1) Double-Click the LSA Chemistry Recharge icon

2) Type in your uniquename, your PI’s uniquename, and your shortcode, and click OK

The MassHunter Data Acquisition program will come up automatically after you login.

3) Load a Method, using the drop-down menu near the top-center of the screen. For small molecule work, use the Student_Small_Molecule method.
4) Click on the On button to turn the instrument on.

5) Click on the Method Editor tab near the bottom of the screen. Click on the TOF tab, Click on the Ref Mass tab, and Click on Apply Now, next to Use Bottle A.

After you have done this, you should see the reference mass ions, m/z 922 & m/z 121, in the spectrum window:
6) On the method editor TOF tab, click on the General Tab. Click on Apply Now under LC Stream to MS.

7) Wait for the TOF status to turn from Yellow to Green, indicating that it is ready to use.
8) When the TOF is ready, click on the Sample Run tab near the bottom of the screen. Choose where to put the data, type in a filename, type in a comment (optional), then click on the Go arrow to start the run.

↓ 4) Click on Go arrow to start run.

9) After you have clicked on the Go arrow to start the run, the TOF status should change to a purple color, for the Prerun state:
10) Make sure that the injector handle is up in the Load position:

Please note:
Your samples need to be in the low micro-molar concentration range! Do not run samples that are more concentrated than this!

11) Rinse the syringe with clean solvent. Then, draw some sample solution into the syringe (around 50 ul). Insert the syringe into the injector valve as far in as it will go, and inject your sample solution into the valve (while the handle is still in the Load position).
12) After you have injected the sample solution, rotate the handle down to the Inject position to start the run:

13) Remove the syringe and solvent rinse the syringe.

14) When the run is completed, you can process the data.

How to Process the Data

1) Open the Qualitative analysis program (unless it is already open).
2) Open your data file.
3) Select a region of the chromatogram for defining a background spectrum. Do this by left-clicking and dragging across the region.
4) Right-click in the region to obtain a menu. Left click on “Extract MS Spectrum to Background”:

5) Highlight your sample peak by left-clicking and dragging across it.
6) Right-click on the selected region to obtain a menu. Left click “Extract MS Spectrum”: 

![Extract MS Spectrum menu screenshot]

- Extract MS Spectrum to Background
- Extract UV Spectrum
- Extract Peak Spectrum
- Extract MS Peak Spectrum from UV Peaks
- Extract Chromatograms...
- Extract Defined Chromatograms
- Use Highlighted Chromatograms
  - Extract Manual Compound(s)
  - Integrate Chromatogram
  - Integrate and Extract Peak Spectra
  - Smooth Chromatogram
  - Subtract Any Chromatogram
  - Calculate Signal-to-Noise

Integration Peak List
- Adjust Peak Threshold
- Set Anchor
  - Clear Anchor
- Assign Ranges to
  - Copy to User Chromatograms
- Clear Results
7) Subtract the background spectrum from your sample spectrum, by right-clicking the spectrum to get a menu. Then left-click “Subtract Background Spectrum”:

8) For printing, the spectrum can be copied and pasted into Microsoft Word.
9) To obtain a mass list, right-click the spectrum to get a menu, and then left-click “MS Spectrum Peak List 1”
How to Shut Down the Instrument When Finished

1) Click on the Off Button on the Data Acquisition page:

2) Close the Data Acquisition software. It will ask if you want to put the instrument in Standby. The answer is always Yes. Once you have closed the data acquisition software, then your account automatically closes, and it stops adding up time you are billed for.