Bruker Amazon SL

ESI-Ion Trap Mass Spectrometer
If Hystar isn’t open when you arrive at the computer, open it using either the shortcut on the desktop or the icon on the start menu.
Open your sample table by selecting the sample table icon
Go to your group’s folder and open your sample table
Open your Sample Table or use the template and SAVE AS yours.
Under the “General” tab you can name your sample, change the vial position, and change the volume of your 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.
Select the solvent mix appropriate for your sample and the polarity of the ionization. This instrument runs an alternating positive and negative ionization method that produces results for both polarities.
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.
Once the instrument is ready and all of the boxes above are green, 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)
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”.

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.
Repeat above with second chromatogram (if you ran Alt Pos/Neg)
Copy to Compound Spectra as before