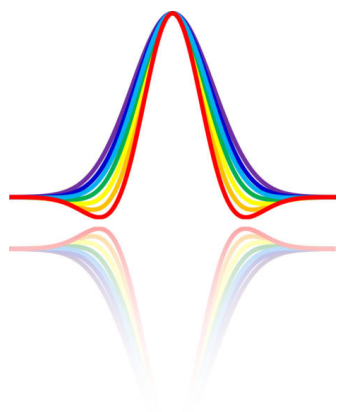


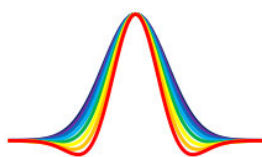
Spectro+swiss

Unlock absorption mode Fourier transform capability
for your FTMS platform, and much more

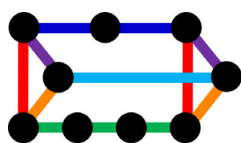


AutoVectis Pro

AutoVectis



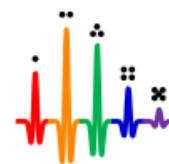
AutoLogis



AutoSeequer



Discharger

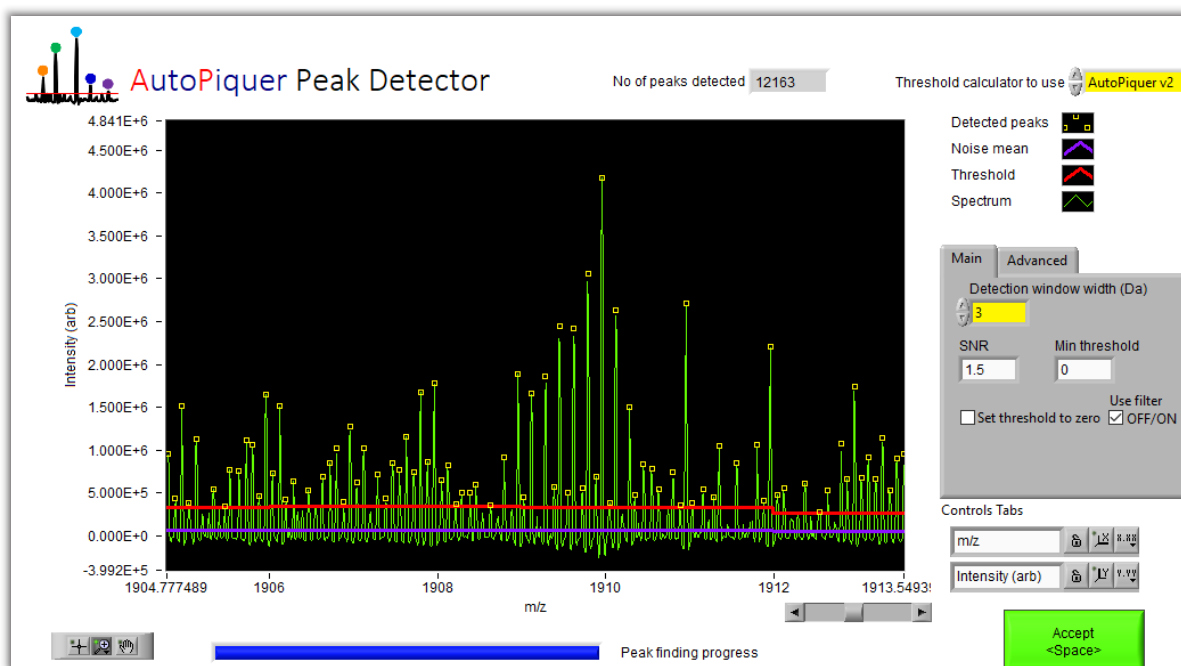
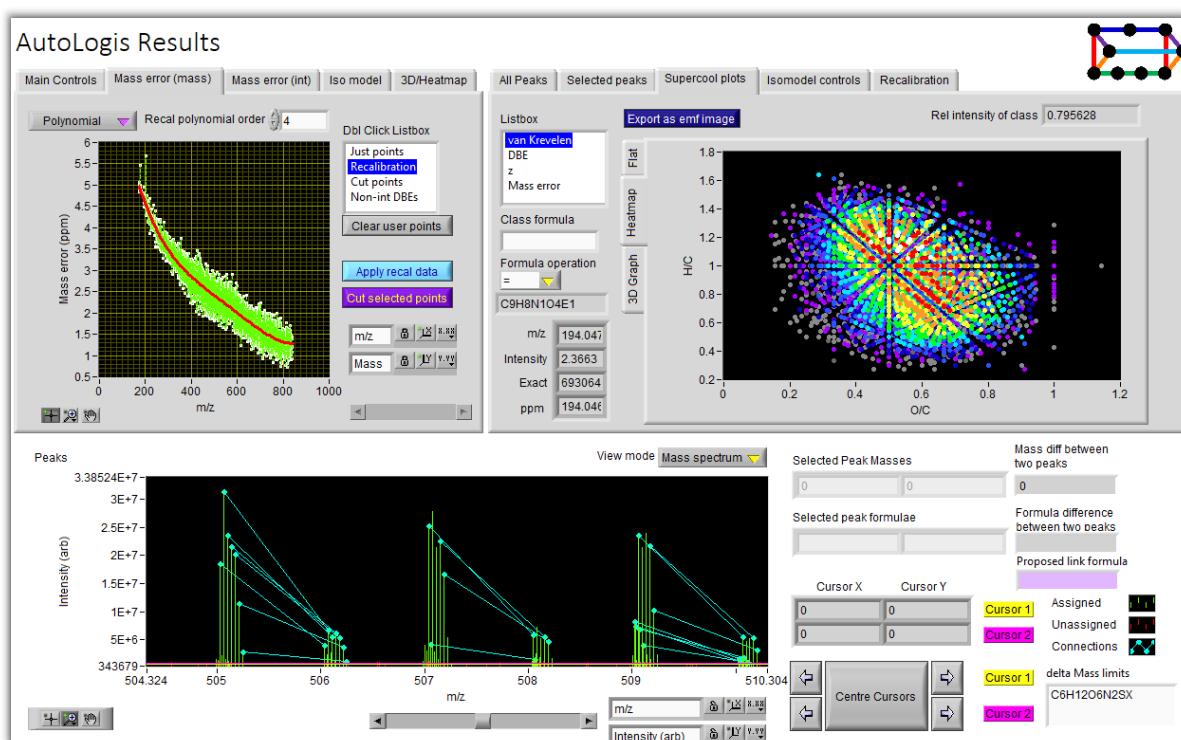


In a partnership with
Dr. David Kilgour
www.kilgourlab.com



AutoVectis Suite

- FTMS data representation in **absorption mode**, instead of the usual magnitude mode, lets you detect more peaks and gives you improved mass accuracy. Or, it lets you record mass spectra up to twice as fast. As a data post processing technique, it does not require any changes to the instrument. Using powerful algorithms, **AutoVectis Pro** automates the steps required to produce and process absorption mode mass spectra so the benefits can be easily enjoyed by everyone.
- A graphical user interface and built-in help system lead users through FTMS absorption mode FT (aFT) data processing (AutoVectis Pro) and low-resolution deconvolution (Discharger).
- Built-in tools include advanced peak detection (AutoPiquer), top-down protein sequencing (AutoSequer), and petroleomic/DOM assignments (AutoLogis).



Key features

- Easy to learn, **absorption mode Fourier transform (aFT)** signal processing for FTMS;
- Advanced capabilities and powerful algorithms, but simple to use;
- Support for single mass spectra, and also LC-MS data and FTMS images;
- Support for data formats of common FTMS instruments and software;
- Configured for petroleomic, proteomic or any high mass accuracy application;
- Is compatible with **Peak-by-Peak**, for easy integration and data code processing;
- Developed in collaboration with **Dr. David Kilgour** – www.kilgourlab.com

Peak Masses - Abs mode - Mass, Int
m/z Int
146755.49 0.0089143706
147575.11 0.0084104817
147840.37 0.011854157
147830.95 0.0371938923
147982.59 0.028666003

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Top-down mass spectrometry:

van der Burgt YE, Kilgour DP, Tsybin YO, Srzentić K, Fornelli L, Beck A, Wuhler M, Nicolardi S. Structural analysis of monoclonal antibodies by ultrahigh resolution MALDI in-source decay FT-ICR mass spectrometry. *Analytical chemistry*. 2018 Dec 20;91(3):2079-85

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Osterholz H, Kilgour DP, Storey DS, Lavik G, Ferdelman TG, Niggemann J, Dittmar T. Accumulation of DOC in the South Pacific Subtropical Gyre from a molecular perspective. *Marine Chemistry*. 2021 Apr 20;231:103955

Native mass spectrometry:

Campuzano ID, Netirojjanakul C, Nshanian M, Lippens JL, Kilgour DP, Van Orden S, Loo JA. Native-MS analysis of monoclonal antibody conjugates by Fourier transform ion cyclotron resonance mass spectrometry. *Analytical chemistry*. 2018 Jan 2;90(1):745-51.

Resources

MS training videos



<https://tinyurl.com/kcue9wkt>

AutoVectis videos



<https://tinyurl.com/4tzz6nw4>



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