Agilent CrossLab
From Insight to Outcome

Quant-My-Way Unknowns Analysis

MassHunter Quantitative Analysis Webinar Series

Howard Sanford
Stephen Harnos
With Tom Barrett & Matt Leyden & Kevin Costalunga

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Quant-My-Way

MassHunter Quantitative Analysis B.09.00

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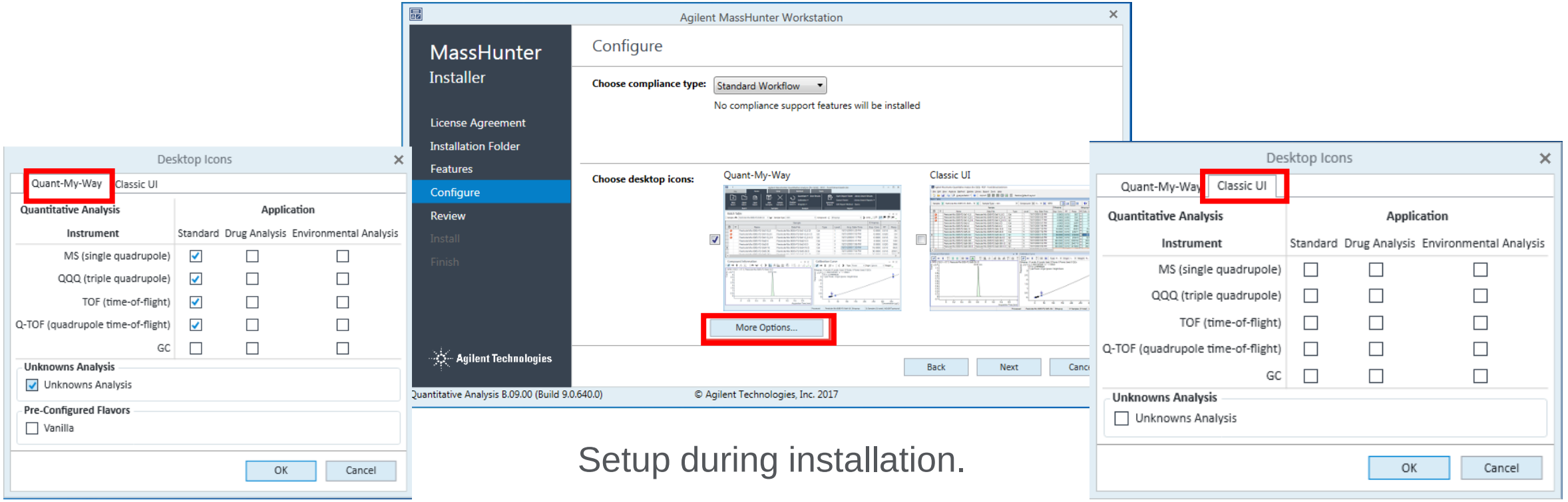
Custom Desktop icons.



Setup during installation.

Quant-My-Way

MassHunter Quantitative Analysis B.09.00

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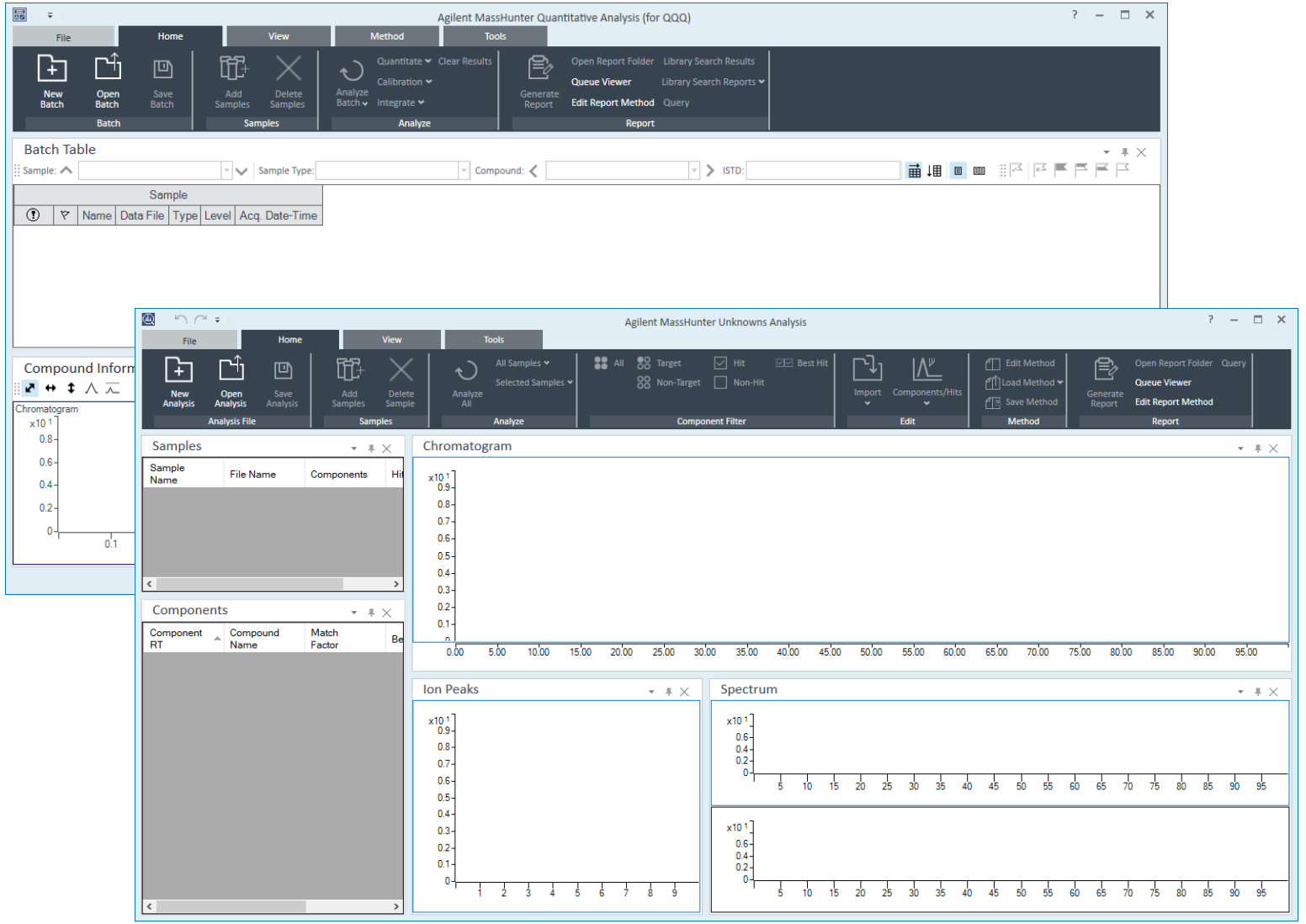
Preconfigured Quantitative and Unknowns Analysis Layouts.

Tools to

- Customize various layouts.
- Save the layouts.
- Share the layouts on other computers.

Customize Display for only relevant tools and menu items.

“OpenLab like” appearance with tabs and ribbons.



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Quant-My-Way

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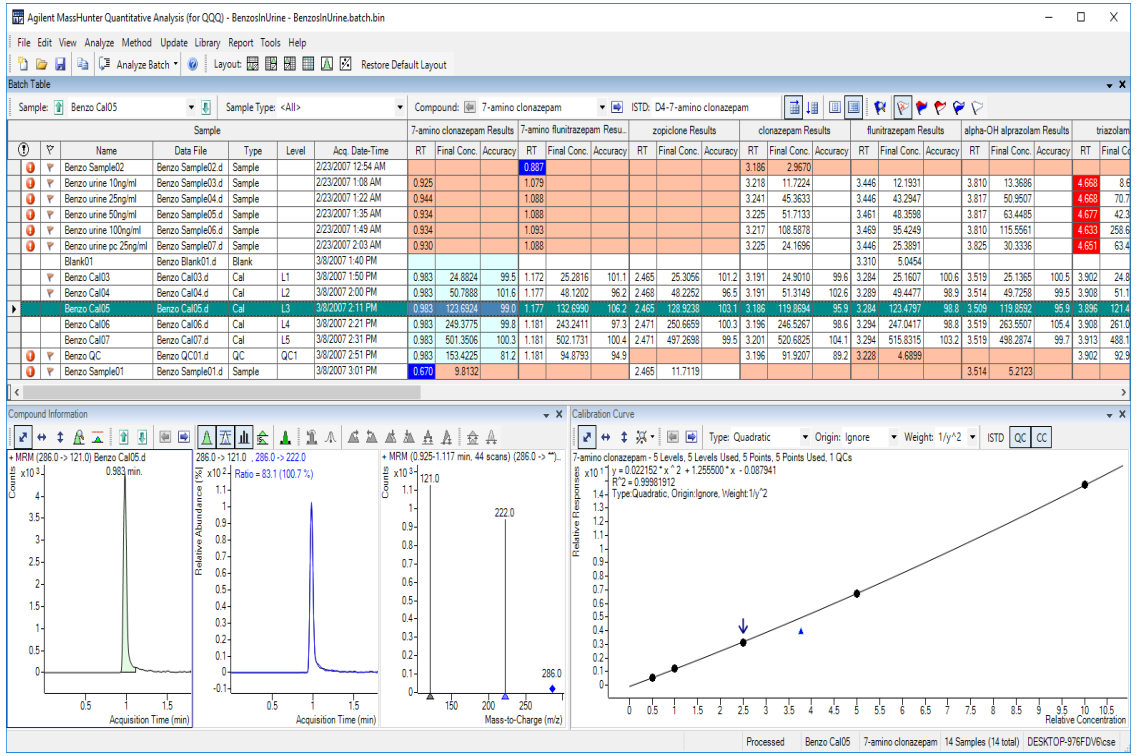
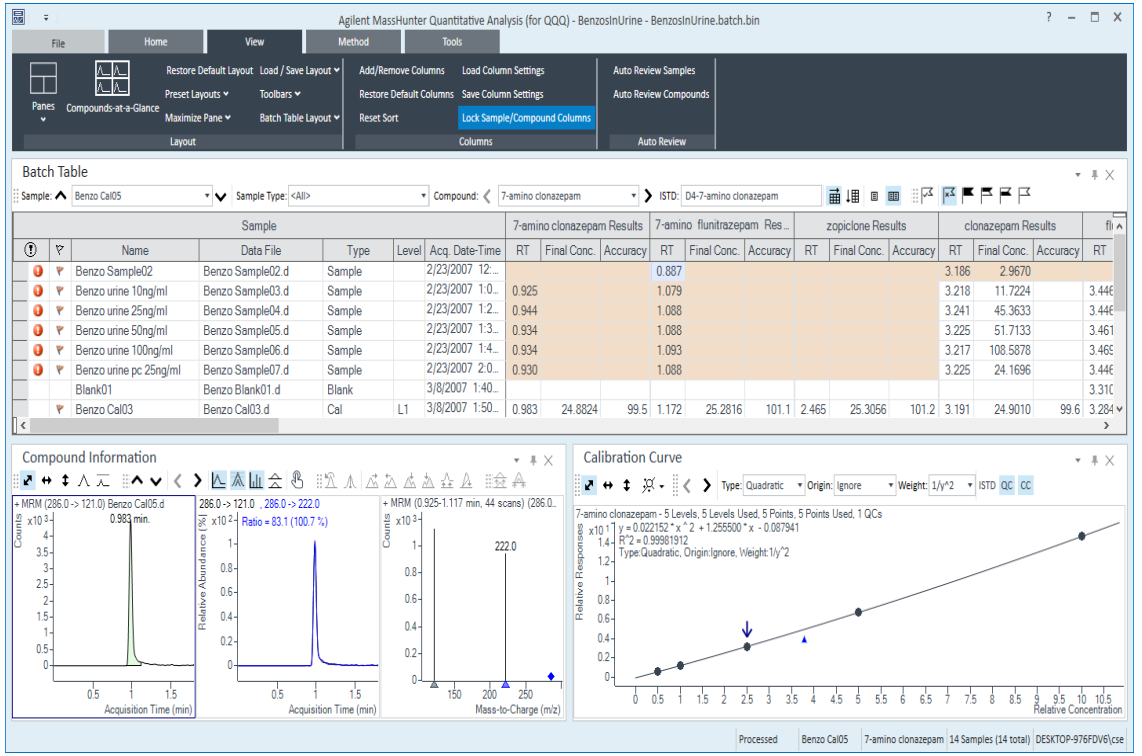
Classic UI



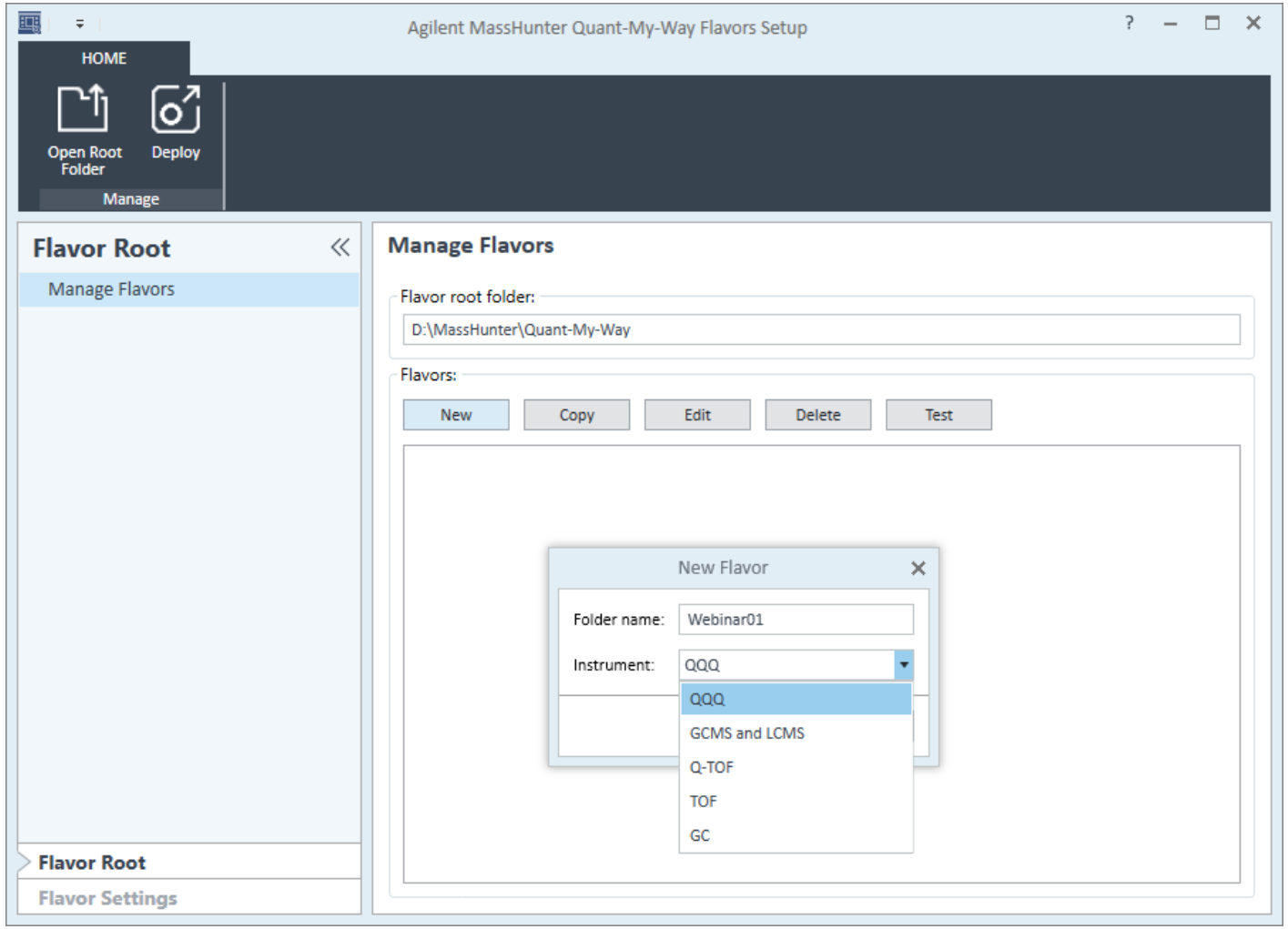
Quant-My-Way



Identical information → different appearance.

Quant-My-Way

Create and Manage Flavors



Click on Quant-My-Way Flavors Setup. Installed from **Start > Agilent MassHunter Quantitative Analysis > Quant-My-Way Flavors Setup.**

Select the Root Folder.

Click New and create a new Flavor for a given instrument type

- or -

Select an existing Flavor name.

Click Edit…..

Quant-My-Way

Edit the Flavor

Step through the various settings.

- General Settings
- Batch Table Settings
- Column Settings

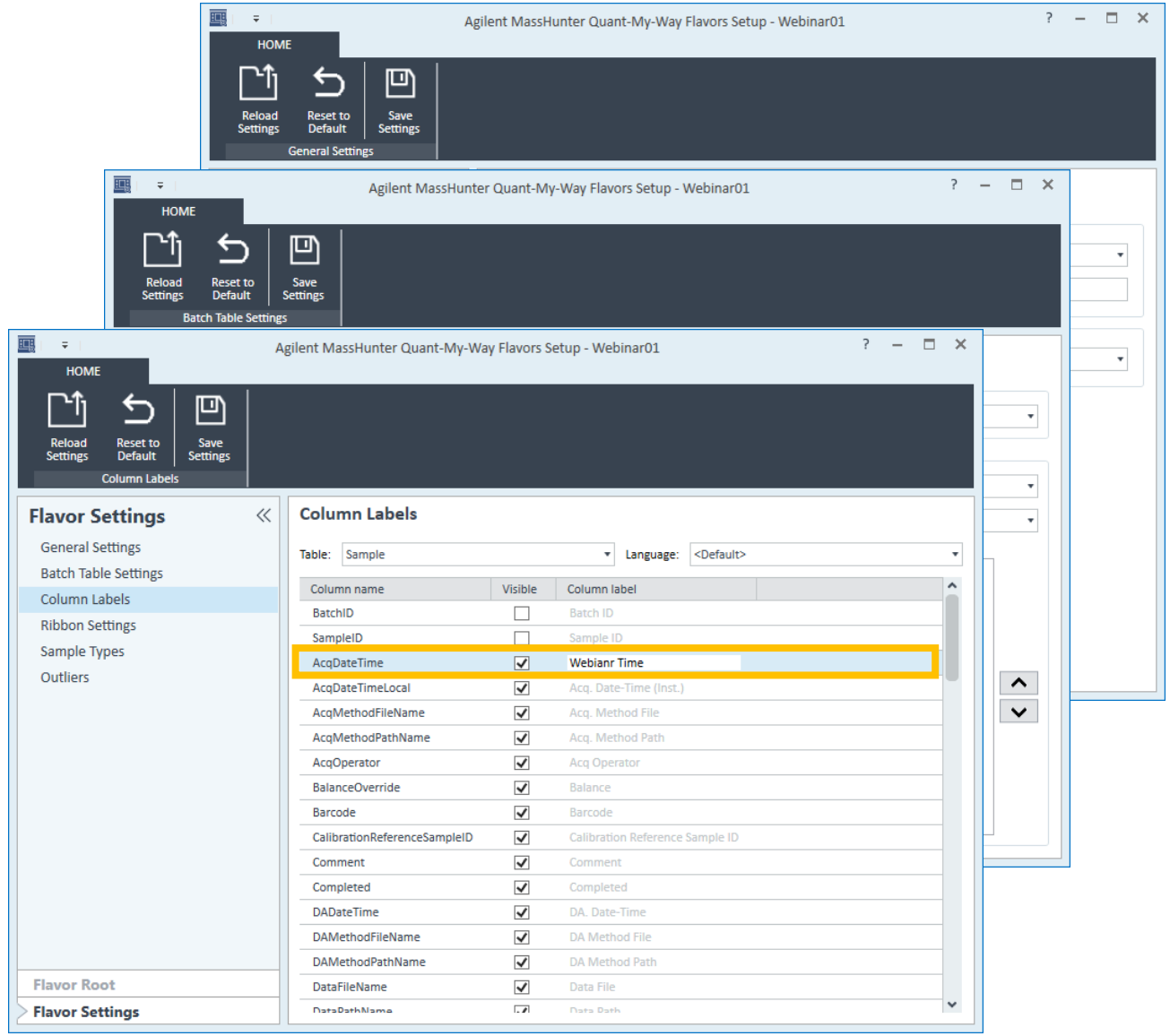
Modify as desired.

- Change AcqDate Time variable → Webinar Time

Save Settings.

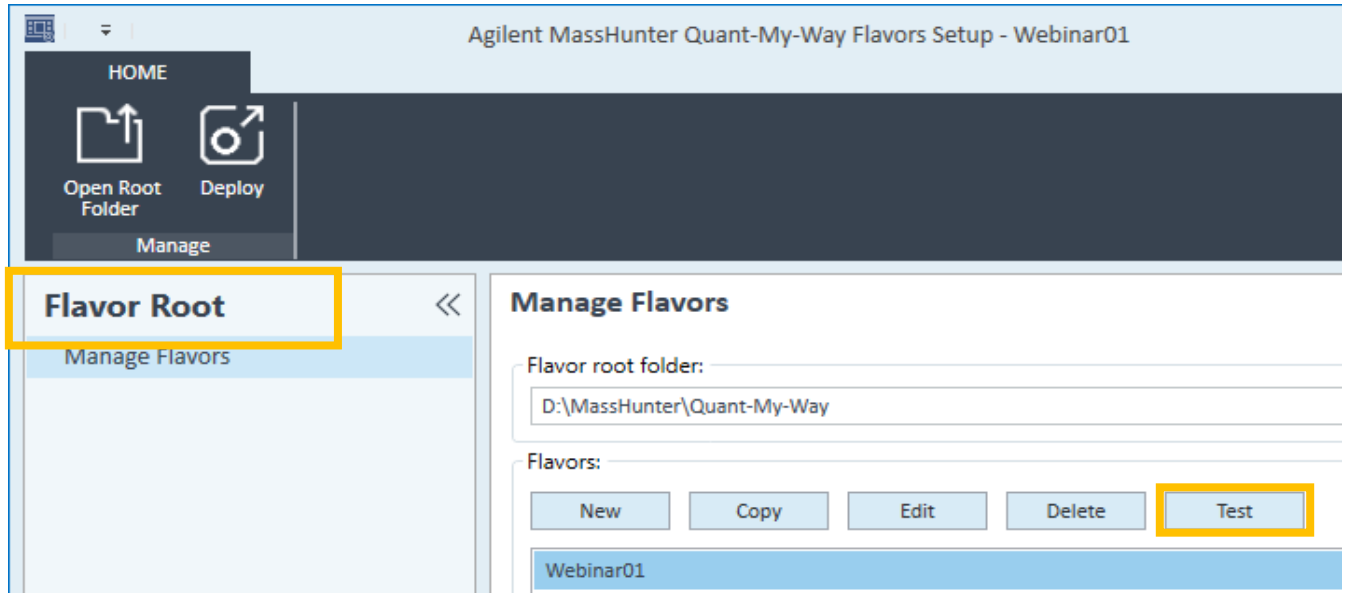
Step back to Flavor Root

Test

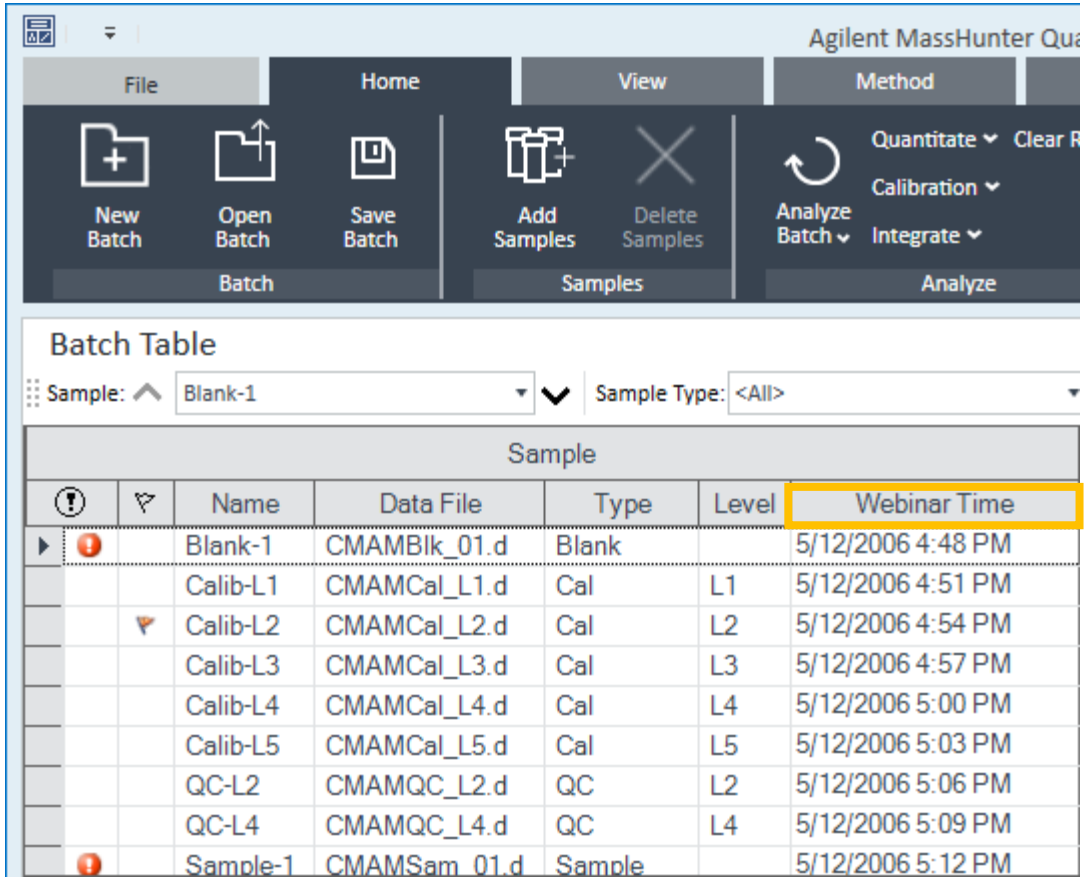


Quant-My-Way

Test the Flavor



Tip: Quant remembers the last configuration -> Restore User Settings.



Test the new flavor.

Automatically opens Quant-My-Way.

New label is present.

Tip: Test at each step of the way.

Quant-My-Way

Ribbon Layout

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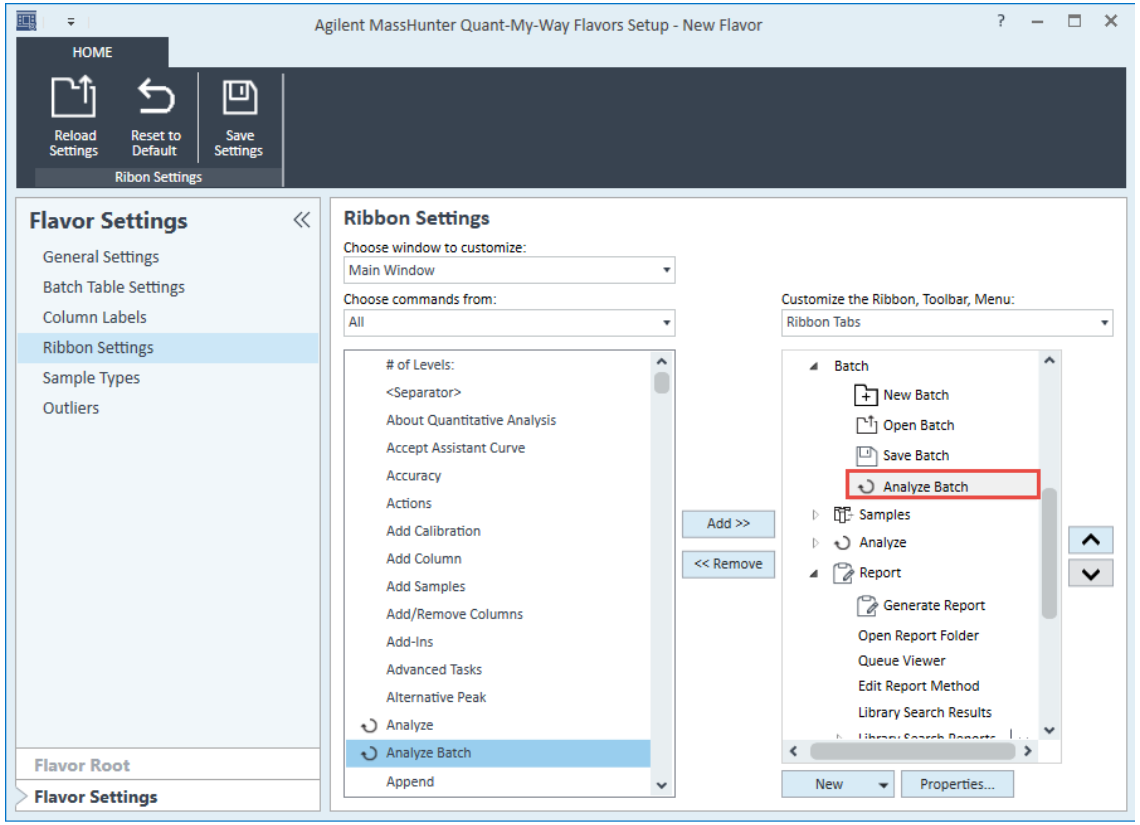
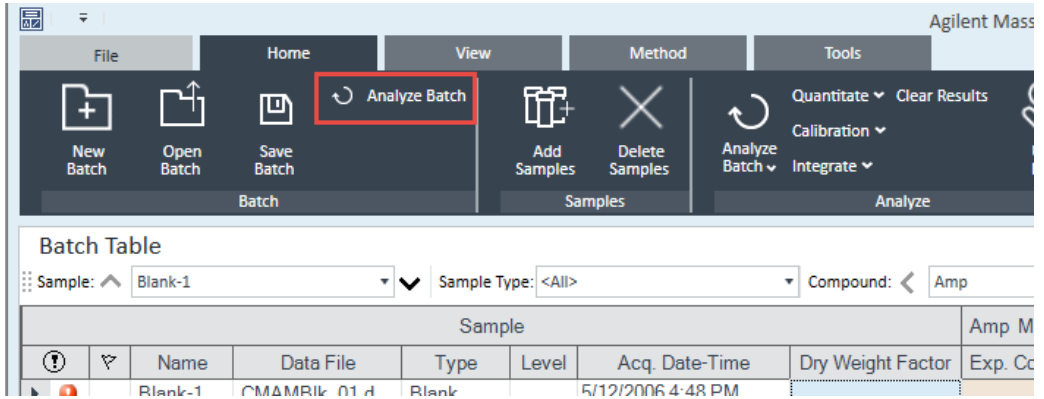


Easy access to frequently used items and features.

Remove unneeded or unused features to reduce clutter.



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Quant-My-Way

Help Files

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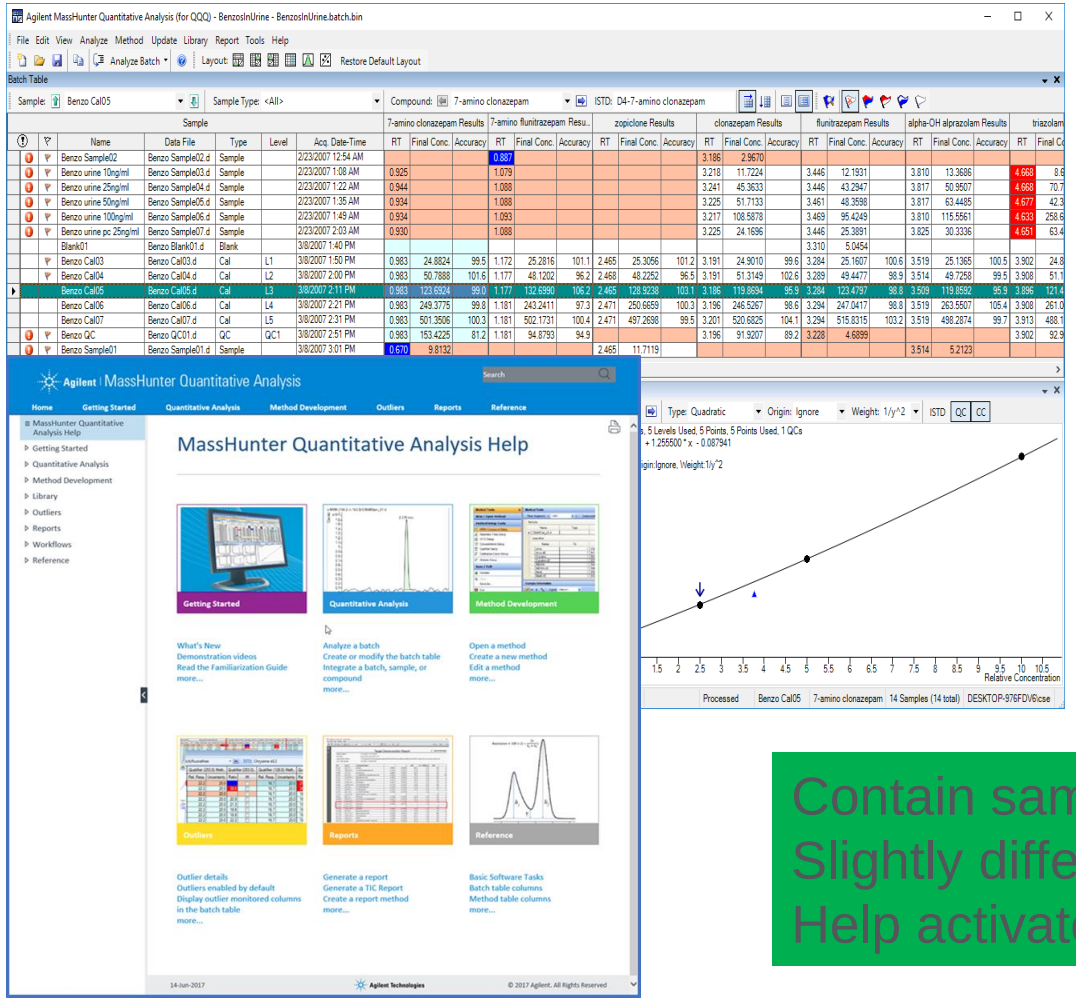
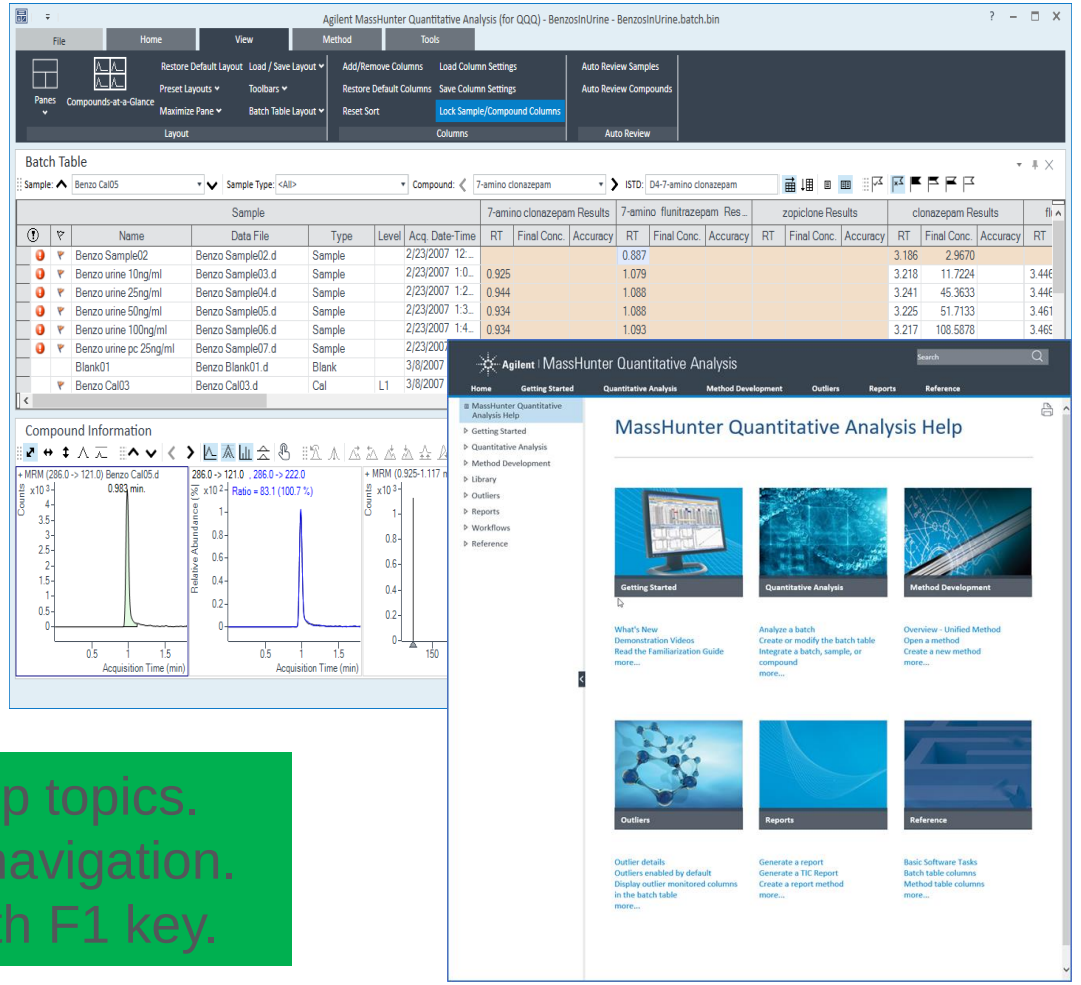
Classic UI



Quant-My-Way



Contain same help topics.
Slightly different navigation.
Help activated with F1 key.

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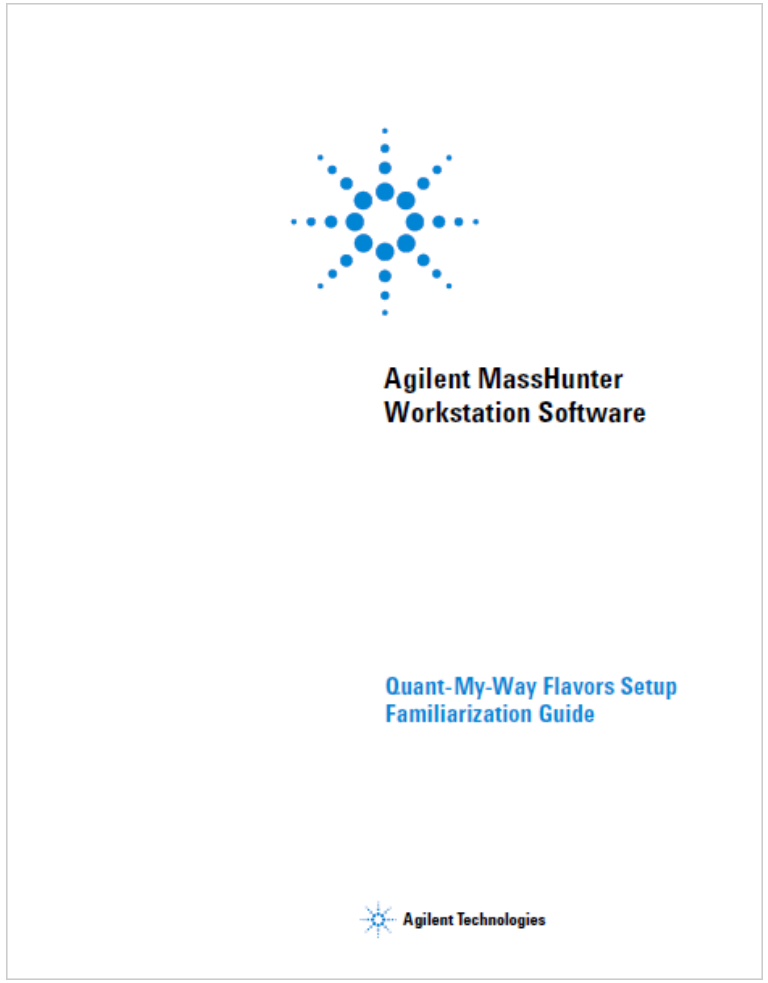
Training Resources

Familiarization Guide and Videos



Supplemental\MassHunter\Manuals\Quant

Name

- Quant-My-Way - Agile Iterative Development - Starter.mp4
- Quant-My-Way - Batch Table Settings - Demo - Advanced.mp4
- Quant-My-Way - Column Labels - Demo - Advanced.mp4
- Quant-My-Way - Compounds-at-a-Glance Demo - Starter.mp4
- Quant-My-Way - Custom Button.mp4
- Quant-My-Way - Deploy Flavors - Advanced.mp4
- Quant-My-Way - Flavors Setup steps - Starter.mp4
- Quant-My-Way - General Settings - Demo - Advanced.mp4
- Quant-My-Way - Introduction - Starter.mp4
- Quant-My-Way - Less is More - Starter.mp4
- Quant-My-Way - Outliers - Demo - Advanced.mp4
- Quant-My-Way - Ribbon Settings - Compounds-at-a-Glance.mp4
- Quant-My-Way - Ribbon Settings - Main Window - Batch Table - Toolbar+Context Menu - Advanced.mp4
- Quant-My-Way - Ribbon Settings - Main Window - Calibration Curve - Toolbar+Context Menu - Advanced.mp4
- Quant-My-Way - Ribbon Settings - Main Window - Compound Info - Toolbar+Context Menu - Advanced.mp4
- Quant-My-Way - Ribbon Settings - Main Window - MethodTable - Toolbar+Context Menu - Advanced.mp4
- Quant-My-Way - Ribbon Settings - Main Window - Others - Toolbar+Context Menu - Advanced.mp4
- Quant-My-Way - Ribbon Settings - Main Window - Ribbon Tabs - Advanced.mp4
- Quant-My-Way - Ribbon Settings - Main Window - Sample Info - Toolbar+Context Menu - Advanced.mp4
- Quant-My-Way - Ribbon Settings introduction - Advanced.mp4
- Quant-My-Way - Sample Types - Demo - Advanced.mp4

Supplemental\MassHunter\Videos\Quant

Quant-My-Way

Time for a demo

Next up:

Unknowns Analysis

Unknowns Analysis
Overview

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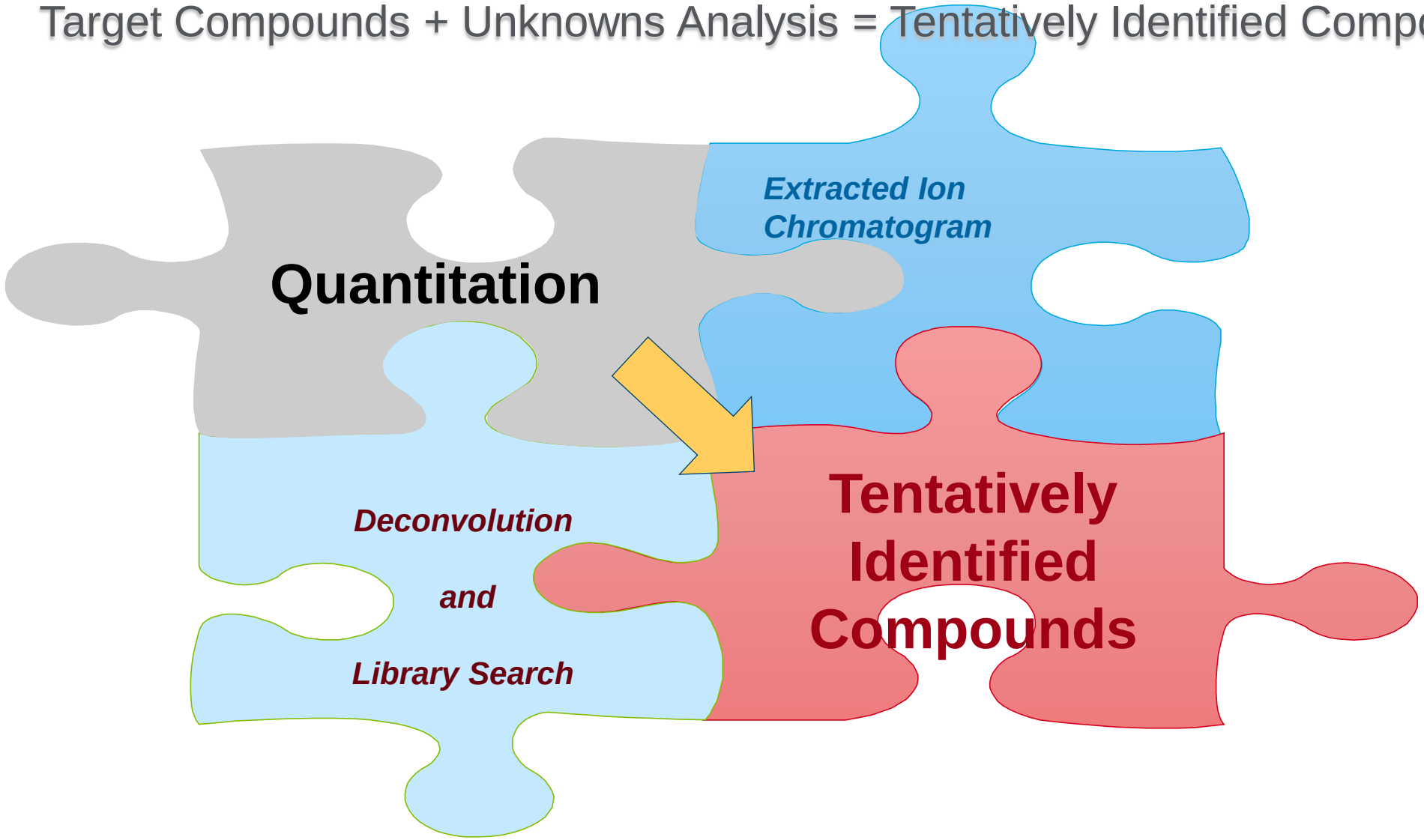
Tentatively Identified Compounds

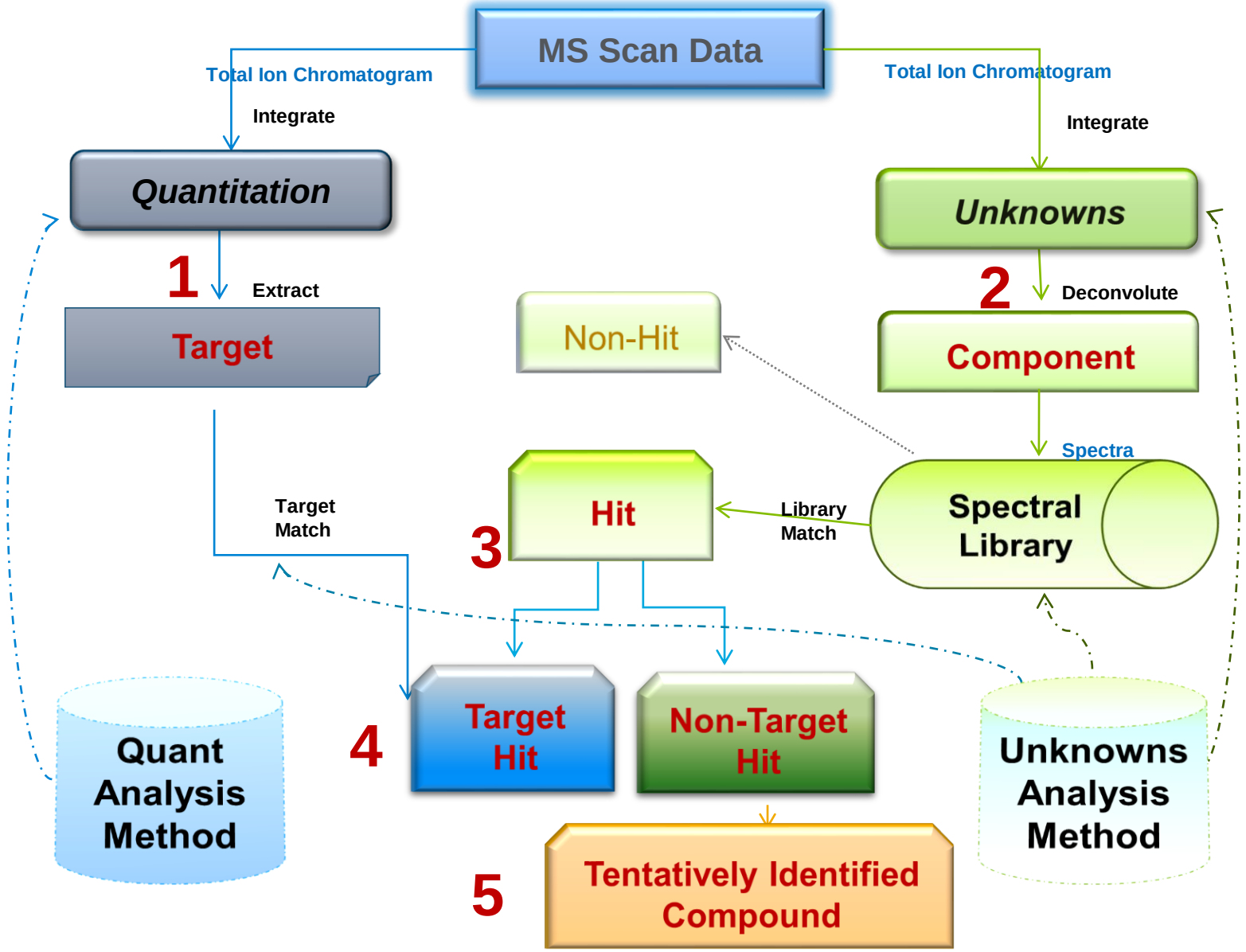
- Method Parameters
  - Peak Detection
  - Library Search
  - Compound Identification
  - Target Match (semi quantitation)
  - Blank Subtraction
- Component Review
- Screening
  - Minimal Sample Prep
  - Fast Chromatography
  - Component found ⇒ Confirmation
- Report Generation
  - PDF Report Builder
  - Queries

Overview of Unknowns Analysis

Target Compounds + Unknowns Analysis = Tentatively Identified Compounds



Quantitative Analysis & Unknowns Analysis Workflow



Unknowns Analysis Workflow

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Tentatively Identified Compounds

- Process the batch of samples in Quantitative Analysis
- Start Unknowns Analysis
- Edit an Unknowns Analysis Method
  - Peak Detection
  - Library Search
  - Compound Identification
  - Target Match (semi quantitation)
  - Blank Subtraction
- Component Review
  - Review component and library spectrum
  - View ion peak shapes vs. component peak shape vs. TIC
  - Run Queries for custom review
- Report Generation
  - PDF Report Builder

Process Batch with Quantitative Analysis

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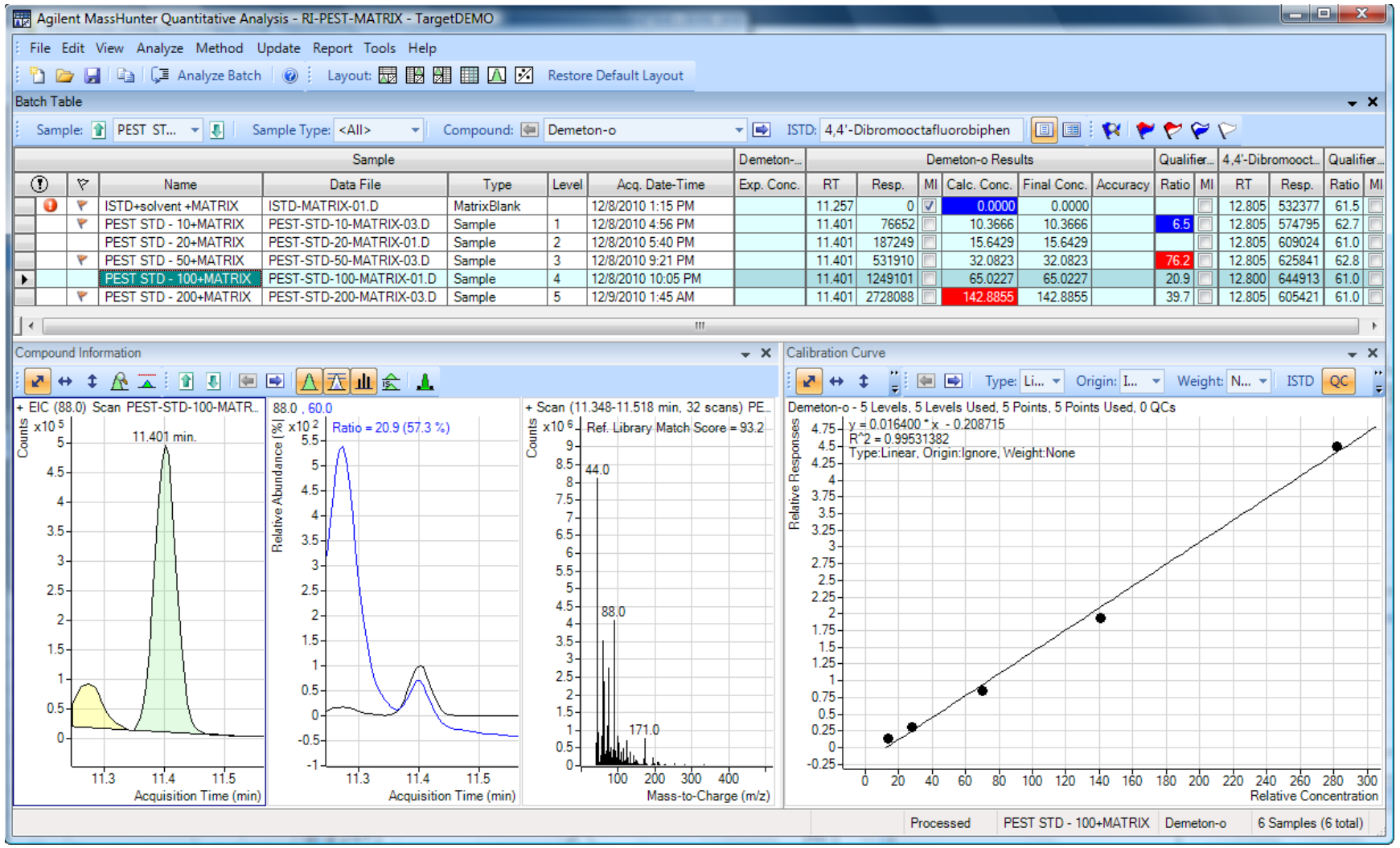
From Insight to Outcome

Information from the batch file (batch.bin) is used in Unknowns Analysis.



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Unknowns Analysis
Startup

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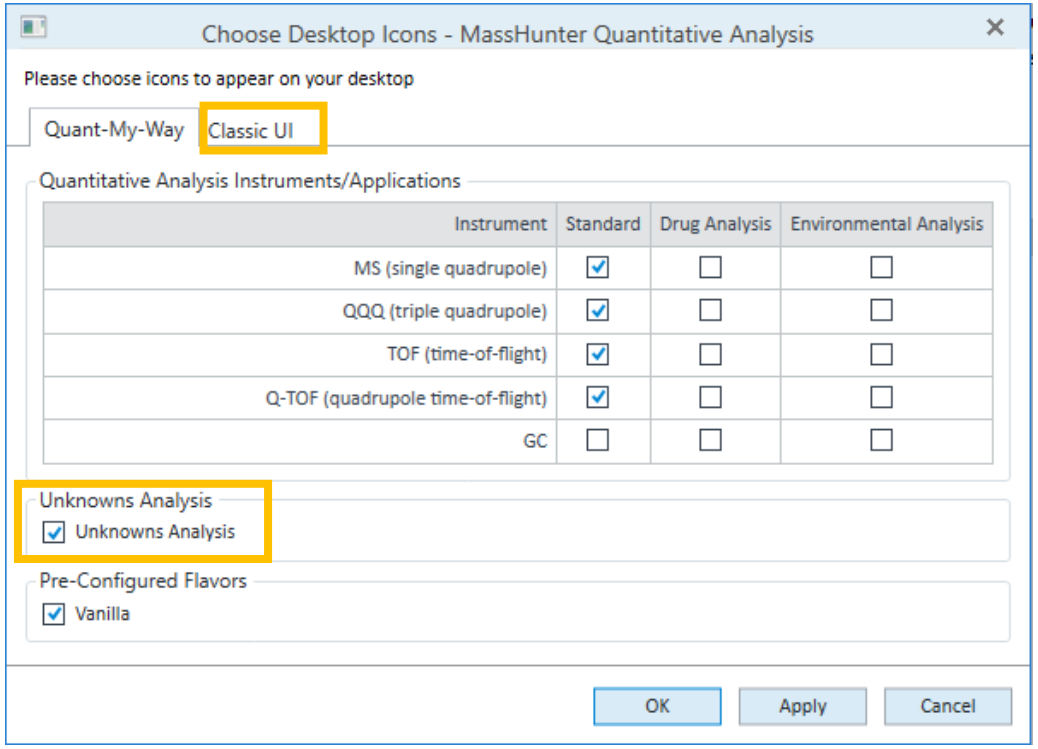
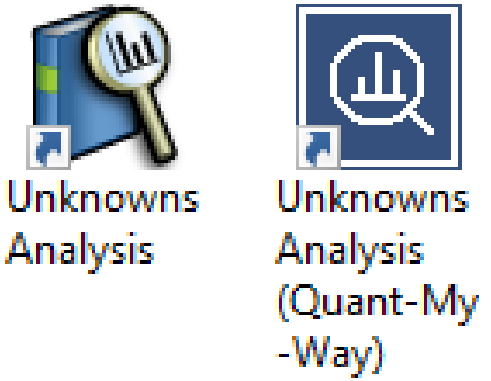
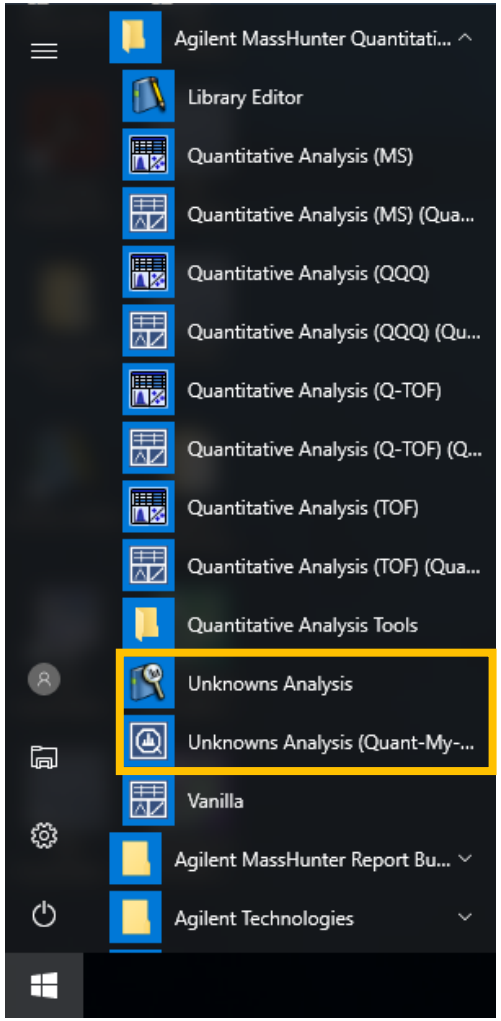


Loaded as part of MassHunter Quantitative Analysis.

As of Quant B.09.00 it will not be displayed in the Start menu unless it is enabled using the Choose Desktop Icons utility.





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Setting Up an Analysis
New Analysis

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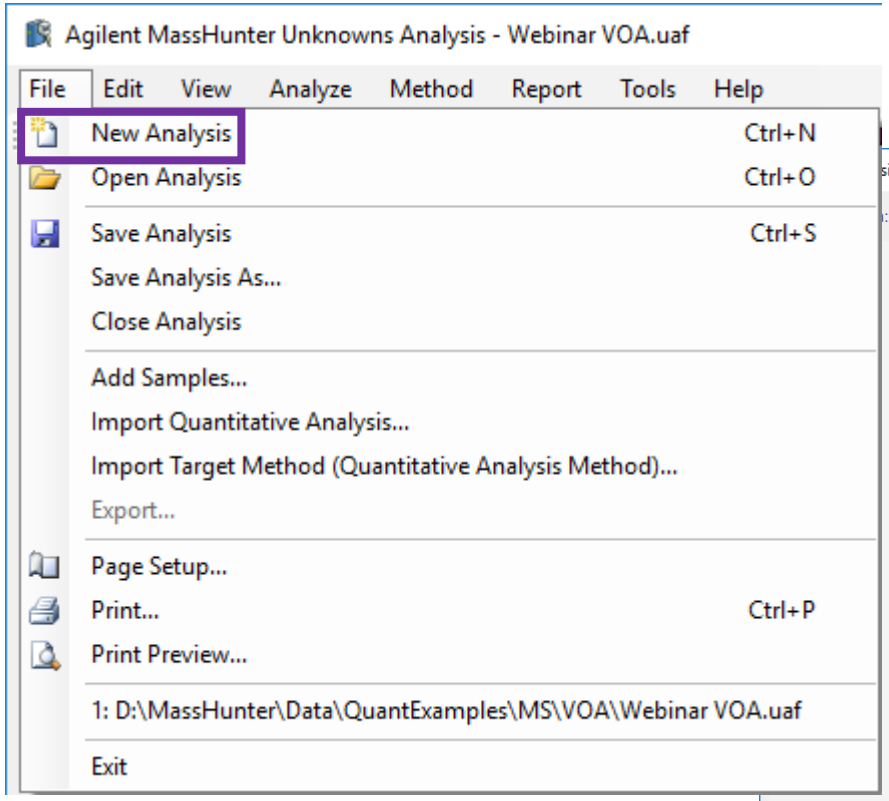
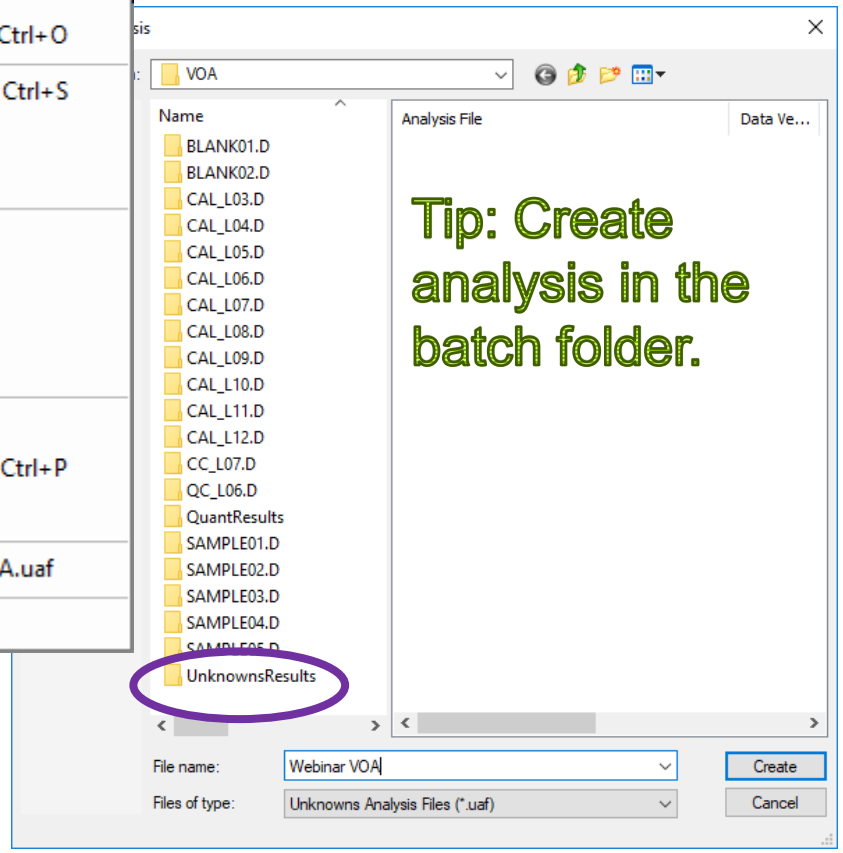
Unknowns Analysis file (.uaf) contains information on

- Quantitative Analysis batch (.batch.bin or .batch.xml)
- Unknowns Analysis Method (.uamethod.xml)
- Sample list (typically from Quantitative Analysis batch)
- Results
  - Components with any identity information.
- Component is the “compound” found in Unknowns Analysis.





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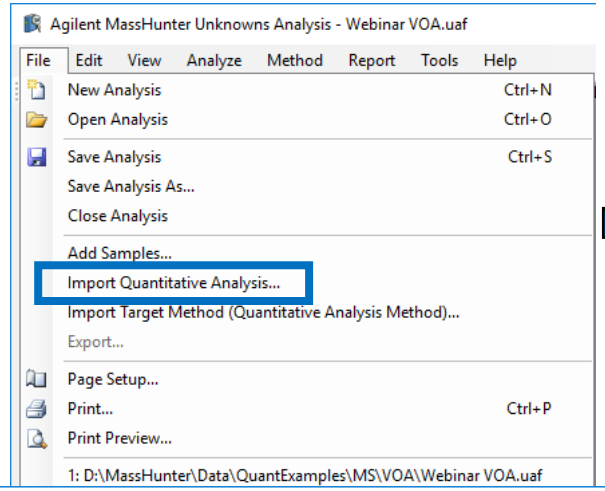
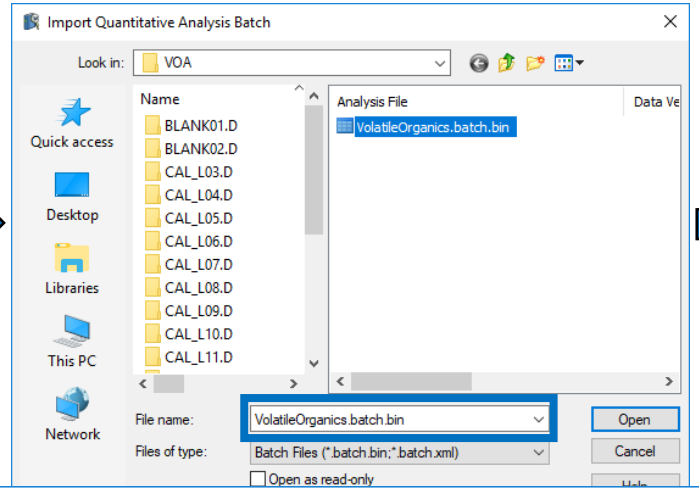
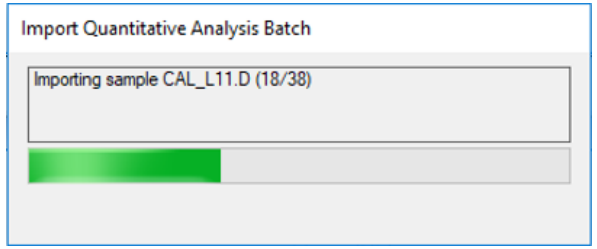
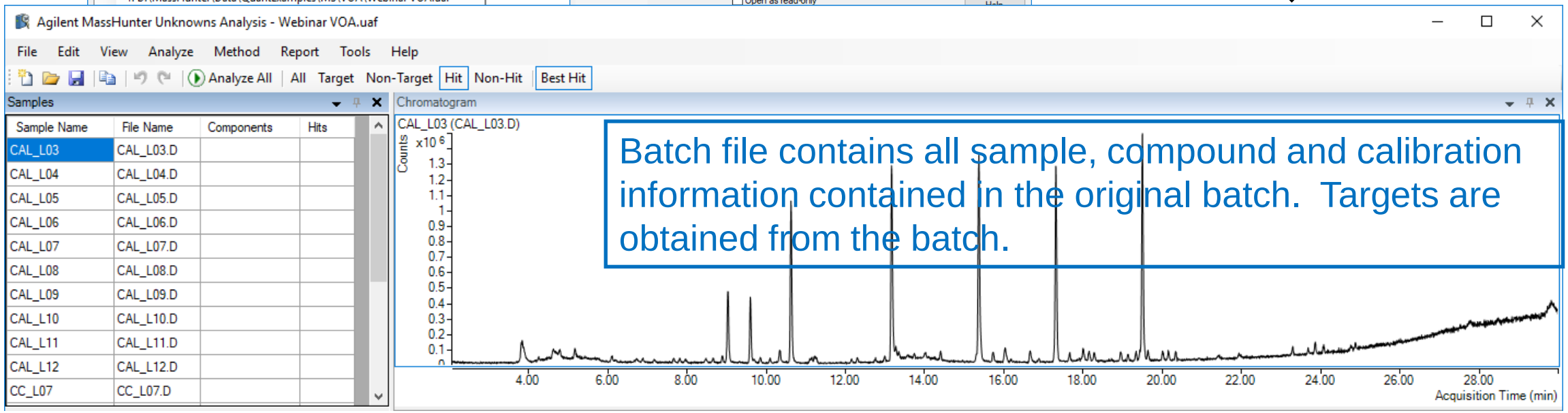
Setting Up an Analysis

Import Quantitative Analysis Batch









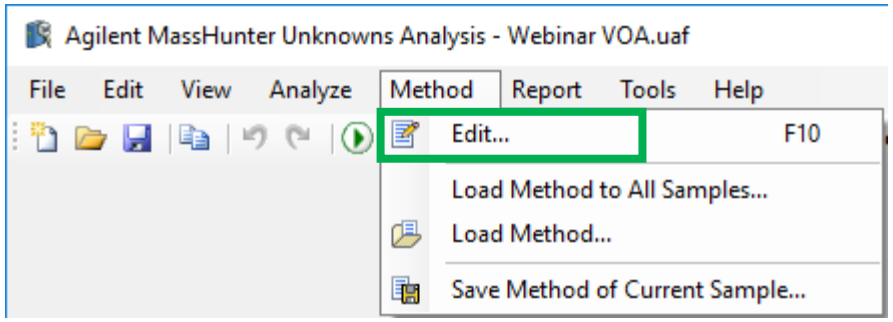
Batch file contains all sample, compound and calibration information contained in the original batch. Targets are obtained from the batch.

Unknowns Analysis

Time for a demo

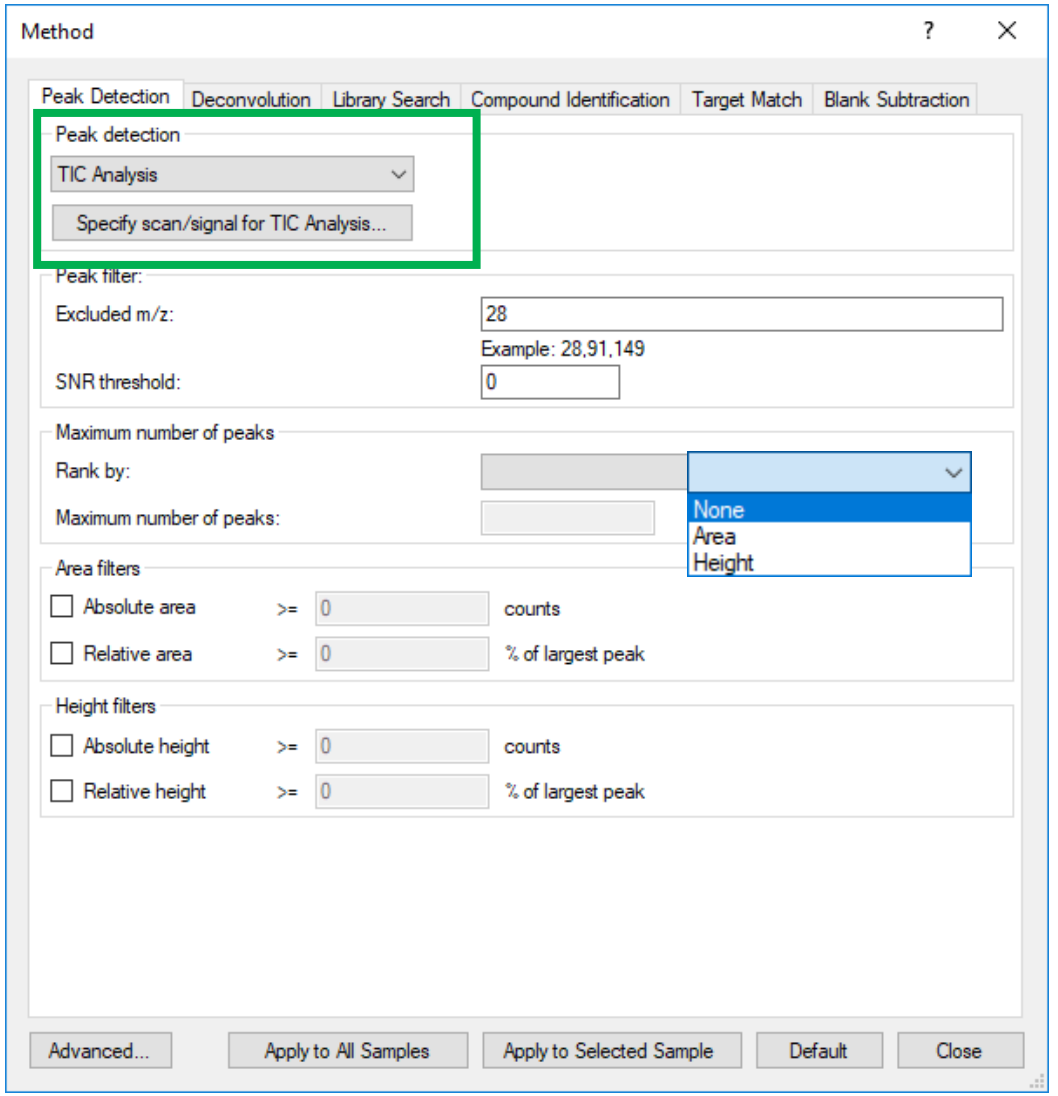
Next up:
Unknowns Analysis Methods

Edit Method
Peak Detection

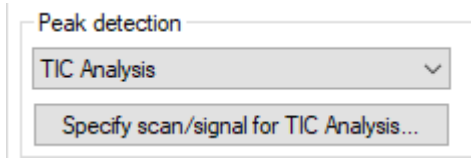


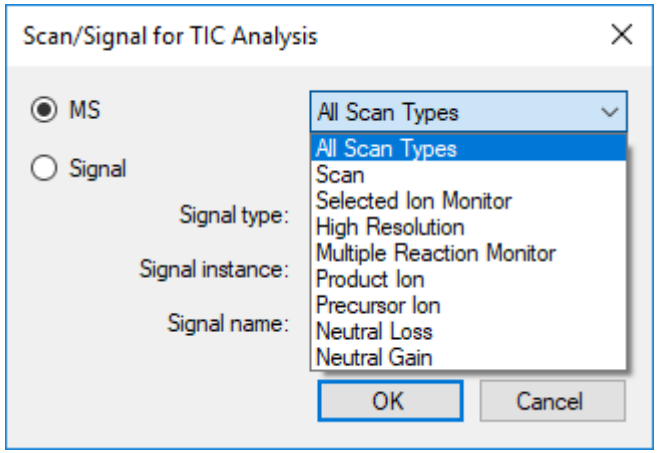
Choose Peak Detection Parameters

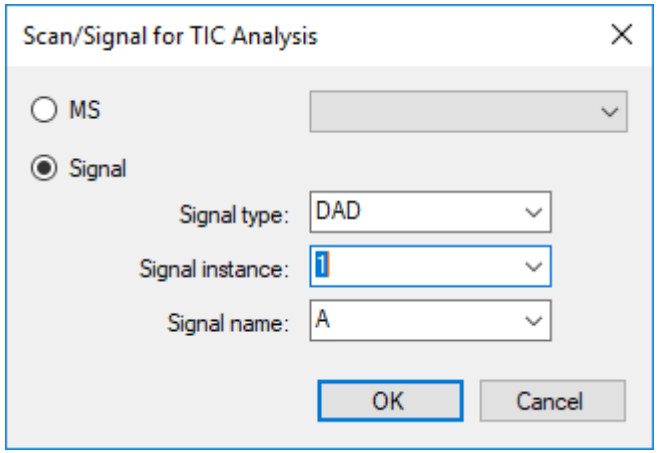
- TIC Analysis locates components by integration.
- Deconvolution locates components using parameters.
- SureMass applicable only to GC QTOF data.
  - Feature Extraction algorithm.
- Can also set Peak Filter parameters based on SNR, area or height.

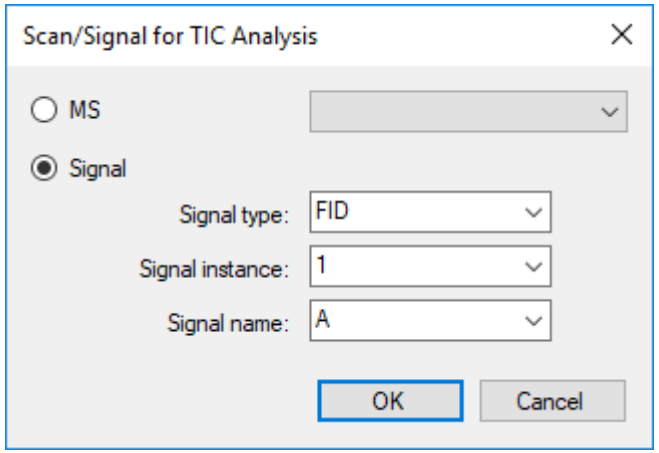


Edit Method
Peak Detection









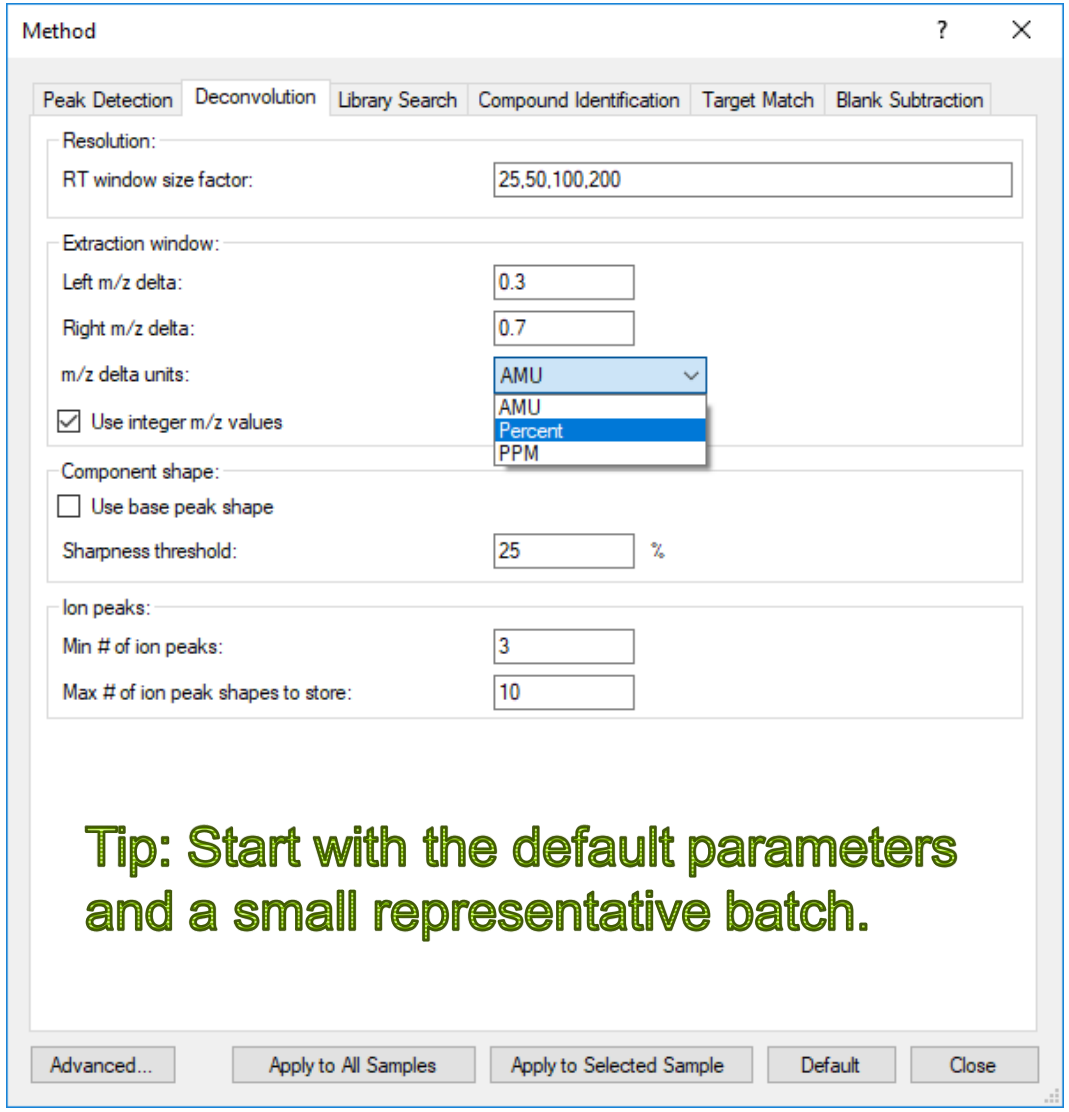
MS
Can focus on various scan types.

UV
Can select various DAD signals.

GC
Can look at various GC signals.

Tip: TIC Analysis uses an integration algorithm.

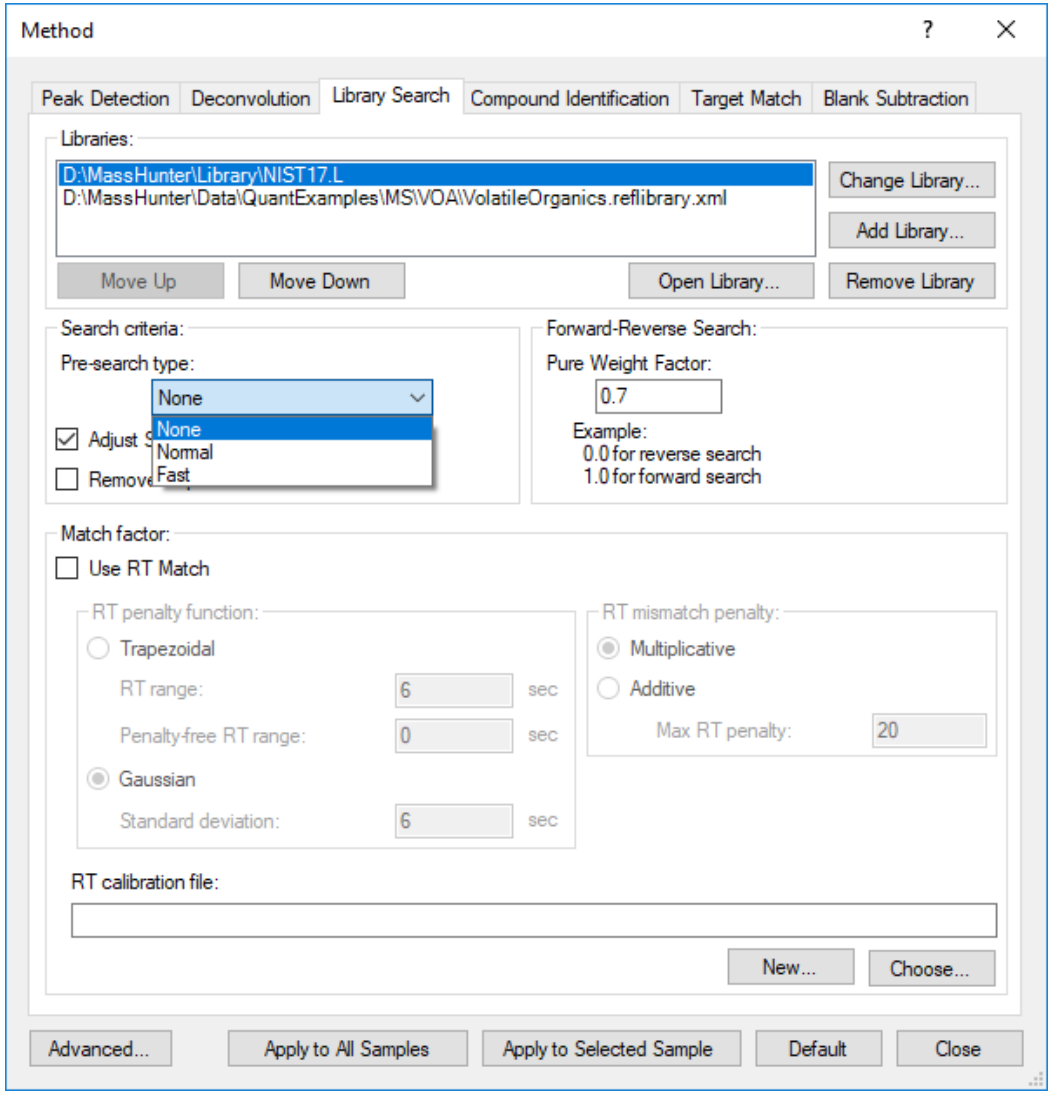
Edit Method
Deconvolution



Deconvolution Parameters

- RT window size factor →Key parameter that controls the grouping of EIC peaks into components.
  - Larger value ⇒ fewer components.
  - Equivalent to RT window in AMDIS, but unitless.
- Extraction window →Allowable mass drift.
  - More applicable to high resolution data.
  - Low resolution data can use integer m/z values.
- Use integer m/z values → Evaluates both rounded (integer) and unrounded m/z values when extracting EICs.
  - Almost always doubles number of components.
- Component shape →Matches the EIC peak shape across the component.
- Ion Peaks→ controls the number of mass spectral peaks (depends on data EI, CI, ESI, APCI, etc.).

Edit Method
Library Search



Library Search Parameters

- Libraries → Multiple Libraries can be searched.
  - Search ordered can be changed.
  - Library can be opened and viewed in Library Editor.
- Search Criteria **Tip: Recommended → Normal**
  - None ⇒ no preliminary search.
  - Normal ⇒ Screens entire library ⇒ 50-100 times faster.
  - Fast ⇒ Uses an index for potential candidates. ⇒ 100-1000 faster
- Forward-Reverse-Search Pure Weight Factor **New Feature**
- Match Factor
  - Uses retention times from library or retention indices (RT calibration file needed).
- Can set different parameters for different libraries.
  - Including different Match factor parameters, RT and RI libraries

Edit Method
Compound Identification

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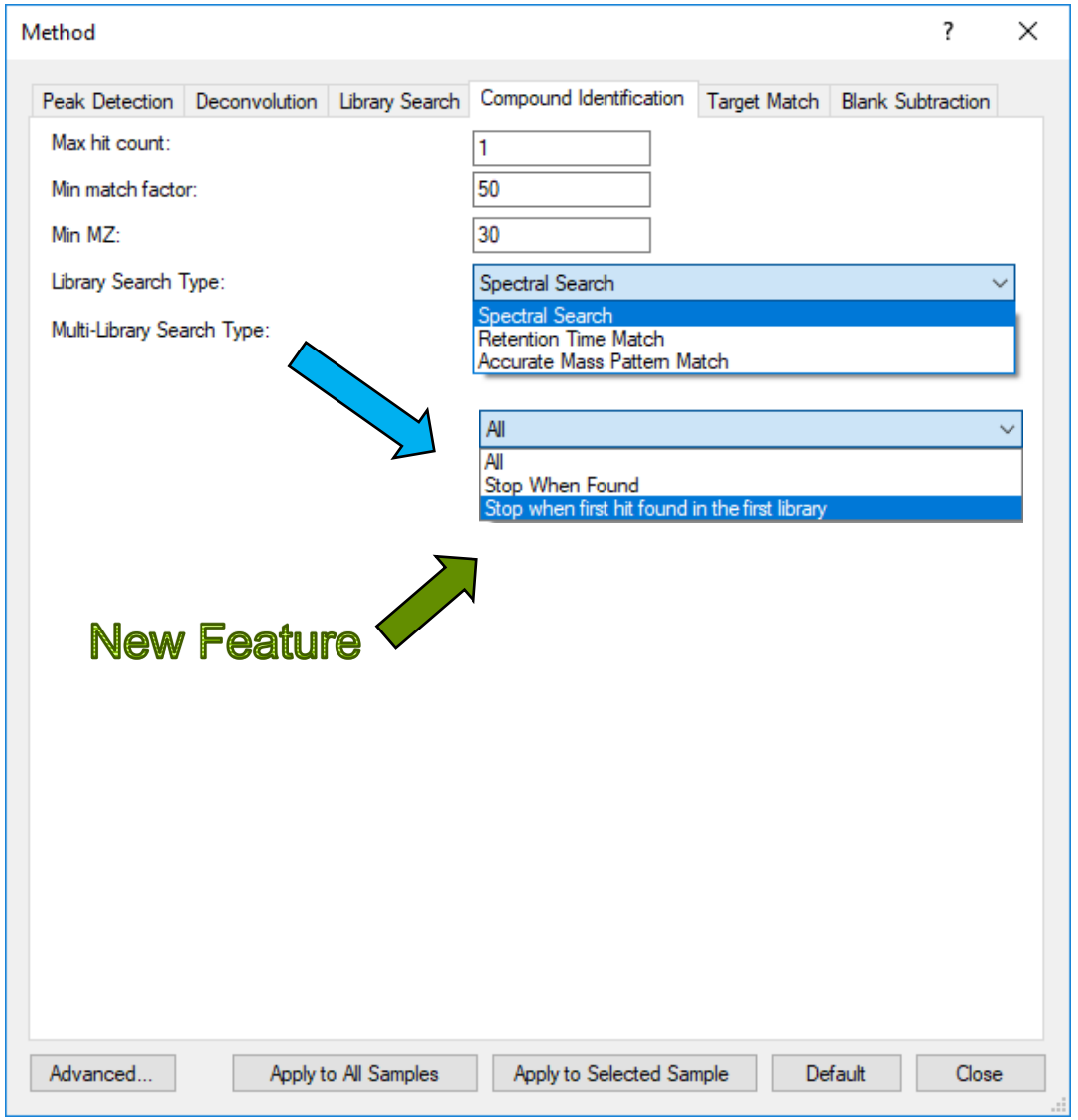
Compound Identification Parameters

- Max hit count ⇒ number of library matches to save.
- Min match factor
- Min MZ ⇒ Important factor
  - Set to minimum scan ranges
  - avoids penalties for low masses that may be in library but not is spectrum.
- Library Search Type
  - Spectral Search used dot product search.
  - Retention Time Match ⇒ for GC, LC 2D data.
  - Accurate Mass Pattern Match ⇒ Isotopic pattern match for TOF only.
- Multi-Library Search Type
  - stop when first hit found in the first library.
  - put a user generated library first.



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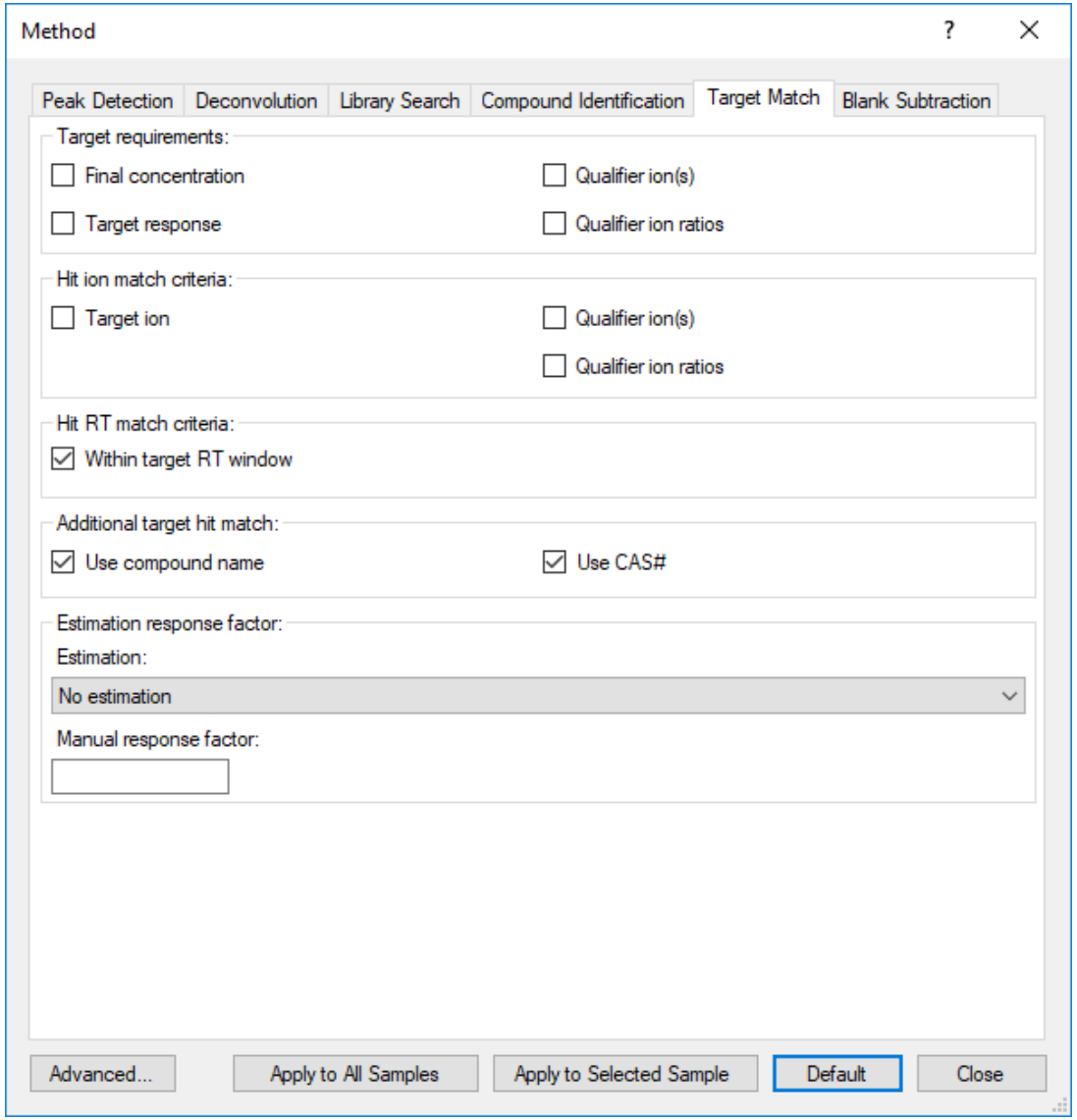
Edit Method

Target Match

Target Match Parameters

- Target requirements ⇒ Filters the quant method compound (target) list.
  - Final/target concentration > 0
  - Qualifier ions found
  - Qualifier ratios in specified ratio
- Hit ion match criteria ⇒ Filters the components list.
  - Target ion > 0
  - Target ion found and/or Qualifier ion(s) found.
  - Qualifier ions in specified ratios.
- Hit RT match criteria ⇒ component within Quant RT window
- Additional target hit match
  - must be present in quant method and match library.

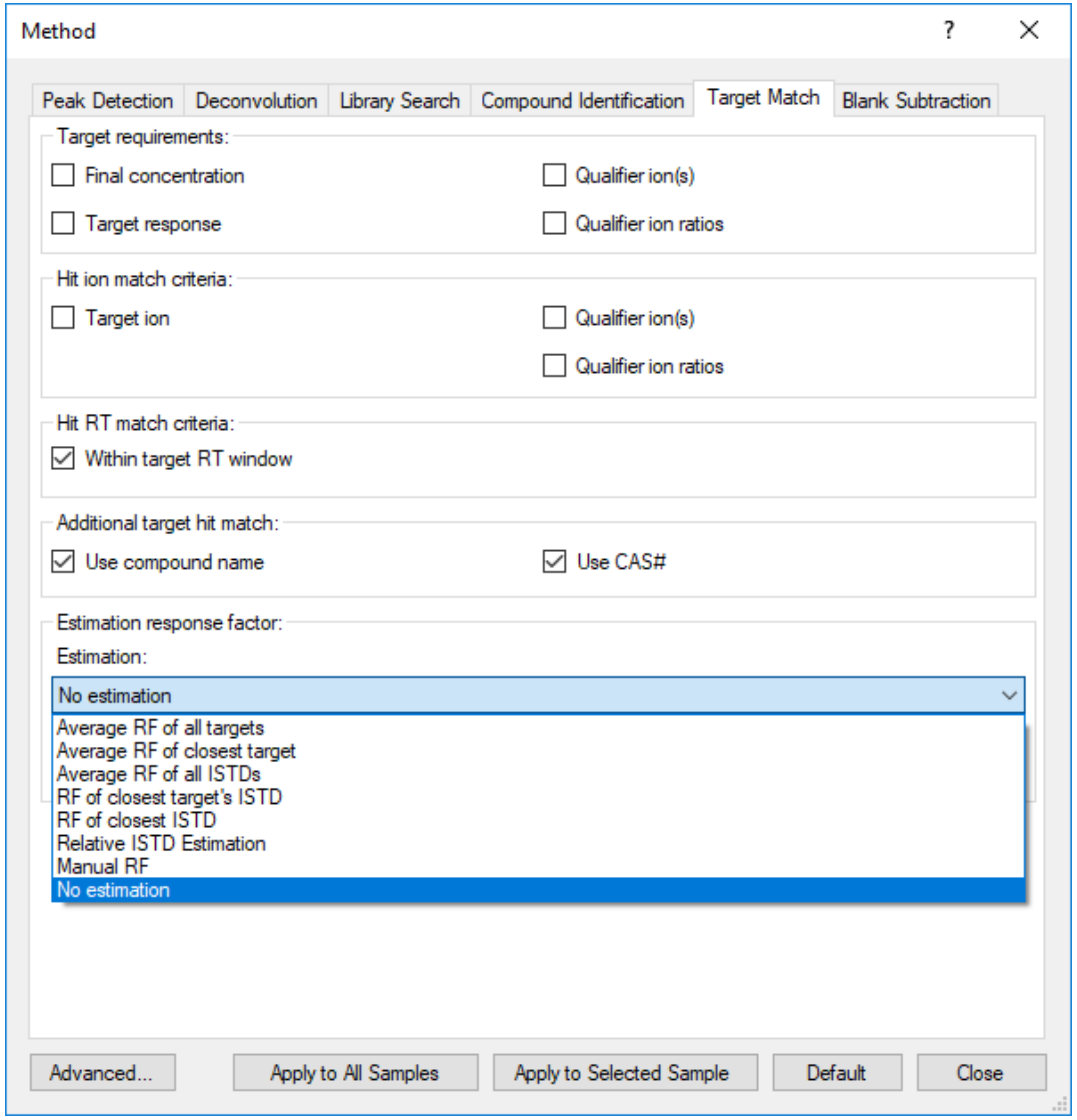


Edit Method

Target Match –Semi Quantitation

Target Match Parameters

- Estimation response factor ⇒ Method of semi quantitation.
  - Based on response factors from Quantitative Analysis.
  - Calculates the estimated concentration based on value chosen.
  - A manual response factor can be chosen for semi quantitation of the components.

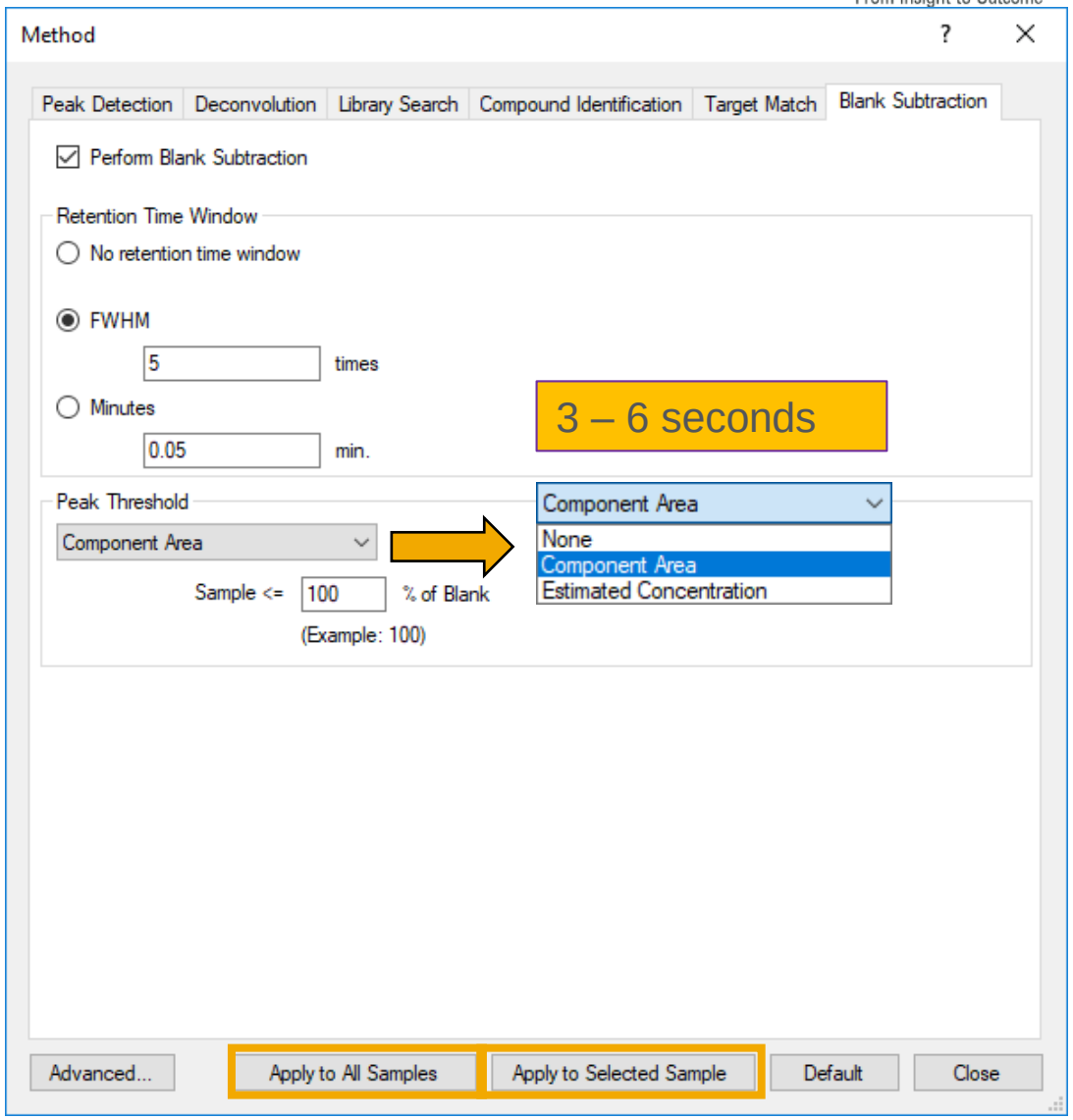


Edit Method

Blank Subtraction

Blank Subtraction Parameters

- Perform Blank Subtraction
  - assumes a blank is present in sample list
  - annotates blank subtracted from sample
- Retention Time Window => allows for RT variation between blank and sample
  - No retention time window active => sample and blank must have ‘same’ retention time to be subtracted.
  - FWHM when checked the blank peak must be within the specified multiple of the sample peaks Full Width at Half Maximum.
  - Minutes when active, blank peak must be specified minutes to the sample.
- Peak Threshold
  - Blank peaks will not be subtracted from sample peaks unless the Component Area/Estimated Concentration exceeds the specified percentage of the samples.



Edit Method

Advanced Parameters

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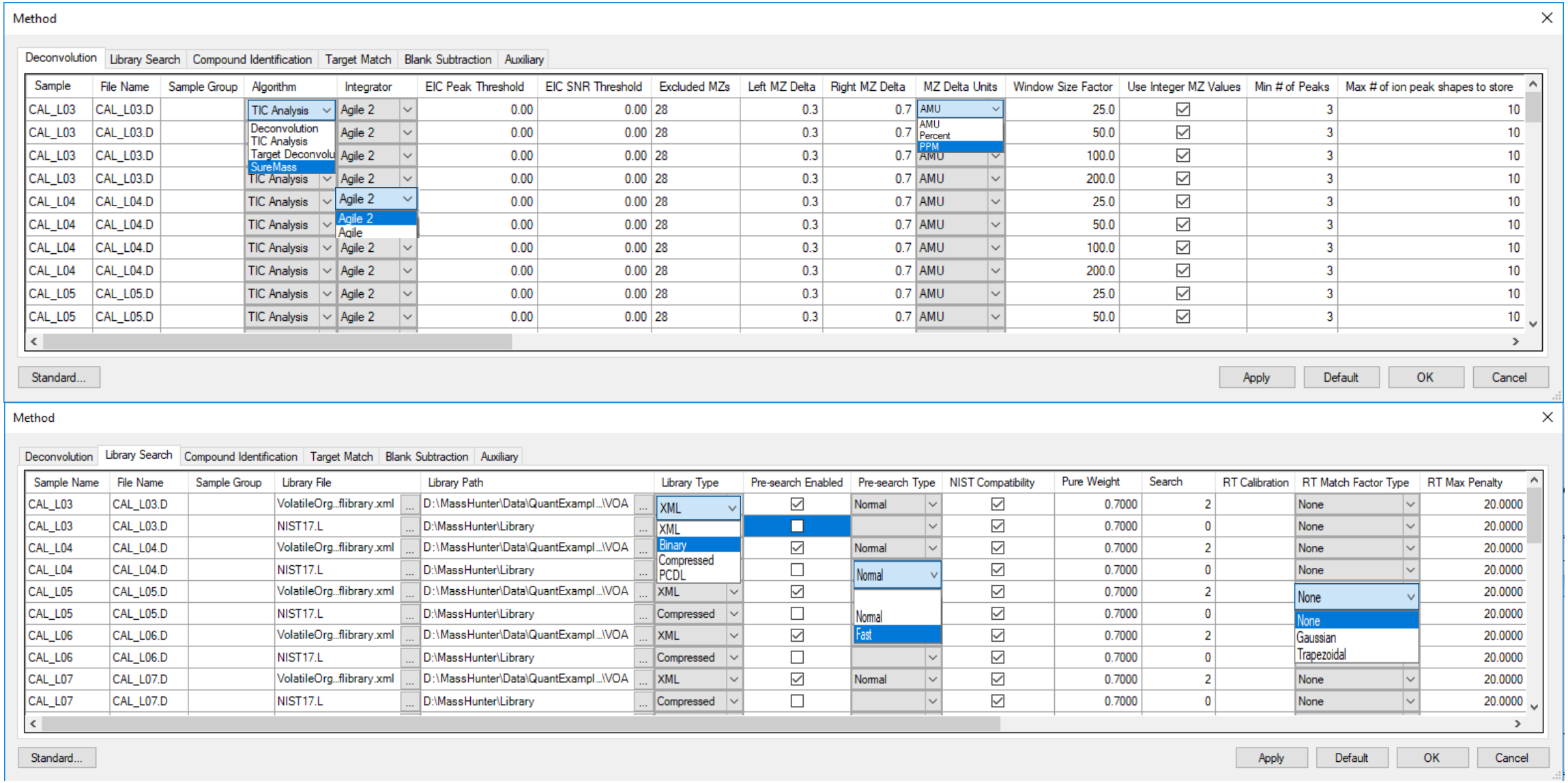

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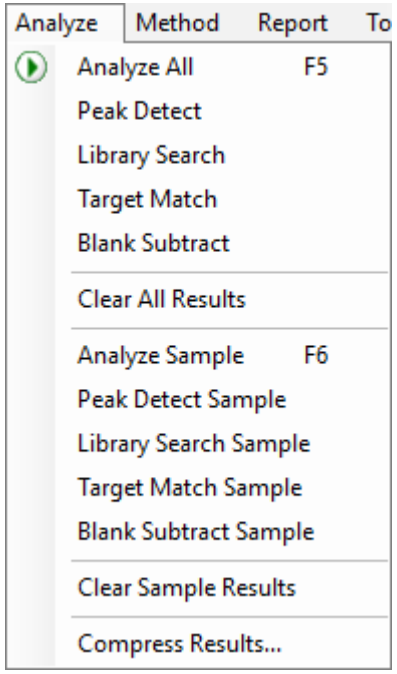
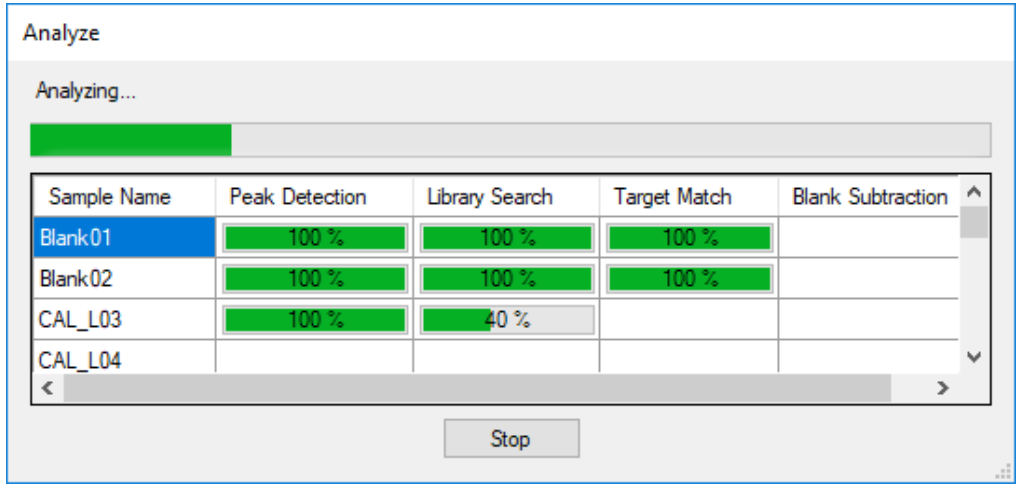
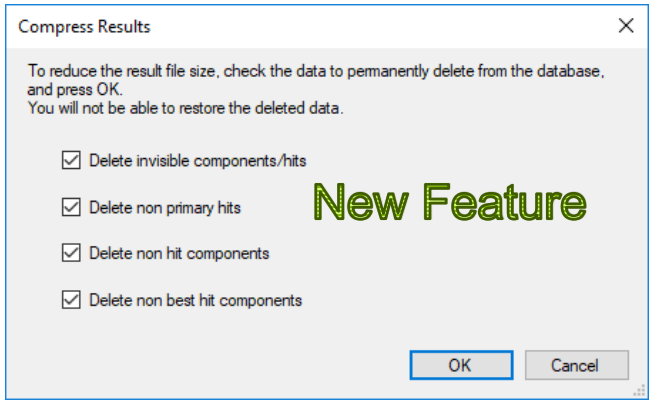
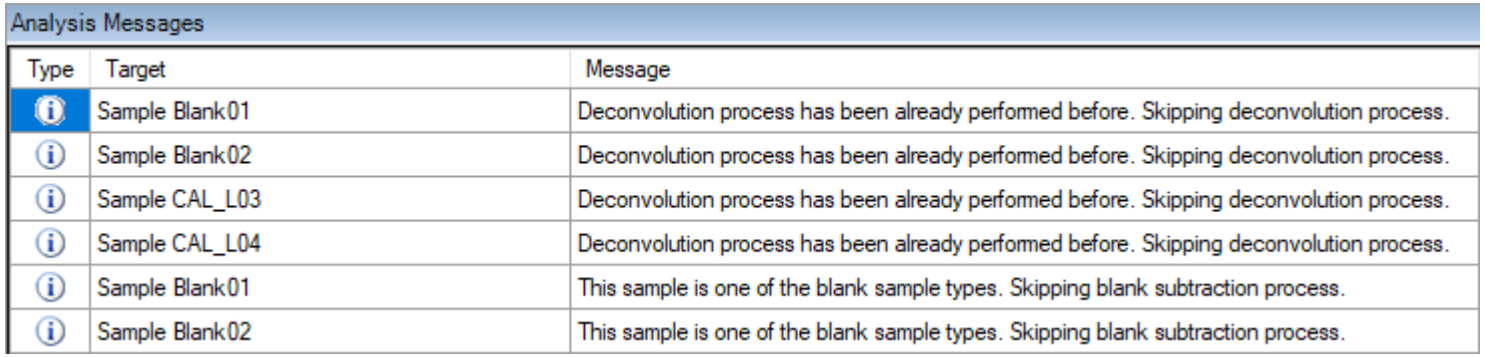
Analyze
Analyze All



Clicking **Analyze All** causes each sample to be fully processed. This step can take several minutes.



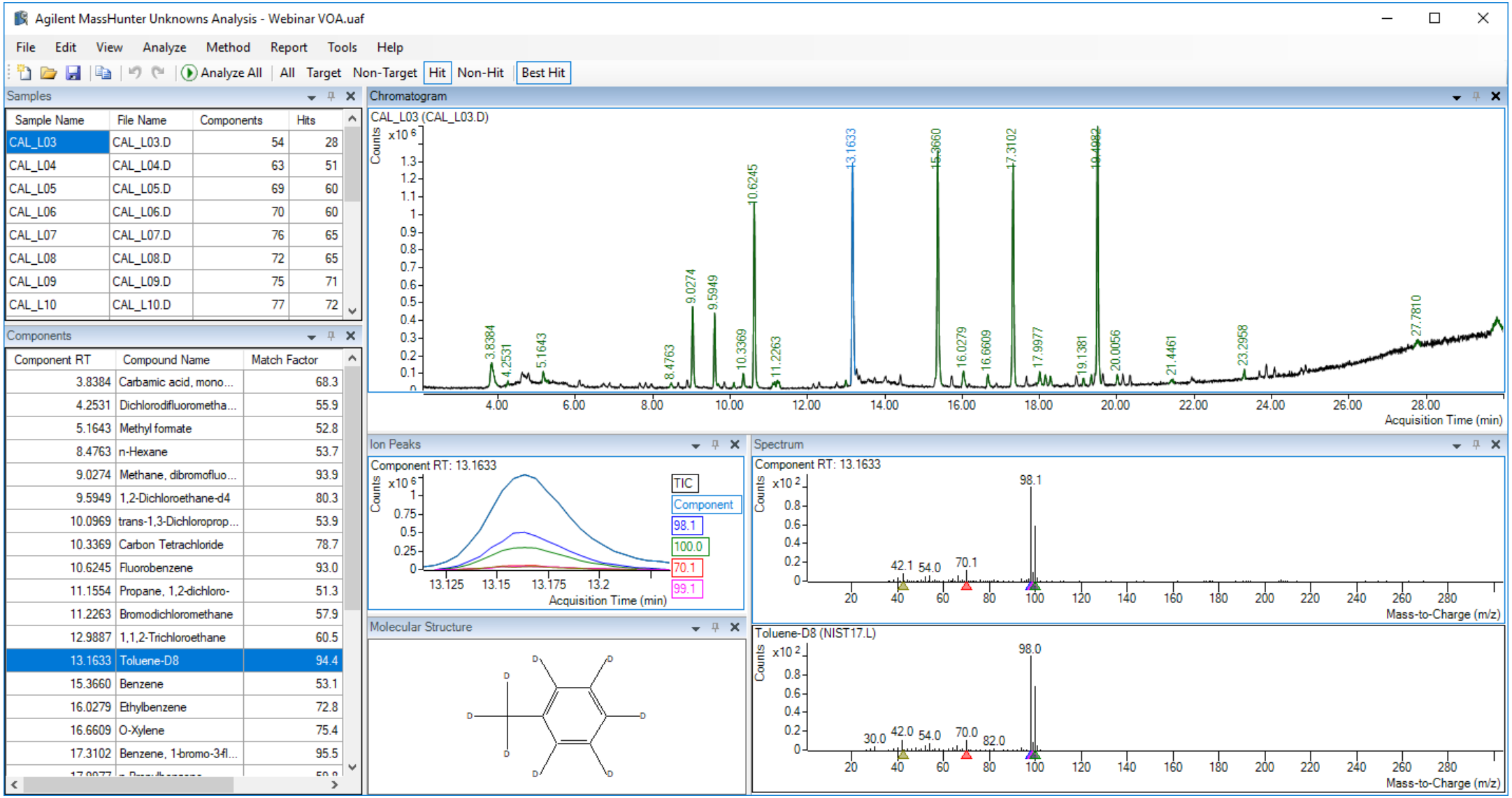




Analysis Messages provide guidance with information and errors.

Component Review

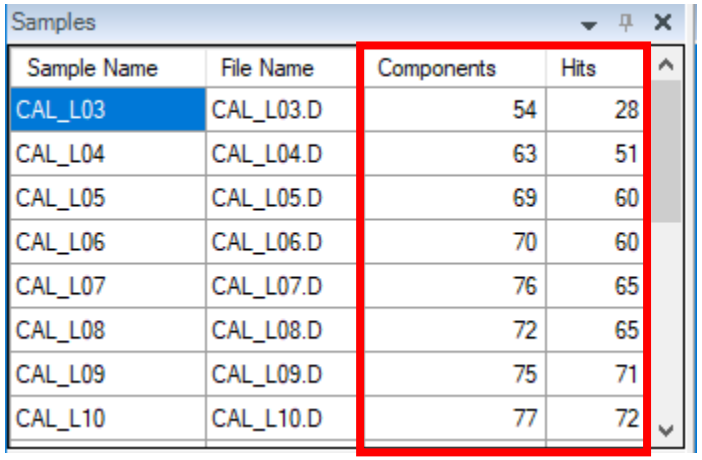
Agilent CrossLab
From Insight to Outcome

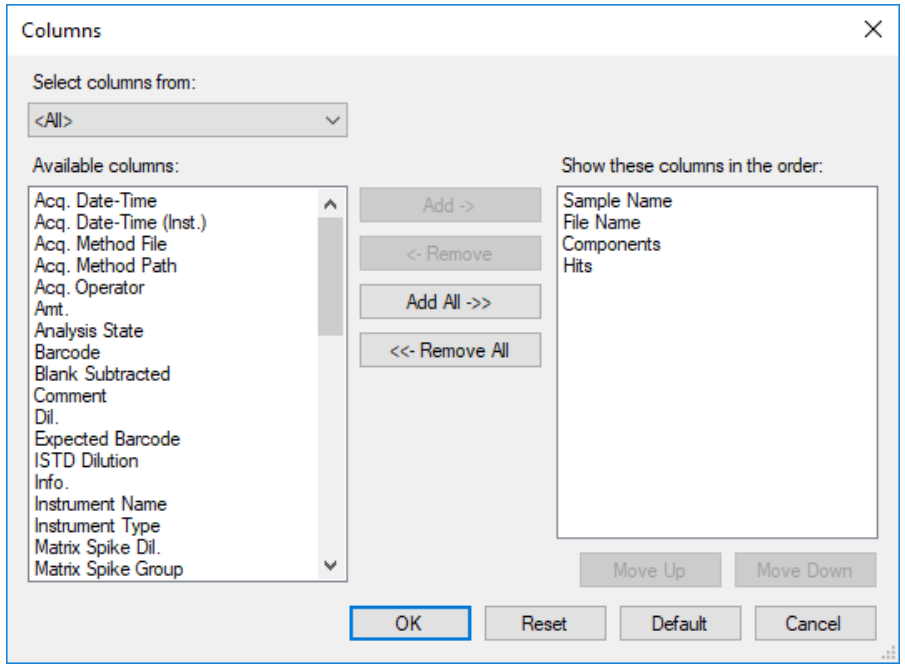


Agilent

Component Review
Sample Table

- Sample table gives summary information on number of components found and number of library matches.
- Used to navigate between samples.
- Samples can be removed or added as needed.
- Additional sample info accessible by Add/Remove Columns.
- Numerous parameters are available in the tables.





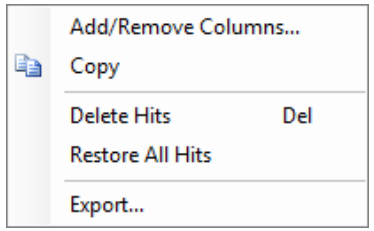
Component Review

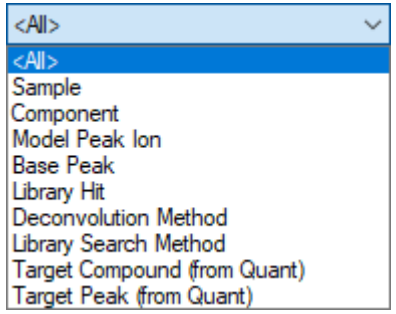
Components Table

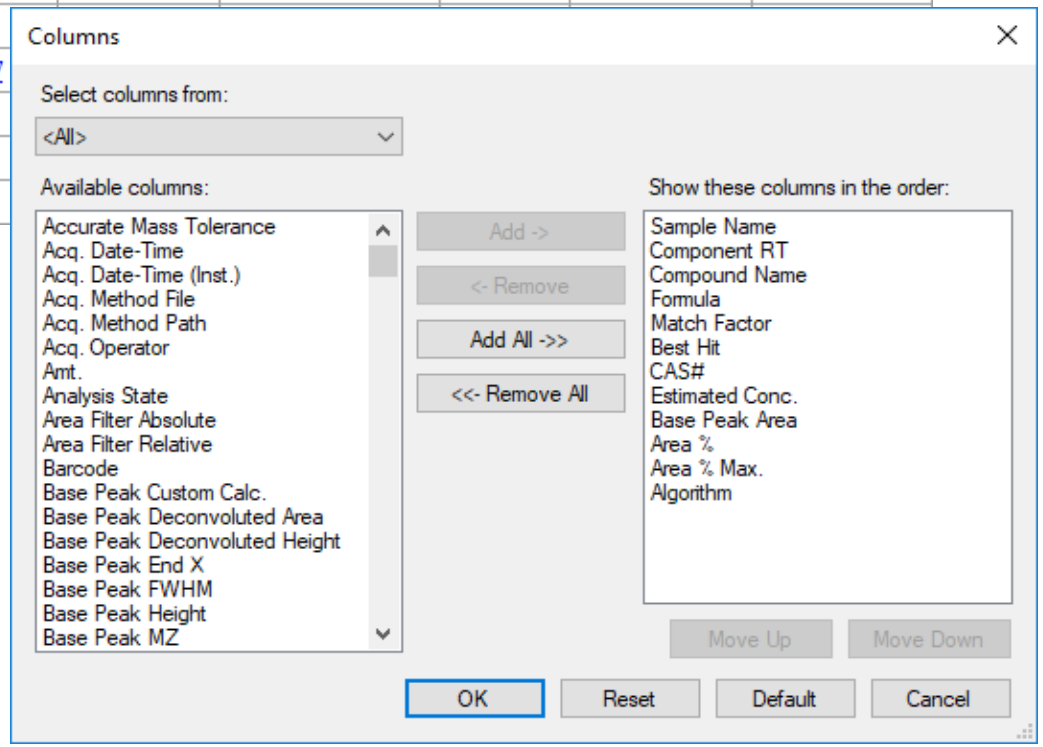
- Displays components and associated data.
- Extensive number of data columns.

Components

Sample Name	Component RT	Compound Name	Formula	Match Factor	Best Hit	CAS#	Estimated Conc.	Base Peak Area	Area %	Area % Max.	Algorithm
CAL_L08	3.8275	(2-Aziridinylethyl)amine	C4H10N2	50.5	☑	4025-37-0	9.003	554638.2	0.259	4.98	TIC Analysis
CAL_L08	4.2476	Dichlorodifluoromethane	CCl2F2	94.6	☑	75-71-8	24.39	965394.4	0.700	13.48	TIC Analysis
CAL_L08	4.4931	Chloromethane	CH3Cl	73.7	☑	74-87-3					
CAL_L08	4.7823	1-Propene, 2-methyl-	C4H8	89.4	☑	115-11-7					
CAL_L08	5.2352	Methane, bromo-	CH3Br	88.4	☑	74-83-9					
CAL_L08	5.4044	Ethyl Chloride	C2H5Cl	81.7	☑	75-00-3					
CAL_L08	6.0973	Trichloromonofluoromethane	CCl3F	95.0	☑	75-69-4					



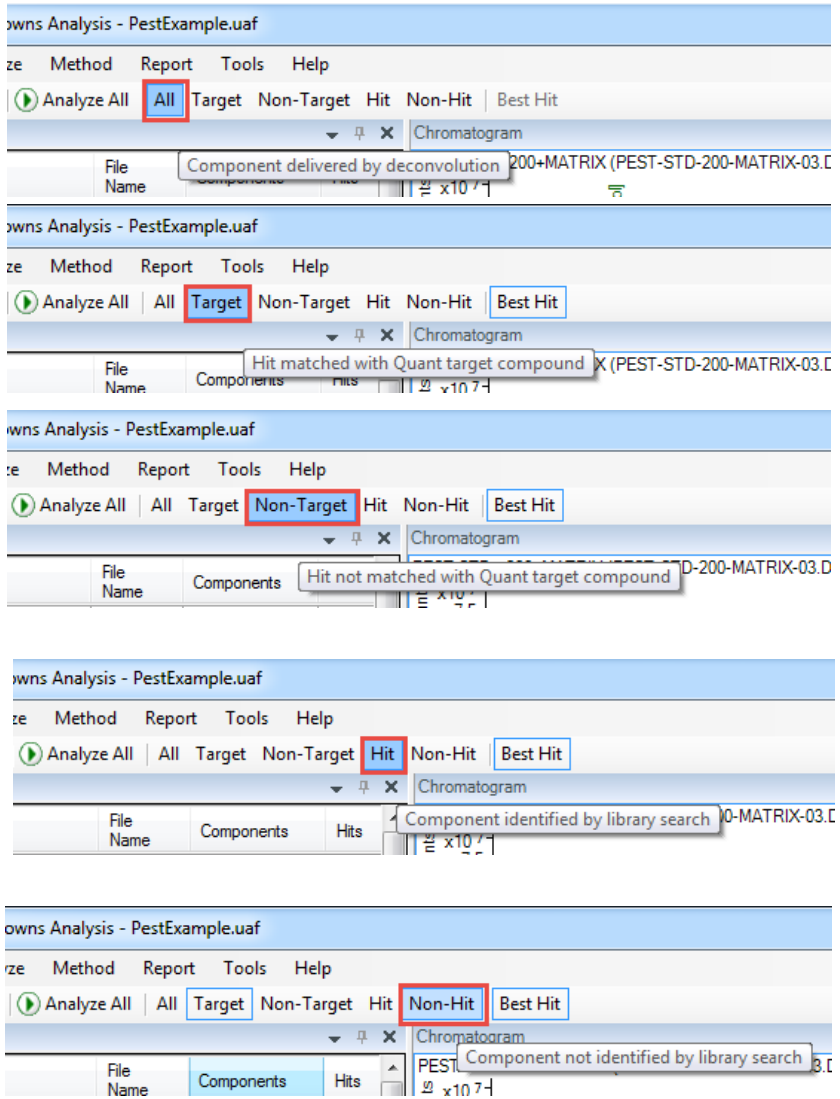




Component Review

Filtering of the Components Table

- All – All components are displayed.
- Target – Components that match a library entry and match Quant Batch compounds.
- Non-Target – Components that match a library entry, but don't match Quant batch compounds.
- Hits – Components that have a library match.
- Non-Hit –Components that don't match any library entry within the defined parameters.



Component Review
Best Hit

When **Best Hit** is **disabled** all library hits are displayed.

When **Best Hit** is **enabled** only the highest Match Factor hit is displayed.

Agilent MassHunter Unknowns Analysis - Webinar VOA 2.uaf

File Edit View Analyze Method Report Tools Help

Analyze All | All Target Non-Target Hit Non-Hit Best Hit

Components

Sample Name	Component RT	Compound Name	Match Factor	Best Hit	CAS#
CAL_L08	7.1777	Carbon disulfide	89.7	☑	75-15-0
CAL_L08	7.1777	Arsine	60.7	☐	7784-42-1
CAL_L08	7.1777	4,4'-Diisothiocyanatostilbene...	61.1	☐	53005-05-3
CAL_L08	7.1777	Carbon disulfide	89.7	☐	75-15-0
CAL_L08	7.1777	Glycine, N-(dithiocarboxy)-N-...	63.4	☐	40520-03-4
CAL_L08	7.6578	Ethylene, 1,2-dichloro-, (Z)-	96.4	☑	156-59-2
CAL_L08	7.6578	Ethylene, 1,2-dichloro-, (Z)-	95.4	☐	156-59-2
CAL_L08	7.6578	Ethylene, 1,2-dichloro-, (E)-	95.7	☐	156-60-5
CAL_L08	7.6578	Ethylene, 1,2-dichloro-, (E)-	96.1	☐	156-60-5
CAL_L08	7.6578	1,2-Dichloroethylene	95.5	☐	540-59-0

Agilent MassHunter Unknowns Analysis - Webinar VOA 2.uaf

File Edit View Analyze Method Report Tools Help

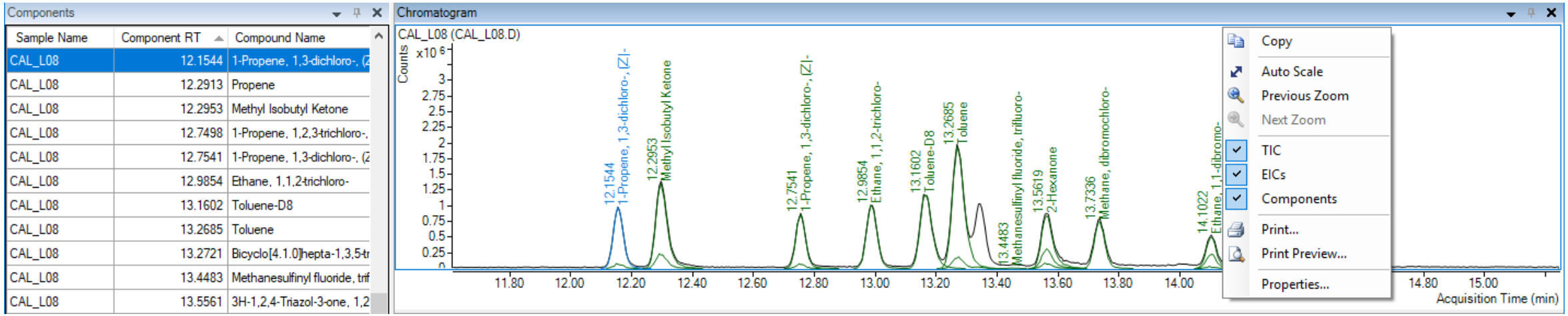
Analyze All | All Target Non-Target Hit Non-Hit Best Hit

Components

Sample Name	Component RT	Compound Name	Match Factor	Best Hit	CAS#
CAL_L08	7.1777	Carbon disulfide	89.7	☑	75-15-0
CAL_L08	7.6578	Ethylene, 1,2-dichloro-, (Z)-	96.4	☑	156-59-2
CAL_L08	7.8052	Propane, 2-methoxy-2-methyl-	92.7	☑	1634-04-4
CAL_L08	7.9579	Ethane, 1,1-dichloro-	94.8	☑	75-34-3
CAL_L08	8.0616	Acetic acid ethenyl ester	80.5	☑	108-05-4
CAL_L08	8.4326	2-Butanone	83.8	☑	78-93-3
CAL_L08	8.6509	Ethene, 1,1-dichloro-	95.2	☑	75-35-4
CAL_L08	8.8910	Trichloromethane	94.8	☑	67-66-3
CAL_L08	9.0056	Propane, 2,2-dichloro-	78.7	☑	594-20-7
CAL_L08	9.3275	Tetrahydrofuran	76.9	☑	109-99-9

Tip: Must have more than 1 Max. hit count.

Component Review
Chromatogram

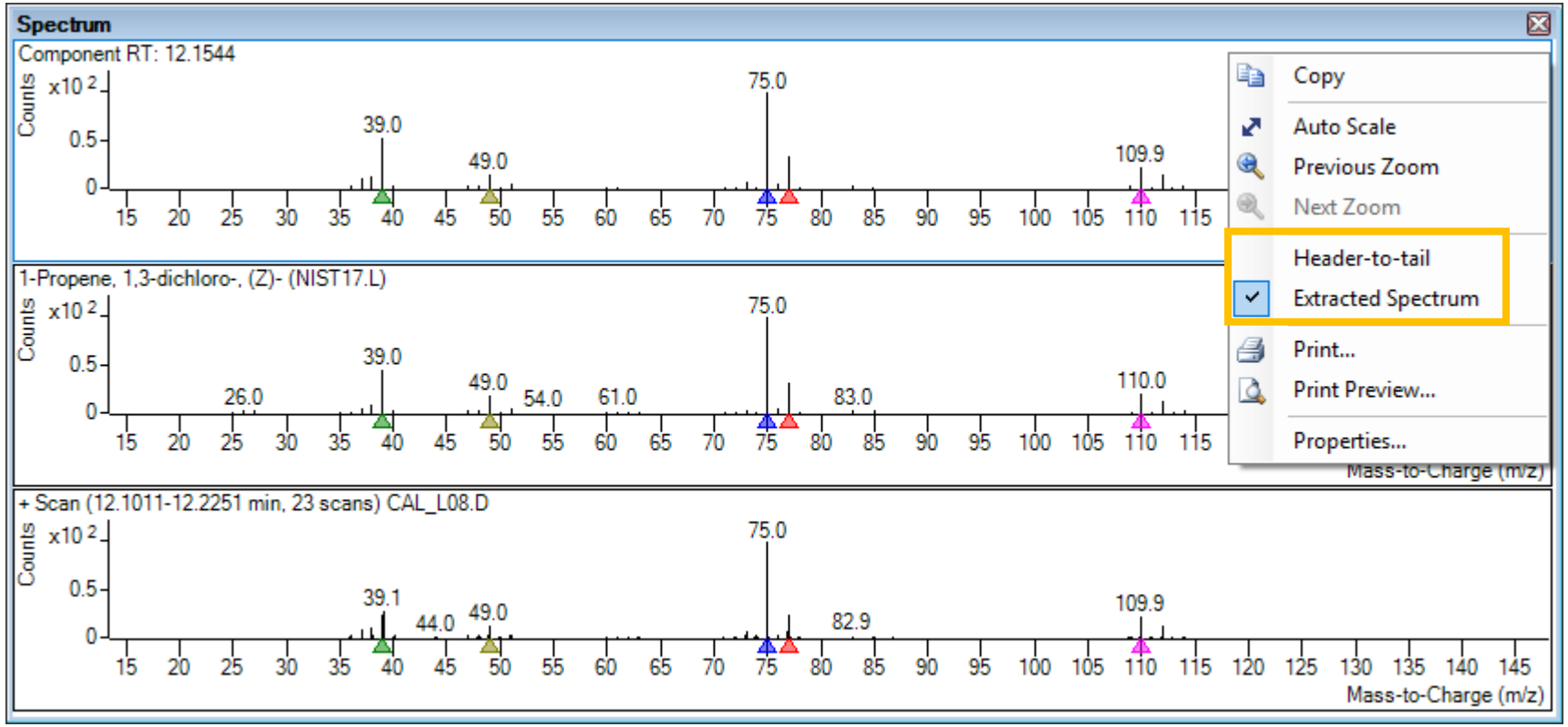


- Various displays of the Chromatogram window are available.
- TIC displayed in Black.
- All non-selected ions (EIC) displayed in Green.
- Chromatogram displays selected component(s) in Blue.
- Clicking in the Chromatogram display selects the nearest peak and selects it in Components table.

Spectrum Views
Extracted Spectrum

Agilent CrossLab
From Insight to Outcome

Allows comparison of the deconvoluted spectrum (top) to the library spectrum (middle) and the averaged spectrum (bottom).

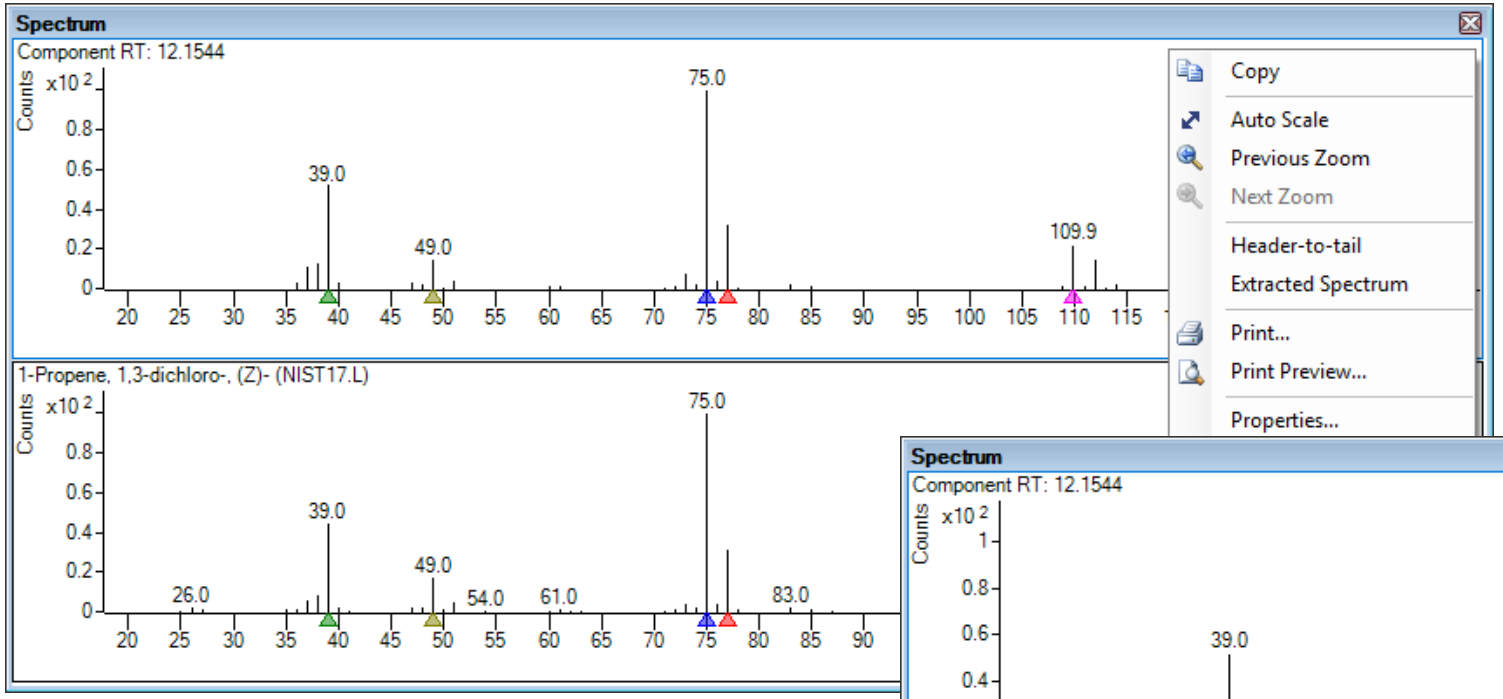


Purity

Agilent

Spectrum Views

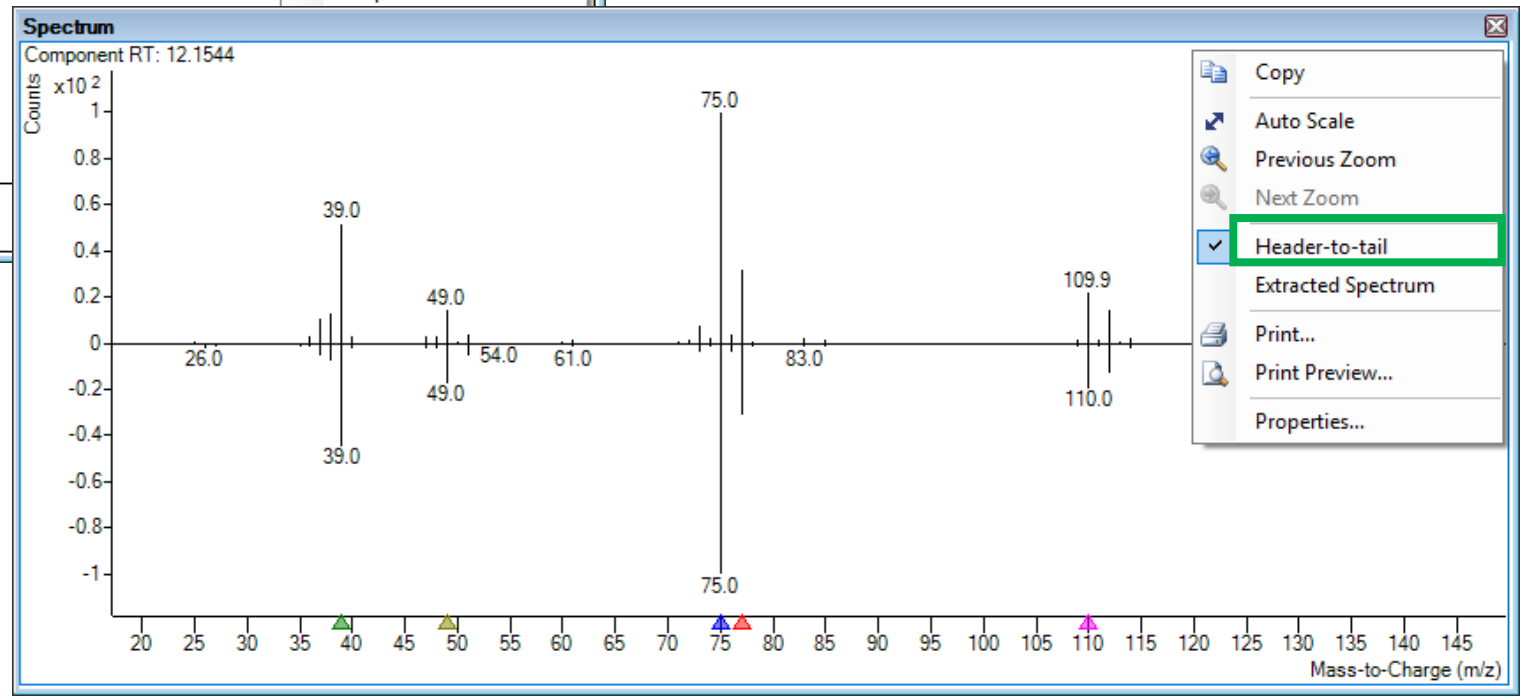
Head-To-Tail



Right click to view Head-to-Tail.

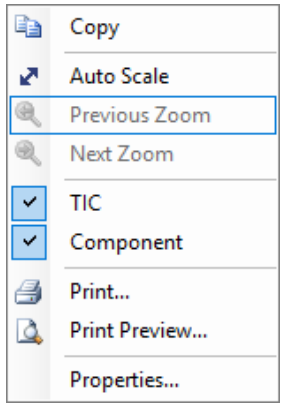
Head to Head View

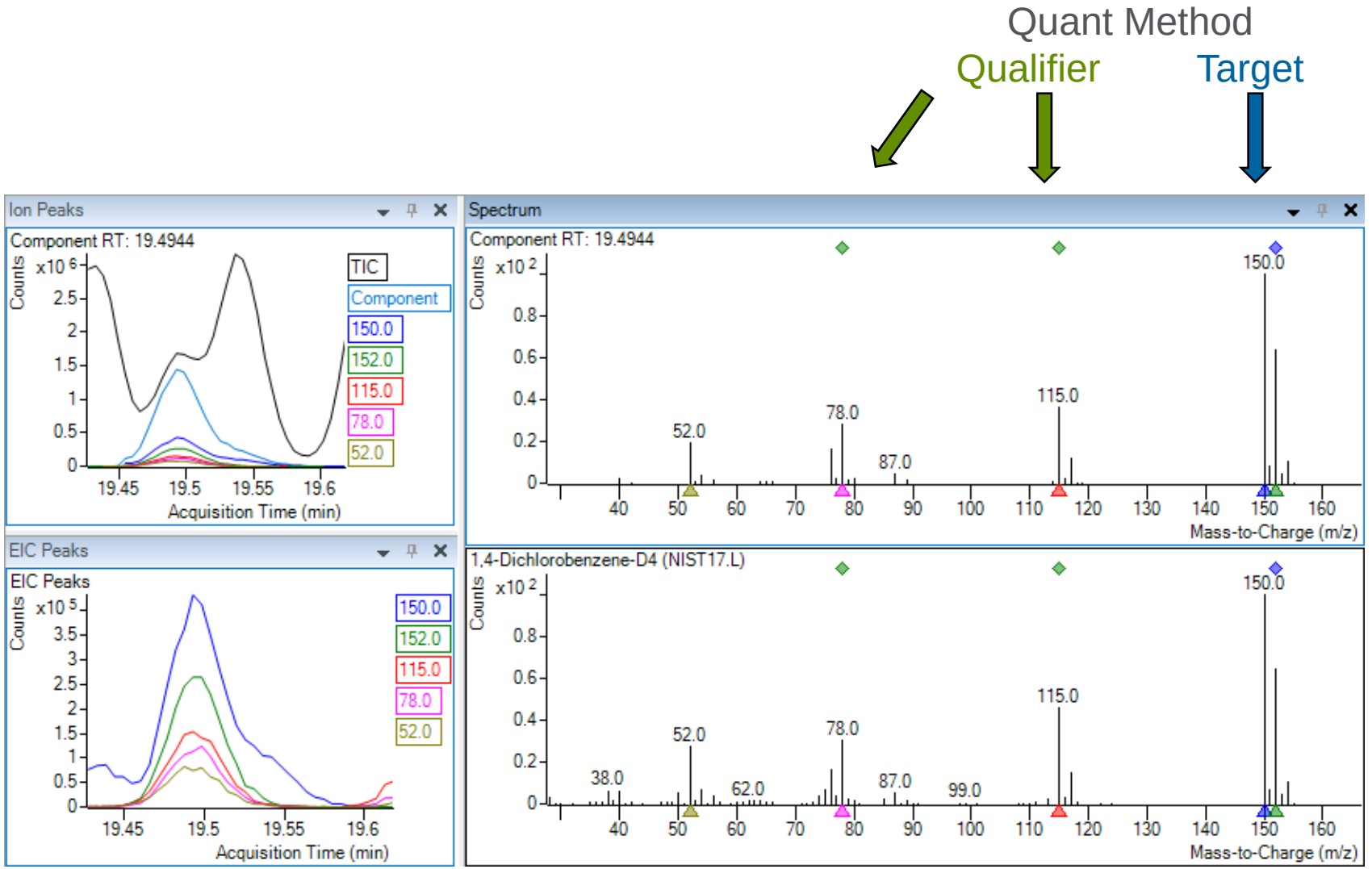
Head to Tail View



Component Review
Ion Peaks and EIC Peaks

- Activated from **View > EIC Peaks.**
- Useful for visualizing co-eluting peaks.
- Click on ion in Spectrum to make it add/remove in Ion Peaks or EIC Peaks.
- Use menu to add TIC & Component.

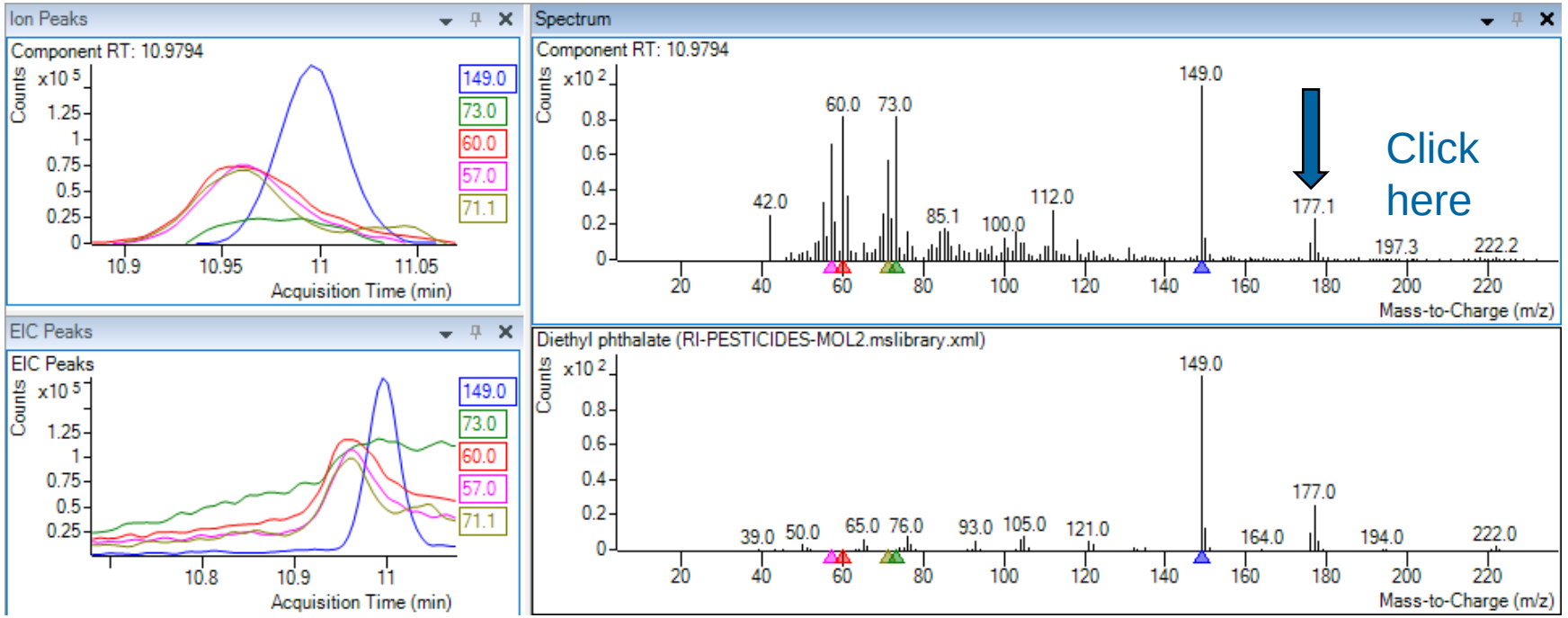




Component Review

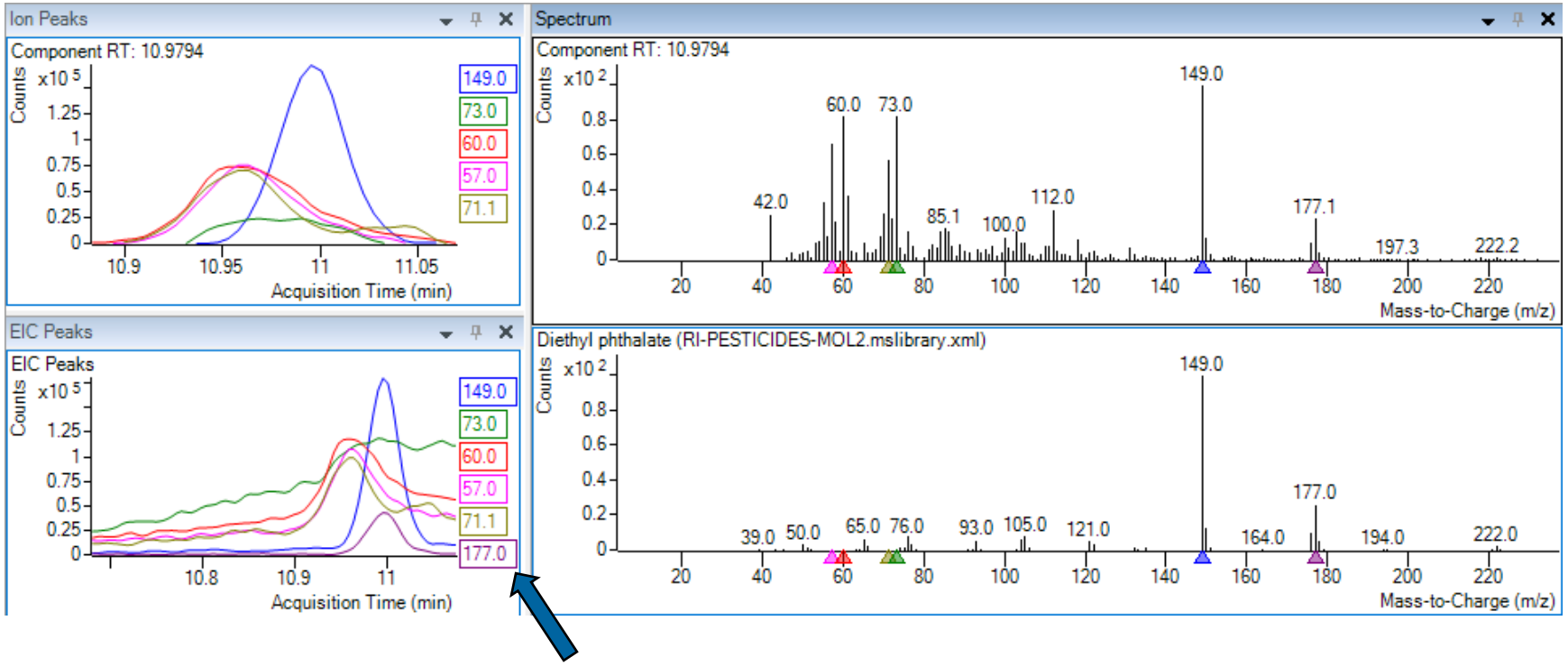
Ion Peaks and EIC Peaks

- Adding another Extracted Ion Chromatogram (EIC)
- Click on the peak in either the component or library window.
- Best done without head-to-tail.
- Is the 177.0 mass part of the first component or the second component?

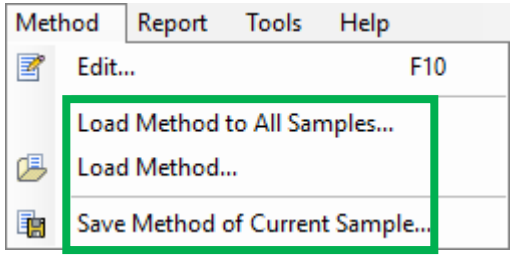


Component Review
Ion Peaks and EIC Peaks

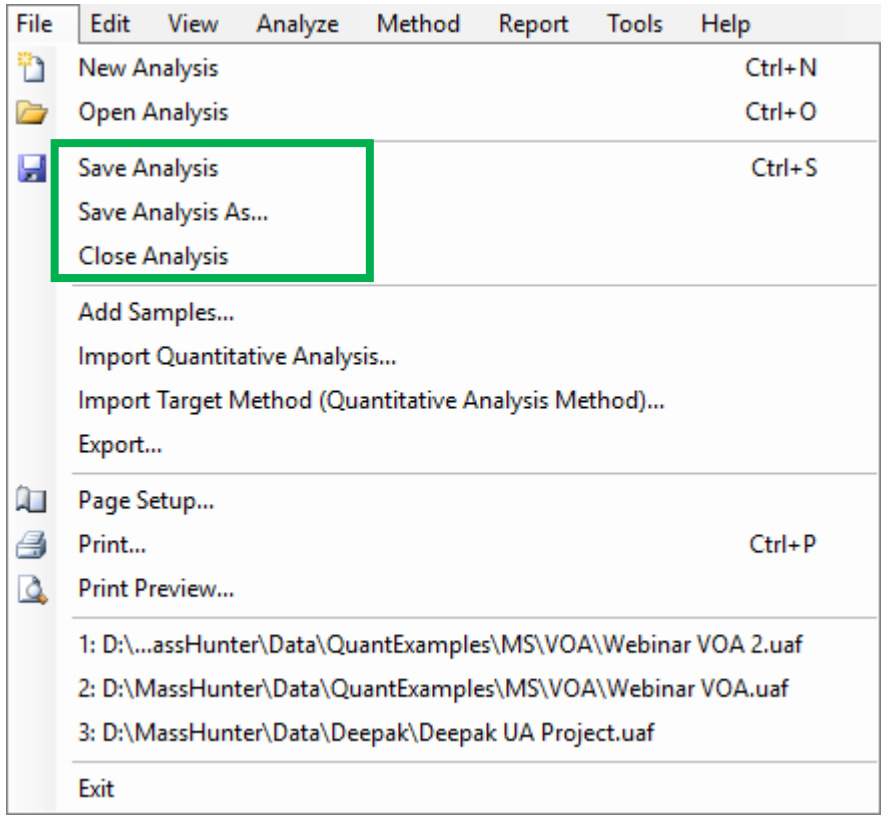
- EIC for mass is displayed in the window.
- Is the 177.0 mass part of the first component or the second component?



Unknowns Analysis Method



- Method can be saved and loaded from .M folder (unified method) or as uamethod.xml file.
- Previously stored methods can be used multiple times.



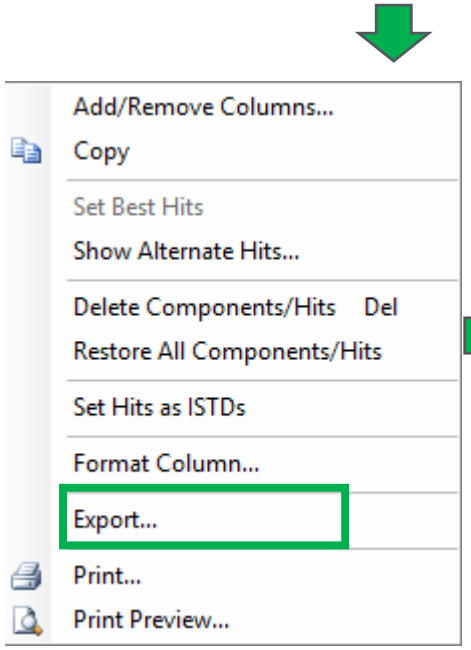
- Method id also saved as part of the Analysis.
- Method is stored in the .uaf file.

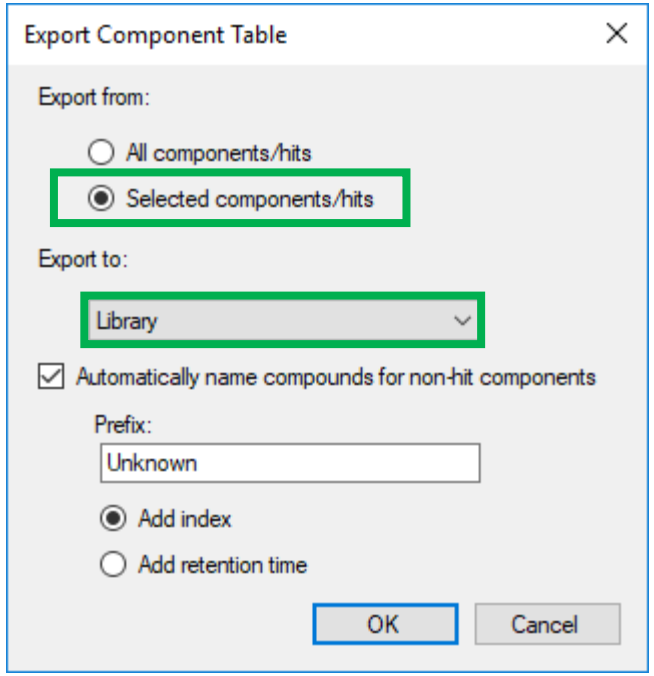
Export Components to Library Editor

Agilent CrossLab
From Insight to Outcome

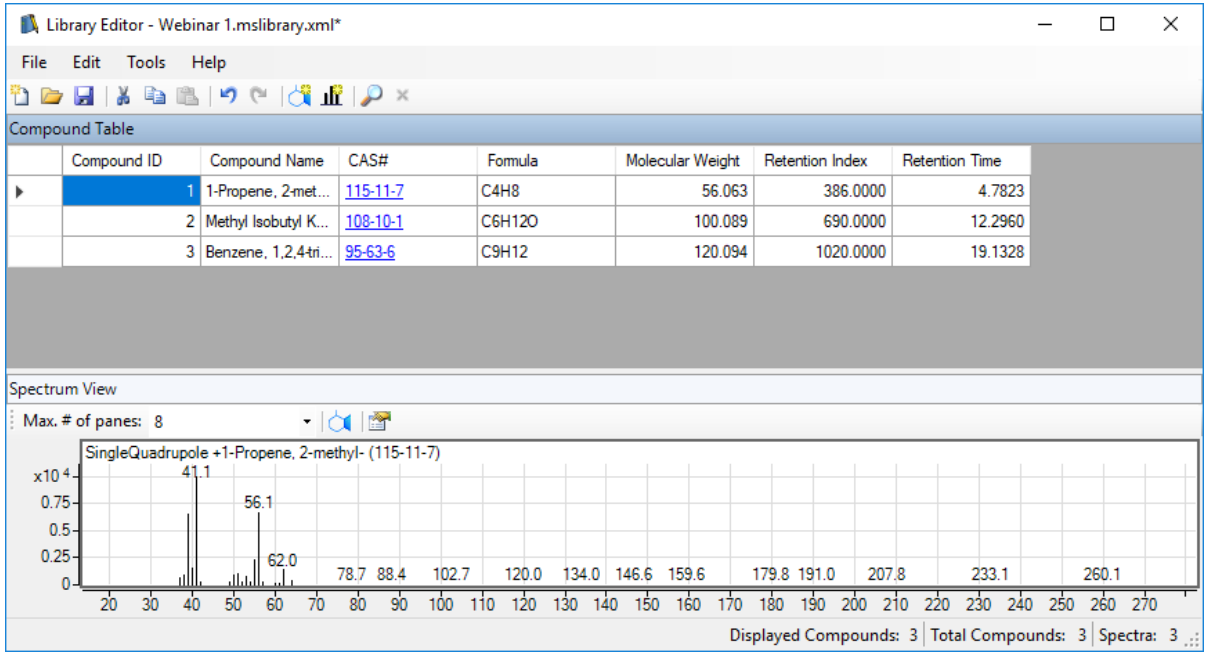
Components

Sample Name	Component RT	Compound Name	Match Factor	Best Hit	Window Size Factor
CAL_L08	3.8275	(2-Aziridinylethyl)amine	50.5	☑	25.0
CAL_L08	4.7823	1-Propene, 2-methyl-	89.4	☑	25.0
CAL_L08	9.5948	Cyclopentene, 1-chl...	62.0	☑	25.0
CAL_L08	12.2960	Methyl Isobutyl Keto...	94.6	☑	25.0
CAL_L08	18.5872	Ethane, pentachloro-	61.1	☑	25.0
CAL_L08	19.1328	Benzene, 1,2,4-trime...	97.7	☑	25.0





- Select desired components (3).
- Right click and select **Export.**
- Choose **Selected Components/Hits.**
- Choose format as **Library.**
- Three components and spectra in library.



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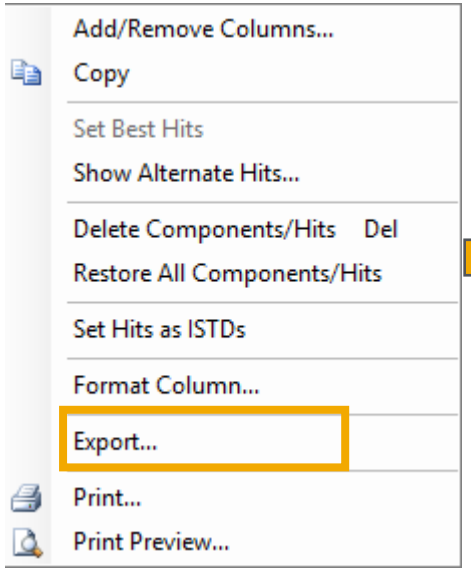
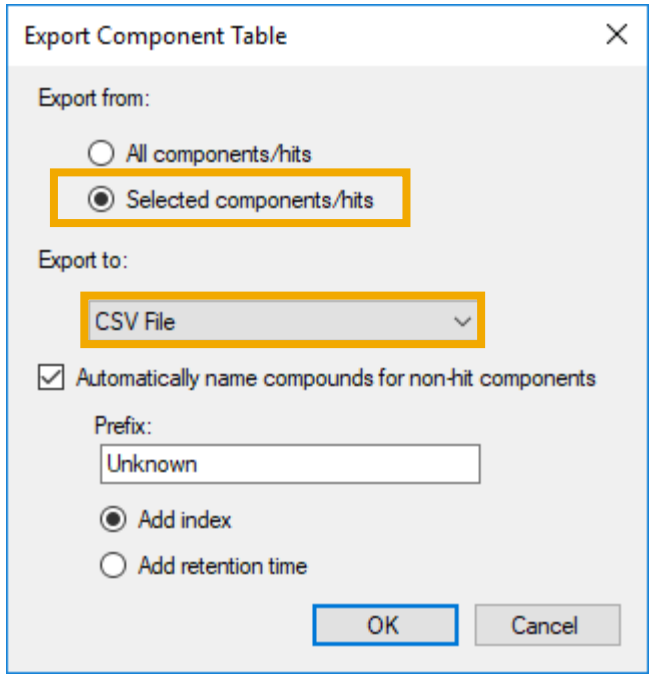
Export Components to .CSV

Components

Sample Name	Component RT	Compound Name	Match Factor	Best Hit	Window Size Factor
CAL_L08	4.2466	Dichlorodifluorometh...	97.7	☑	200.0
CAL_L08	4.4921	Chloromethane	98.6	☑	200.0
CAL_L08	4.6131	2-(Dibromomethane)...	55.4	☑	25.0
CAL_L08	4.7325	Ethene, chloro-	95.3	☑	100.0
CAL_L08	4.7821	2-Butene	99.3	☑	200.0
CAL_L08	4.7871	2-Butyne	59.2	☑	25.0





- Select three different components.
- Right click and select **Export.**
- Choose **Selected Components/Hits.**
- Choose format as **CSV File.**
- Three components in CSV File.

	A	B	C	D	E	F	G
1	Sample Nar	Component RT	Compound Nam	Match Facto	Best Hit	Window Size Factor	
2	CAL_L08	4.492109814	Chloromethane	98.603205	TRUE	200	
3	CAL_L08	4.732524655	Ethene, chloro-	95.327862	TRUE	100	
4	CAL_L08	4.787117711	2-Butyne	59.193042	TRUE	25	

Export Components to Quantitative Analysis Method

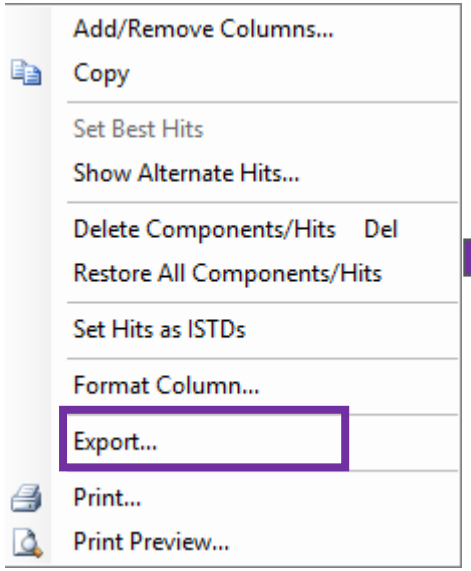
Agilent CrossLab
From Insight to Outcome

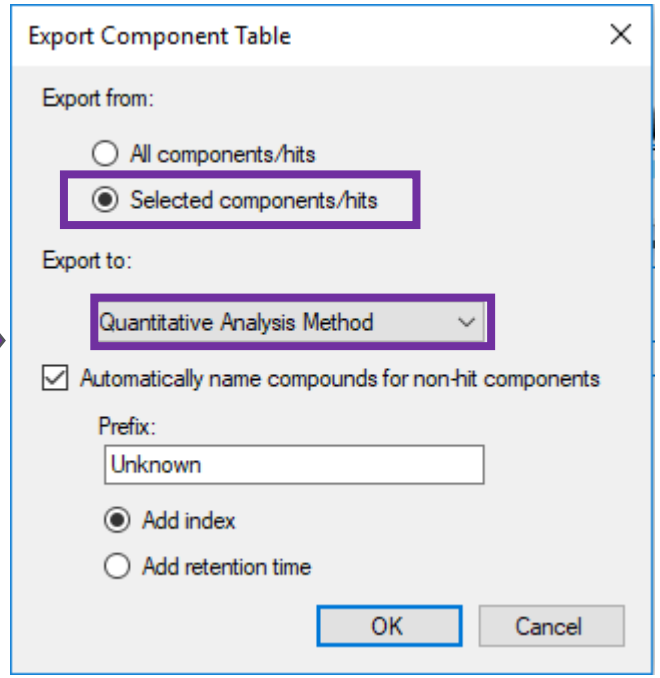
One compound added to QDB

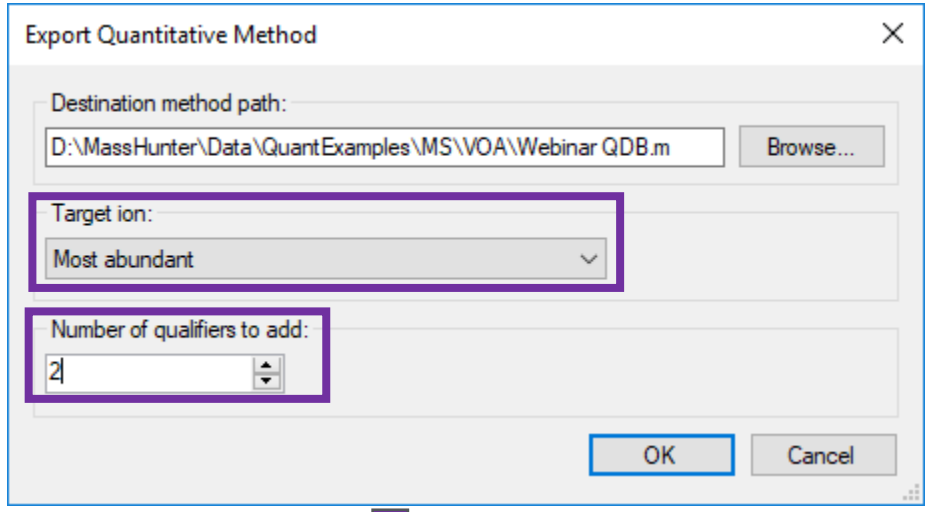
With two Qualifiers

Components

Sample Name	Component RT	Compound Name	Match Factor	Best Hit	Window Size Factor
CAL_L08	4.2466	Dichlorodifluorometh...	97.7	☑	200.0
CAL_L08	4.4921	Chloromethane	98.6	☑	200.0
CAL_L08	4.6131	2-(Dibromomethane)...	55.4	☑	25.0
CAL_L08	4.7325	Ethene, chloro-	95.3	☑	100.0
CAL_L08	4.7821	2-Butene	99.3	☑	200.0
CAL_L08	4.7871	2-Butyne	59.2	☑	25.0







Sample

Name	Data File	Type	Level
CAL_L08	CAL_L08.D	Cal	8

Quantifier

Name	TS	Scan	Type	MZ	Uncertainty
2-(Dibromometh...	1	Scan	Target	45.0	Relative

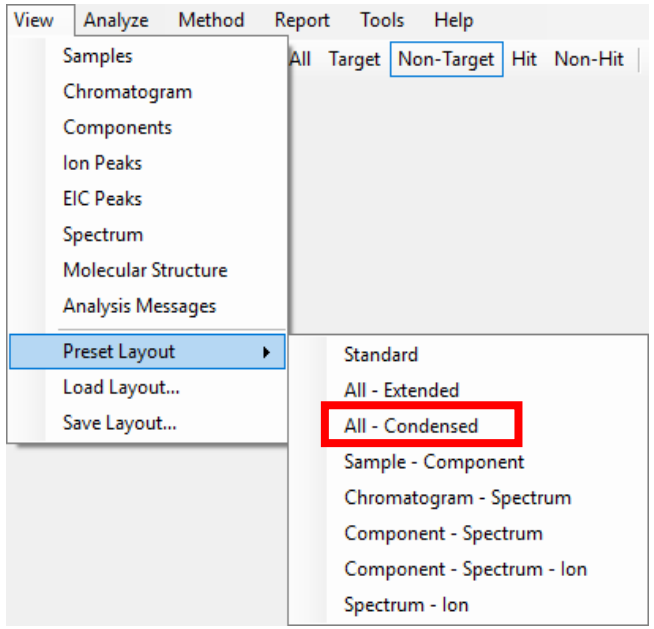
Qualifier

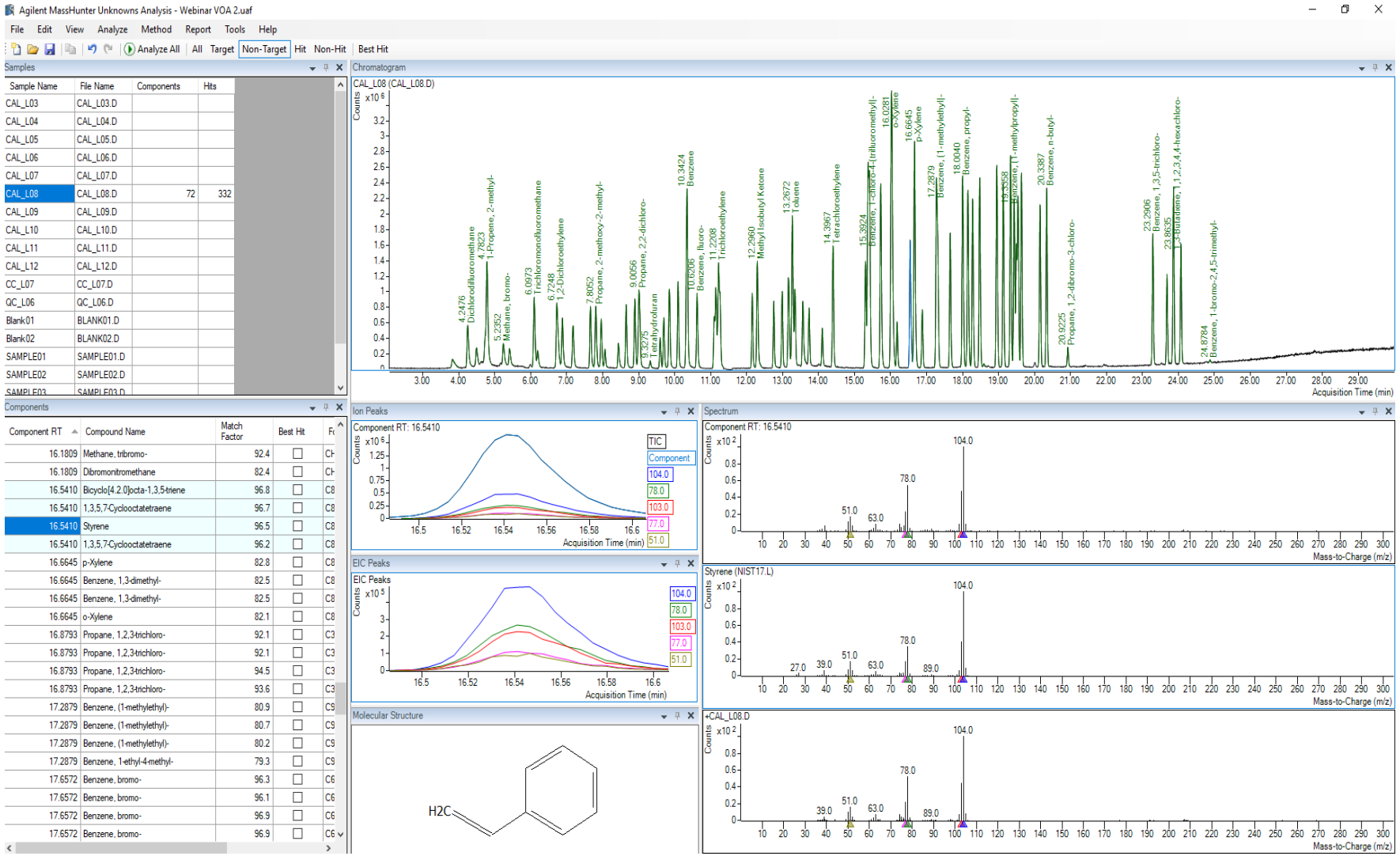
MZ	Rel. Resp.	Uncertainty	Area Sum
219.9	46.3	20.0	☐
217.8	13.5	20.0	☐

Agilent

Layouts

- Preset Layouts
- Create custom layouts





Unknowns Analysis

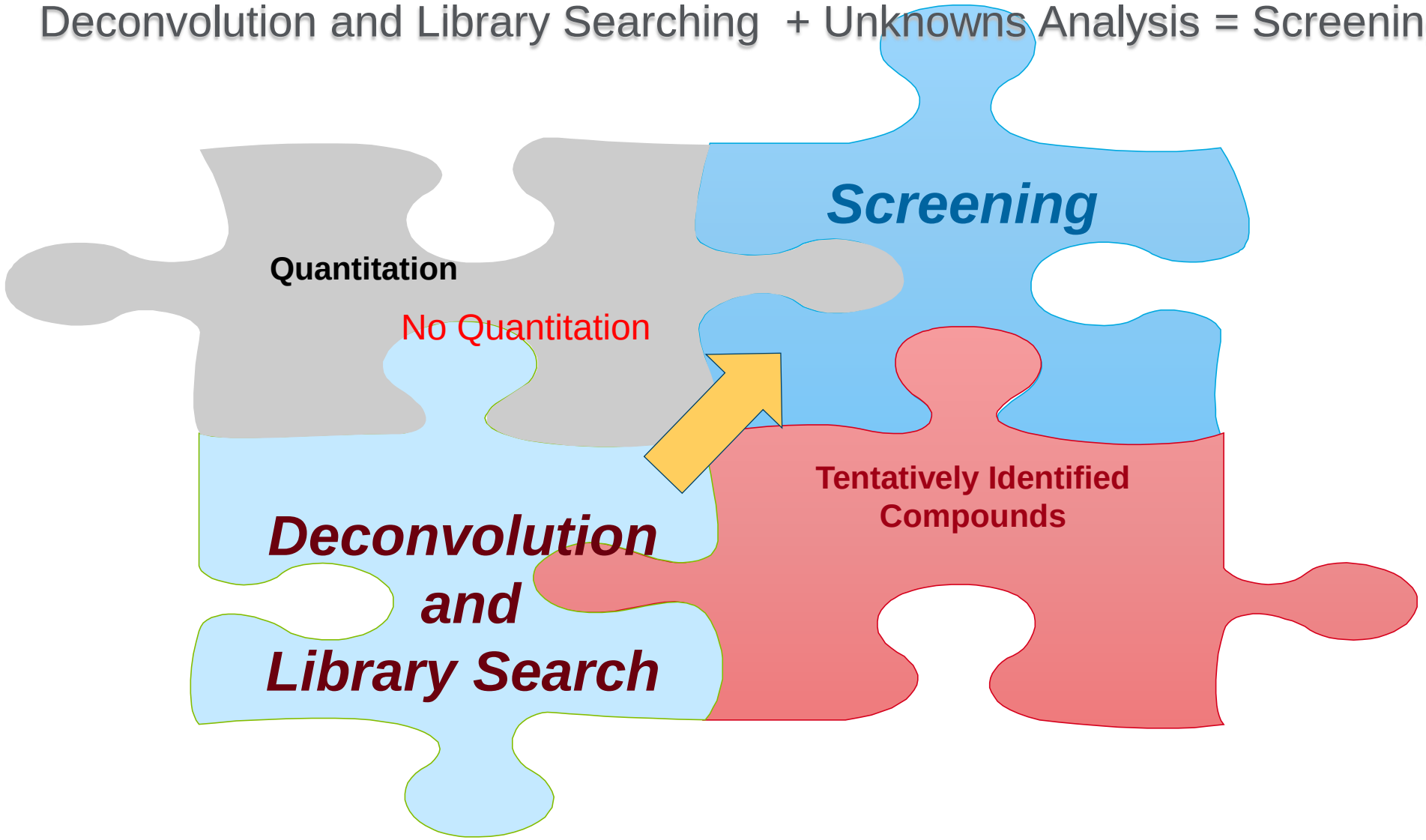
Time for a demo

Next up:
Unknowns Screening

Overview of Unknowns Analysis

Screening

Deconvolution and Library Searching + Unknowns Analysis = Screening



Screening
Workflow

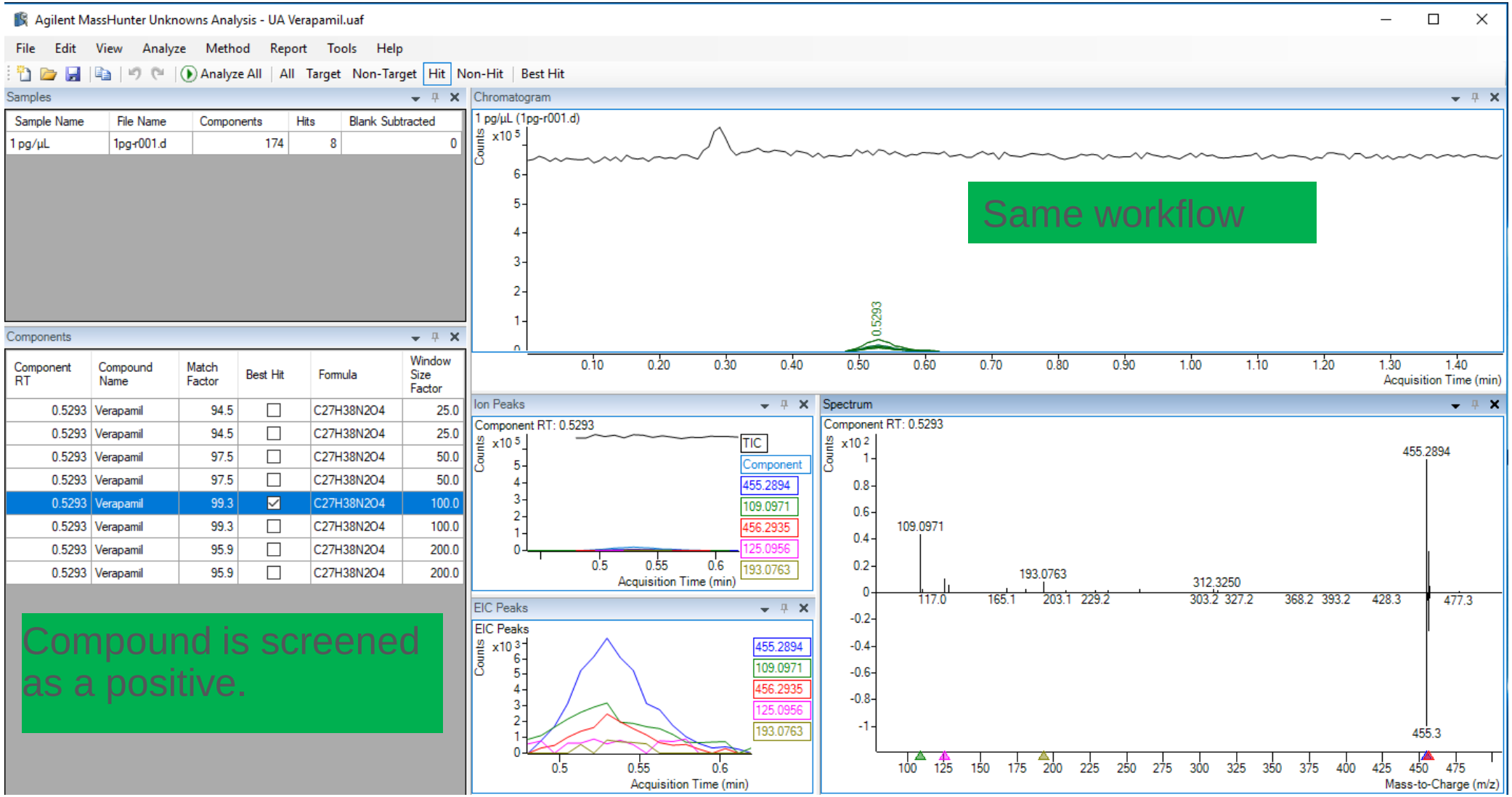
Agilent CrossLab
From Insight to Outcome

Screening methodology

- May require minimal sample preparation.
- Does not require Quantitative Analysis.
- Shorter chromatographic runs.
  - Deconvolution algorithm does most of the ‘dirty’ work.
  - Use multiple RT Window Size Factors to extract targets.
  - Applicable to low resolution and high resolution data.
  - Most appropriate with scan data.
- Library Searching
  - Can be commercial library.
  - Better with a smaller user generated library with ‘targets’.
- Screens positive → Confirmation.
- Improves sample throughput.

Screening
Workflow

Agilent CrossLab
From Insight to Outcome



Agilent

Unknowns Analysis

Time for a demo

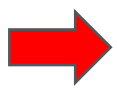
Next up:
Reporting

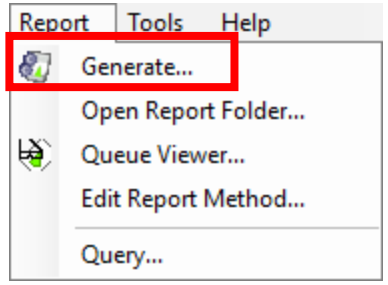
Generate Reports

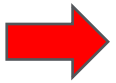
Agilent CrossLab
From Insight to Outcome

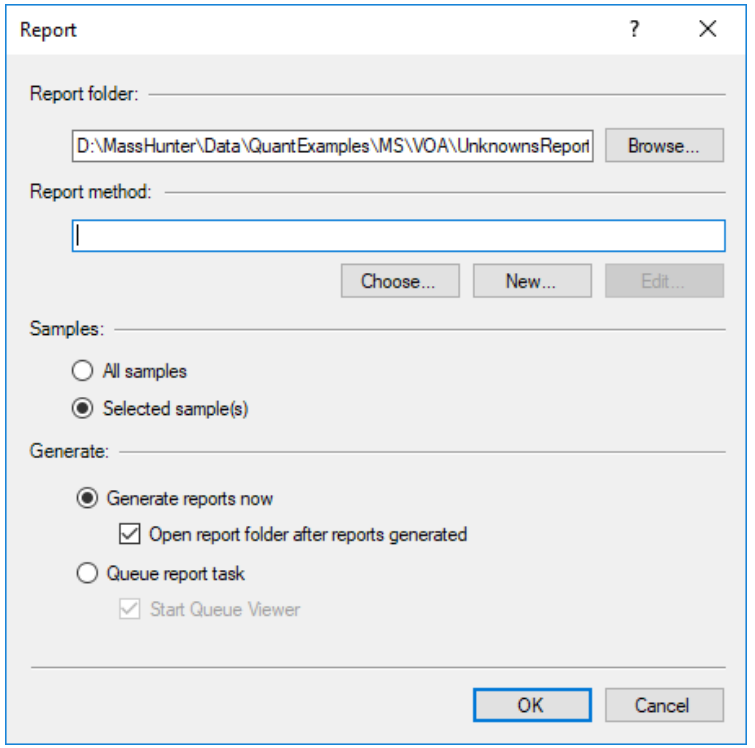
Samples

Sample Name	File Name	Components	Hits
CAL_L03	CAL_L03.D		
CAL_L04	CAL_L04.D		
CAL_L05	CAL_L05.D		
CAL_L06	CAL_L06.D		
CAL_L07	CAL_L07.D		
CAL_L08	CAL_L08.D	72	69
CAL_L09	CAL_L09.D		
CAL_L10	CAL_L10.D		
CAL_L11	CAL_L11.D		
CAL_L12	CAL_L12.D		





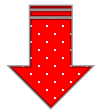




- Must “Save Analysis” first.
- If only a subset of samples is wanted select them in Samples.

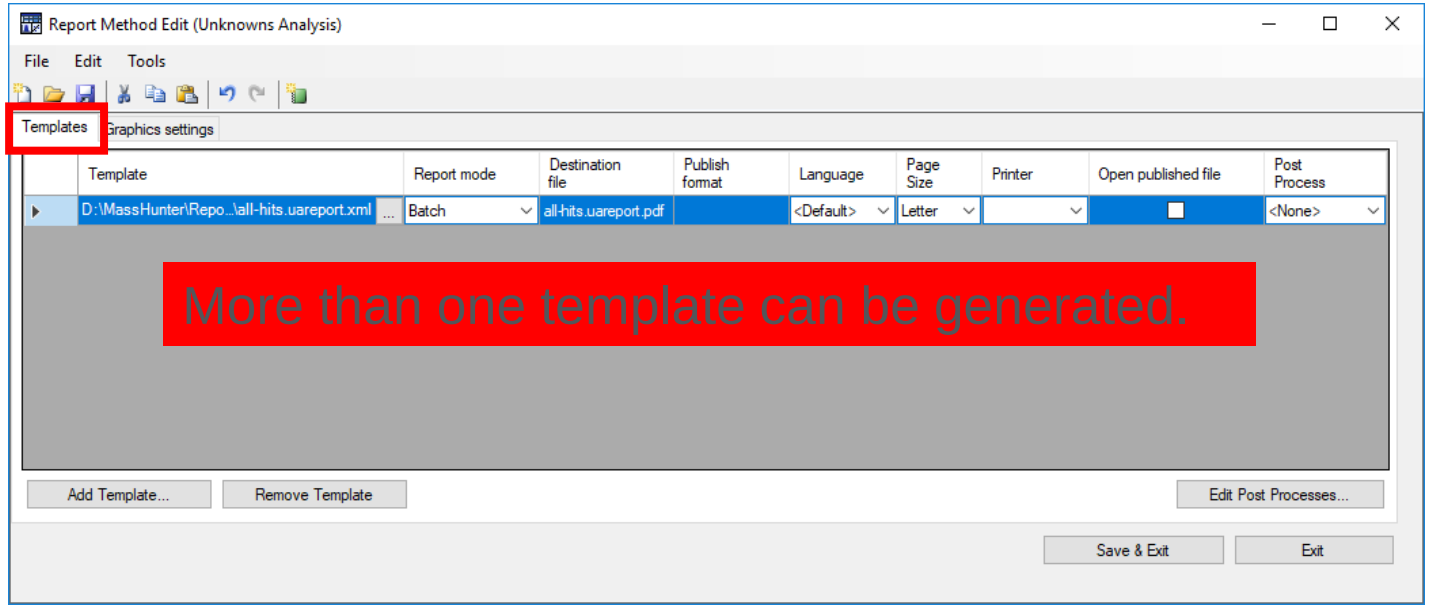
Report > Generate

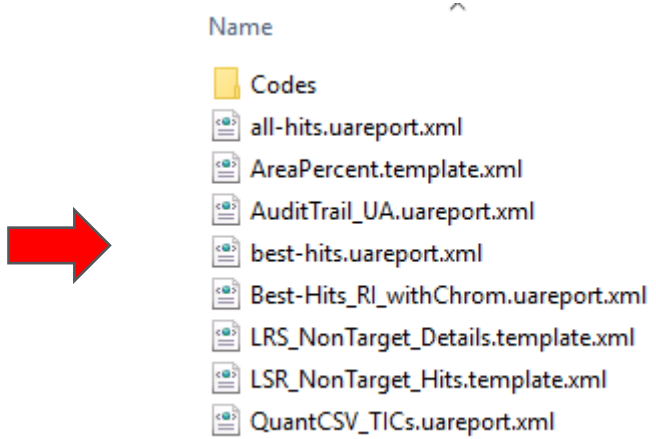
Choose, create or edit a Unknowns Analysis Report Method.

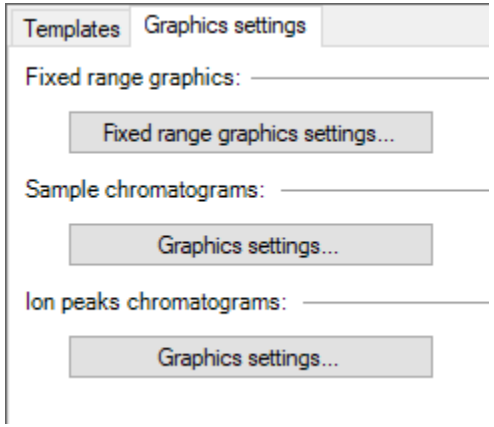


Agilent

Generate Reports

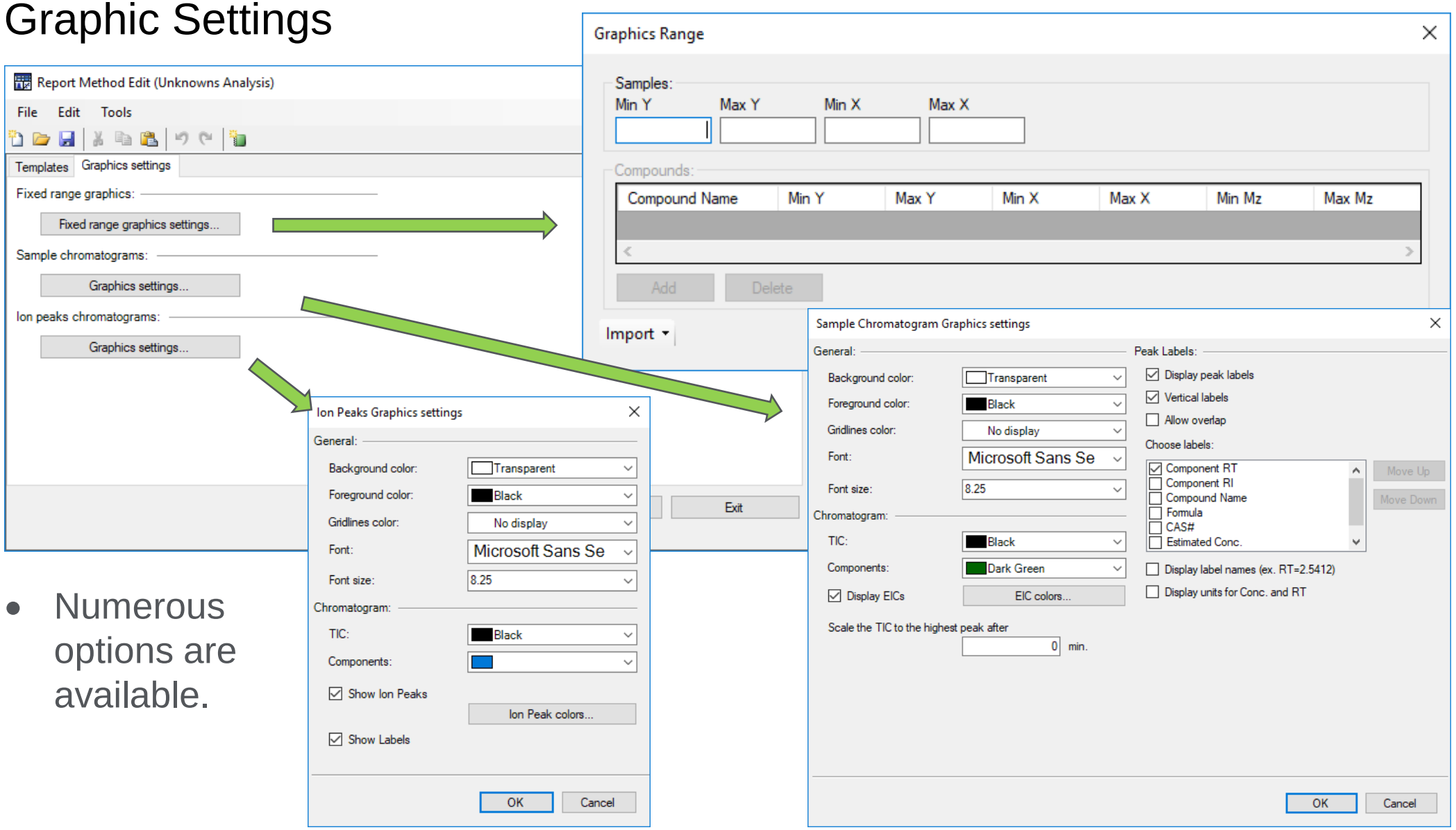






- Select the report(s).
- Numerous PDF style reports are available.
- Determine or modify the graphic settings.
- Generate the report.

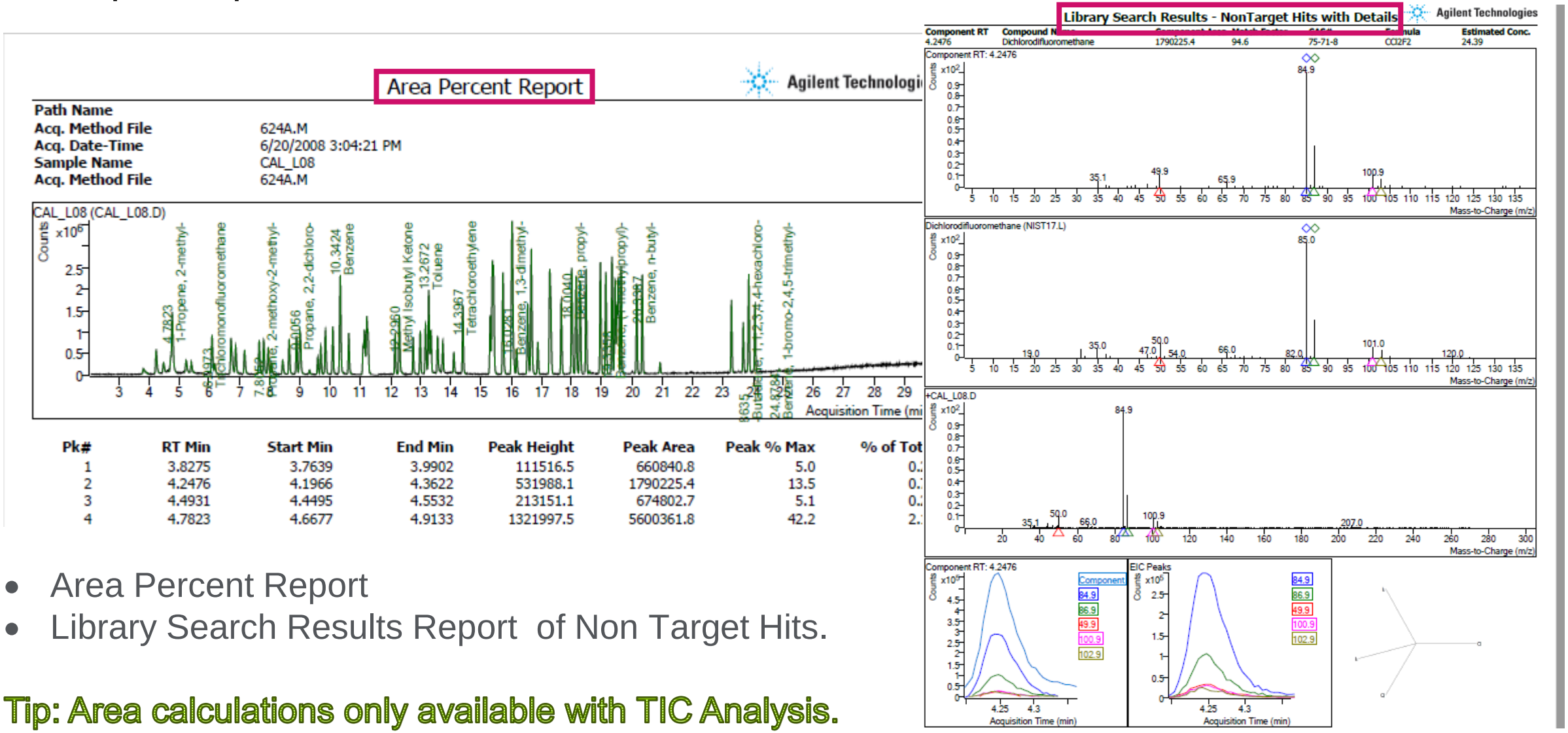
Generate Reports
Graphic Settings



- Numerous options are available.

Generate Reports

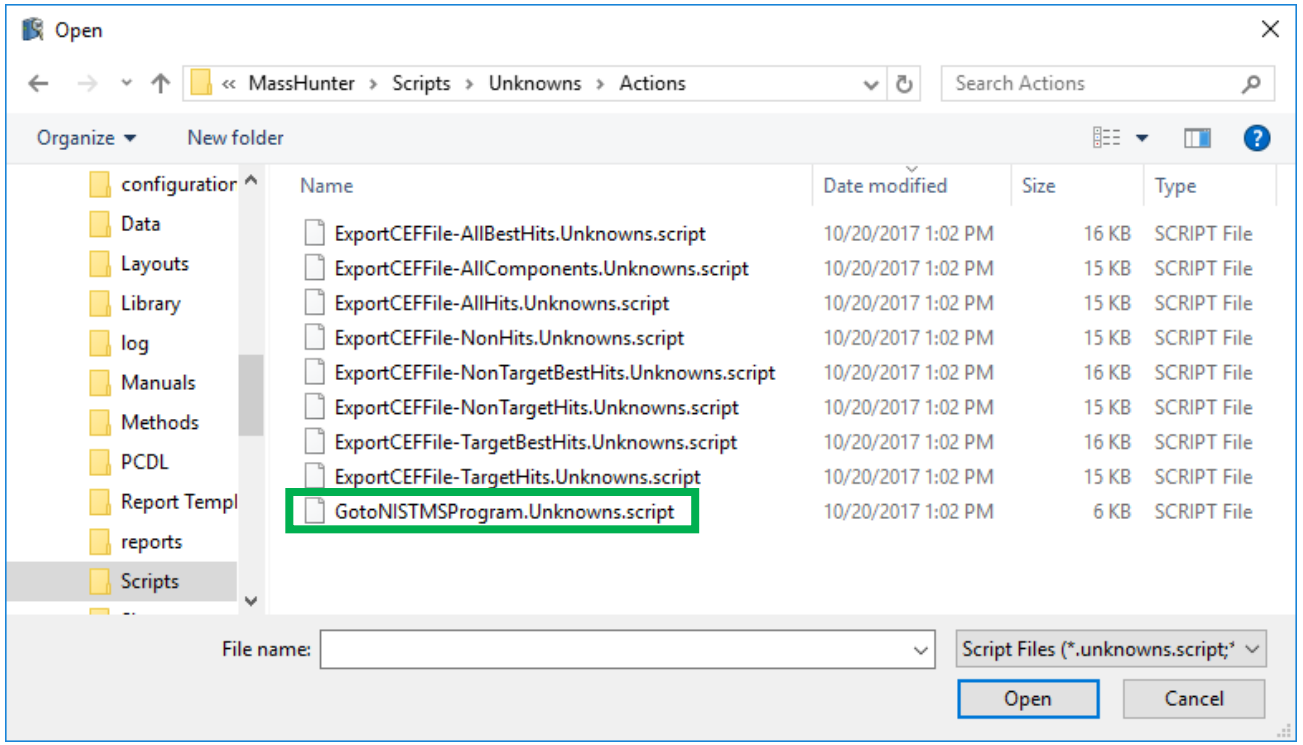
Example Reports

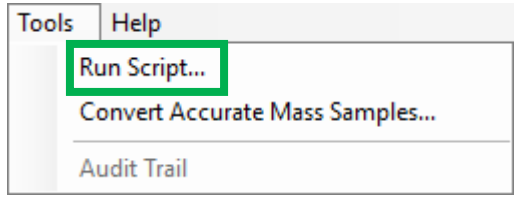


- Area Percent Report
- Library Search Results Report of Non Target Hits.

Tip: Area calculations only available with TIC Analysis.

Generate CEF Files



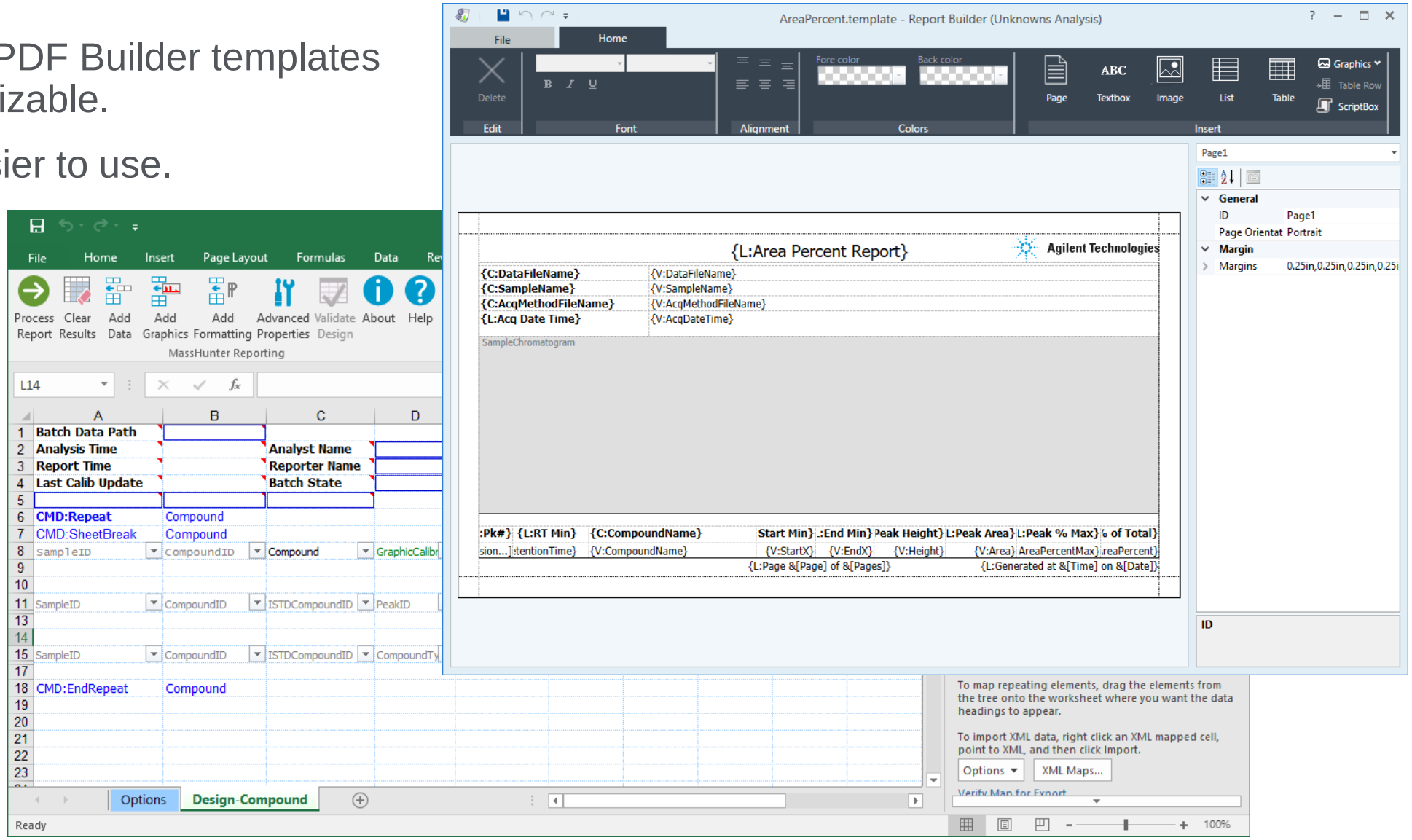


- Activated from **Tools > Run Script.**
- CEF Files (Common Exchange Format) used for exchanging data among programs, Quant, MPP, etc.
- Script to go to NIST programs. **New Feature.**
- Application – essential oils.

Customizable Report Templates

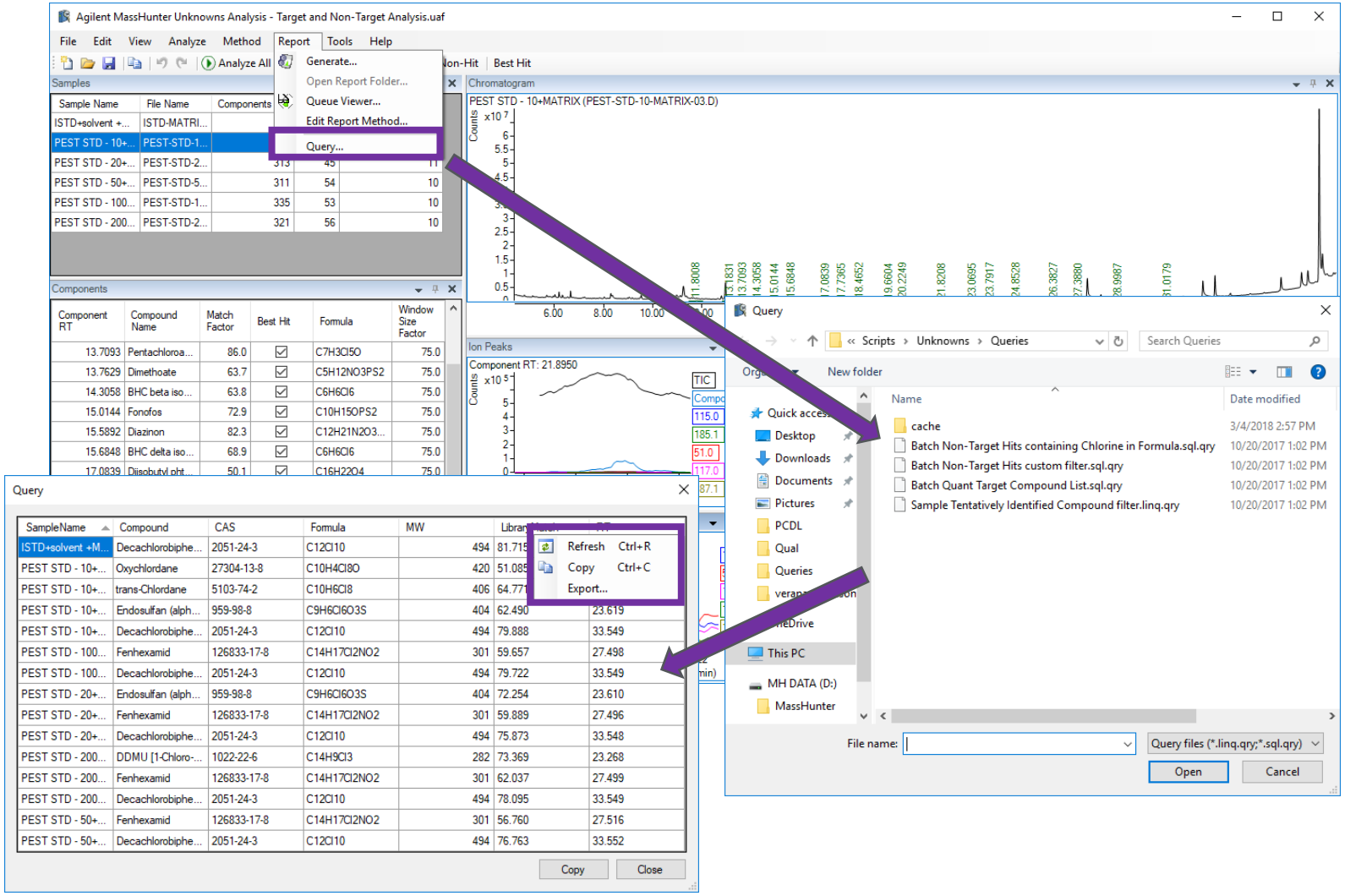
PDF Report Builder

- Both Excel and PDF Builder templates are user customizable.
- PDF Builder easier to use.



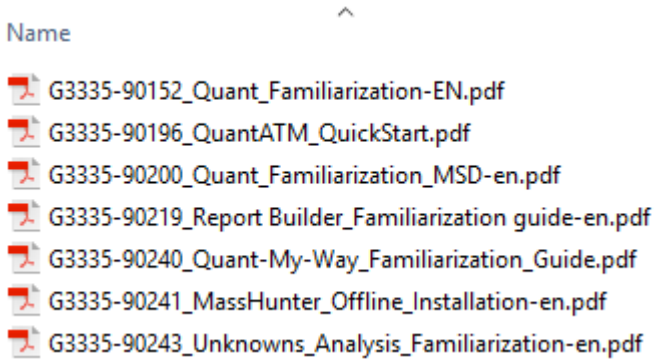
Custom Data Review
Queries

- **Report > Query**
- Queries are useful to review data.
- Data can be viewed in subsets.
- Can Copy all the data.
- Can Copy selected data.
- Can Export Data to csv file.
- Review tentatively identified compounds or positive screening compounds.
- Requires expert programming skills (LINQ,SQL,C#)



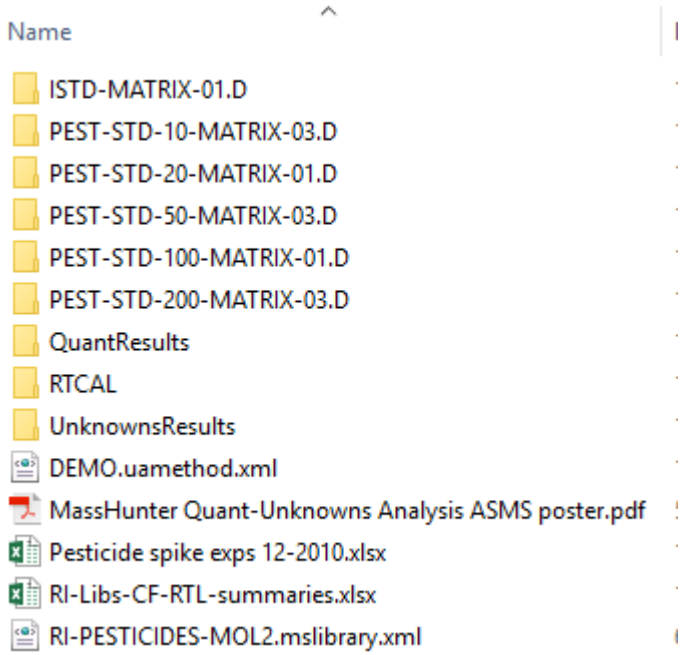
Training Resources

Familiarization Guide



- Familiarization Guide on USB drive in \Supplemental\MassHunter\Manuals\Quant
- Familiarization Guide covers basic operations.

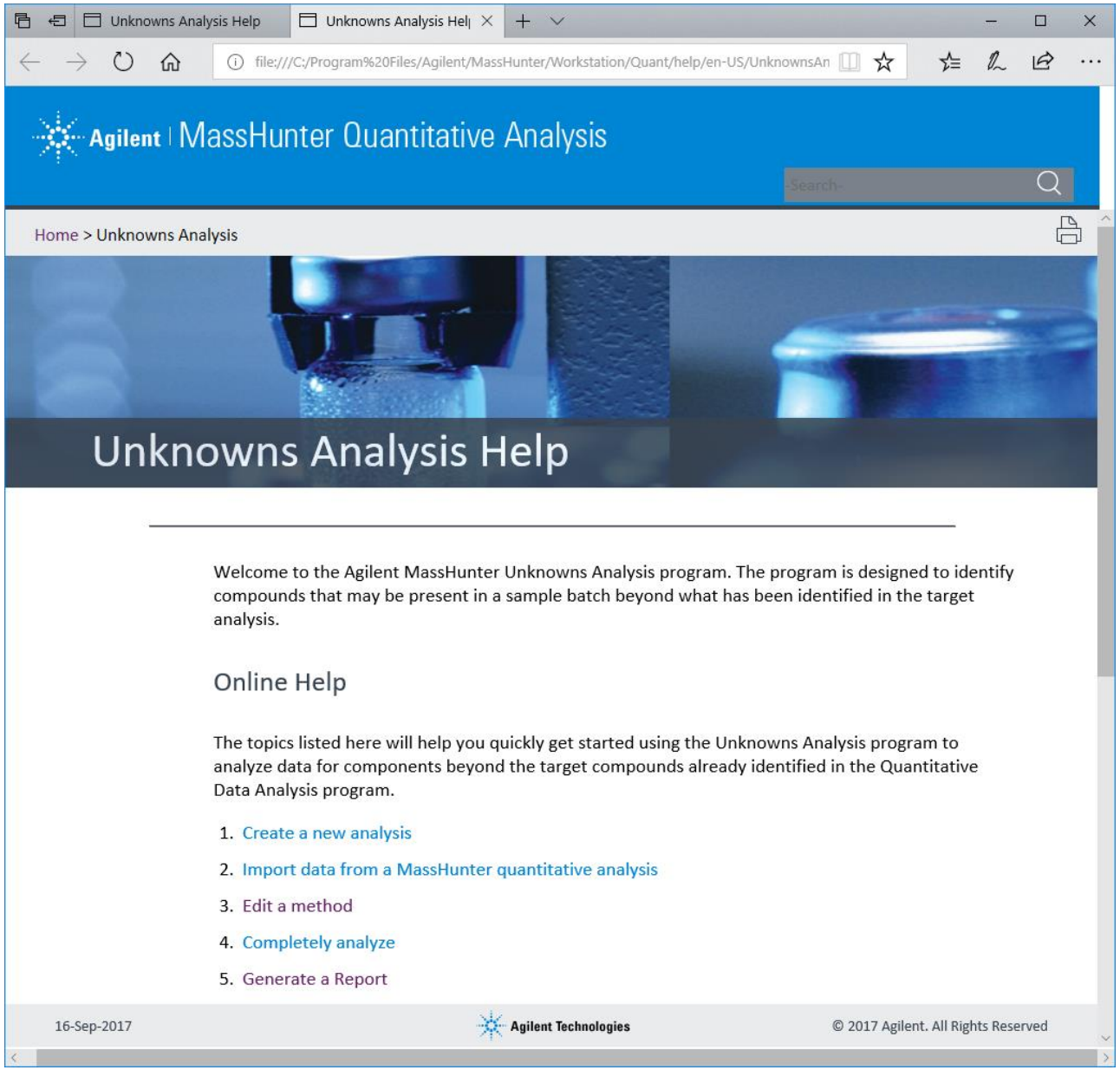
- Uses example data located on USB in \Supplemental\MassHunter\Data\QuantExamples\MS\RI-PEST-MATRIX
- Example data can be loaded with Supplemental installer (Supplemental.msi)
- Includes RI Library and RT Calibration files.



Training Resources

Help

- Help is now compiled HTML based.
- Available with a Context sensitive links.
- Searchable.



Training Resources
Available Training Resources

Agilent CrossLab
From Insight to Outcome

Convenient Training

In our classrooms, at your site or online.

From a team of industry experts that deliver a high quality learning experience.

Classroom Training

Introductory level to in-depth, hands-on for laboratory instrumentation and software.

Customized On-Site Training

Effective learning environment designed to achieve operational excellence and employ development without the need to travel.

Online

Offerings from foundation level to expert delivered at your own pace.

Agilent University

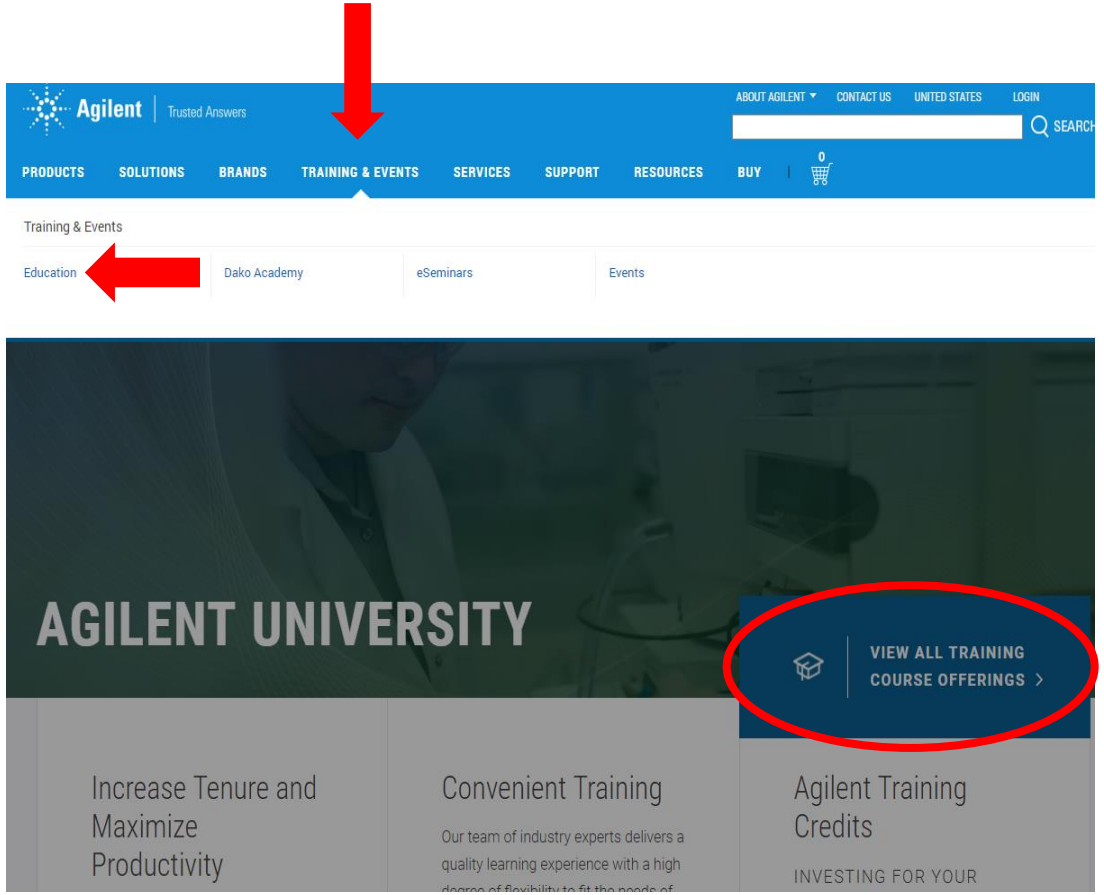
Access From Home Page

Upgraded customer experience
- Search and find courses that meet your interests and needs in the format they require.

Introduce new eLearning capabilities
- Recorded and video-based learning
- Virtual online classes

Expanded portfolio
- Foundational subjects
- Intermediate subjects
- Advanced subjects
- Workflow and applications

Helping customers
- Educate your employees on Agilent instruments and software.
- From new hires to the most seasoned scientists.



Agilent Community

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Agilent Community

community.agilent.com

Get answers. Share insights. Build connections.

Collaborate *- Ask and answer questions.*

Connect *- Interact with other Agilent users.*

Discover *- Find relevant discussions, documents, and videos.*

Share *- Contribute your insights.*