

Gas Chromatography/
Mass Spectrometry**Key Features:**

- Full data review with multiple views
- Proprietary deconvolution algorithms identify and quantify compounds even if they co-elute
- Diagnostic tools monitor instrument health and performance

Chromion Software for Evaluation of Mass Spectral Data

PerkinElmer introduces Chromion® Release 2.0, a complete GC/MS analytical PC software package with quantitation capabilities, advanced proprietary peak deconvolution and customized peak identification algorithms creating a powerful tool for evaluation of mass spectral data. Operation of the software is

simple, and assessment of the results is accomplished using this easy-to-learn Windows-based graphical user interface.

Chromion software directly interfaces with PerkinElmer's field portable GC/MS, the Torion® T-9. Even though the T-9 operates as a standalone system during field operations, Chromion allows the user to manage the instrument's system functions on a computer through the Ethernet. Mass spectral data can be viewed in a wide variety of ways including TIC, RIC, background subtracted and deconvoluted spectra. The capabilities of the new software release include internal, external and averaged standard calibration, multiple curve fitting and quantitation using selected ions. Individual compounds can be identified and quantified from complex matrices with ease and speed using Chromion software.

Vast Library of Information for Simple to Complex Compounds

The capability of searching mass spectra from unidentified compounds against the NIST standard reference library is integrated into Chromion software. It is easy to add a compound to either the Chromion target compound library or a general library by right clicking on any spectral window and selecting the 'add-to-library' function. Existing libraries can be imported into the software for editing. Edited or created libraries can then be exported for use on the Torion T-9 GC/MS for in-field identification. Libraries contain detailed information about compounds including compound name, CAS #, formula, retention index, and molecular weight. Complex data are processed using a combination of proprietary deconvolution and library matching algorithms.

The Torion T-9 GC/MS uses ion trap technology to create analyte spectra. Ion trap spectra are not always identical to traditional libraries like NIST. Using a new proprietary search algorithm, results of unknown compound identification with accuracies similar to data obtained from other types of mass spectrometers, such as quadrupoles, is realized. Search results are displayed in a graphical format where the various deconvolved peaks have an assigned color. The spectra for the deconvolved peaks are displayed in the same color making it easy to identify which masses belong to a specific peak. The results are displayed in a simple-to-use format that shows the identified target compounds, as well as unknown compounds. Unknown compounds are sorted on the quality of the spectral match.

Additional Features

Method Parameters	Complete control of method parameters
Library Search (Compares Retention Time, Retention Index and Mass Fragments)	AMDIST-NIST (1100 compounds) comes standard; NIST 14 library available for extra cost
Quantitation Features	Calibration: internal standard, external standard, selected ions, 10 levels possible with calibration data
	Curve fitting: linear, quadratic, average, etc.
Calibration	Mass, retention time, and retention index
Control of Auxiliary Devices	Other than GC/MS
Batch Reprocessing	All data files can be reprocessed with new calibration parameters
Library Editor	Easy-to-customize library by adding new compounds
File Manager	Transfer files to PC as needed for processing
Compatibility	Runs under Windows 8, and Windows 10

Evaluate your data more effectively with Chromion Software for Torion T-9 GC/MS.

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