

# **Bruker Amazon X**

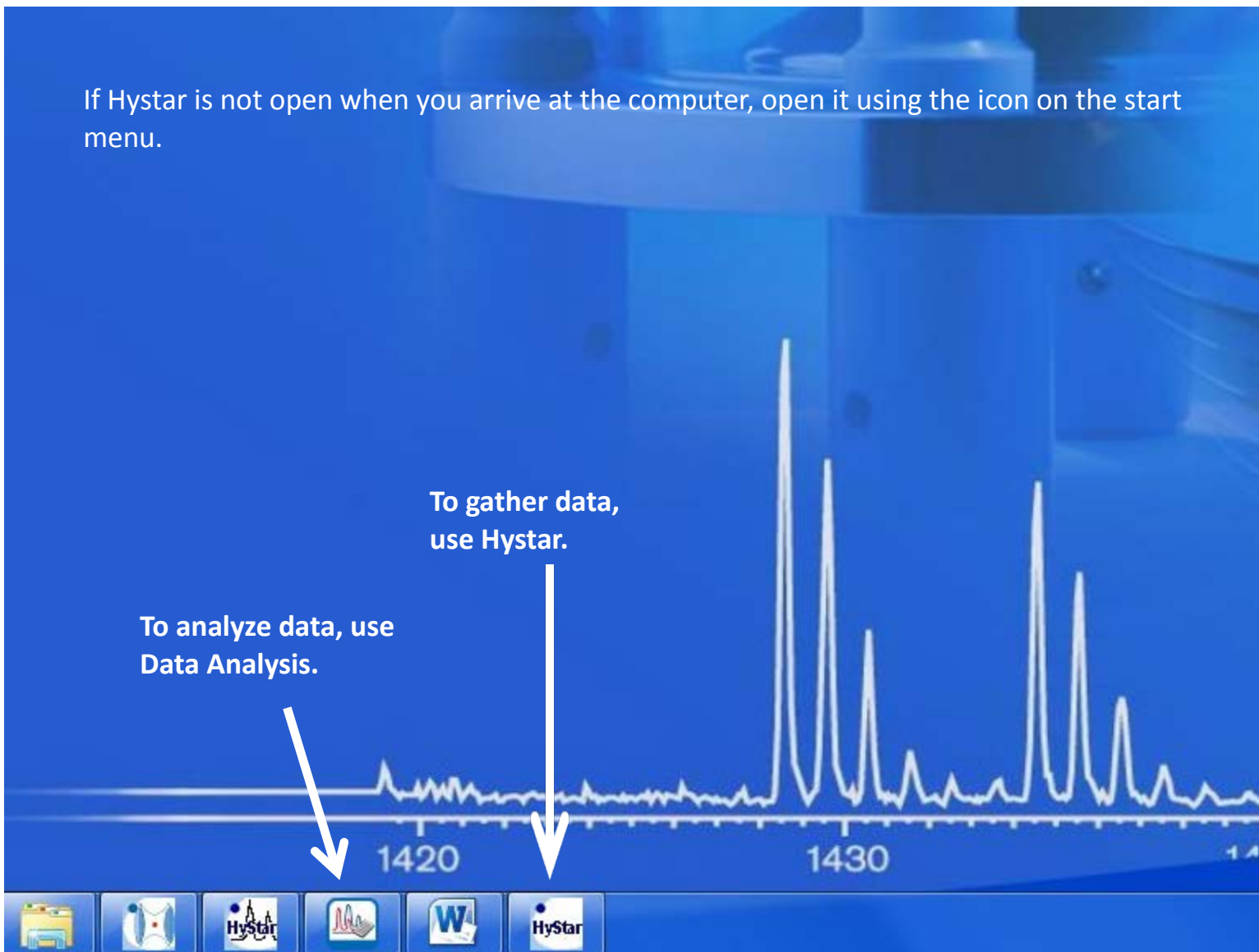
**ESI-Ion Trap Mass Spectrometer**

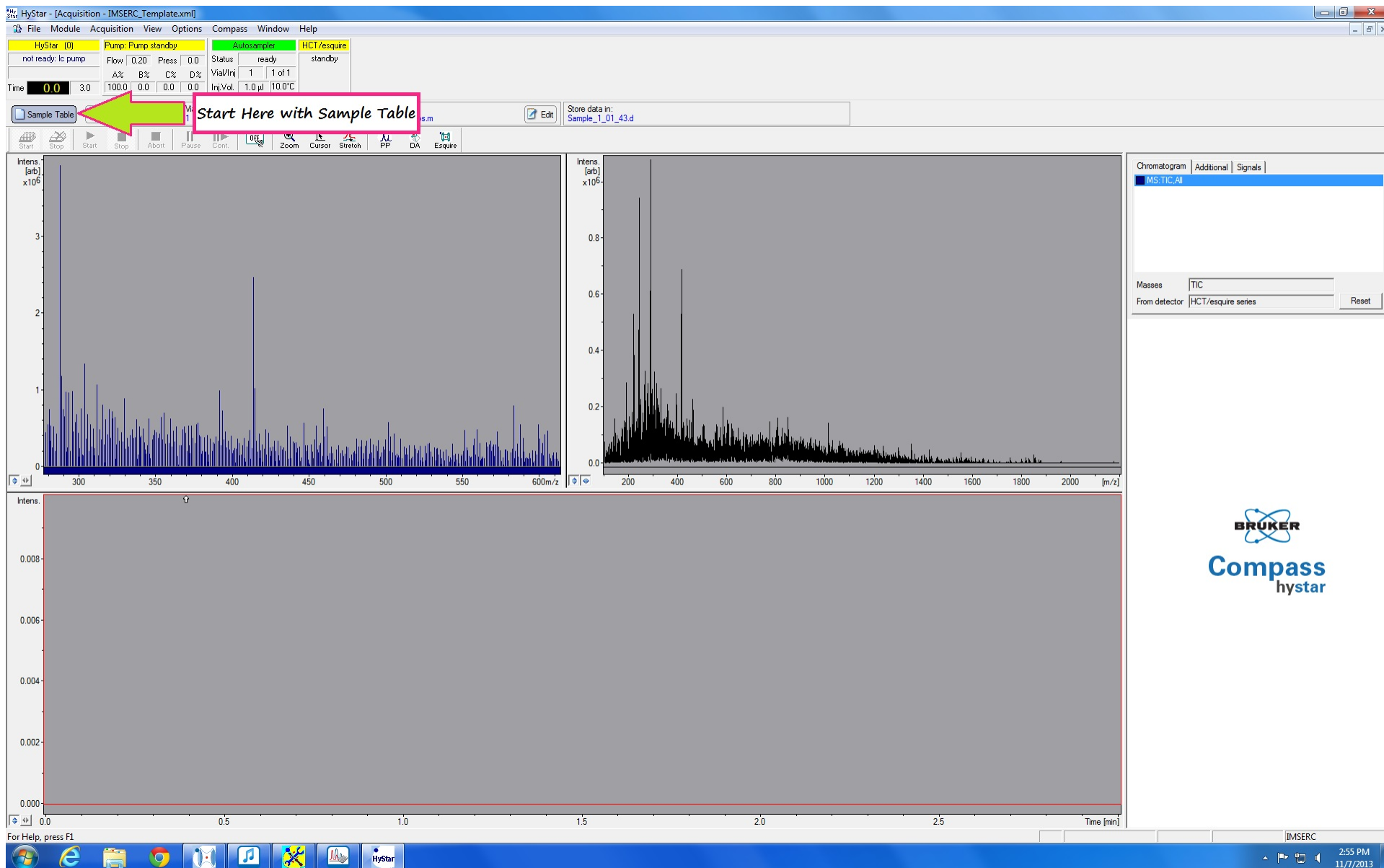
**Direct Injection**

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

To analyze data, use  
Data Analysis.

To gather data,  
use Hystar.





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.)

HyStar - [Acquisition - tempsample.xml]

File Module Acquisition View Options Compass Window Help

HyStar (1) Pump: Pump standby Autosampler: HCT/esquire  
 not ready: lc pump Flow: 0.20 Press: 0.0 Status: injected standbu  
 A% B% C% D% Vial/Inj 4 Inj.Vol. 5.0 µl

Time 0.0 2.0

Sample Table

D:\Methods\AmazonLCMS.m\IMSERC\_Template.xml

Line	Vial	Status	Sample ID	Inj.	Volume [µl]	Amount [µg]	Data Path	Method	LC Method Part	Autosampler Method Part	MS Acquisition Method Part	DataAnalysis Method Part
<input checked="" type="checkbox"/>	1	1	Test_Sample1	1	2.000	0.000	meoh_100_pos	MeOH-100_Pos.m	Standard		MS_Basic_POS_2013_10_31.m	

For Each Line:

- Make sure Box is checked to run sample
- Below, under General: Enter Sample Name (Identifier), Vial Position and Volume (for injection)

General | Methods | Details | Add. Parameters

Sample description  
 Sample Identifier: Test\_Sample1 (max. 30 letters)  
 Sample Weight [mg]: 0 Dilution [ml]: 1 Internal Standard [mg]: 0

Autosampler Parameters  
 Vial Position: 1 (Vial) Number of Injections: 1 Volume [µl]: 2 Pre-run [min]: 2  
 e.g. 1 Amount [µg]: 0.00

Result Data Path  
 Standard Path: D:\Data  
 Subdirectory: [ ] ←

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 hystar

Chromatogram x = 0.06 y = 0.01 IMSERC

For Help, press F1

5:13 PM 11/5/2013

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.

HyStar - [Acquisition - temp-sample.xml]

File Module Acquisition View Options Compass Window Help

HyStar (1) Pump: Pump standby Autosampler: HCT/esquire

not ready: lc pump Flow: 0.20 Press: 0.0 Status: injected standard

A% B% C% D% 100.0 0.0 0.0 0.0

Vial/Inj: 4 Inj.Vol: 5.0 µl

Time: 0.0 2.0

Sample Table

Start Stop Start Stop Abort Pause Cont. Off

Intens. [arb.] x10<sup>6</sup>

5 4 3 2 1 0

300 350 400

Intens.

0.008 0.006 0.004 0.002 0.000

0.0 0.2 0.4 0.6 0.8 1.0 1.2 1.4 1.6 1.8

Time [min]

For Help, press F1

Chromatogram x = 0.06 y = 0.01 IMSERC

D:\Methods\AmazonLCMS.m\IMSERC\_Template.xml

File View Edit Compass Help

Open SaveAs Acquisition Print Reload DB Gel Results

Line	Vial	Status	Sample ID	Inj.	Volume [µl]	Amount [µg]	Data Path	Method	LC Method Part	Autosampler Method Part	MS Acquisition Method Part	Data Analysis Method Part
1	1		Test_Sample1	1	2.000	0.000		meoh_100_pos	MeOH_100_Pos.m	Standard	MS_Basic_POS_2013_10_31.m	

For Each line also Under Method Tab:

- Open Method folder Icon
- Choose Folder IMSERC METHODS
- Choose appropriate method you want to use

General Methods Details Add. Parameters

Standard Path: D:\Methods

Use Method meoh\_100\_pos.m

Method Parts

LC MeOH\_100\_Pos.m

Autosampler (for Agilent G1329A Autosample) Standard Edit

MS (HCT/esquire) MS\_Basic\_POS\_2013\_10\_31.m

Data Analysis

Bio Tools

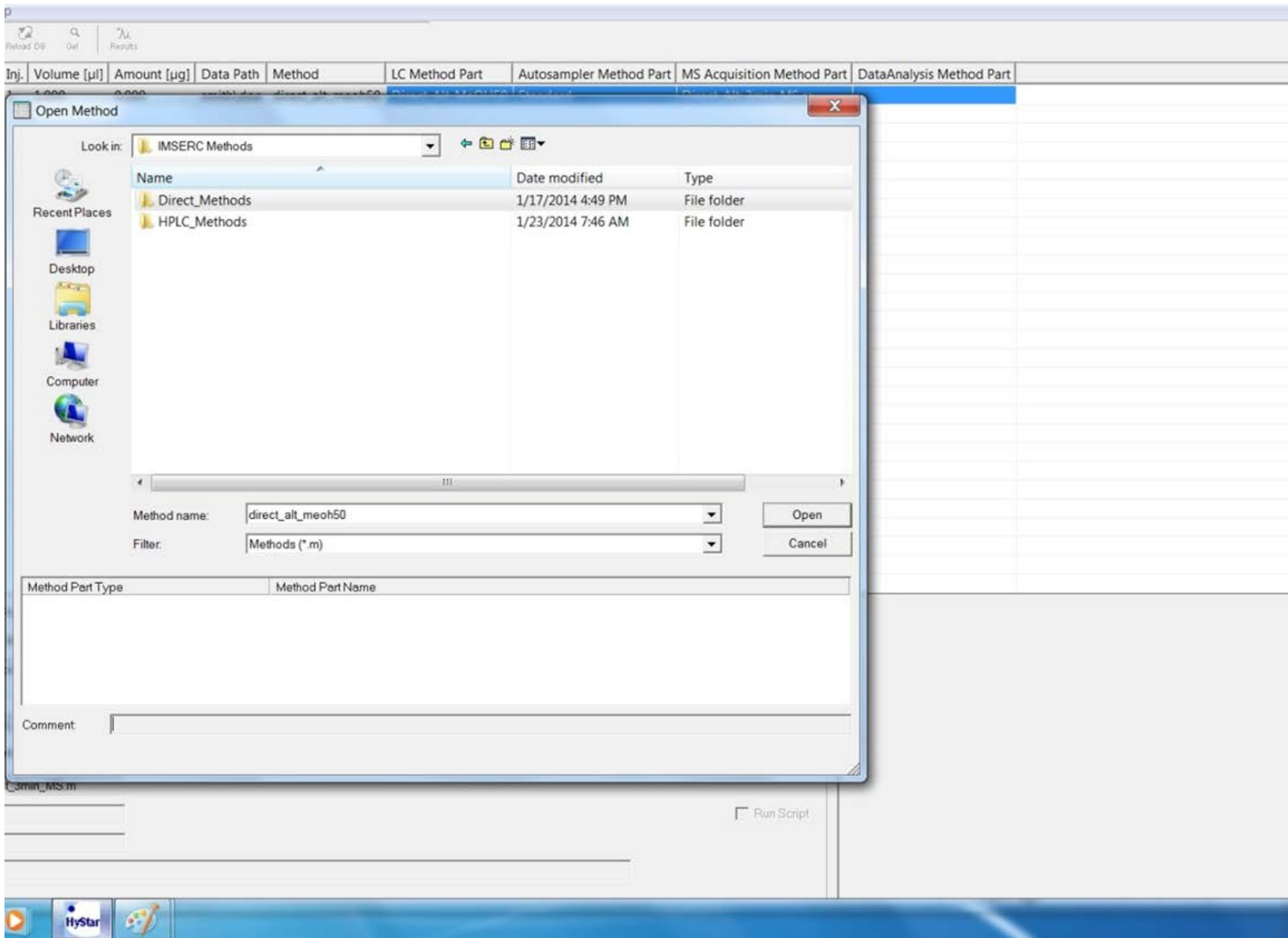
Switches

Run Script

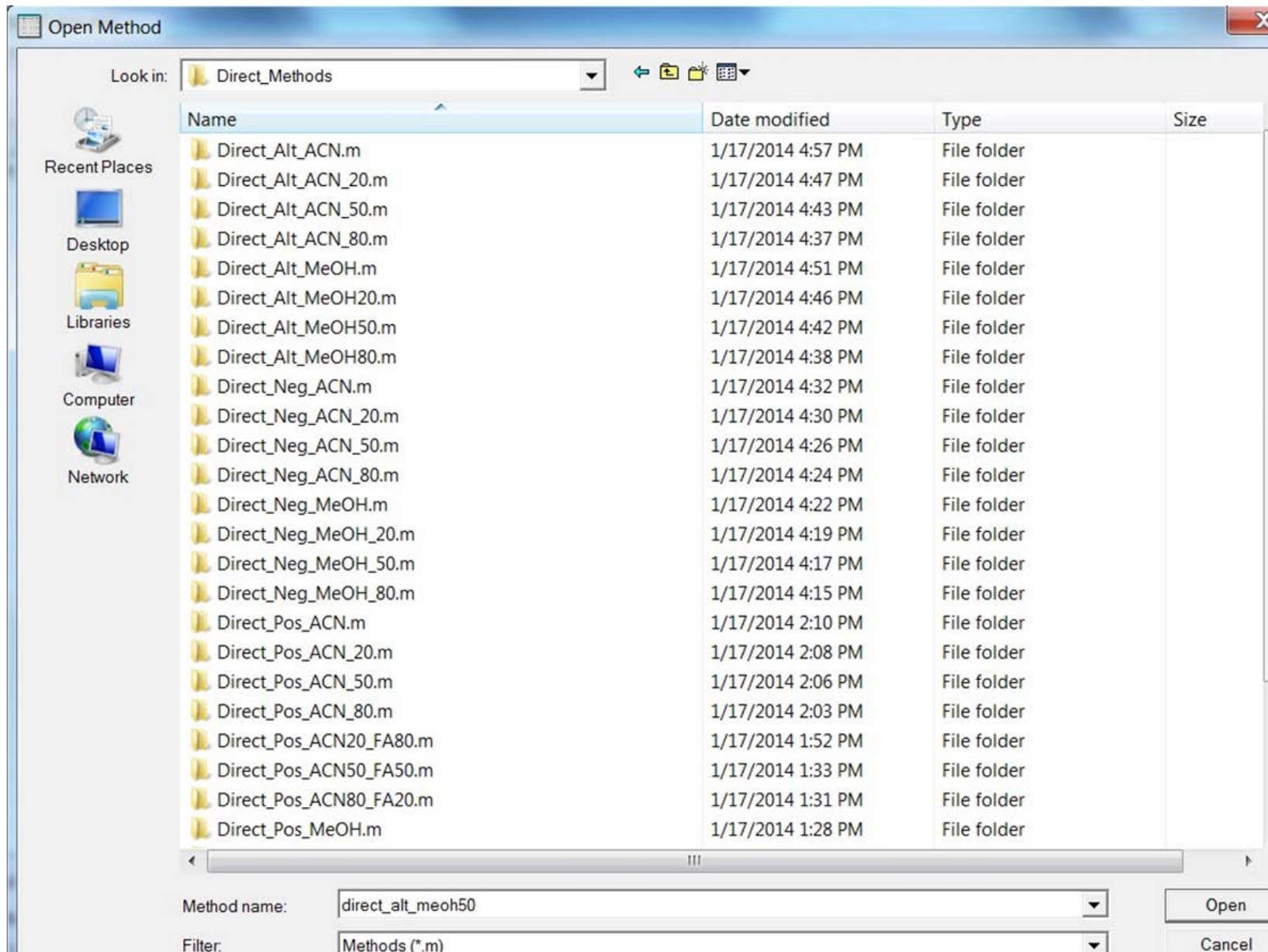
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Compass  
hystar

5:18 PM  
11/5/2013

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.

The screenshot displays the HyStar software interface for acquisition. The main window shows a sample table with the following data:

Line	Vial	Status	Sample ID	Inj.	Volume [µl]	Amount [µg]	Data Path	Method	LC Method Part	Autosampler Method Part	MS Acquisition Method Part	DataAnalysis Method Part
1	1		Sample	1	1.000	0.000		.imserc lc m...	MeOH-100_ALT...	Standard	MS_Basic_ALT_POS_NEG_2...	

A context menu is open over the first row of the table, with the 'Add New Samples...' option highlighted. A pink callout box with a green arrow points to this option, containing the text: "Click to add new samples and lines to the table and Enter the number of samples you want to add".

The interface also includes a chromatogram on the left showing intensity (Intens. [arb] x10<sup>6</sup>) versus time (Time [min]). The bottom panel shows method configuration details, including the standard path, method parts (LC, Autosampler, MS, DataAnalysis, BioTools, Switches), and a 'Run Script' checkbox.

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



The screenshot displays the HyStar software interface for an IMISERC acquisition. The main window shows a chromatogram on the left and a data table in the center. A dialog box titled "Add selected Samples" is open, allowing the user to specify the number of iterations and whether to increment the vial position. A pink box with a green arrow points to the "Iterations" field, with a text box explaining its function. The bottom of the interface shows the Bruker Compass hystar logo and the system tray with the date and time (3:44 PM, 11/7/2013).

Line	Vial	Status	Sample ID	Inj.	Volume [µl]	Amount [µg]	Data Path	LC Method Part	Autosampler Method Part	MS Acquisition Method Part	DataAnalysis Method Part
1	1		Sample	1	1.000	0.000	.imserc lc m...	MeOH_100_ALT...	Standard	MS_Basic_ALT_POS_NEG_2...	

**Add selected Samples**

Iterations:

Increment Position

OK Cancel

*You can enter the number of samples to add and increment the vial position and sample name*

Standard Path: D:\Methods

Use Method: .imserc lc methods\meoh\_100\_alt\_pos\_neg.m

Method Parts

LC: MeOH\_100\_ALT\_Pos\_Neg.n

Autosampler: for Agilent G1329A Autosample Standard

MS (HCT/esquire se): MS\_Basic\_ALT\_POS\_NEG\_...

DataAnalysis:

BioTools:

Switches:

Run Script

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

The screenshot displays the Bruker Compass hyStar software interface. The top menu bar includes File, Module, Acquisition, View, Options, Compass, Window, and Help. The status bar at the top shows 'HyStar (1)', 'Pump: Pump standby', 'Autosampler: HCT/esquire', and 'HCT/esquire'. The main window is titled 'D:\Methods\AmazonLCMS.m\IMSERC\_Template.xml' and contains a table with the following data:

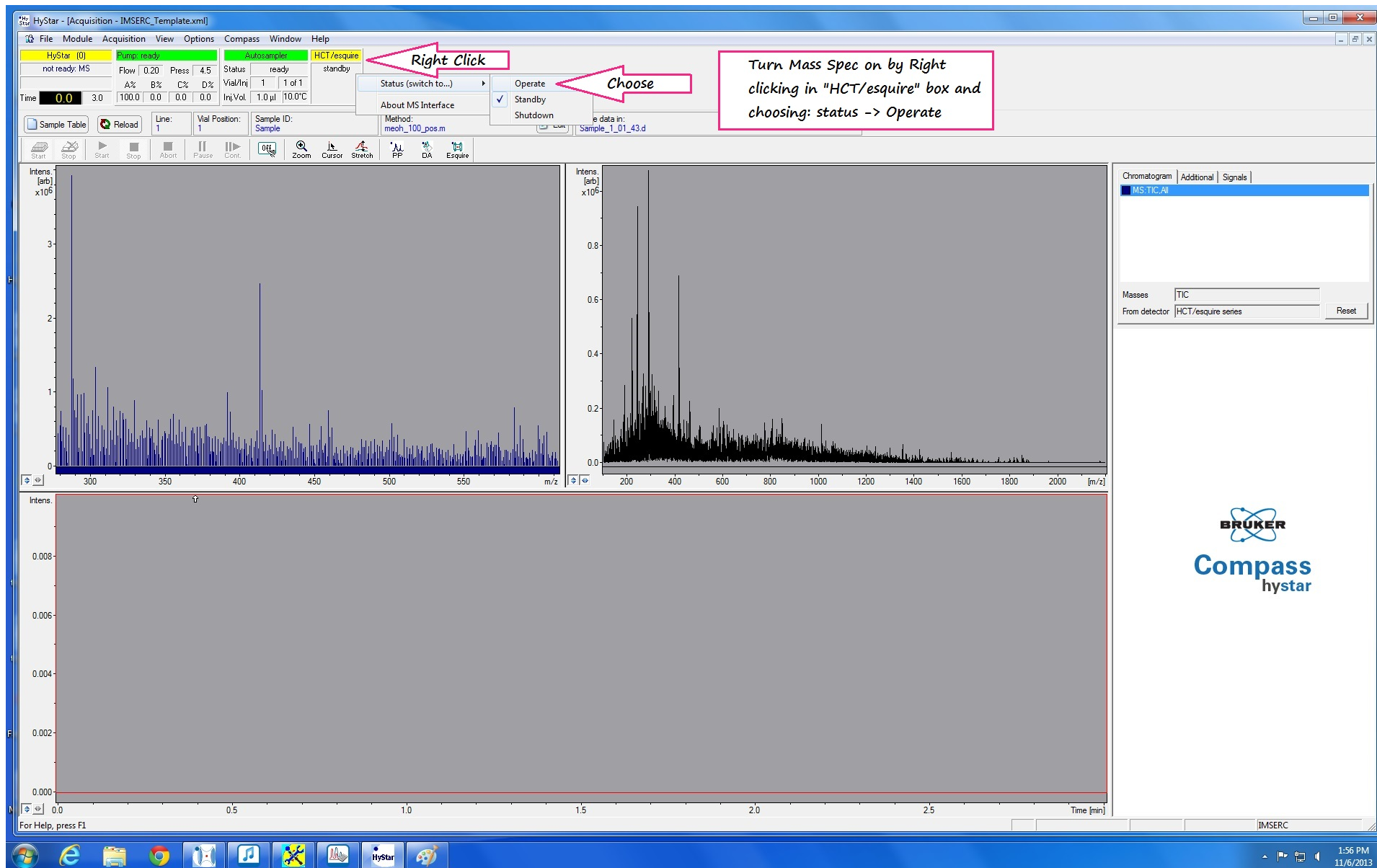
Line	Vial	Status	Sample ID	Inj. Vol.	Vol.	LC Method Part	Autosampler Method Part	MS Acquisition Method Part	DataAnalysis Method Part	
1	1		Test_Sample1	1	2.000	0.000	meoh_100_pos	MeOH_100_Pos.m	Standard	MS_Basic_POS_2013_10_31.m
2	2		Test_Sample1	1	2.000	0.000	meoh_100_pos	MeOH_100_Pos.m	Standard	MS_Basic_POS_2013_10_31.m
3	3		Test_Sample1	1	2.000	0.000	meoh_100_pos	MeOH_100_Pos.m	Standard	MS_Basic_POS_2013_10_31.m
4	4		Test_Sample1	1	2.000	0.000	meoh_100_pos	MeOH_100_Pos.m	Standard	MS_Basic_POS_2013_10_31.m

Annotations in the image include:

- A pink box around the 'Acquisition' button in the top menu bar with the text: "2) When Ready Click Acquisition".
- A pink box around the 'meoh\_100\_pos' text in the 'Use Method' field of the 'Details' tab with the text: "1) You can edit each line as you did previously, with new Name, Injection Volume, Method... etc."

The interface also features a chromatogram on the left, a 'Sample Table' button, and a 'Chromatogram' panel on the right showing 'MS: TIC.A1' and 'TIC' as the mass filter. The Bruker logo and 'Compass hyStar' branding are visible in the bottom right corner.

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.)

The screenshot displays the HyStar software interface for an IMSERC system. At the top, the status bar shows 'HyStar [0]', 'Pump: ready', 'Autosampler: ready', and 'HCT/esquire: ready', all in green. A pink arrow points to this status bar with the text: "When all modules are GREEN (ready) you can Click START to start running the sample table". Below the status bar, the 'Sample Table' button is highlighted with a pink arrow. The main display area contains three chromatograms: a top-left plot of Intensity (arb) x 10<sup>6</sup> vs. Time (min) from 300 to 600; a top-right plot of Intensity (arb) x 10<sup>5</sup> vs. m/z from 200 to 2000; and a bottom-left plot of Intensity (arb) x 10<sup>8</sup> vs. Time (min) from 0.0 to 2.5. The right-hand panel shows 'Chromatogram | Additional | Signals' with 'IMS:TIC,All' selected. Below this, there are fields for 'Masses' (TIC) and 'From detector' (HCT/esquire series), along with a 'Reset' button. The Bruker Compass hystar logo is visible in the bottom right. The Windows taskbar at the bottom shows the system time as 3:54 PM on 11/7/2013.

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

HyStar - [Acquisition - IMSERC\_Template.xml]

File Module Acquisition View Options Compass Window Help

HyStar [0] Pump: ready Autosampler: HCT/esquire

ready Flow: 0.20 Press: 6.2 Status: ready operate

A% B% C% D% Vial/Inj: 1 1 of 1 Inj.Vol: 1.0 µl 10.0°C

Time: 0.0 3.0 100.0 0.0 0.0

Sample Table Reload Line: 1 Vial Position: 1 Sample ID: Sample Method: meoh\_100\_pos.m Store data in: Sample\_1\_01\_43.d

Start Stop Start Stop Abort Pause Cont. Off Zoom Cursor Stretch PP DA Esquire

Intens. [arb] x10<sup>9</sup>

Intens. [arb] x10<sup>5</sup>

Intens. x10<sup>8</sup>

Time [min]

Chromatogram | Additional | Signals

IMS:TIC,All

Masses: TIC From detector: HCT/esquire series Reset

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hystar

IMSERC

For Help, press F1

4:01 PM 11/7/2013

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

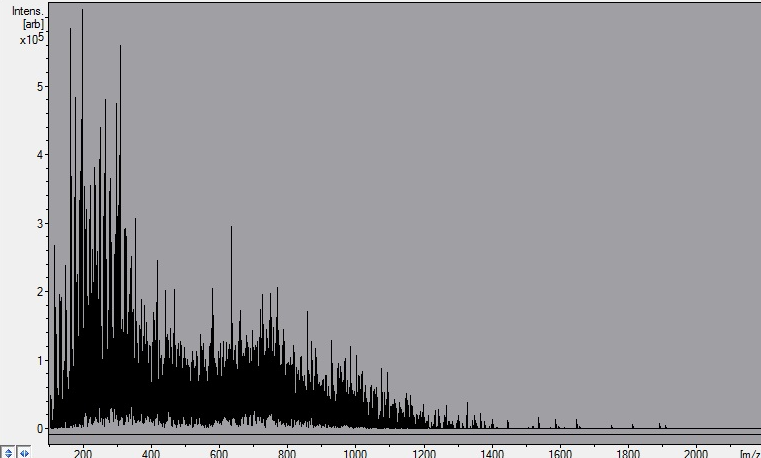
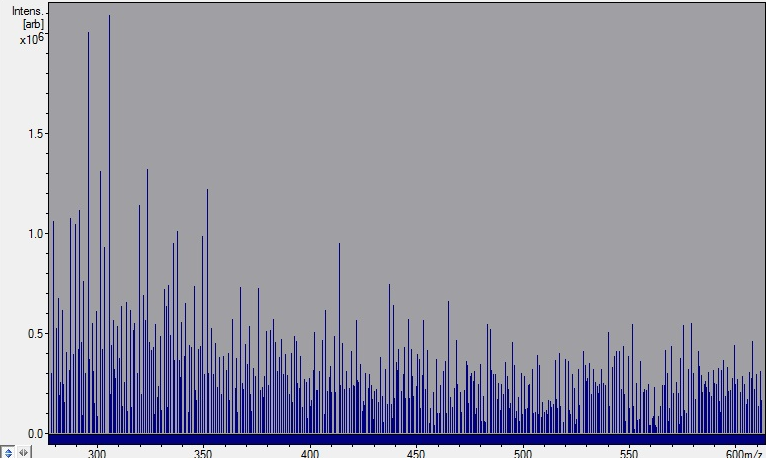
HyStar - [Acquisition - Ruby.xml]

File Module Acquisition View Options Compass Window Help

HyStar (1)	Pump: Pump standby	Autosampler	HCT/esquire
not ready: lc pump	Flow 0.20 Press 0.0	Status injected	standby
	A% B% C% D%	Vial/Inj 41 1 of 1	
Time 0.0 3.0	100.0 0.0 0.0 0.0	Inj.Vol. 2.0 µl 10.0°C	

Sample Table processed. Load a new Sample Table

Start Stop Start Stop Abort Pause Cont. [OFF] Zoom Cursor Stretch [PP] [DA] [Esquire]




Chromatogram | Additional | Signals

IMS:TIC,All

Masses TIC

From detector HCT/esquire series

Reset



Compass hystar

Compass DataAnalysis - RK2-185B\_18hrs\_41\_01\_43.d (acquiring) [DataAnalysis Ion Trap Default.m (modified)]

Compass DataAnalysis - RK2-18...

For Help, press F1

DATA ANALYSIS

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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

HyStar (1)	Pump: Pump standby	Autosampler	HCT/esquire
not ready: lc pump	Flow: 0.20 Press: 0.0	Status: injected	standby
	A% B% C% D%	Vial/Inj: 41 1 of 1	
Time: 0.0 3.0	100.0 0.0 0.0 0.0	Inj.Vol: 2.0 µl 10.0°C	

Sample Table processed. Load a new Sample Table

Start Stop Start Stop Abort Pause Cont. OFF Zoom Cursor Stretch PP DA Esquire

Intens. [arb.] Chromatogram Additional Signals

Compass DataAnalysis - Untitled

File Edit Find Mask Site 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 /

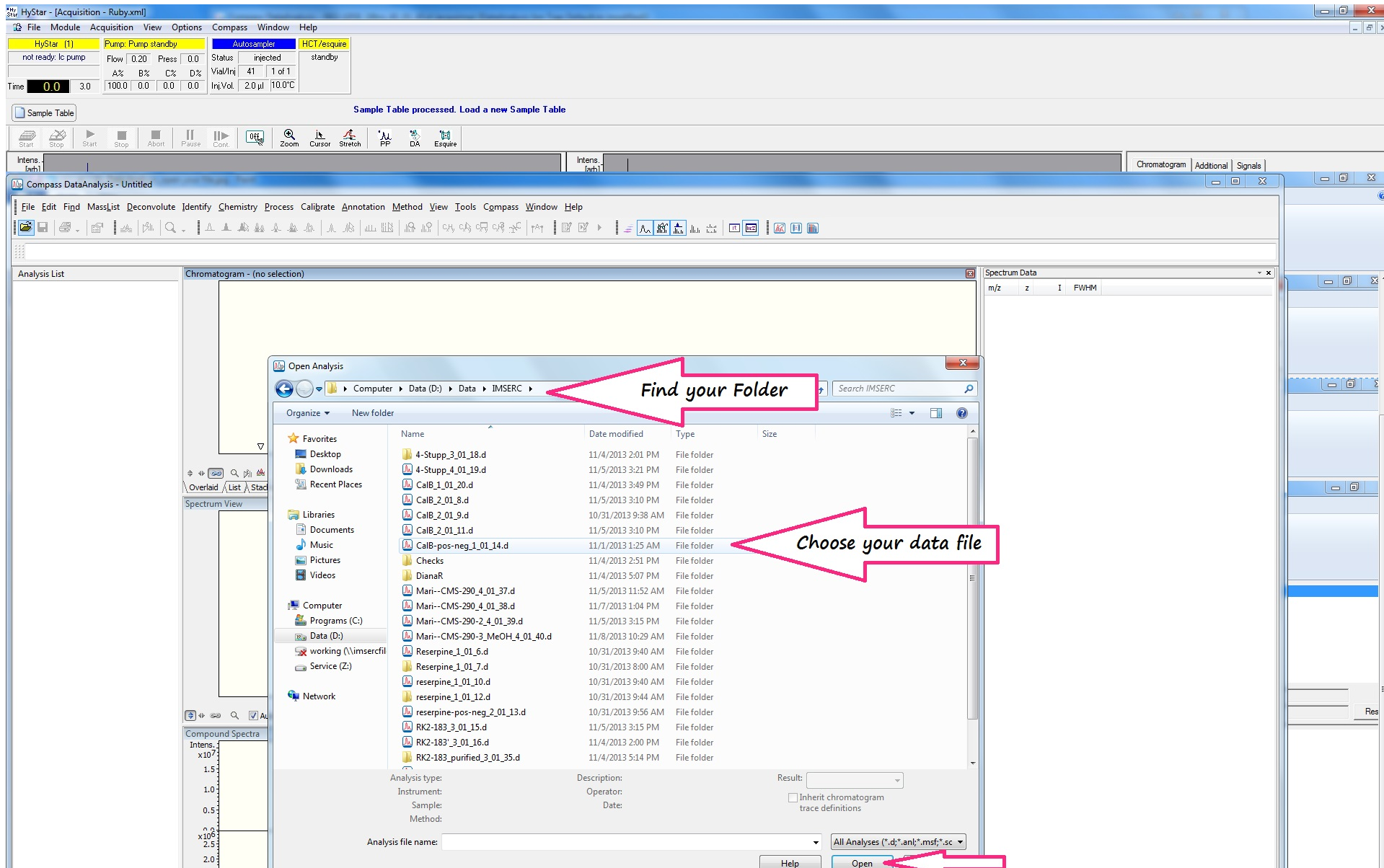
Spectrum View

Compound Spectra

Intens. x10<sup>7</sup>

1.5  
1.0  
0.5  
0.2  
x10<sup>8</sup>  
2.5  
2.0

RES



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



HyStar - [Acquisition - Ruby.xml]

HyStar (1)	Pump: Pump standby	Autosampler	HCT/esquire
not ready: lc pump	Flow: 0.20 Press: 0.0	Status: injected	standby
	A% B% C% D%	Vial/Inj: 41 1 of 1	
Time: 0.0 3.0	100.0 0.0 0.0 0.0	Inj.Vol: 2.0 µl 10.0°C	

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
  - Compound Spectra

Chromatogram - CalB\_1\_01\_44.d: (multiple selection)

Intens. x10<sup>8</sup>

Time [min]

Spectrum Data

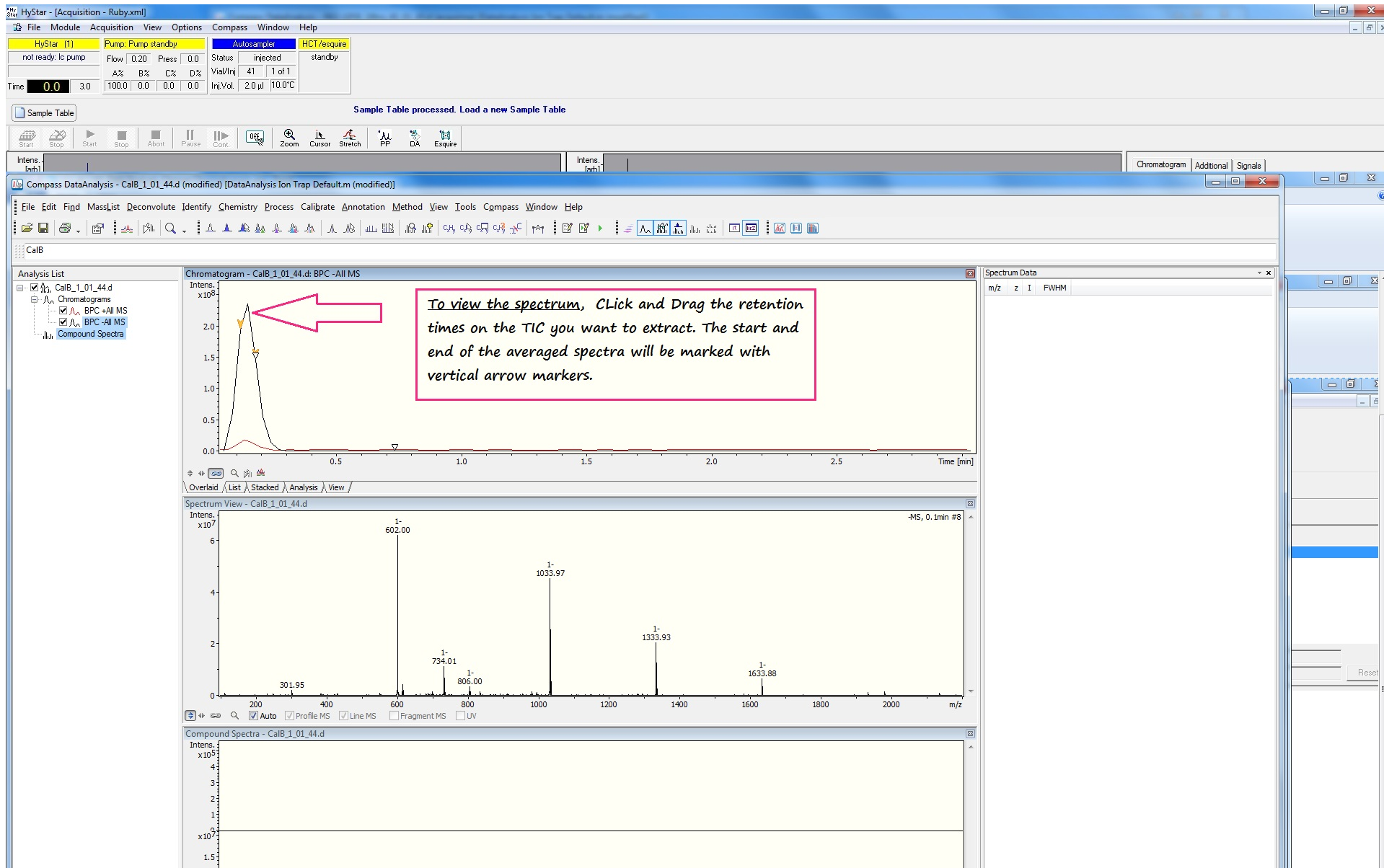
m/z	z	I	FWHM

Compound Spectra - CalB\_1\_01\_44.d

Intens. x10<sup>8</sup>

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ass  
ystar

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.

The screenshot displays the HyStar software interface. At the top, there's a menu bar (File, Module, Acquisition, View, Options, Compass, Window, Help) and a status bar showing system parameters like flow rate (0.20), pressure (0.0), and temperature (10.0°C). Below this is a toolbar with various icons for starting/stopping the run, pausing, and zooming. The main window is titled 'Compass DataAnalysis - CalB\_1\_01\_44.d (modified)'. It features an 'Analysis List' on the left, a 'Chromatogram - CalB\_1\_01\_44.d: BPC - All MS' plot in the center, and a 'Spectrum View - CalB\_1\_01\_44.d' plot at the bottom. The spectrum view shows a mass spectrum with a base peak at m/z 602.00 and other peaks at 301.95, 734.01, 806, and 1633.88. A context menu is open over the spectrum, with 'Copy to Compound Spectra' selected. A pink callout box with an arrow pointing to the menu contains the following text:

To keep the spectra of interest and work with it, you need to move it from here to a permanent buffer the "Compound Spectra" window below. Click left mouse button in spectrum to get the option to Copy it.

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

HyStar - [Acquisition - Ruby.xml]

File Module Acquisition View Options Compass Window Help

HyStar (1) Pump: Pump standby Autosampler: HCT/esquire

not ready: lc pump Flow: 0.20 Press: 0.0 Status: injected standby

Vial/Inj: 41 1 of 1

Inj.Vol: 2.0 µl 10.0°C

Time: 0.0 3.0 100.0 0.0 0.0 0.0

Sample Table processed. Load a new Sample Table

Start Stop Start Stop Abort Pause Cont. Off Zoom Cursor Stretch All PP DA Esquire

Intens. [arb.] Intens. [arb.] Chromatogram Additional Signals

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

Chromatogram - CalB\_1\_01\_44.d: BPC +All MS

Intens. x10<sup>8</sup>

Time [min]

Choose the second chromatogram to work with by putting box on it and clicking. Extract the chromatogram the same way by dragging the left mouse button, to get the new spectra in Spectrum View window

Spectrum Data

m/z	z	I	FWHM
112.92	794983	0.27	
142.81	43061	0.26	
148.70	25262	0.33	
152.81	103403	0.28	
154.85	306023	0.37	
156.93	117533	0.24	
158.81	24025	0.24	
172.82	88771	0.27	
180.82	26784	0.28	
186.93	57522	0.26	
194.93	41648	0.23	
197.75	276728	0.48	
198.80	23458	0.27	
202.81	69589	0.23	
204.93	41808	0.17	
205.26	24094	0.22	
206.96	37877	0.34	
210.71	33737	0.32	
214.84	28677	0.34	
216.72	49132	0.42	
219.81	67878	0.28	
223.07	86851	0.32	
226.77	22945	0.23	
230.87	28676	0.34	
233.07	517918	0.37	
234.05	115542	0.21	
234.94	35110	0.24	
236.69	26296	0.26	
237.80	67777	0.31	
238.94	50971	0.27	
240.83	37780	0.47	
247.16	73996	0.24	
248.89	455540	0.43	
250.81	141995	0.28	
251.94	21909	0.24	
252.85	106620	0.51	
255.10	63350	0.44	
256.08	26468	0.32	
264.94	85280	0.26	
267.32	120545	0.29	
269.16	184039	0.24	
272.93	26276	0.20	
274.84	39026	0.34	
277.20	61908	0.45	
278.19	56305	0.25	
280.96	70129	0.41	
283.20	262751	0.41	

Spectrum View - CalB\_1\_01\_44.d

Intens. x10<sup>6</sup>

m/z

Second Spectrum- POS Ion

Compound Spectra - CalB\_1\_01\_44.d

Intens. x10<sup>7</sup>

m/z

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

HyStar - [Acquisition - Ruby.xml]

File Module Acquisition View Options Compass Window Help

HyStar (1)	Pump: Pump standby	Autosampler	HCT/esquire
not ready: lc pump	Flow   0.20 Press   0.0	Status   injected	standby
	A%   B%   C%   D%	Vial/Inj   41   1 of 1	
Time   0.0   3.0	100.0   0.0   0.0   0.0	Inj.Vol.   2.0 µl   10.0°C	

Sample Table processed. Load a new Sample Table

Start Stop Start Stop Abort Pause Cont. Off Zoom Cursor Stretch All PP DA Esquire

Intens. [arb.] Intens. [arb.] Chromatogram Additional Signals

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

Chromatogram - CalB\_1\_01\_44.d: BPC +All MS

Spectrum Data

m/z	z	I	FWHM
112.92	794983	0.27	
142.81	43061	0.26	
148.70	25262	0.33	
152.81	103403	0.28	
154.85	306023	0.37	
156.93	117533	0.24	
158.81	24025	0.24	
172.82	88771	0.27	
180.82	26784	0.28	
186.93	57522	0.26	
194.93	41648	0.23	
197.75	276728	0.48	
198.80	23458	0.27	
202.81	69589	0.23	
204.93	41808	0.17	
205.26	24094	0.22	
206.96	37877	0.34	
210.71	33737	0.32	
214.84	28677	0.34	
216.72	49132	0.42	
219.81	67878	0.28	
223.07	86851	0.32	
226.77	22945	0.23	
230.87	28676	0.34	
233.07	517918	0.37	
234.05	115542	0.21	
234.94	35110	0.24	
236.69	26296	0.26	
237.80	67777	0.31	
238.94	50971	0.27	
240.83	37780	0.47	
247.16	73996	0.24	
248.89	455540	0.43	
250.81	141995	0.28	
251.94	21909	0.24	
252.85	106620	0.51	
255.10	63350	0.44	
256.08	26468	0.32	
264.94	85280	0.26	
267.32	120545	0.29	
269.16	184039	0.24	
272.93	26276	0.20	
274.84	39026	0.34	
277.20	61908	0.45	
278.19	56305	0.25	
280.96	70129	0.41	
283.20	262751	0.41	

Spectrum View - CalB\_1\_01\_44.d

Compound Spectra - CalB\_1\_01\_44.d

Context menu for Spectrum View:

- 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

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

Spectrum Data

m/z	z	I	FWHM
100.14		164228	0.28
108.09		80040	0.30
109.17		117636	0.26
111.11		115687	0.44
123.16		113982	0.21
125.06		89796	0.26
126.97		115927	0.38
129.06		154840	0.40
130.17		77917	0.20
138.05		202953	0.20
141.06		170791	0.36
141.95		106984	0.30
143.18	2+	98528	0.22
143.93	2+	90205	0.24
145.00	1+	235586	0.34
145.98	1+	131427	0.30
147.01	1+	71839	0.42
152.05		99193	0.19
153.08		88826	0.41
156.15		92643	0.22
157.04		93489	0.29
158.93		226701	0.40
160.95		164743	0.32
163.18	2+	71846	0.52
163.93	2+	124106	0.22
164.95		102229	0.31
167.01		76773	0.40
167.97		104893	0.36
169.15		142151	0.30
171.00		186990	0.31
172.93	1+	238394	0.29
173.97	1+	98873	0.29
181.03		91120	0.58
185.05		416409	0.42
186.96		182401	0.46
188.05		78660	0.21
188.93		114452	0.33
190.94		71527	0.29
191.99		187249	0.26
192.88		248995	0.29
193.84	1+	510283	0.37
194.99	1+	123862	0.31
196.12		161945	0.25
197.06	2+	156368	0.33
197.80	2+	81979	0.50
199.00	1+	202476	0.32
199.96	1+	95469	0.38
200.41		90476	0.14
200.98	1+	281323	0.39
202.06	1+	108280	0.21
203.05	1+	105007	0.33
205.03		93402	0.38
206.07		75687	0.28

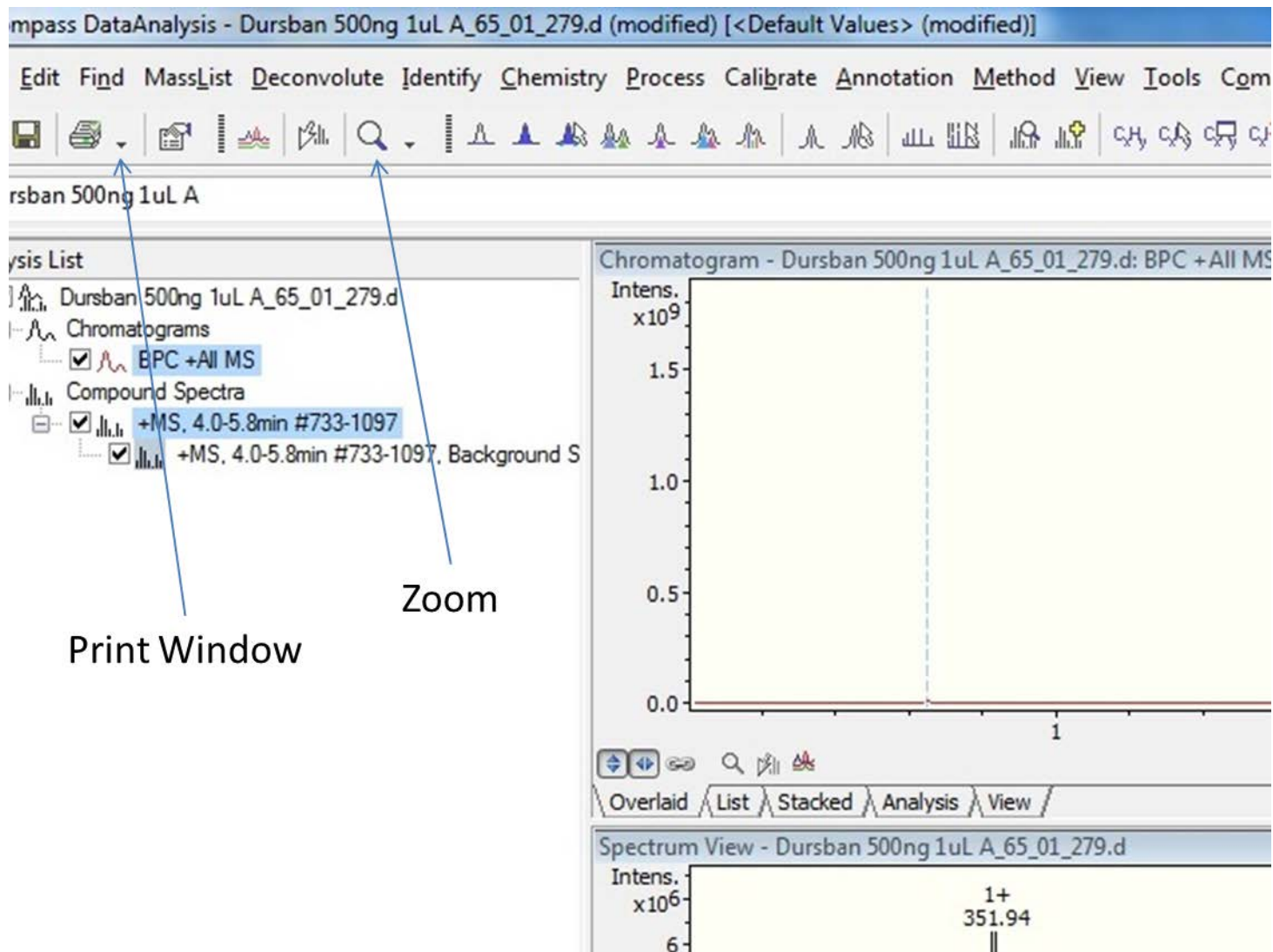
Spectrum View - CalB\_1\_01\_44.d

Compound Spectra - CalB\_1\_01\_44.d

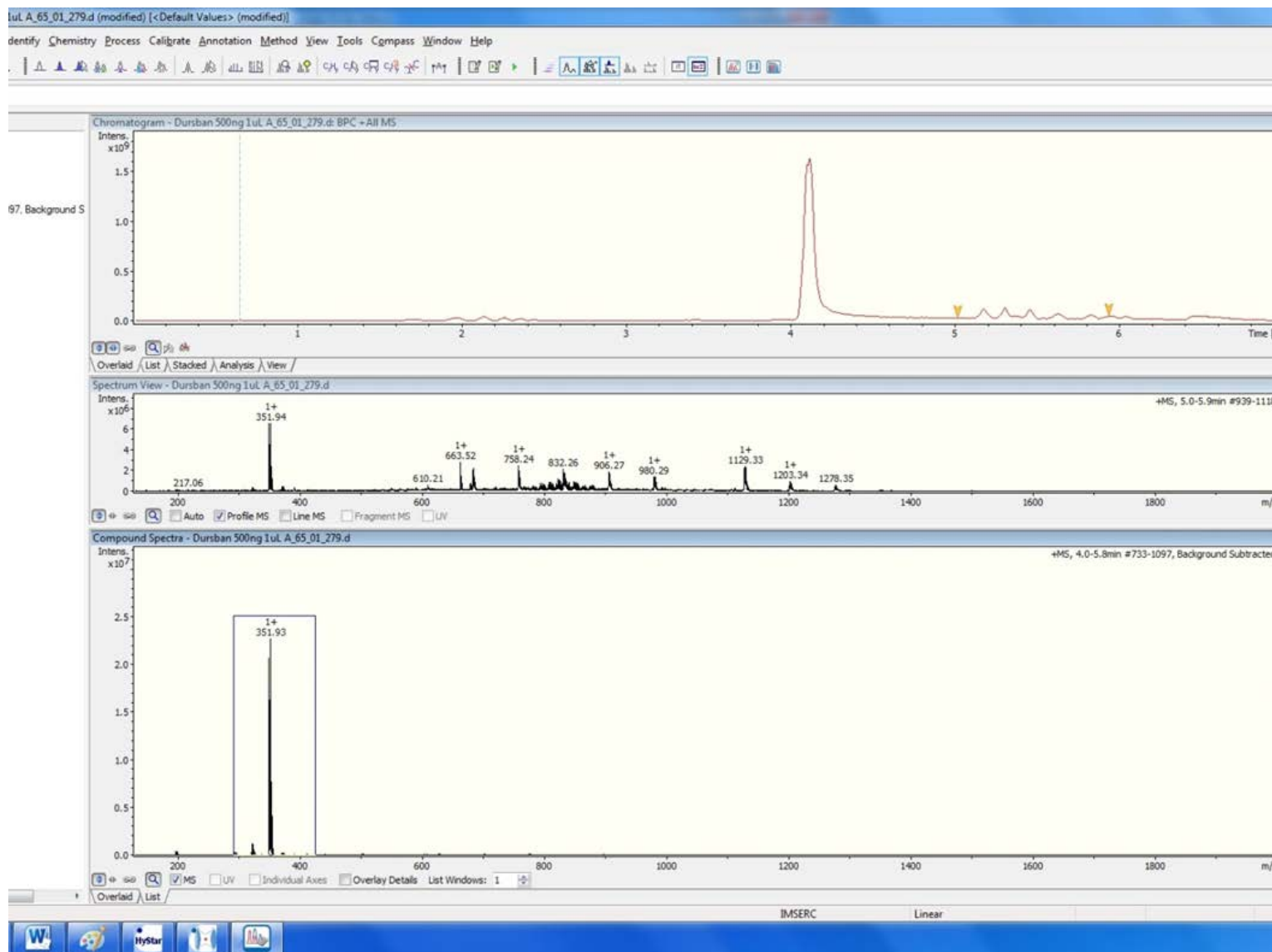
For Help, press F1

IMSRC Linear 0.7 min 2390910

Windows taskbar: 1420, 1430, 1440, 3:35 PM 11/8/2013

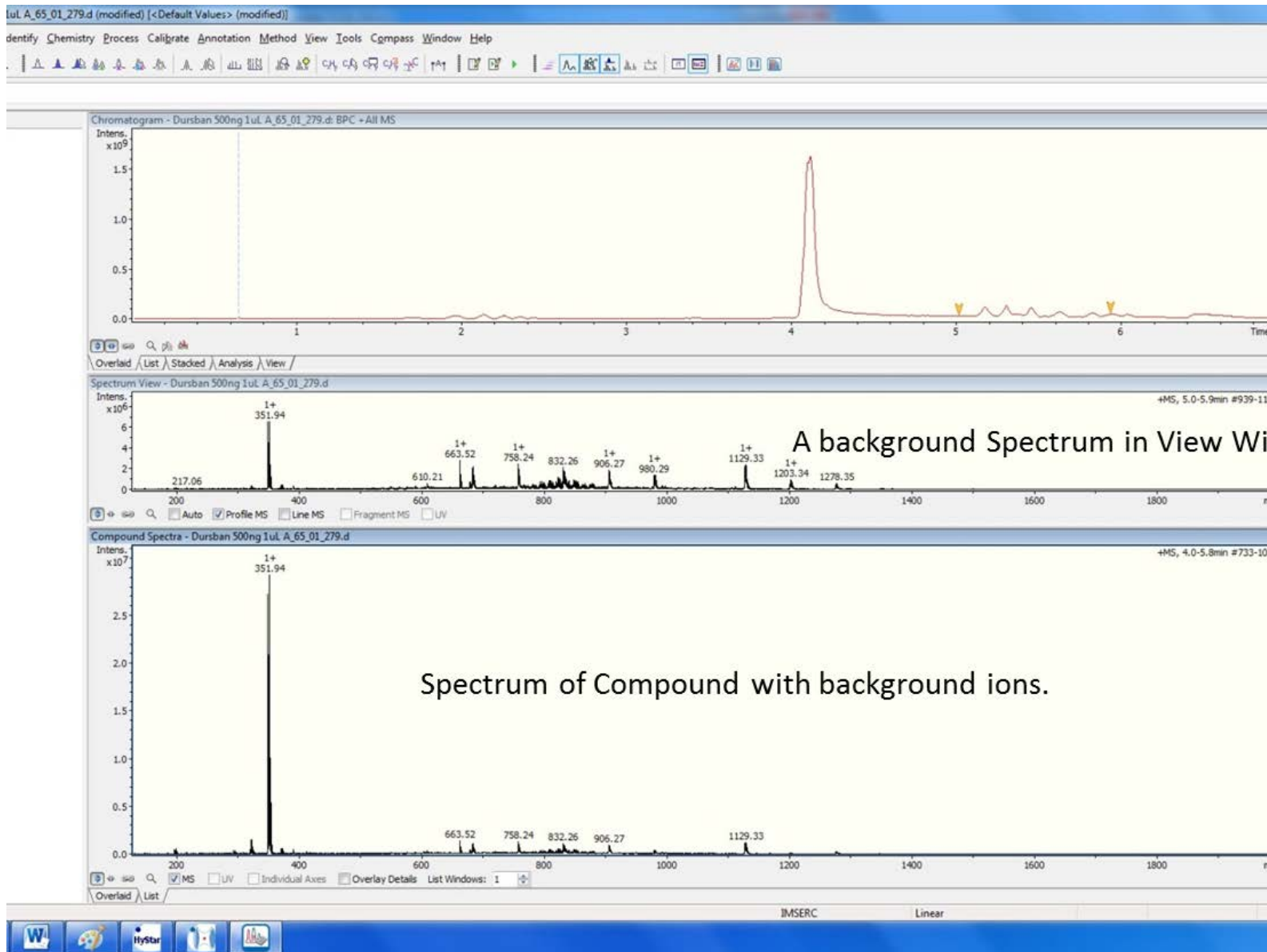


Zoom and Print. To print a single window, click on the arrow to the right of the printer icon and select print window. The highlighted window will be printed.



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.

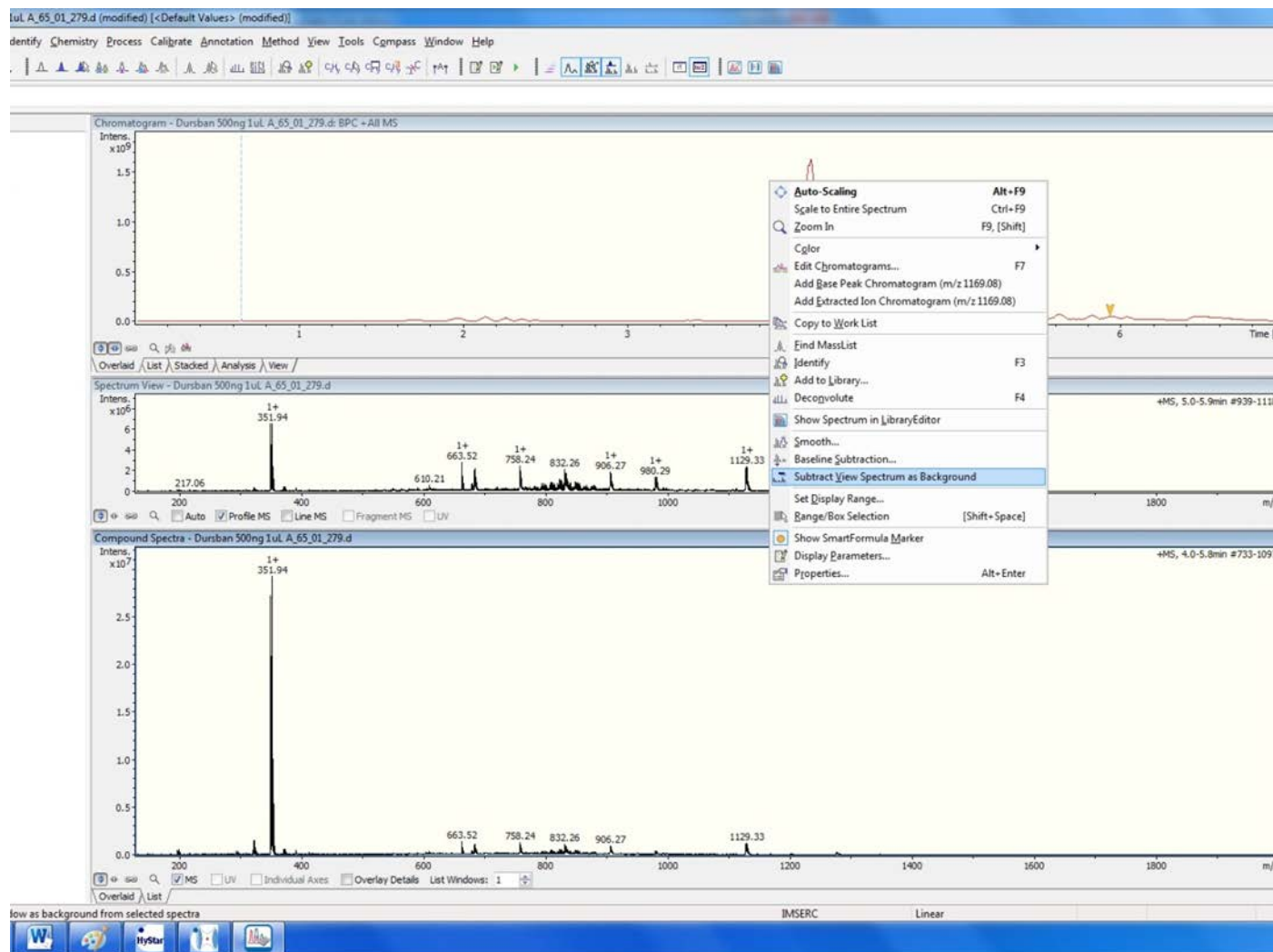




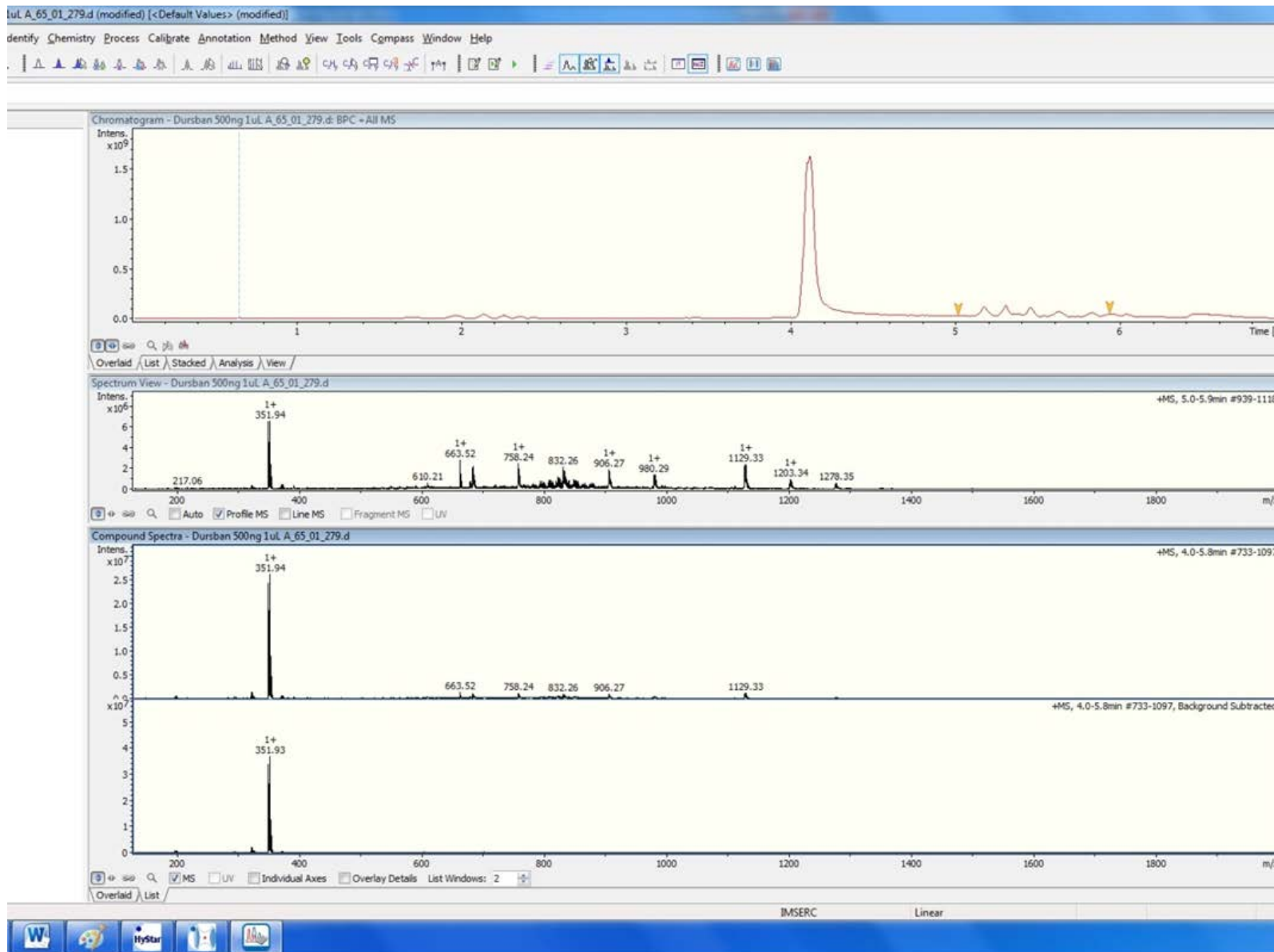
A background Spectrum in View Window

Spectrum of Compound with background ions.

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.