Getting Started with **mMass**: An Open Source Mass Spectrometry Tool

Go to www.mmass.org and download the appropriate version of **mMass** for your computer.
Versions are available for Linux, Windows, and Mac OSX.

File → Open
mMass will open its own files (.msd) and ASCII files (.txt). When you open an ASCII (.txt) file, save it as (save as) a .msd file.

Control-click (right-click) the cursor over an area of the spectrum to enlarge that area. Double-click on the spectrum to return to the full spectrum.

Tools → Label Peak : Cursor is now labeled with a small green +. Pull the cursor across the top of a peak, and a label appears on the spectrum and in a list to the right of the spectrum.
To delete a label, highlight it in the peak list, and hit delete.

View → Canvas Properties
m/z precision, intensity precision, bars height, gel height, canvas font size, label font size, notation length

Tools → Mass Calculator → Isotope Pattern window

File → Export → Export Spectrum Image
Choose size, resolution, font scale, line scale, format (PNG, JPEG, or TIFF).

To change color of spectrum: control-click (right-click) on the colored dot for that spectrum → colour

Other:

View → Peak Labels → vertical/horizontal

View → Peak List → lots of choices

Sequence → New → Sequence Editor (This is all about peptides and proteins.)

Processing → Peak Picking → wrench button Check and see if your data fits any of the types listed.
Processing means treating a batch of spectra all the same way.

If you use images generated with mMass in publications, reports or posters, be sure to say you used mMass and cite it.

mMass 3: A Cross-Platform Software Environment for Precise Analysis of Mass Spectrometric Data Strohalm M, Kavan D, Novák P, Volný M, Havlíček V *Anal Chem* 82 (11), 4648-4651 (2010).

mMass Data Miner: an Open Source Alternative for Mass Spectrometric Data Analysis Strohalm M, Hassman M, Košata B, Kodíček M *Rapid Commun Mass Spec* 22 (6), 905-908 (2008).

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