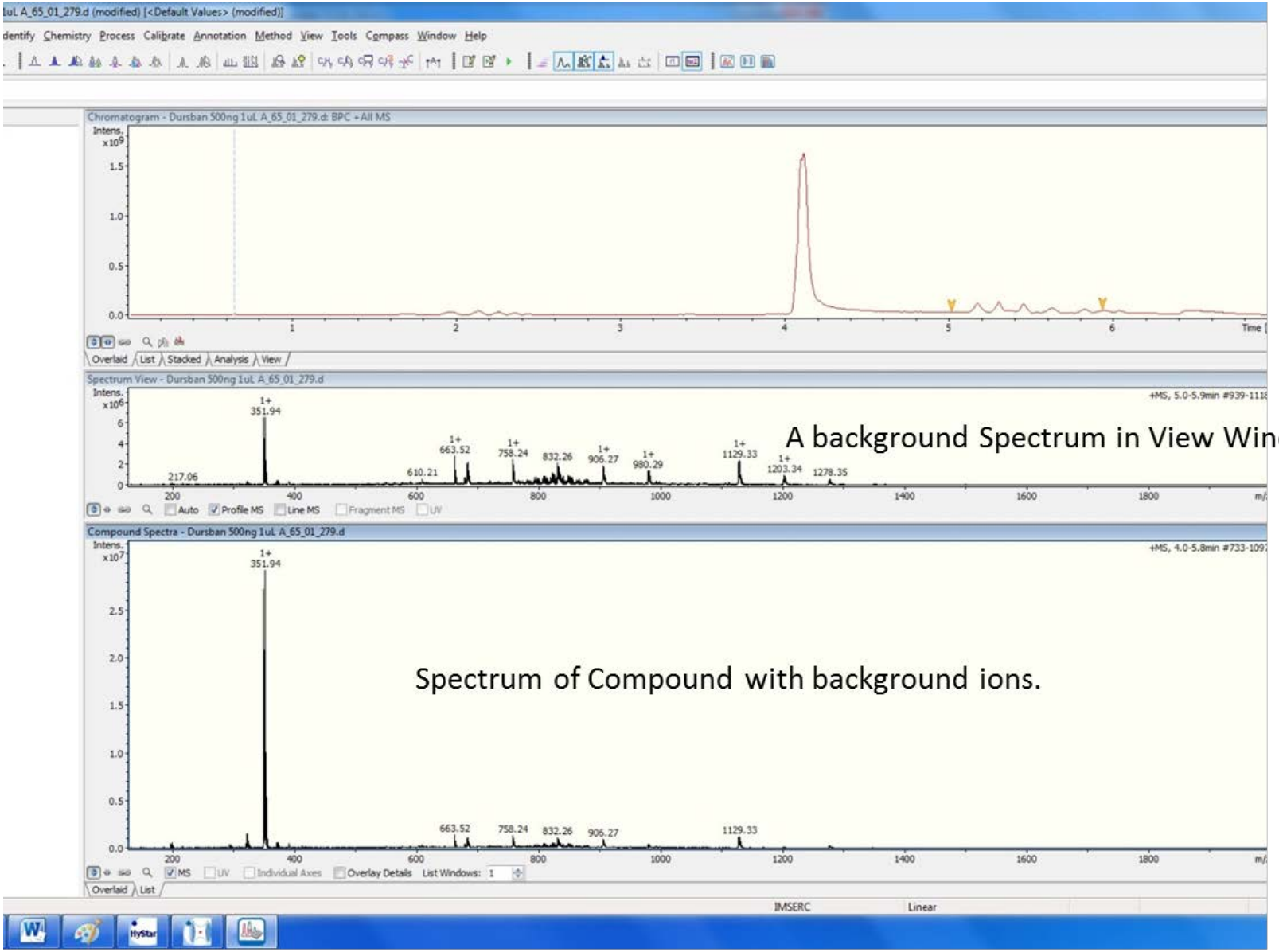

Compass DataAnalysis - CalB_1_01_44.d (modified) [DataAnalysis Ion Trap Default.m (modified)]
File Edit Find MassList Deconvolute Identify Chemistry Process Calibrate Annotation Method View Tools Compass Window Help
CalB
Analysis List
CalB_1_01_44.d
Chromatograms
BPC +All MS
BPC -All MS
Compound Spectra
-MS, 0.1min #8
+MS, 0.1-0.2min #5-9
Chromatogram - CalB_1_01_44.d: BPC +All MS
Intens.
Time [min]
Overlaid List Stacked Analysis View
Spectrum View - CalB_1_01_44.d
+MS, 0.1-0.2min #5-9
m/z
Auto Profile MS Line MS Fragment MS UV
Compound Spectra - CalB_1_01_44.d
-MS, 0.1min #8
+MS, 0.1-0.2min #5-9
MS UV Individual Axes Overlay Details List Windows: 2
Overlaid List
Spectrum Data
m/z z I FWHM
Mass List Deconvolution Results
For Help, press F1
IMSERC
Linear
0.7 min
2390910
1420
1430
3:35 PM
11/8/2013



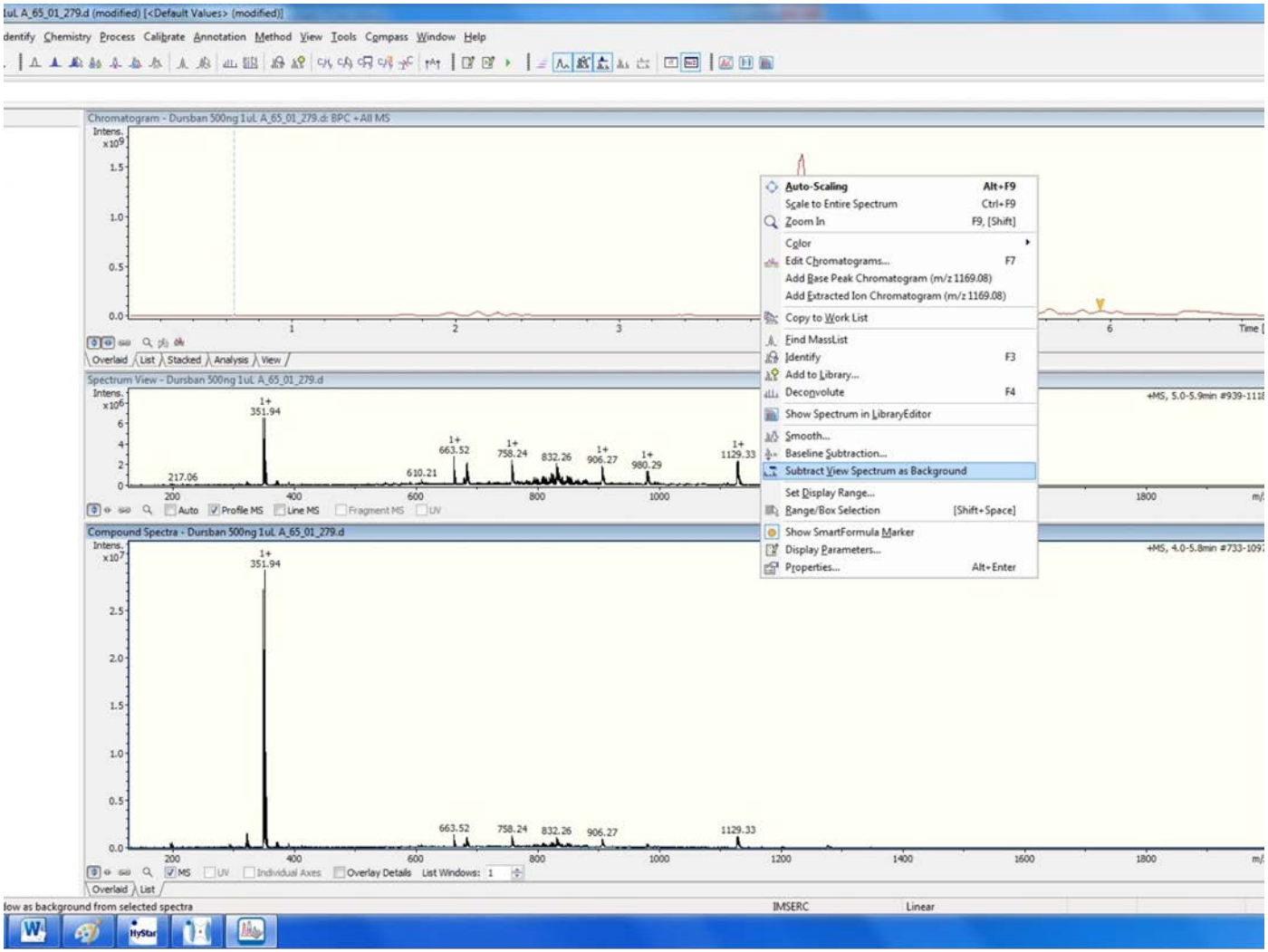
Zoom and Print. To print a single window, click on the arrow to the right of the printer icon and select print window. The highlighted window will be printed.



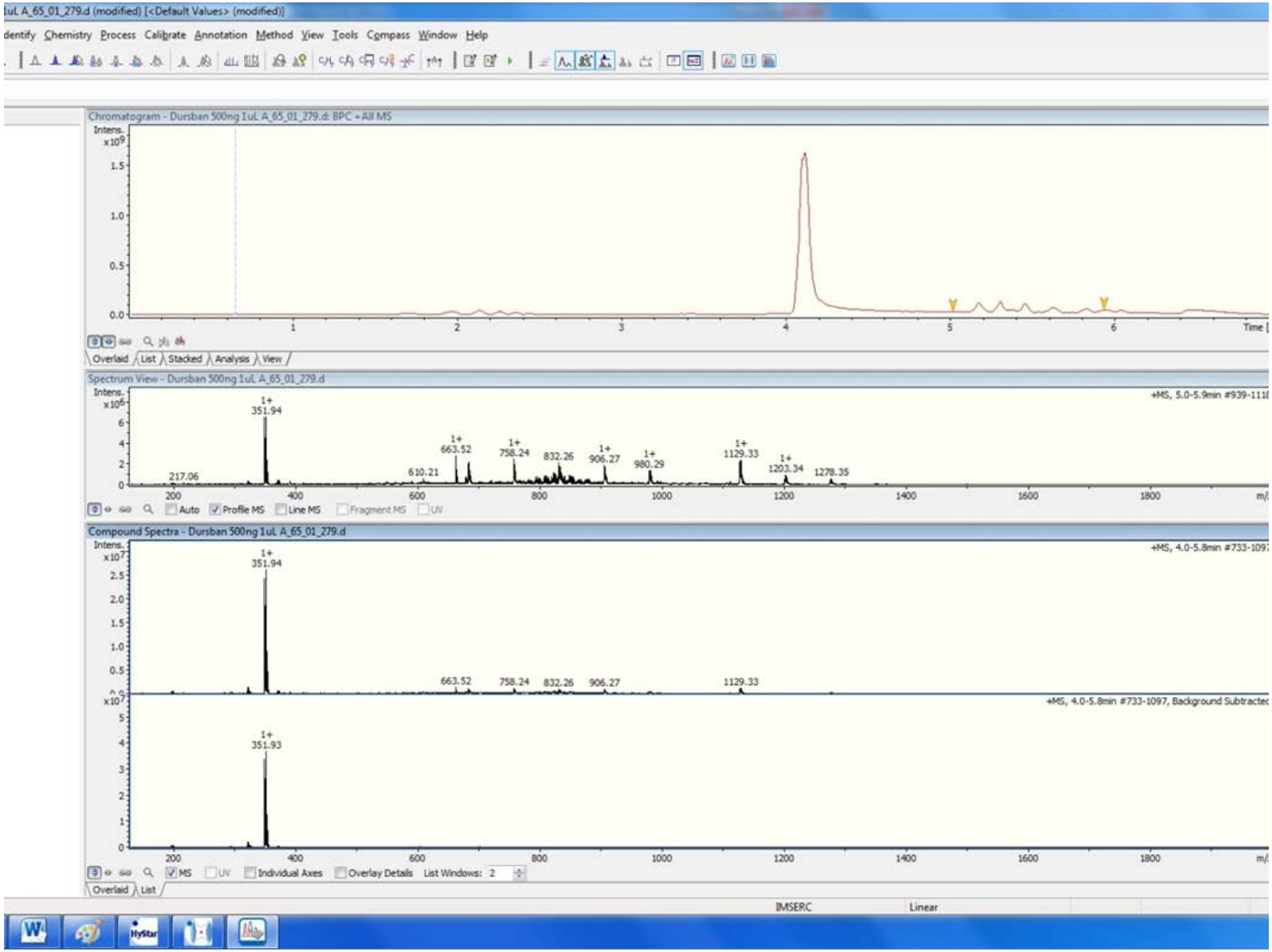
To Zoom, after clicking on the magnifying glass, draw a box around the area that you want to zoom in on. Unzoom by clicking below or to the left of the axes.



Background Subtracting



Subtracting the View Spectrum from the Compound Spectrum: "Subtract View Spectrum as Background"



A new window appears in the Compound Spectrum Window with the cleaner subtracted spectrum.