Open Internet Explorer on any PC within Chemistry (you can use the Login PCs in the MS lab – these will already be linked to RA).

Enter RA address http://152.78.196.118/RemoteAnalyzer/login.aspx

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Click on Results



Here you should see all the results for your samples

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Note under instrument you will see the description of the mass spectrometer used and next to it the ionisation method information. Under Sample ID you will find your reference code.

Click on the data and time entry to review the data

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To view the mass spectrum for a given peak in the chromatogram box, click on the retention time (RT minutes). *E.g.* for the largest peak in this example chromatogram this is 8.90 minutes. (Note the largest peak can also be identified by the largest number for Area or Height.)



This takes you to the spectrum viewer



A list of the ions and abundances is also given at this stage. When you have finished viewing your data please sign out.

Note the software that processes the data will deconvolve all peaks in the chromatogram, there should be no need to reprocess the data. In the event that the automated processing has missed a peak please see us.

All data is archived and can be retrieved when required.