

TASQ 2025B

What is new in TASQ 2025b

TASQ 2025b – Features

- Processing and quantification of UV-VIS data
 - UV-VIS data collected and stored by HyStar is supported (chromatography-data.sqlite)
 - MS data must also be acquired

TASQ 2025b – Features

- Processing
 - Load single wavelength UV-VIS chromatograms
 - Extract UV-VIS chromatograms from DAD spectra
 - Smooth traces
 - Perform peak detection and integration
 - Valley to valley option is currently not supported!
 - S/N filter currently not performed
 - Store peak data and group them to a determination
- Manual integration of UV-VIS chromatogram

TASQ 2025b – Features

- Quantification
 - Use UV-VIS area or height for regression calculation and calculation of quantities
 - Obey UV-VIS area or height of internal standard accordingly



TASQ 2025b: UV-VIS Processing Result Presentation – Result Tables

- Result table add Area/Height for Quantification (UV) column as summary on determination level
- Available columns for result tables

Area (UV) for Quantification

Sum of UV area values of all quantifier ions

Area for Quantification [IS] (UV)

Area of UV chromatogram peak for internal standard

Height (UV) for Quantification

Sum of UV height values of all quantifier ions

Height for Quantification [IS] (UV)

Height for Quantification [IS] (UV)

Rel. Area UV

Area UV relative to internal standard

Rel. Height UV

Height UV relative to internal standard

Rel. Quantity (UV Area)

Relative quant based on IS $c = (S_A \text{ for Quantification UV} / S_{IS_A} \text{ UV}) * c_{IS}$

Rel. Quantity (UV Height)

Relative quant based on IS $c = (S_H \text{ for Quantification UV} / S_{IS_H} \text{ UV}) * c_{IS}$

	Analyte Name	Formula	MRSQC	Δm/z [mDa]	ΔRT [min]	mSigma	Quantity	Quantity expe...	Area (UV) for Quantification	Area for Quantification [IS] (UV)	Height (UV) for Quantification	Height for Quantification [IS] (UV)	Rel. Area UV	Rel. Height UV	Rel. Quantity (UV Area)	Rel. Quantity (UV Height)	A/H	Visited	Review State
1	Caffeine	C ₈ H ₁₀ N ₄ O ₂		0.09	0.18	3.1	2510.7 ng/mL	2500.0 ng/mL	708		200						6.7	<input checked="" type="checkbox"/>	ACCEPTED
2	Theobromine Mob1	C ₇ H ₈ N ₂ O ₂		0.27	0.15	1.7	2772.1 ng/mL	2500.0 ng/mL	125	708	31	200	0.157	0.176	439.8 ng/mL	392.1 ng/mL	6.7	<input checked="" type="checkbox"/>	ACCEPTED
3	Reserpine	C ₃₃ H ₄₆ N ₂ O ₉		-0.28	0.40	9.2	264.8 ng/mL	250.0 ng/mL		708			200				8.3	<input type="checkbox"/>	NONE
4	Alprazolam	C ₁₇ H ₁₂ ClN ₄		-0.28	0.26	14.3	26.2 ng/mL	25.0 ng/mL									7.7	<input type="checkbox"/>	NONE

TASQ 2025b: UV-VIS Processing Result Presentation – Detailed UV Results View

- New Detailed UV Results view available – displays results for the different UV-VIS traces specified for each analyte

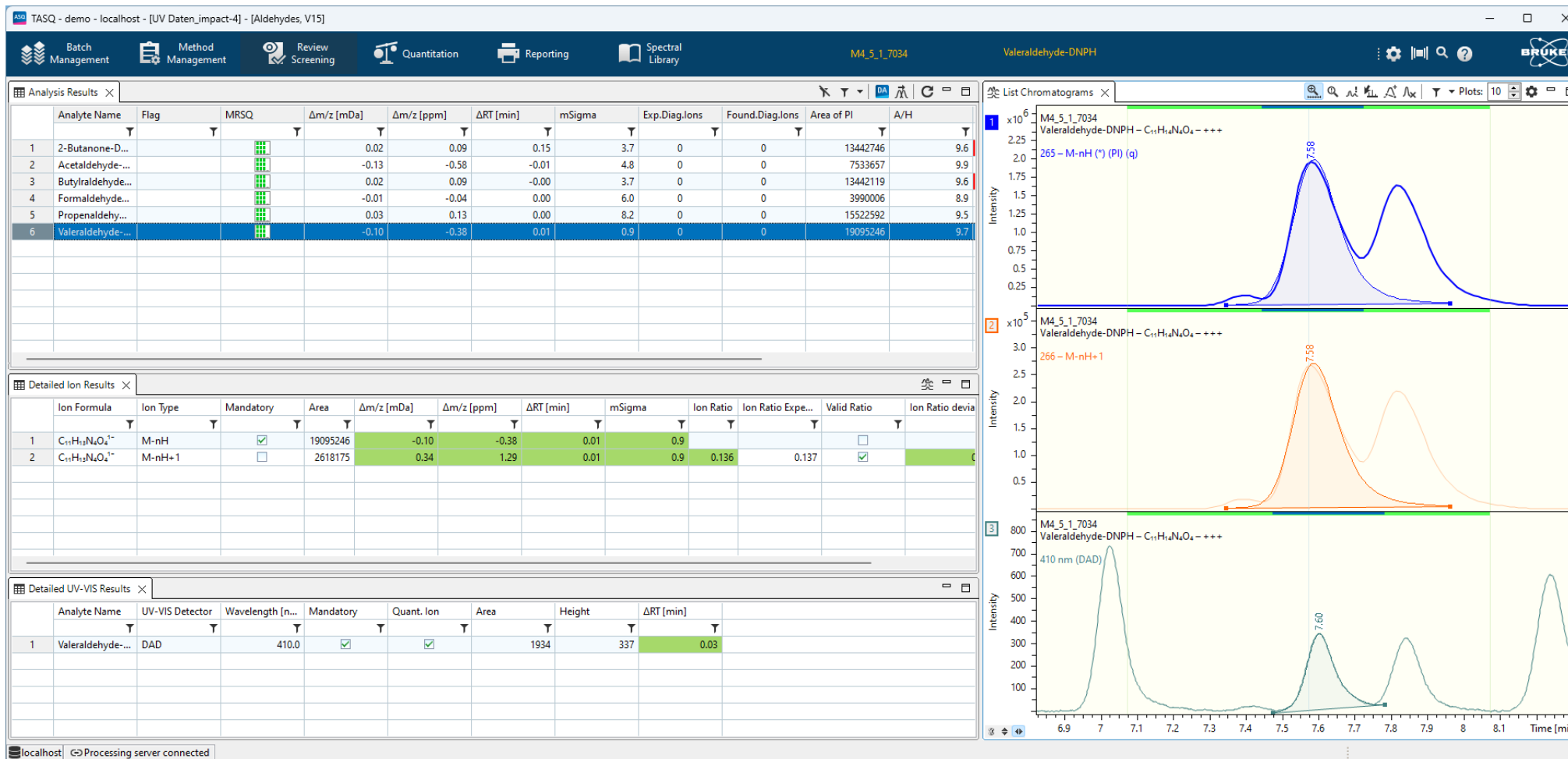
Detailed UV Results																			
	Analyte Name	Wavelength [nm]	UV Detector	Status	RT expected [min]	RT [min]	RT Score	ΔRT [min]	FWHM [s]	Quant. Ion	Mandatory	Man.	Area	Height	Intensity	A/H	S/N	Noise	Found
1	Caffeine	280.0	DAD		4.27	4.45	++	0.18	3.30	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	708	200	189	3.5	200	1	<input checked="" type="checkbox"/>

TASQ 2025b: UV-VIS Processing Result Presentation

- New Detailed UV Results view available – displays results for the different UV-VIS traces specified for each analyte

A/H	Area to height ratio indicates whether this is a real chromatographic peak.
Analyte	Name of analyte
Area	Area of detected chromatographic peak for ion trace
FWHM [s]	Chromatographic peak width at half height in seconds
Found	Status information whether analyte has been identified or not
Height	Height of detected chromatographic peak for ion trace
Intensity	Intensity of detected chromatographic peak for ion trace
Man.	Flag whether peak has been integrated manually
Mandatory	Mandatory ion
Noise	Back calculated noise from S/N and S
Quant. Ion	Quantifier ion
RT Score	Retention time score
RT [min]	Observed retention time in minutes
RT expected [min]	Expected retention time in minutes
S/N	Signal-to-noise level of chromatographic peak for finding
Status	Status of measurement
UV Detector	Shows the used source of UV data (channel trace or DAD spectra)
Wavelength [nm]	Wavelength setting of UV chromatogram
Δ RT [min]	Absolute retention time deviation of finding relative to expected retention time

TASQ 2025b: Detailed UV-VIS Results View Available

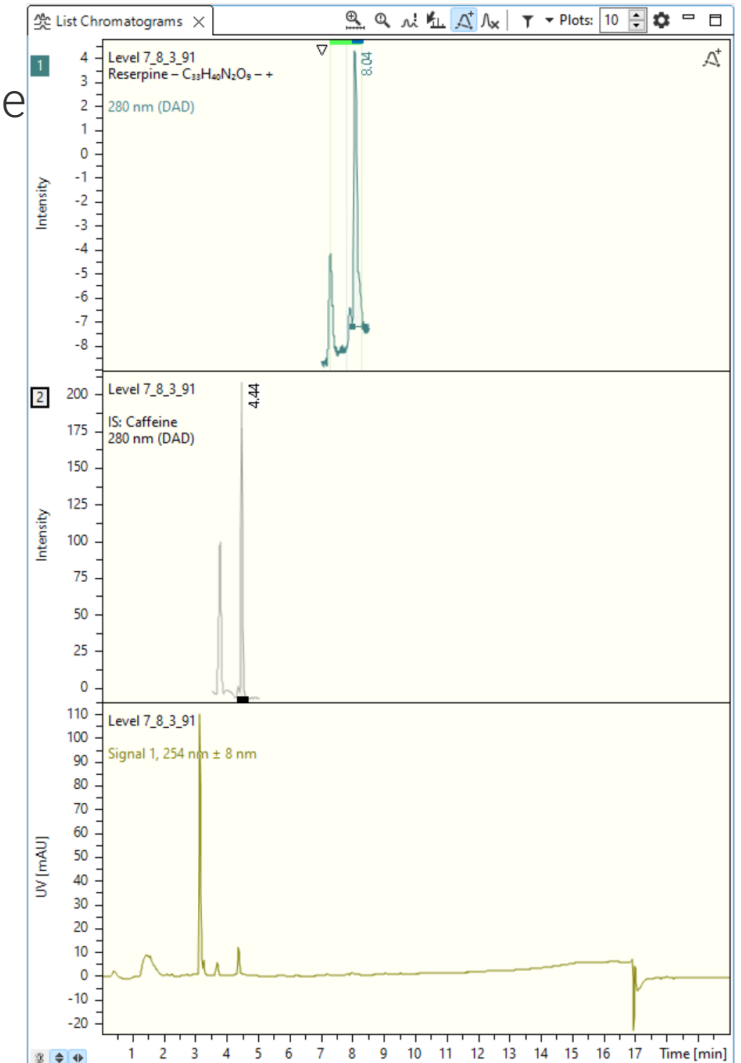
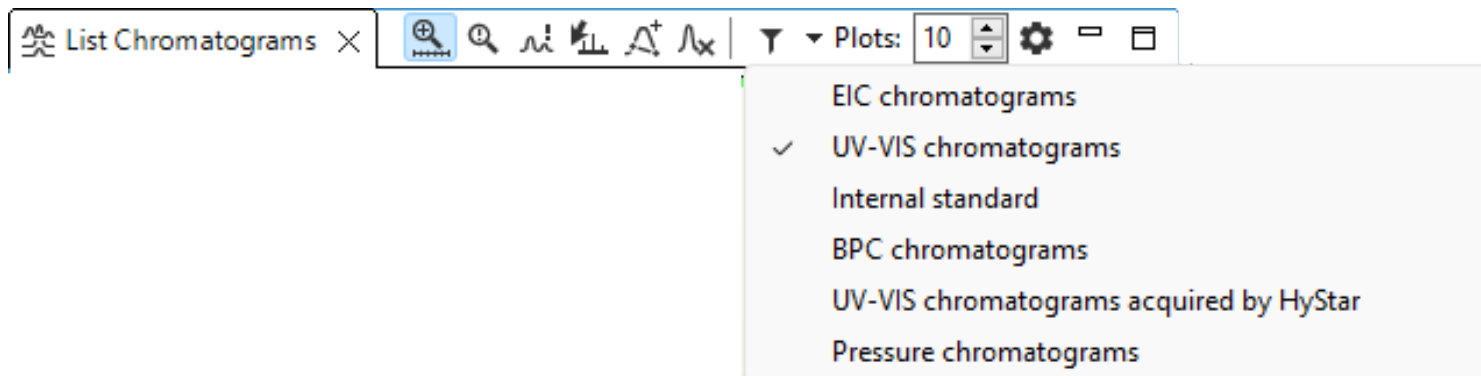


TASQ 2025b: UV-VIS Processing Result Presentation – List Chromatograms View

- List Chromatograms view displays the chromatographic traces and detected peaks for the specified UV-VIS traces
 - List Chromatograms view allows to integrate manually the peaks of the UV-VIS traces
- Show optionally UV-VIS traces of associated internal standard

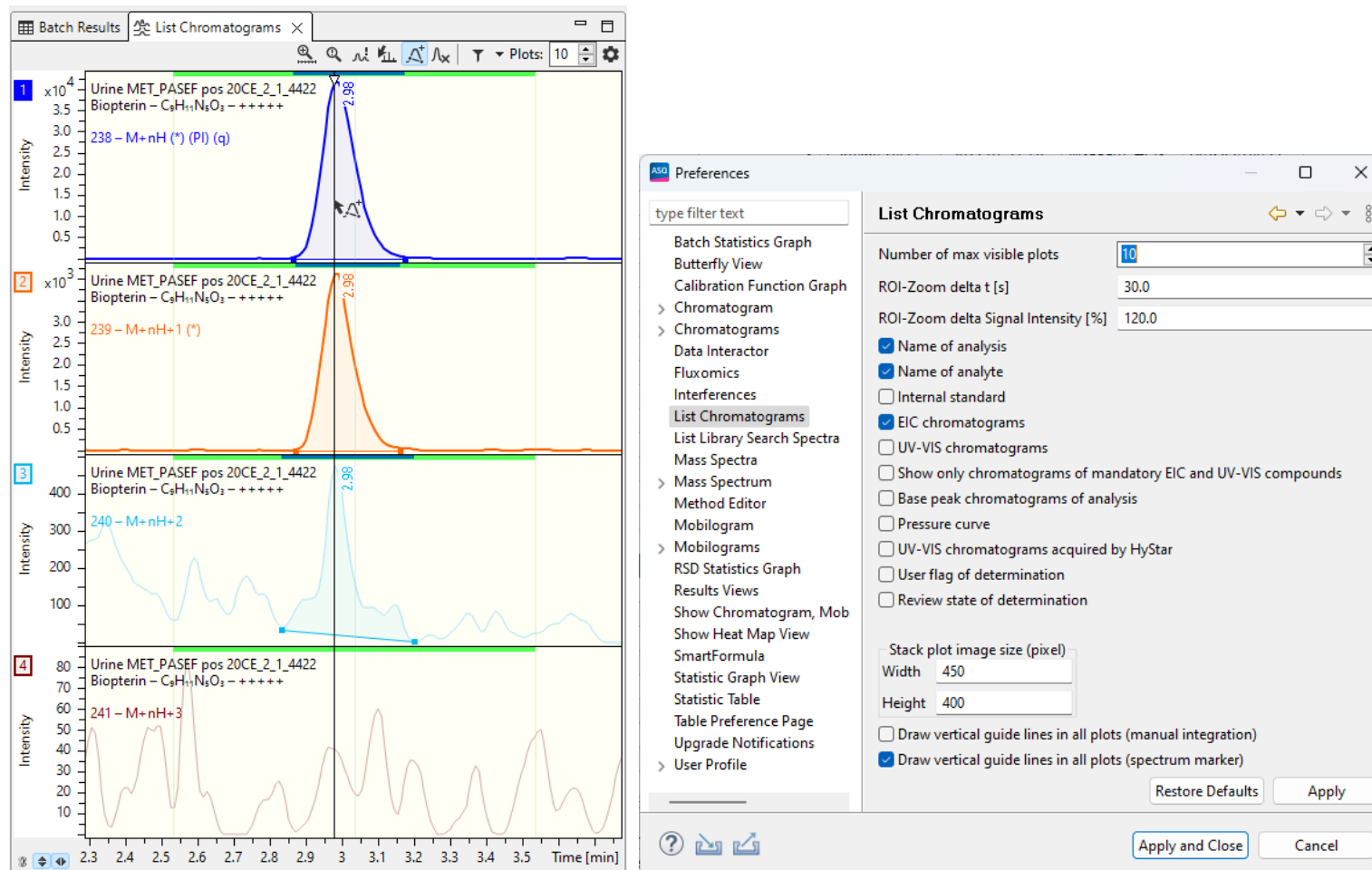
TASQ 2025b: List Chromatogram View – UV-VIS chromatograms / Internal Standard

- Show all UV-VIS chromatograms available from chromatography-data.sqlite
- Show UV-VIS compound traces of selected analyte and optionally related internal standard
- Option to show / hide EIC chromatogram of selected determination



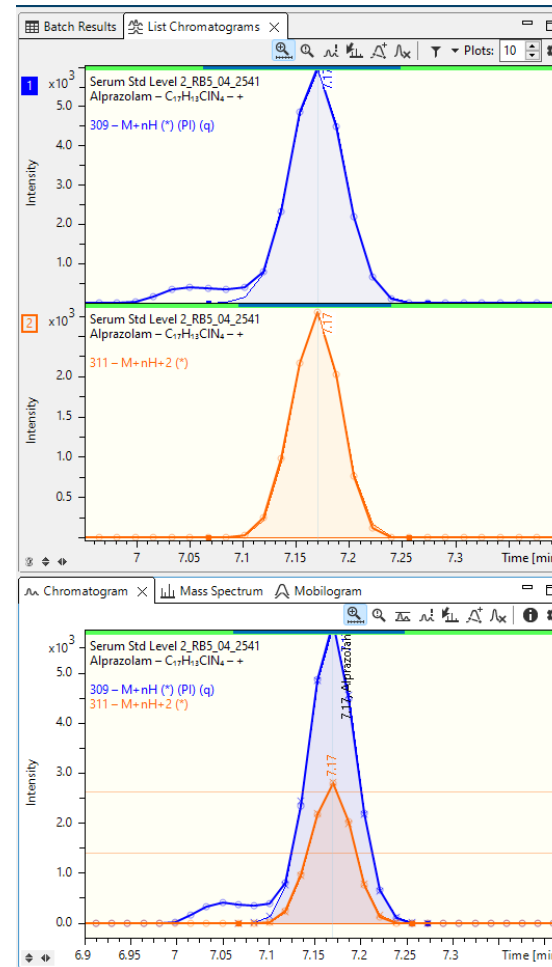
TASQ 2025b: List Chromatograms View – Vertical Guidelines

- Show vertical rulers in all views simultaneously to compare as a guide for comparison the various traces

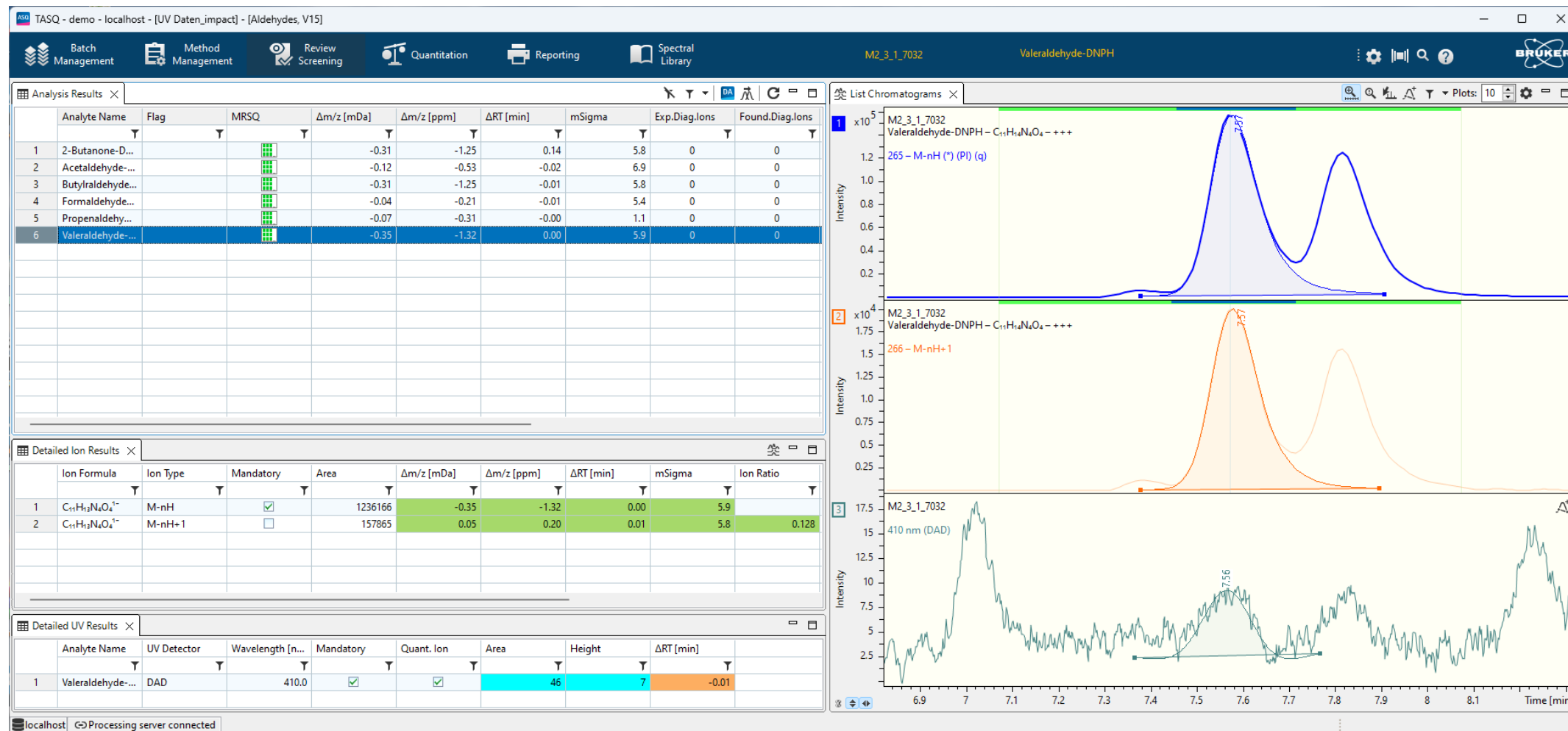


TASQ 2025b: List Chromatograms View: Show EMG Fitted Curves

- As in Chromatogram/s, Mobilogram/s view



TASQ 2025b: Detailed UV Results View Available



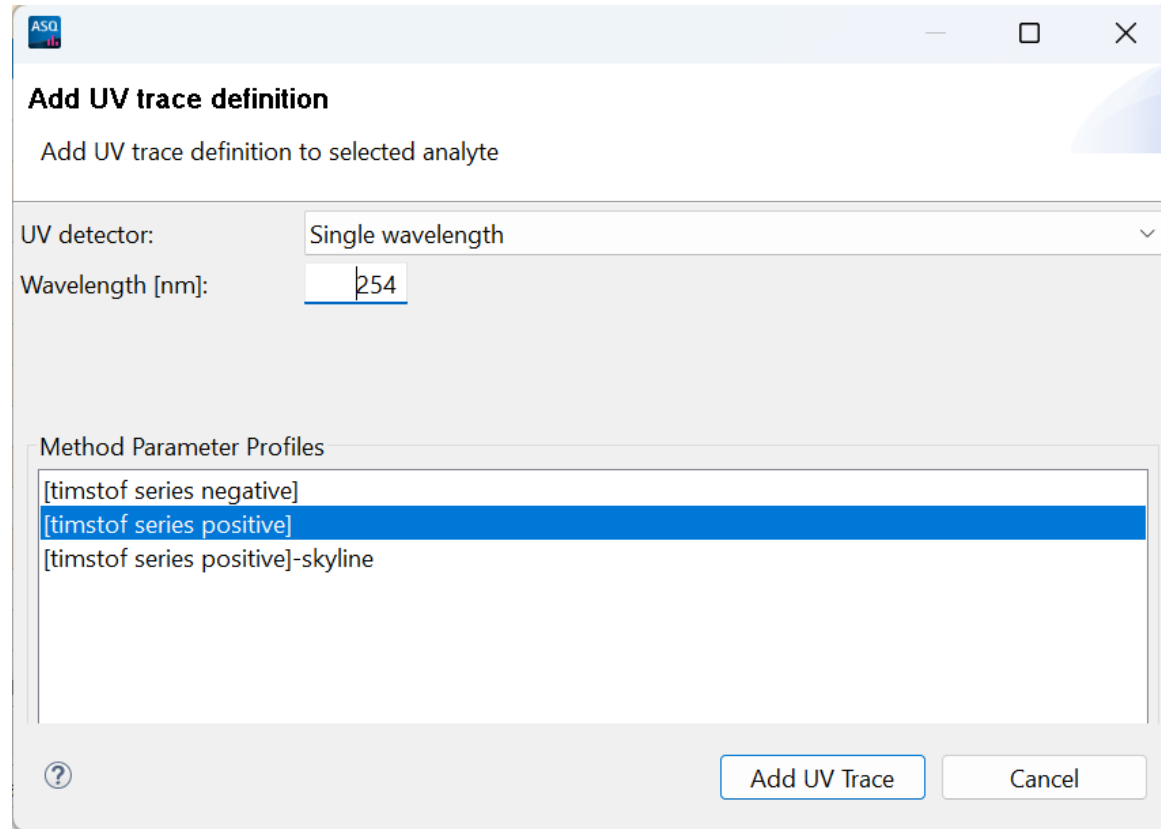
TASQ 2025b – UV-VIS Method Parameters

- In General Method Settings is a new group for detector configuration
 - If UV-VIS data is available specify the retention time offset of clock of the UV-VIS detector and the MS detector
- In the Analytes settings tab is a new sub tab beside of the Ions tab
 - Specify here the settings for loading or extracting UV-VIS chromatograms for single wavelength or DAD chromatograms

Ions	UV-VIS	Ion Ratios	Rules										
	Analyte	UV-VIS Detector	Wavelength [n...	Wavelength wi...	Mandatory	Quant. UV-VIS ...	Area thr.	Height thr.	Sens. [%]	Min peak valle...	Smoothing wi...		
	⌵	⌵	⌵	⌵	⌵	⌵	⌵	⌵	⌵	⌵	⌵		
1	Caffeine	DAD	280	10	<input type="checkbox"/>	<input checked="" type="checkbox"/>	0	0	90	4.0	0.10		
2	Reserpine	DAD	280	10	<input type="checkbox"/>	<input checked="" type="checkbox"/>	0	0	90	4.0	0.10		
3	Theobromine ...	DAD	280	10	<input type="checkbox"/>	<input checked="" type="checkbox"/>	0	0	90	4.0	0.10		
4	Theobromine ...	DAD	254	10	<input type="checkbox"/>	<input checked="" type="checkbox"/>	0	0	90	4.0	0.10		

TASQ 2025b – UV-VIS Method Parameters: Add a UV-VIS Trace

- UV-VIS chromatograms can be acquired as single wavelength chromatograms stored by HyStar or
- Extracted UV-VIS chromatograms calculated from DAD UV-VIS spectra



ASQ
Add UV trace definition
Add UV trace definition to selected analyte

UV detector: Single wavelength

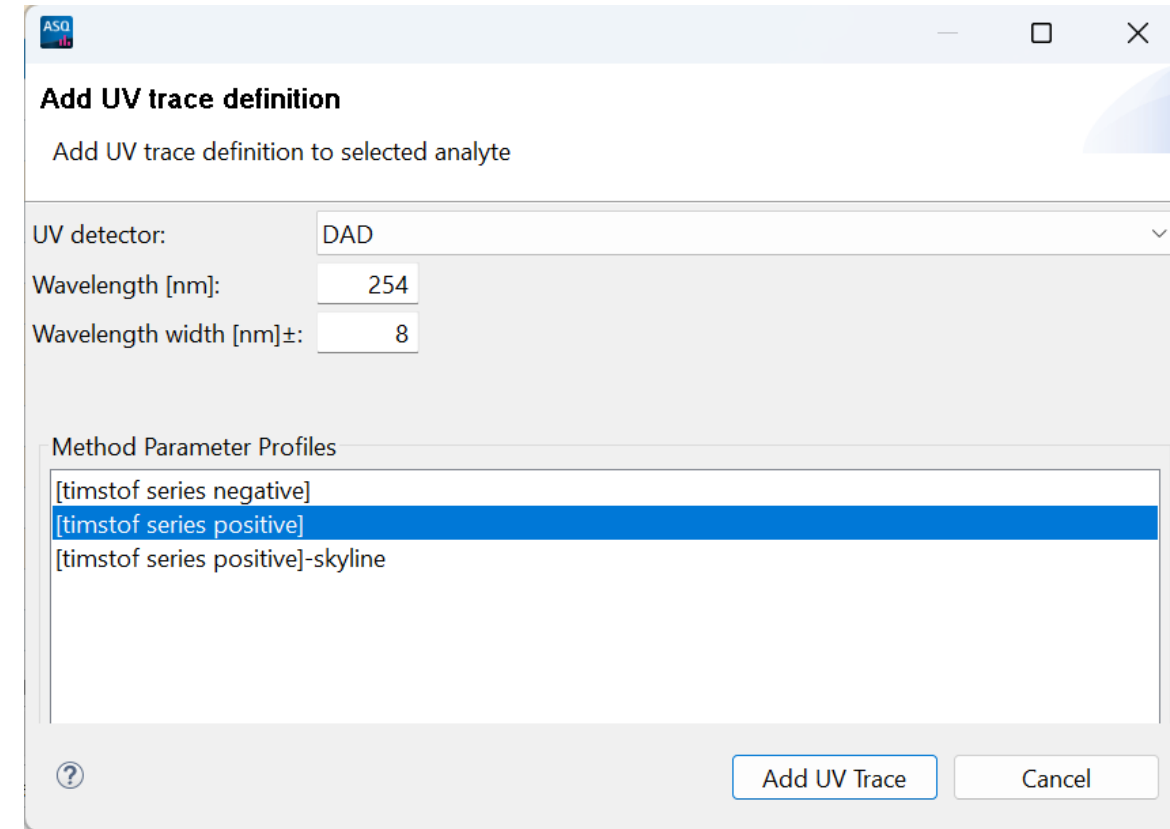
Wavelength [nm]: 254

Method Parameter Profiles

- [timstof series negative]
- [timstof series positive]
- [timstof series positive]-skyline

?

Add UV Trace Cancel



ASQ
Add UV trace definition
Add UV trace definition to selected analyte

UV detector: DAD

Wavelength [nm]: 254

Wavelength width [nm]±: 8

Method Parameter Profiles

- [timstof series negative]
- [timstof series positive]
- [timstof series positive]-skyline

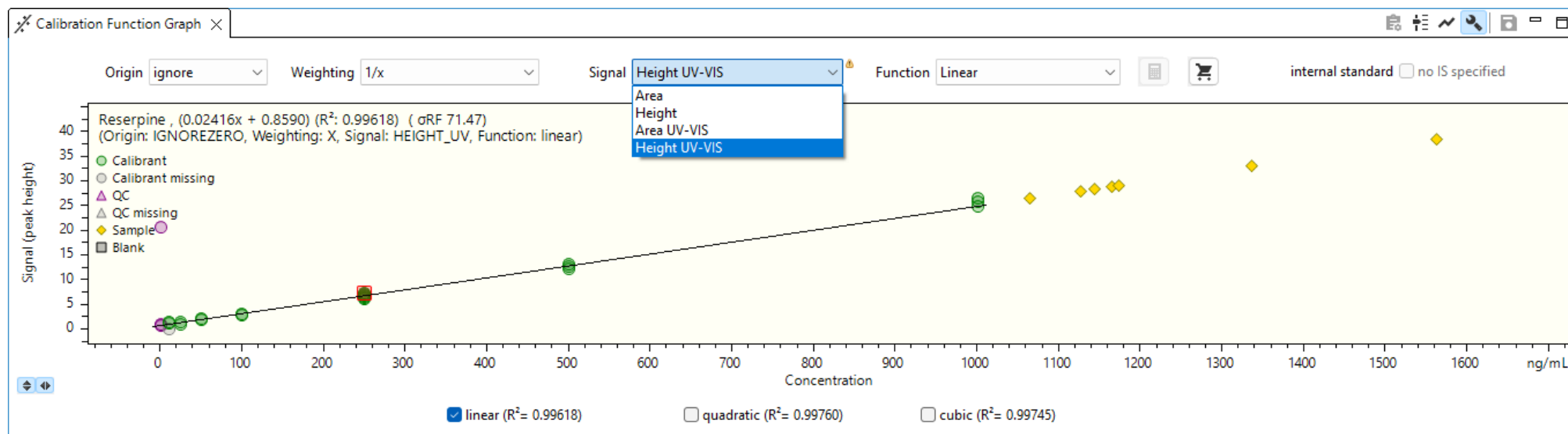
?

Add UV Trace Cancel

TASQ 2025b – UV-VIS Quantitation Parameters

- For quantification specify Area or Height UV to use the UV-VIS derived signal values

	Analyte	Function type	Weighting	Origin	Signal	Principal Ion	Quantitation ...	Correction fact...	Referenced an...	Tags	Legacy Calibra...	Interferences	Batch origin
1	Caffeine	Linear	None	Force	Area	M+nH	IN_BATCH	1.000	Caffeine				
2	Reserpine	Linear	1/x	Ignore	Area	M+nH	IN_BATCH	1.000	Reserpine				
3	Theobromine ...	Linear	1/x	Ignore	Height	M+nH	IN_BATCH	1.000	Theobromine ...				
4	Theobromine ...	Linear	1/x	Ignore	Area UV-VIS Height UV-VIS	M+nH	IN_BATCH	1.000	Theobromine ...				



TASQ 2025b – Method Creation in MetaboScope

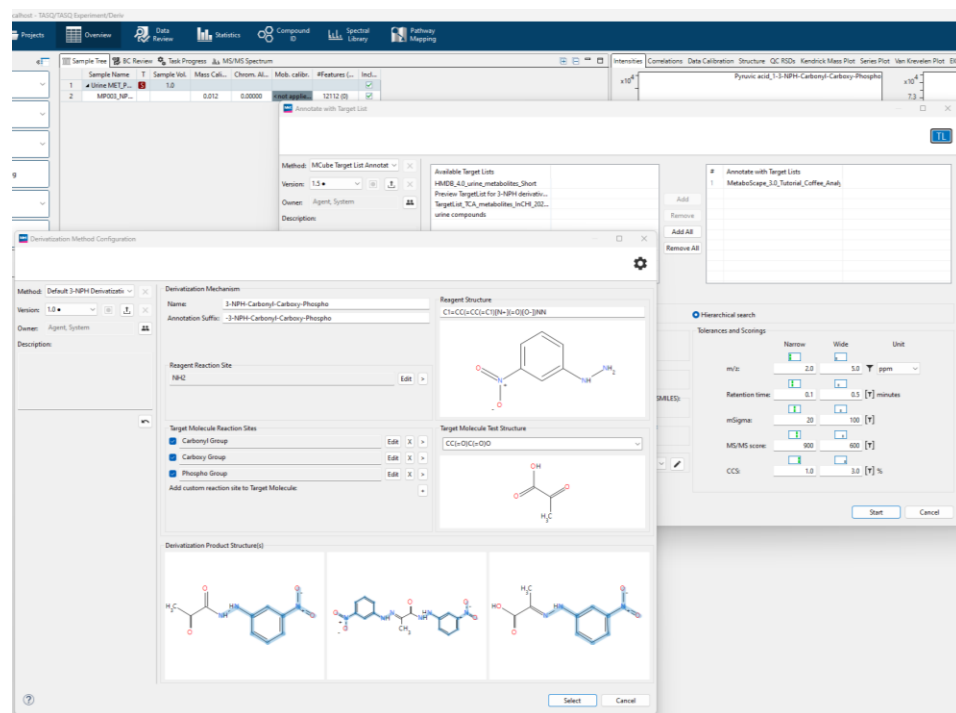
- Extension for fluxomics/derivatisation – Create TASQ method from MetaboScope
 - Support for fluxomics w/ or w/o derivatisation

Analyte	Formula	Mass [Da]	RegID	RT expected [min]	RT tol. [min]	RT narrow [min]	RT wide [min]	Rules	Tags	Comment	Principal Ion
1	2-(Hydroxyme...	C ₈ H ₁₀ O ₅	162.0528	0.40	0.50	0.25	0.40	15 / 16			A+0
2	N-Methylnicot...	C ₈ H ₉ N ₂ O ₂	137.0477	0.33	0.50	0.25	0.40	15 / 16			A+0
3	N-Methylnicot...	C ₈ H ₉ N ₂ O ₂	137.0477	0.35	0.50	0.25	0.40	15 / 16			A+0
4	Quinic acid	C ₇ H ₁₂ O ₆	192.0634	0.36	0.50	0.25	0.40	15 / 16			A+0
5	Quinic acid_1	C ₇ H ₁₂ O ₆	192.0634	0.34	0.50	0.25	0.40	15 / 16			A+0

Ion	Ion formula	m/z	Spectrum type	Mandatory	Quant. ion	Reference ion	Ion ratio	Ion ratio tol. [%]	Area thr.	Height thr.	Sens. [%]
1	A+0	¹² C ₇ H ₁₂ O ₆ ⁺	193.0707	FullScan	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>			3000	1500	99
2	A+1	¹³ C ¹ ₇ H ₁₂ O ₆ ⁺	194.0740	FullScan	<input type="checkbox"/>	<input type="checkbox"/>			3000	1500	99
3	A+2	¹³ C ² ₇ H ₁₂ O ₆ ⁺	195.0774	FullScan	<input type="checkbox"/>	<input type="checkbox"/>			3000	1500	99
4	A+3	¹³ C ³ ₇ H ₁₂ O ₆ ⁺	196.0807	FullScan	<input type="checkbox"/>	<input type="checkbox"/>			3000	1500	99
5	A+4	¹³ C ⁴ ₇ H ₁₂ O ₆ ⁺	197.0841	FullScan	<input type="checkbox"/>	<input type="checkbox"/>			3000	1500	99
6	A+5	¹³ C ⁵ ₇ H ₁₂ O ₆ ⁺	198.0874	FullScan	<input type="checkbox"/>	<input type="checkbox"/>			3000	1500	99
7	A+6	¹³ C ⁶ ₇ H ₁₂ O ₆ ⁺	199.0908	FullScan	<input type="checkbox"/>	<input type="checkbox"/>			3000	1500	99
8	A+7	¹³ C ⁷ ₇ H ₁₂ O ₆ ⁺	200.0941	FullScan	<input type="checkbox"/>	<input type="checkbox"/>			3000	1500	99

TASQ 2025b – Method Creation in MetaboScape

- Extension for fluxomics/derivatisation – Create TASQ method from MetaboScape
 - Support for fluxomics w/ or w/o derivatization – the moiety introduced by derivatization will not be considered for generation of isotopologous



General method settings		Calibration settings		Analytes settings		Quantitation settings		Library search settings		General library search settings		Internal standards		Number formats		Colors definition		Workflow settings	
Analyte	Formula	Mass [Da]	Reg.ID	RT expected [...]	RT tol. [min] ±	RT narrow [mi...] ±	RT wide [min] ±	Rules	Tags	Comment	Principal Ion								
1	cis-Aconitic ac...	C ₁₂ H ₁₄ N ₂ O ₅	444.1030	6.42	0.50	0.25	0.40	15 / 16			A+U								
2	cis-Aconitic ac...	C ₁₂ H ₁₄ N ₂ O ₅	579.1462	7.54	0.50	0.25	0.40	15 / 16			A+0								
3	Citric acid_2-3...	C ₁₈ H ₁₈ N ₂ O ₅	462.1135	10.64	0.50	0.25	0.40	15 / 16			A+0								
4	Citric acid_3-3...	C ₂₄ H ₂₂ N ₂ O ₁₀	597.1568	7.16	0.50	0.25	0.40	15 / 16			A+0								
5	Fumaric acid_1...	C ₁₀ H ₈ N ₂ O ₅	251.0542	4.33	0.50	0.25	0.40	15 / 16			A+0								
6	Fumaric acid_2...	C ₁₆ H ₁₄ N ₂ O ₅	386.0975	6.51	0.50	0.25	0.40	15 / 16			A+0								
7	L-Lactic acid	C ₃ H ₄ O ₃	90.0317	4.81	0.50	0.25	0.40	15 / 16			A+0								
8	L-Lactic acid_1...	C ₉ H ₁₁ N ₂ O ₈	225.0750	4.09	0.50	0.25	0.40	15 / 16			A+0								
9	Malic acid_2-3...	C ₁₆ H ₁₈ N ₂ O ₇	404.1080	8.12	0.50	0.25	0.40	15 / 16			A+0								
10	Oxalacetic aci...	C ₁₆ H ₁₄ N ₂ O ₇	402.0924	9.15	0.50	0.25	0.40	15 / 16			A+0								
11	Oxalacetic aci...	C ₂₂ H ₁₉ N ₂ O ₇	537.1357	8.72	0.50	0.25	0.40	15 / 16			A+0								
12	Oxoglutaric ac...	C ₁₇ H ₁₄ N ₂ O ₇	416.1080	8.49	0.50	0.25	0.40	15 / 16			A+0								
13	Oxoglutaric ac...	C ₂₃ H ₁₈ N ₂ O ₇	551.1513	8.67	0.50	0.25	0.40	15 / 16			A+0								
14	Pyruvic acid_1...	C ₈ H ₈ N ₂ O ₄	223.0593	6.88	0.50	0.25	0.40	15 / 16			A+0								
15	Pyruvic acid_2...	C ₁₄ H ₁₄ N ₂ O ₅	358.1026	9.03	0.50	0.25	0.40	15 / 16			A+0								
16	Succinic acid_...	C ₁₄ H ₁₄ N ₂ O ₅	388.1131	6.08	0.50	0.25	0.40	15 / 16			A+0								

Ions		UV settings		Ion Ratios		Rules												
Ion	Ion formula	m/z	Spectrum type	Mandatory	Quant. ion	Reference ion	Ion ratio	Ion ratio tol. [...]	Area thr.	Height thr.	Sens. [%]							
1	A+0	C ₈ ¹² C ₃ H ₈ N ₂ O ₄ ⁺	224.0677	FullScan	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>			3000	1500	99							
2	A+1	C ₈ ¹² C ₃ ¹³ H ₈ N ₂ O ₄ ⁺	225.0710	FullScan	<input type="checkbox"/>	<input type="checkbox"/>			3000	1500	99							
3	A+2	C ₈ ¹² C ₂ ¹³ C ₂ H ₈ N ₂ O ₄ ⁺	226.0744	FullScan	<input type="checkbox"/>	<input type="checkbox"/>			3000	1500	99							
4	A+3	C ₈ ¹² C ₁ H ₈ N ₂ O ₄ ⁺	227.0777	FullScan	<input type="checkbox"/>	<input type="checkbox"/>			3000	1500	99							

TASQ 2025b – User Workflow – Process Batch

- Add Perform Library Search and Apply Evaluation Rules as separate workflow steps to Workflow Settings tab

General method settings | Calibration settings | Analytes settings | Quantitation settings | Library search settings | General library search settings | Internal standards | Number formats | Colors definition | Workflow settings

Execute settings: These parameters steers execution of report generation or LIMS export during automatic workflow in context of batch acquisition.

Perform library search Calculate calibration functions and quantify Perform LIMS export
 Apply evaluation rules Create reports

LIMS export settings:

Root folder for LIMS export: ...

Substitute text for n.a.:

Format:

Report missings

Single file for batch

TASQ 2025b: Checks Whether a Batch can be Processed

ASQ Batch Processing

Select method for processing UV IS 1

Please select a method to process your batch.

Applied filter: None

	TASQ Method	Version	Type	Read-
185	TSQ-9247-Demo Data Quant	1	TOF	
186	TSQ-9464 Bre-24-2042_Quant	1	TOF	
187	TSQ-9693 EPA PFAS 20min PFAS Kit bbCID 70 for TargetScreener KAWE finalize	3	timsTOF	
201	UV IS (V2) 1	1	timsTOF	

Processing service status

Processing server not connected on station [No station id]. Processing not possible.

< Back Next > Finish Cancel

201	UV IS (V2) 1	1	timsTOF
-----	--------------	---	---------

Batch status processing

You can't start batch processing as long the batch has status running.

Purge task queues of batch

< Back Next > Finish Cancel

ASQ Set to Batch Parameters

Method differences

Change batch parameters "Caffeine-UV Quant-import-as-TOF (V3)" to new method "Caffeine-UV Quant-import-as-TOF (V4)" requires the following steps:

Component	Necessary step
Caffeine	Reprocess analyte
Reserpine	Reprocess analyte
Theobromine Mob1	Reprocess analyte
Theobromine Mob2	Reprocess analyte

Workflow options

Perform screening Calculate calibration functions and quantify Perform LIMS export
 Replay manual integration Apply evaluation rules
 Perform library search

Batch status processing

You can't start batch processing as long the batch has status running.

Purge task queues of batch

TASQ 2025b: Improvements

- DART – make use of area / intensity threshold for detection of analytes
- TASQ method: disable Peak Fit option if DART processing is selected

TASQ 2025b: Export Parameter Settings of Selected Analytes

- Export all processing parameter of selected analytes in a TASQ method as a tab separated text file
- This parameter sets can be modified in any text editor or Excel

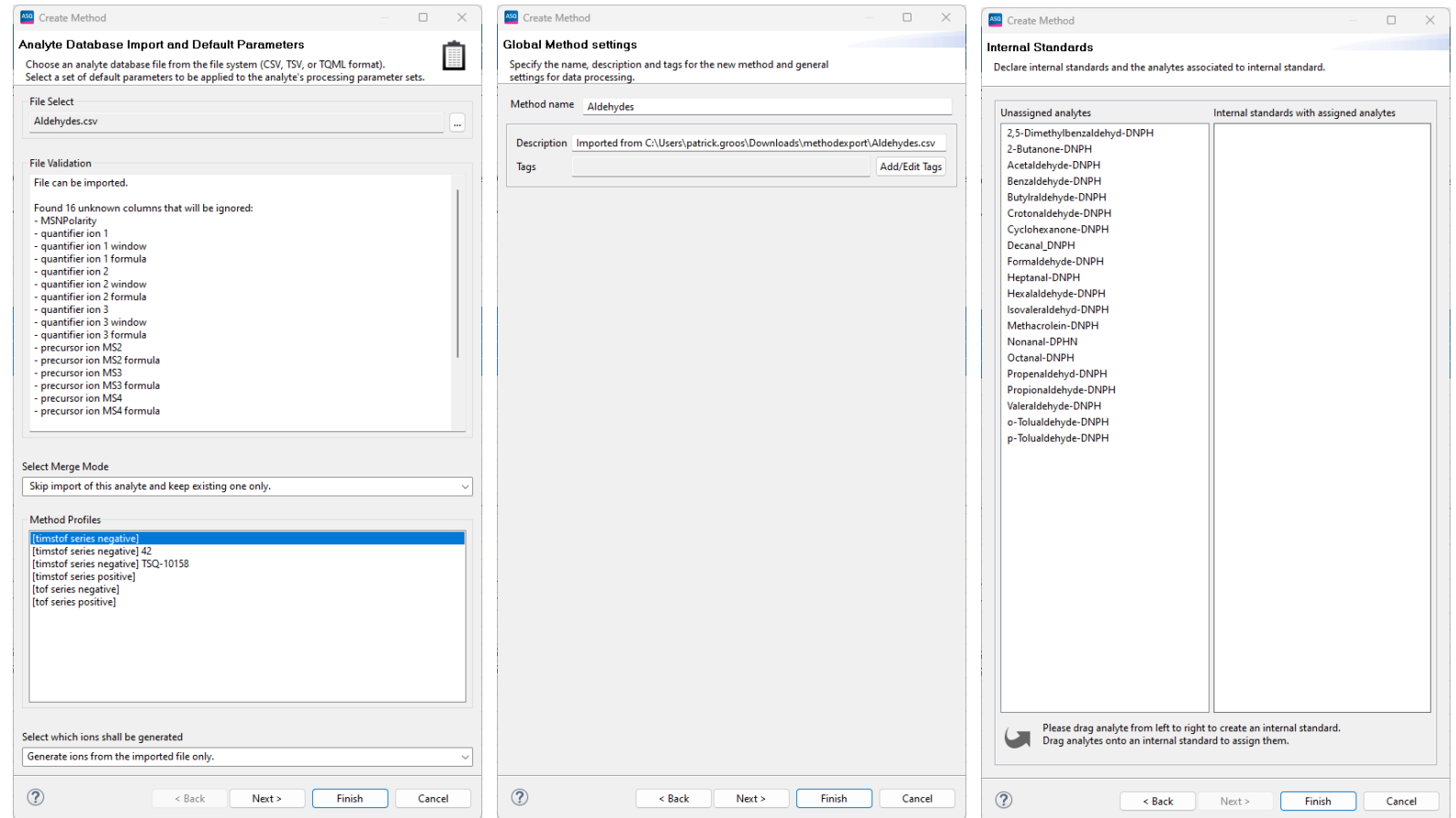
General method settings		timsTOF settings		Calibration settings		Analytes settings		Quantitation settings		Library search settings	
	Analyte	Formula	Mass [Da]	Reg.ID	RT expected [...]	RT tol. [min] ±	RT n				
1	10-Hydroxycar...	C ₉ ¹³ C ₈ H ₁₄ N ₂ O ₂	260.1257	29331-92-8		0.00	0.50				
2	2-Hydroxyethy...	C ₁₇ D ₄ H ₁₀ ClFN ₂ O ₂	336.0979	1397209-35-6		0.00	0.50				
3	4-ANPP D5	C ₁₉ D ₅ H ₁₉ N ₂	285.2253	1189466-15-6		0.00	0.50				
4	4-Fluoroisobut...	C ₂₃ D ₇ H ₂₂ FN ₂ O	375.2703	2747917-34-4		0.00	0.50				
5	6-MAM D6	C ₁₉ D ₆ H ₁₈ NO ₄	333.1847	152477-90-2		0.00	0.50				
6	7-Aminoclona...	C ₁₅ D ₃ H ₂					0.50				
7	7-Aminoflunitr...	C ₁₆ D ₇ H ₁₂					0.50				
8	7-Hydroxyque...	C ₂₀ ¹³ C					0.50				
9	8-Aminoclona...	C ₁₇ D ₄ H ₂					0.50				
10	9-Hydroxyrisp...	C ₂₃ D ₄ H ₂					0.50				
11	AB-CHMINAC...	C ₂₀ D ₄ H ₂					0.50				
12	Acetyl Fentany...	C ₂₁ D ₅ H ₂					0.50				
13	Acetyl Norfent...	C ₁₃ D ₃ H ₁					0.50				
14	Acrylfentanyl D5	C ₂₂ D ₅ H ₂					0.50				
15	ADB-Butinaca ...	C ₁₈ D ₉ H ₁					0.50				
16	alpha-Hydroxy...	C ₁₇ D ₃ H ₄					0.50				

Ions		UV-VIS	Ion Ratios	Rules
	Ion		Ion fo	
1	M-nH		C ₁₅ D ₃ F	
2	M-nH+2		C ₁₅ D ₃ F	
3	M-nH		C ₁₆ D ₇ F	
4	M-nH+1		C ₁₆ D ₇ F	
5	M-nH		C ₂₀ ¹³ C	
6	M-nH+1		C ₂₀ ¹³ C	
7	M-nH		C ₁₇ D ₄ F	
8	M-nH+2		C ₁₇ D ₄ F	

Set Tags to Selected Analytes
Add Analyte
Remove Analytes
Paste Analytes
Copy selected Analytes
Add Library Search Configuration to selected Analytes
Delete Library Search Configuration from selected Analytes
Add Missing Ion Ratios
Change Retention Times Offset...
Delete Sigma and Tau Values of all Analytes
Select Evaluation Rules
Clone Method for selected Analytes
Clone Method for Fluxomics for selected Analytes
Export selected Analytes for MetaboScope Target List
Generate prm-PASEF CSV file from selected Analytes
Create processing Method for prm-PASEF
Create processing Method for dia-PASEF
Export selected analytes as TSV
Fill Down
Copy
Export to Excel

TASQ 2025b: Import new TSV File for Creating a TASQ Method

- Import modified parameter sets as a new method



The image displays three sequential screenshots of the 'Create Method' wizard in the TASQ software.

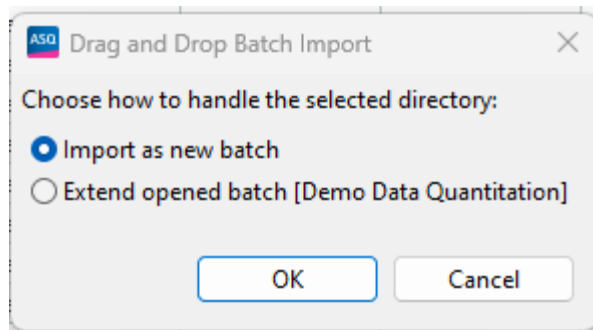
Step 1: Analyte Database Import and Default Parameters
This window shows the process of importing a TSV file. The 'File Select' section shows 'Aldehydes.csv' is chosen. The 'File Validation' section indicates the file can be imported but lists 16 unknown columns to be ignored, including various quantifier and precursor ion parameters. The 'Method Profiles' section shows a list of profiles, with '[tmstof series negative]' selected. The 'Select Merge Mode' dropdown is set to 'Skip import of this analyte and keep existing one only.' The 'Select which ions shall be generated' dropdown is set to 'Generate ions from the imported file only.'

Step 2: Global Method settings
This window allows for specifying the method name and general settings. The 'Method name' is 'Aldehydes'. The 'Description' is 'Imported from C:\Users\patrick.groos\Downloads\methodexport\Aldehydes.csv'. There is an 'Add/Edit Tags' button.

Step 3: Internal Standards
This window is for declaring internal standards. It features two columns: 'Unassigned analytes' and 'Internal standards with assigned analytes'. The 'Unassigned analytes' list includes various aldehydes such as 2,5-Dimethylbenzaldehyd-DNPH, 2-Butanone-DNPH, Acetaldehyde-DNPH, Benzaldehyde-DNPH, Butyraldehyde-DNPH, Crotonaldehyde-DNPH, Cyclohexanone-DNPH, Decanal-DNPH, Formaldehyde-DNPH, Heptanal-DNPH, Hexalaldehyde-DNPH, Isovaleraldehyd-DNPH, Methacrolein-DNPH, Nonanal-DPHN, Octanal-DNPH, Propenaldehyd-DNPH, Propionaldehyde-DNPH, Valeraldehyde-DNPH, o-Tolualdehyde-DNPH, and p-Tolualdehyde-DNPH. A note at the bottom states: 'Please drag analyte from left to right to create an internal standard. Drag analytes onto an internal standard to assign them.'

TASQ 2025b: Drag & Drop – Acquired Data, TASQ Method, BRKRAR

- Import .brkrar file on **drag & drop** from file explorer to Batch Summary view
 - Import batch – drag & drop folder containing .d data sets
 - Extend batch –drag & drop .d folders
 - Import .tasqMethod
 - Import .brkrar (**new**)
- Create TASQ processing method by drag & drop of .csv, .tsv, or .tqml analyte specifications (**new**)

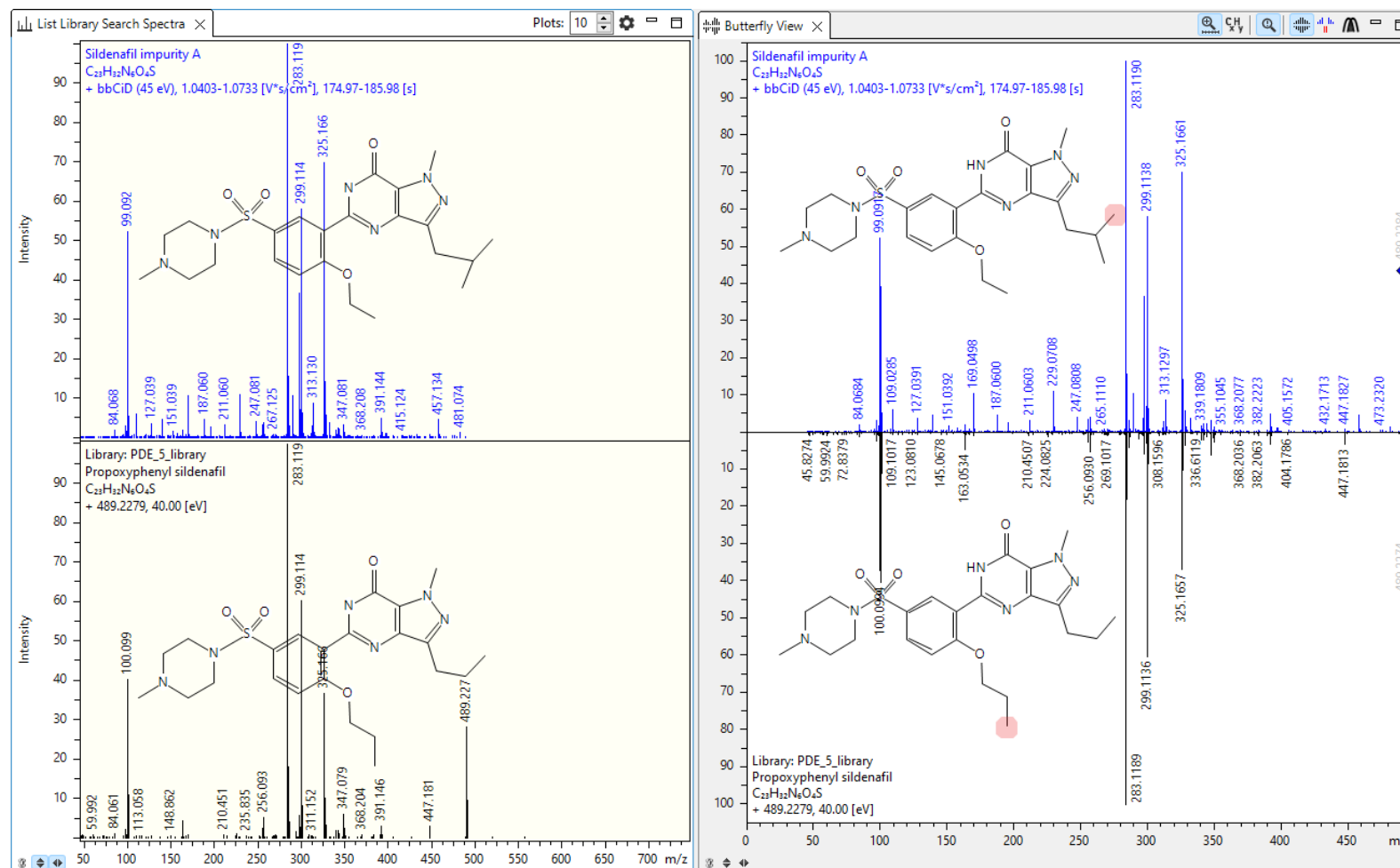


TASQ 2025b: Library Search

- Show structure of TASQ method compound or library search compound in List Library Search Spectra view
- Optionally highlight common or different structure moieties in chemical structure in Butterfly view
- Added Smart Formula pointer to Butterfly view
 - Click on a peak in acquired spectrum or library spectrum to generate elemental compositions and optionally add the identified fragment peak to TASQ method
- New method parameter on General library search settings tab – Fragment mass tolerance [mDa] for matching MS/MS peaks in library search spectrum
- Extend library search result info with time stamp when library search was performed
- When cloning a TASQ method add name and version of source to description

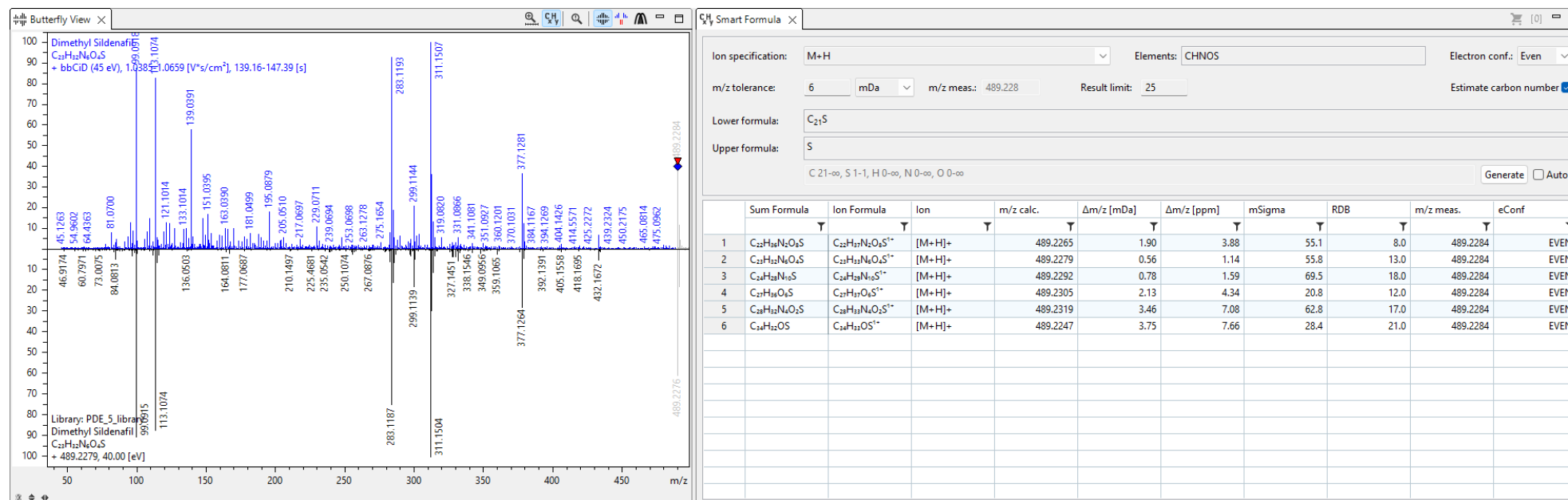
TASQ 2025b: news

- Library Search Spectra list view
 - Show structure of compound
- Butterfly view
 - Show structure of compounds
 - TASQ method compound
 - Library spectrum compound
- Highlight common substructure optionally
- Highlight non-common substructure optionally



TASQ 2025b: SmartFormula from Butterfly View

- Peform SmartFormula from Butterfly view
- Click on a peak in measured spectrum or library spectrum and review results
- Add ions from SmartFormula view to TASQ method

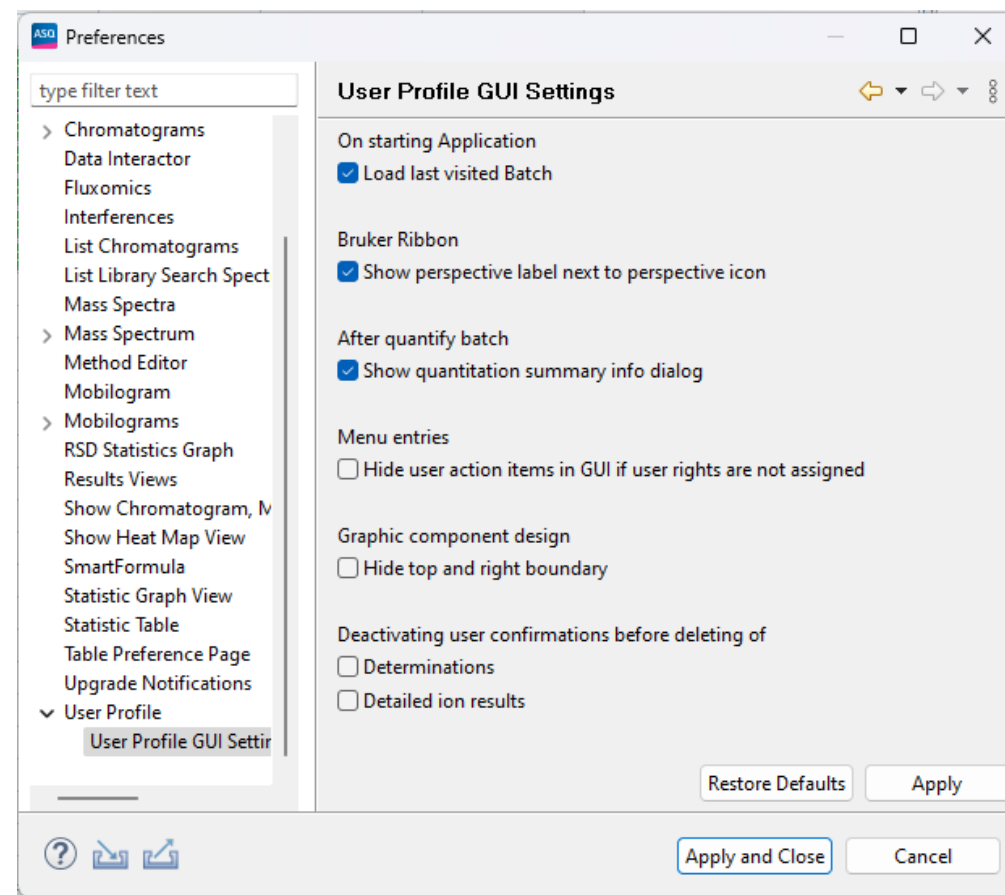
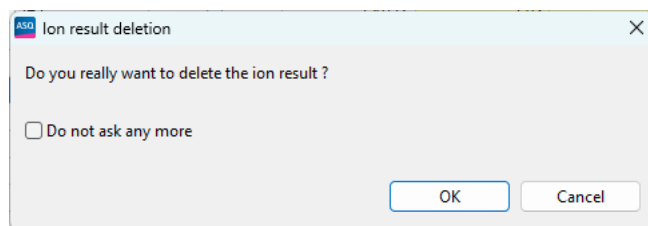
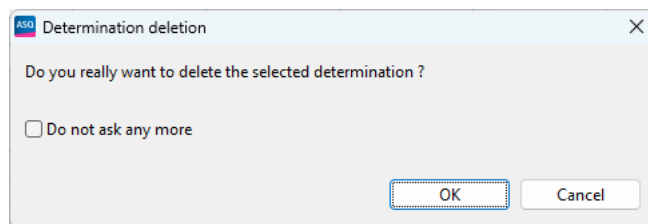


TASQ 2025b: Miscellaneous

- Task Progress view can show tasks running on other stations optionally
- Ongoing improvements on handling context menu
- Ongoing work on import TASQ method from tsv file
- When cloning a TASQ method add name and version of source to description

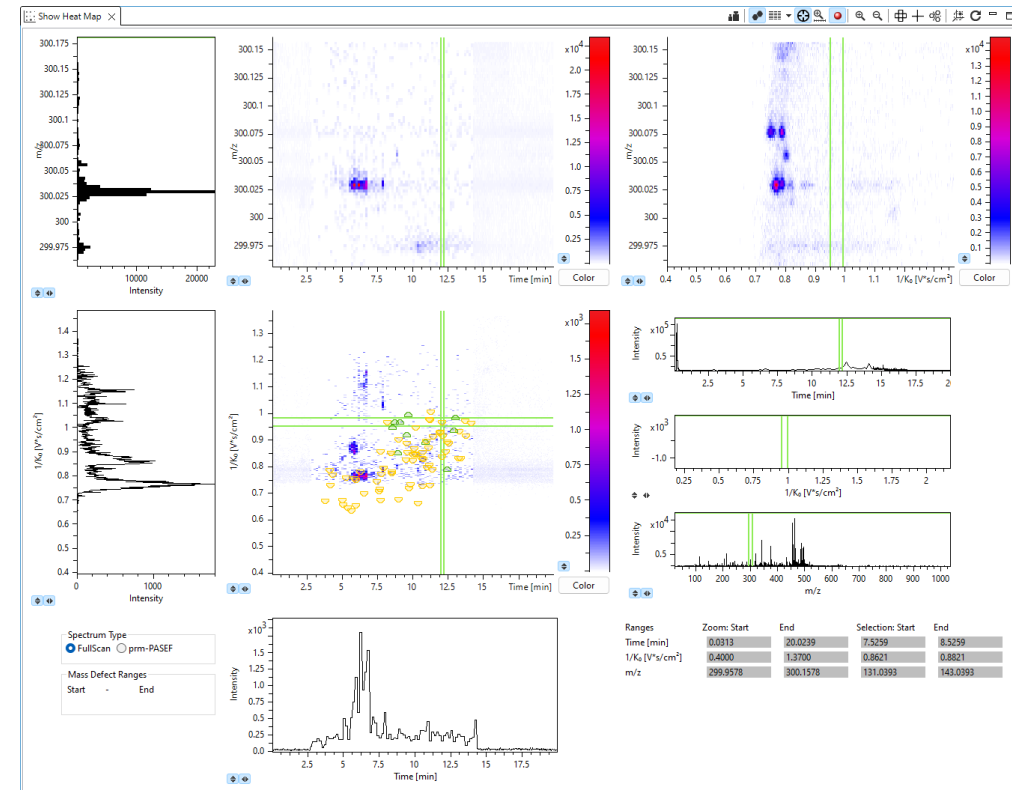
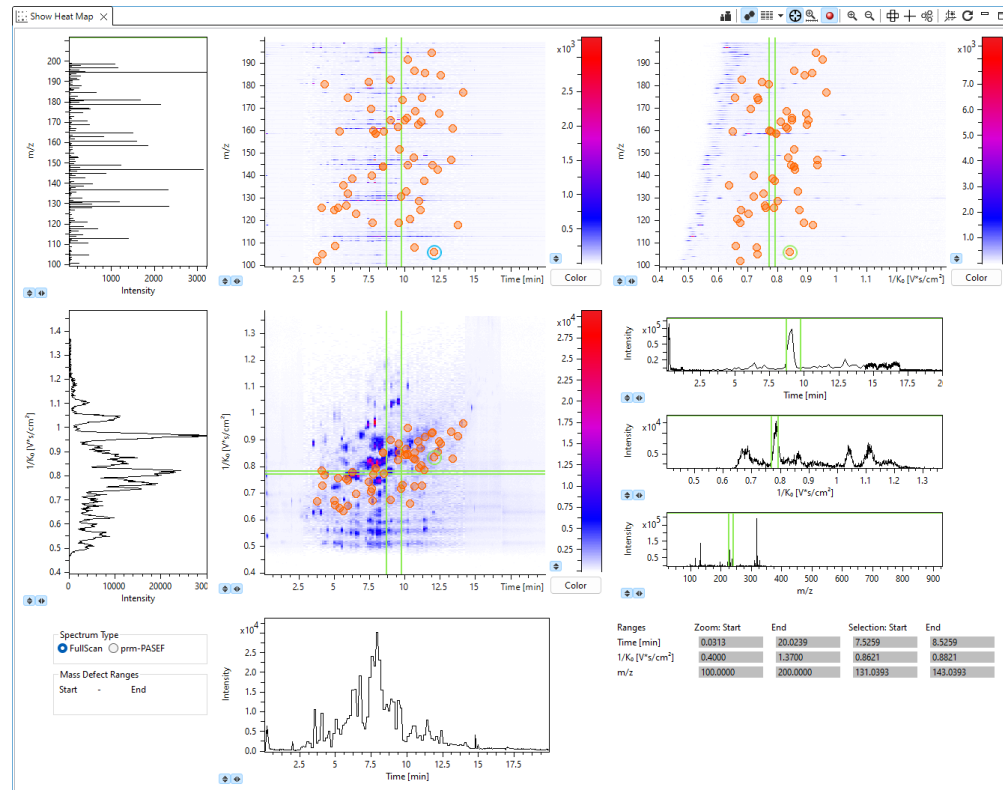
TASQ 2025b: Miscellaneous

- Make behavior of Delete Ion Results and Delete Determination similar:
 - Show pop up dialog „really delete?“ in both cases
 - Add option to hide dialog next time
 - Can be switched on/off in Preferences as well



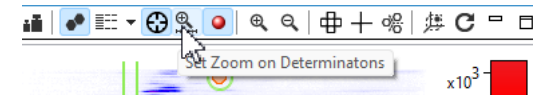
TASQ 2025b: HeatMap view

- Change z-Axis zoom with [CTRL]-LMB on a determination
- The respective z-axis coordinate will be changed to the z-value of selected determination +/- offset



TASQ 2025b: HeatMap view

- Zoom in to show only bounding ranges of all determinations
- Zoom changes on selecting a determination
 - Create a sliced zoom with [Ctrl]-LMB on a determination
 - Move zoom range with [SHIFT]-LMB on a determination
- Edit zoom ranges and selection ranges manually

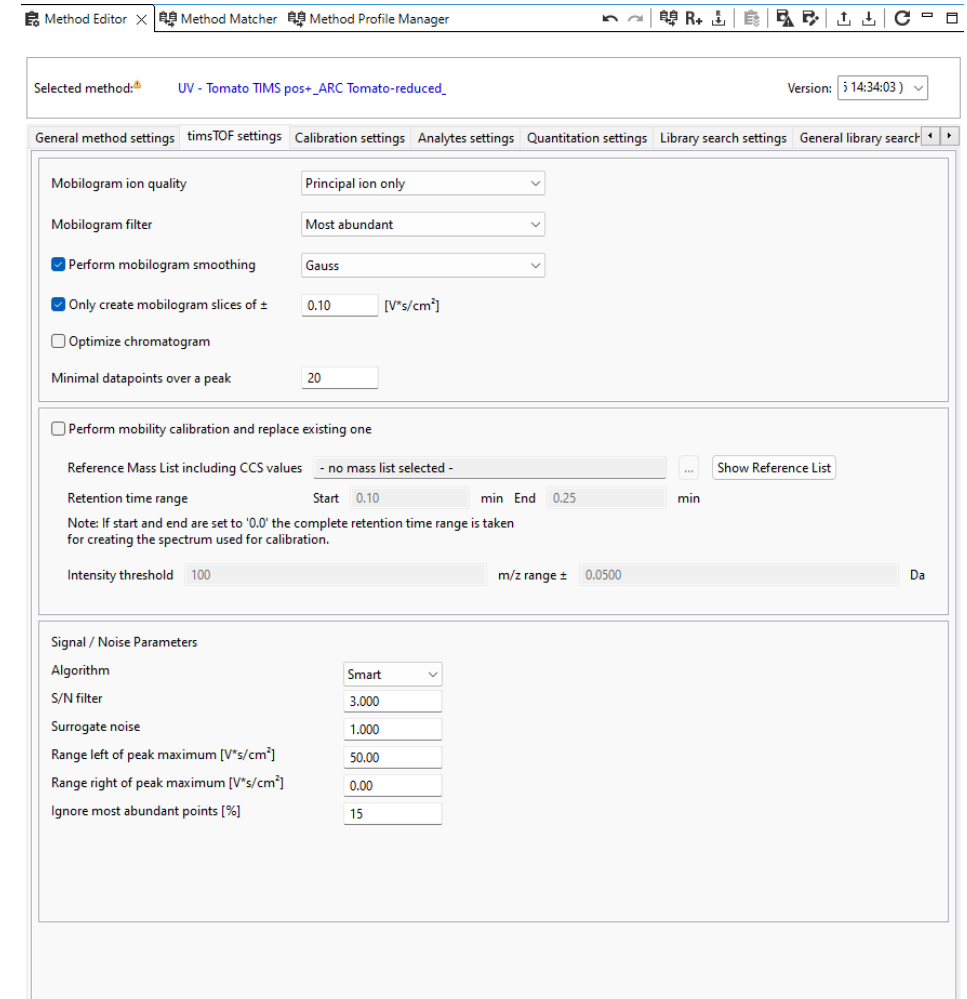


Ranges	Zoom: Start	End	Selection: Start	End
Time [min]	0.0313	20.0239	7.5259	8.5259
1/K ₀ [V*s/cm ²]	0.4000	1.3700	0.8621	0.8821
m/z	250	350	131.0393	143.0393

Ranges	Zoom: Start	End	Selection: Start	End
Time [min]	0.0313	20.0239	7.5259	8.5259
1/K ₀ [V*s/cm ²]	0.4000	1.3700	0.8621	0.8821
m/z	250	100	131.0393	143.0393

TASQ 2025b: TASQ Method Extensions for timsTOF Data Processing

- Added S/N threshold for mobilogram peak detection
- Optionally show Smart noise trace in mobilogram view
- Added minimum data points for mobilogram peak detection



The screenshot displays the 'Method Editor' window for a method named 'UV - Tomato TIMS pos+ _ARC Tomato-reduced_'. The interface is divided into several tabs: 'General method settings', 'timsTOF settings', 'Calibration settings', 'Analytes settings', 'Quantitation settings', 'Library search settings', and 'General library search'. The 'timsTOF settings' tab is active, showing the following parameters:

- Mobilogram ion quality:** Principal ion only
- Mobilogram filter:** Most abundant
- Perform mobilogram smoothing:** Gauss
- Only create mobilogram slices of \pm :** 0.10 [V*s/cm²]
- Optimize chromatogram:**
- Minimal datapoints over a peak:** 20

Below these settings, there is a section for 'Perform mobility calibration and replace existing one' with the following options:

- Reference Mass List including CCS values:** - no mass list selected - (with a 'Show Reference List' button)
- Retention time range:** Start 0.10 min, End 0.25 min
- Note:** If start and end are set to '0.0' the complete retention time range is taken for creating the spectrum used for calibration.
- Intensity threshold:** 100
- m/z range \pm :** 0.0500 Da

The 'Signal / Noise Parameters' section at the bottom includes:

- Algorithm:** Smart
- S/N filter:** 3.000
- Surrogate noise:** 1.000
- Range left of peak maximum [V*s/cm²]:** 50.00
- Range right of peak maximum [V*s/cm²]:** 0.00
- Ignore most abundant points [%]:** 15

TASQ 2025B: Filter Options for Mobilogram Peak Assignment

- Determination ion quality:
 - New option: Principal ion and at least one mandatory ion and the same in mobilogram:
 - The principal ion and at least one mandatory ion must be detected on the chromatogram. In addition, for each chromatogram peak, the matching mobilogram peak must be found too. Otherwise, the determination will be discarded
- Mobilogram filter:
 - New option: Most mandatories and closest to CCS
 - The determination containing the principal ion (or any qualifier if not present) being closest to the expected CCS will remain
 - New option: Most mandatories and most abundant
 - The determination containing the principal ion (or any qualifier if not present) having the largest area will remain

TASQ 2025b: Determination Filter: Principal Ion and at Least one Mandatory Ion in Chromatogram and Mobilogram

Determination ion quality

Principal ion and at least one mandatory ion and the same in mobilogram

Keep all

Principal ion only

Principal ion and at least one mandatory ion

Principal ion and at least one mandatory ion within expected ion ratio

Principal ion and at least one mandatory ion found and all of them within expected ion ratio

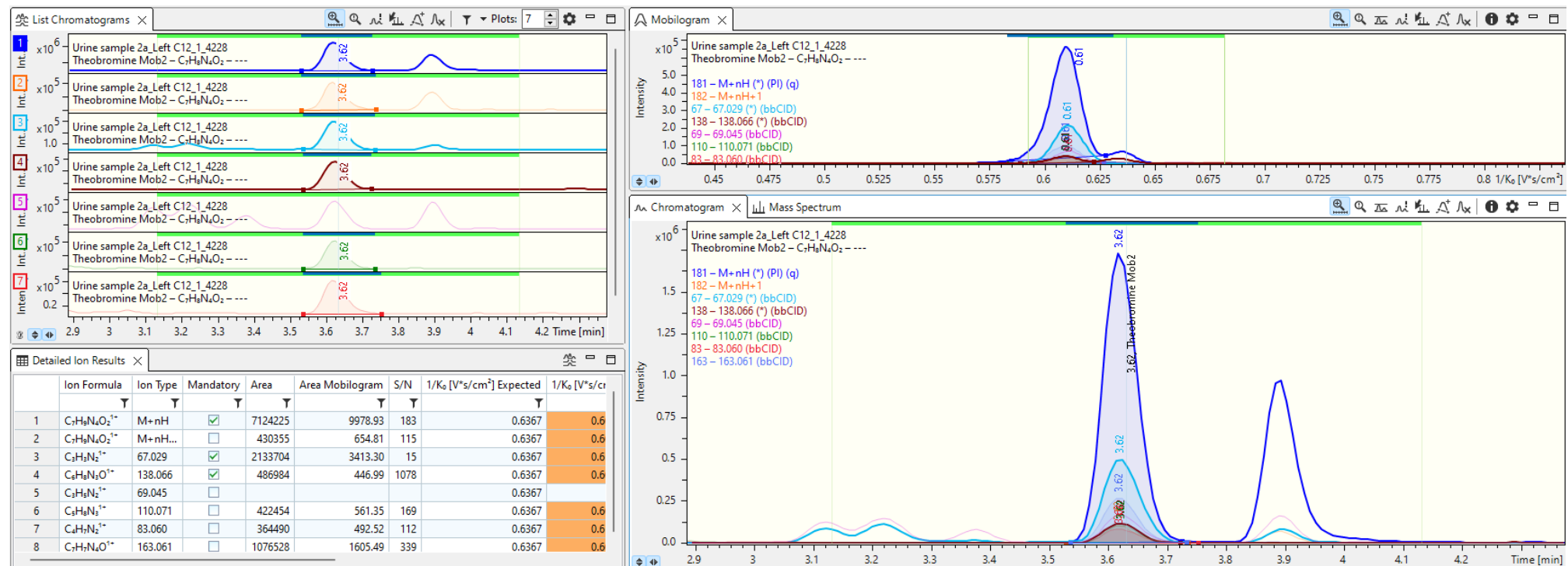
Principal ion and all mandatory ions

Principal ion and all mandatory ions within expected ion ratio

Principal ion and at least one mandatory ion and the same in mobilogram

Detailed Ion Results									
	Ion Formula	Ion Type	Mandatory	Area	Area Mobilogram	S/N	1/K ₀ [V*s/cm ²] Expected	1/K ₀ [V*s/cm ²]	
1	C ₃ F ₇ O ₂ ¹⁻	I	<input checked="" type="checkbox"/>	722849	712.4821	2372	0.5594	0.5585	
2	C ₃ F ₇ O ₂ ¹⁻	I+1	<input checked="" type="checkbox"/>	24854	24.3971	64	0.5594	0.5584	
3	C ₃ F ₇ O ₂ ¹⁻	200.979	<input checked="" type="checkbox"/>				0.7332		
4	CF ₃ O ¹⁻	84.991	<input checked="" type="checkbox"/>				0.5594		
5	CF ₃ O ¹⁻	84.991...	<input checked="" type="checkbox"/>				0.7360		
6	C ₂ F ₅ O ¹⁻	134.99	<input type="checkbox"/>				0.7360		
7	C ₅ F ₉ O ₄ ¹⁻	3,6-O...	<input type="checkbox"/>	151892	143.7809	262	0.7360	0.7346	

TASQ 2025b: Mobilogram Filter: Most Mandatories and Closest to CCS

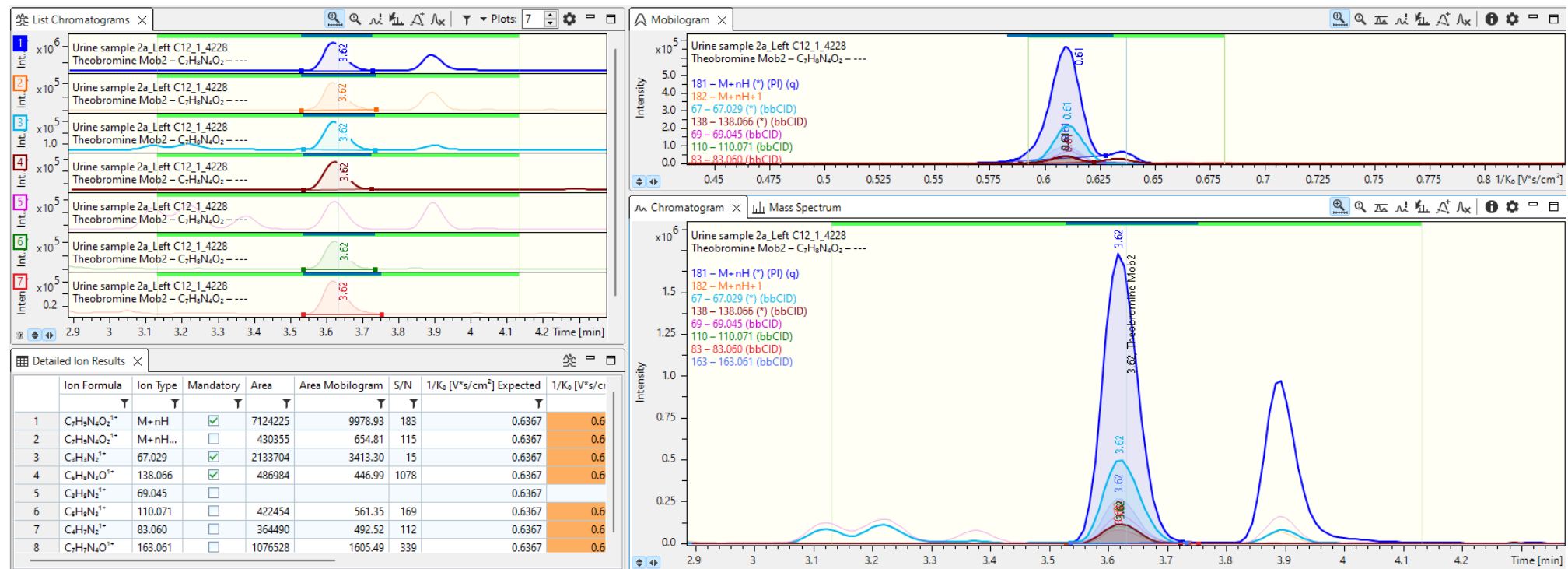


- The mobilogram peaks on the left hand side were chosen as there are more ions covered than with the peaks at the right hand side

Mobilogram filter

- Perform mobilogram smoothing
- Only create mobilogram slices of ± 0.30 [V*s/cm²]

TASQ 2025b: Mobilogram Filter: Most Mandatories and most Abundant



Mobilogram filter

- Perform mobilogram smoothing
- Only create mobilogram slices of +

Most mandatories and most abundant

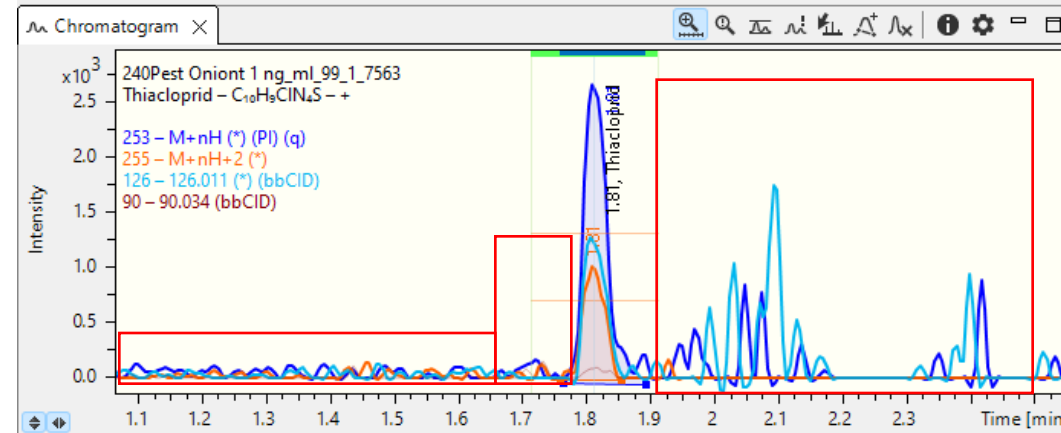
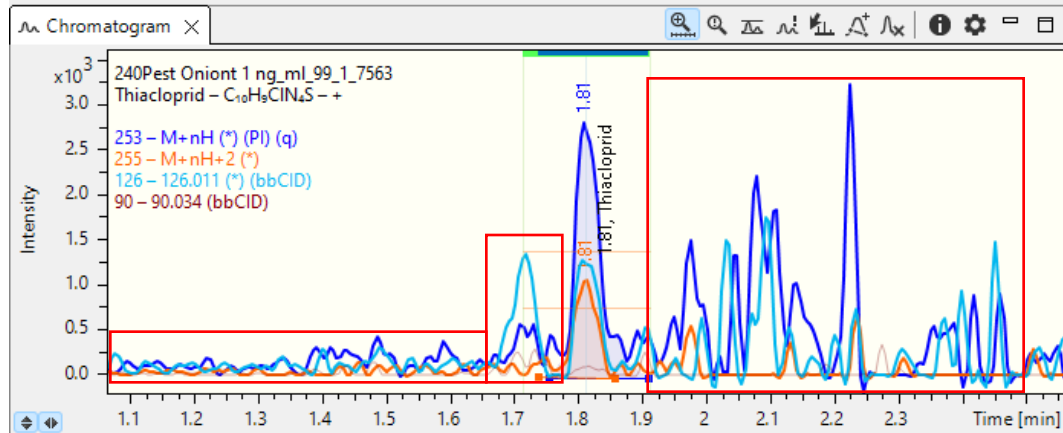
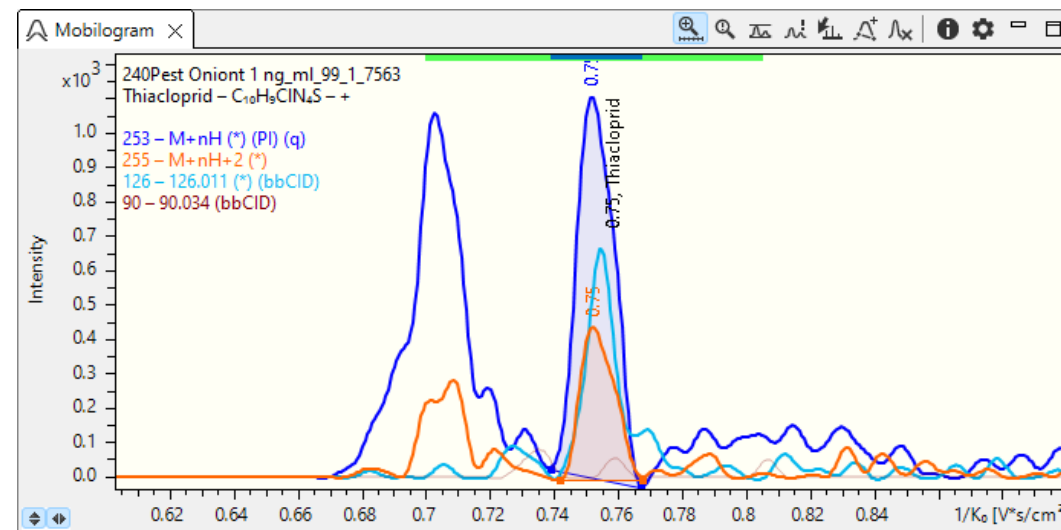
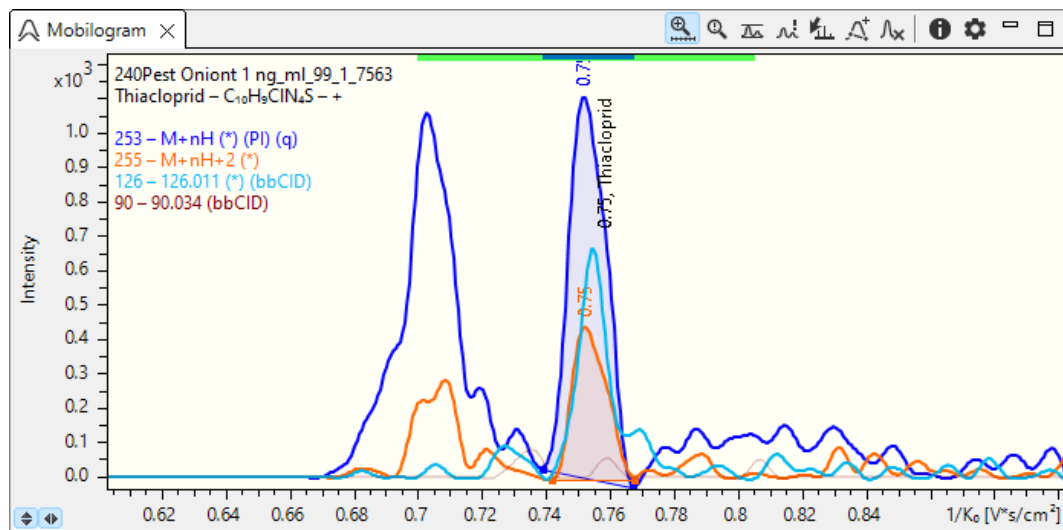
- Most abundant
- Closest CCS value
- Most mandatories and closest to CCS
- Most mandatories and most abundant

TASQ 2025b: Optimize Chromatogram

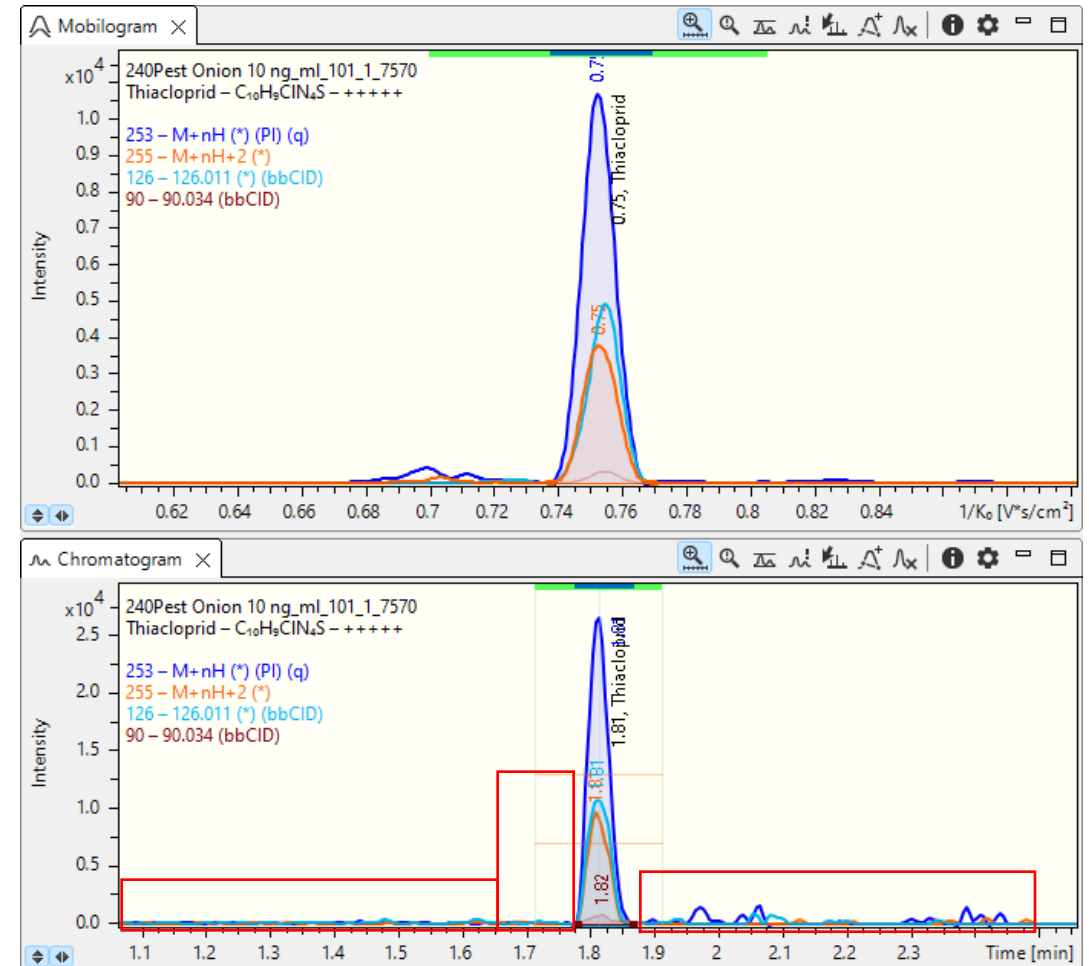
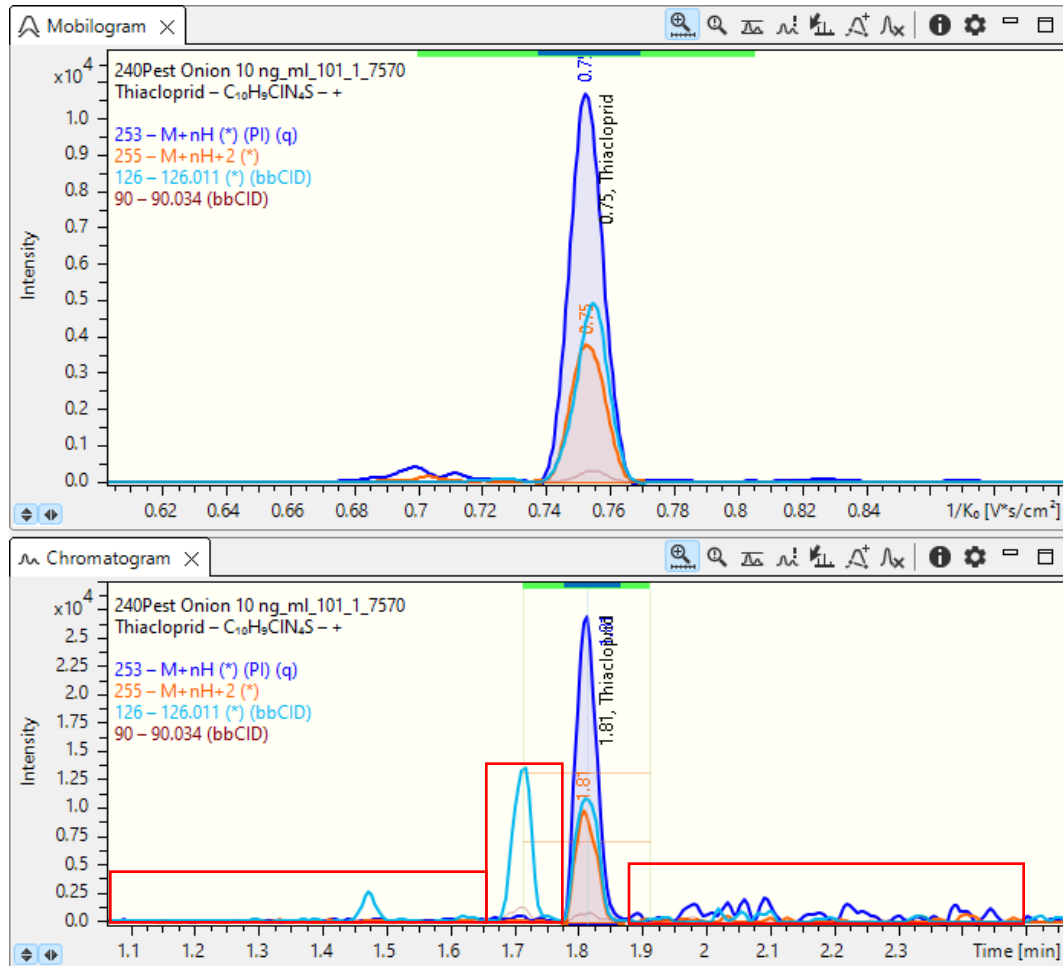
- In timsTOF settings a new parameter **Optimize chromatogram** is available
- After detection of mobilogram peak the EIC 1/K0 width will be adopted to the peak width of mobilogram peak

General method settings	timsTOF settings	Calibration settings	Analy
Mobilogram ion quality	Principal ion only		
Mobilogram filter	Closest CCS value		
<input checked="" type="checkbox"/> Perform mobilogram smoothing	Savitzky Golay		
<input checked="" type="checkbox"/> Only create mobilogram sl	0.07	[V*s/cm ²]	
<input checked="" type="checkbox"/> Optimize chromatogram			
Minimal datapoints over a p	5		

TASQ 2025b: Optimize Chromatogram – Thiacloprid 1 ng/mL

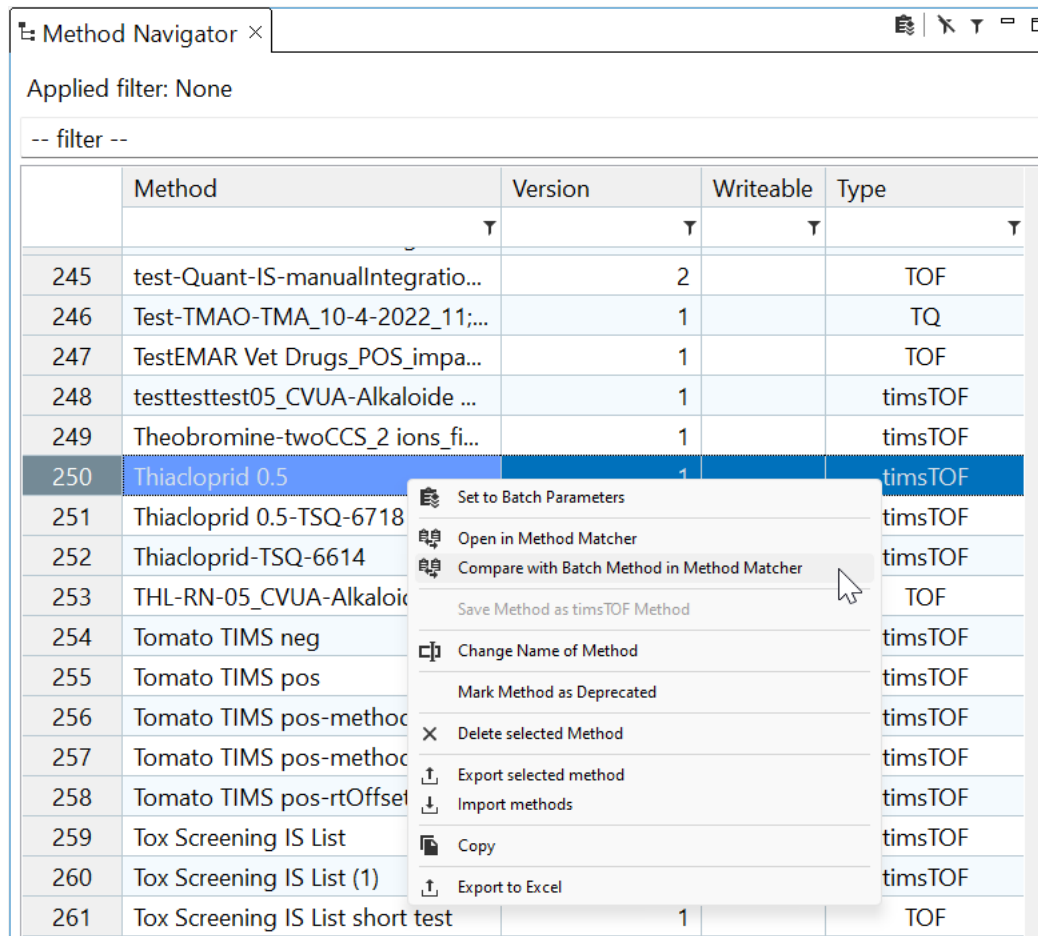


TASQ 2025b: Optimize Chromatogram – Thiacloprid 10 ng/mL



TASQ 2025b: Method Navigator – New Command Compare Batch Method with Selected Method

- Compare any method listed in the Method Navigator directly with the method assigned to the selected batch



Method Navigator x

Applied filter: None

-- filter --

	Method	Version	Writeable	Type
245	test-Quant-IS-manuallIntegratio...	2		TOF
246	Test-TMAO-TMA_10-4-2022_11;...	1		TQ
247	TestEMAR Vet Drugs_POS_impac...	1		TOF
248	testtesttest05_CVUA-Alkaloide ...	1		timsTOF
249	Theobromine-twoCCS_2 ions_fi...	1		timsTOF
250	Thiacloprid 0.5	1		timsTOF
251	Thiacloprid 0.5-TSQ-6718			timsTOF
252	Thiacloprid-TSQ-6614			timsTOF
253	THL-RN-05_CVUA-Alkaloic			TOF
254	Tomato TIMS neg			timsTOF
255	Tomato TIMS pos			timsTOF
256	Tomato TIMS pos-method			timsTOF
257	Tomato TIMS pos-method			timsTOF
258	Tomato TIMS pos-rtOffset			timsTOF
259	Tox Screening IS List			timsTOF
260	Tox Screening IS List (1)			timsTOF
261	Tox Screening IS List short test	1		TOF

Context menu options:

- Set to Batch Parameters
- Open in Method Matcher
- Compare with Batch Method in Method Matcher
- Save Method as timsTOF Method
- Change Name of Method
- Mark Method as Deprecated
- Delete selected Method
- Export selected method
- Import methods
- Copy
- Export to Excel

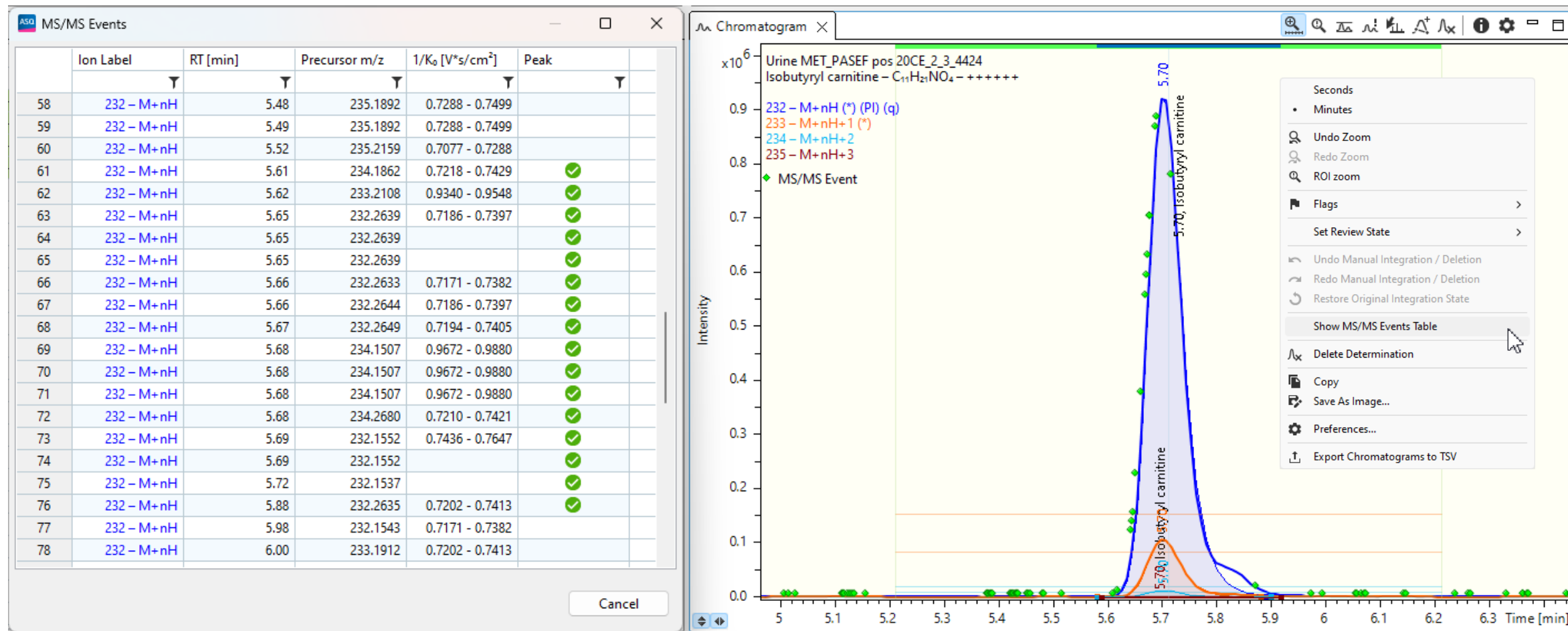
TASQ 2025b: Miscellaneous

- Show MS/MS events for selected determination
 - List all MS/MS events which matches to the ions specified for the respective analyte
 - In Chromatogram view call Show MS/MS events to review which MS/MS spectra are available
 - Enable MS/MS events option in Preferences>Chromatogram
 - Loading MS/MS events for a chromatogram takes some time and will be loaded each time the chromatogram view is updated (selection change)

	Ion Label	RT [min]	Precursor m/z	1/K ₀ [V*s/cm ²]	Peak
58	232 - M+nH	5.48	235.1892	0.7288 - 0.7499	
59	232 - M+nH	5.49	235.1892	0.7288 - 0.7499	
60	232 - M+nH	5.52	235.2159	0.7077 - 0.7288	
61	232 - M+nH	5.61	234.1862	0.7218 - 0.7429	✓
62	232 - M+nH	5.62	233.2108	0.9340 - 0.9548	✓
63	232 - M+nH	5.65	232.2639	0.7186 - 0.7397	✓
64	232 - M+nH	5.65	232.2639		✓
65	232 - M+nH	5.65	232.2639		✓
66	232 - M+nH	5.66	232.2633	0.7171 - 0.7382	✓
67	232 - M+nH	5.66	232.2644	0.7186 - 0.7397	✓
68	232 - M+nH	5.67	232.2649	0.7194 - 0.7405	✓
69	232 - M+nH	5.68	234.1507	0.9672 - 0.9880	✓
70	232 - M+nH	5.68	234.1507	0.9672 - 0.9880	✓
71	232 - M+nH	5.68	234.1507	0.9672 - 0.9880	✓
72	232 - M+nH	5.68	234.2680	0.7210 - 0.7421	✓
73	232 - M+nH	5.69	232.1552	0.7436 - 0.7647	✓
74	232 - M+nH	5.69	232.1552		✓
75	232 - M+nH	5.72	232.1537		✓
76	232 - M+nH	5.88	232.2635	0.7202 - 0.7413	✓
77	232 - M+nH	5.98	232.1543	0.7171 - 0.7382	
78	232 - M+nH	6.00	233.1912	0.7202 - 0.7413	

Cancel

TASQ 2025b: Show MS/MS Event on Chromatogram Traces



TASQ 2025b: Statistic Table

- Statistic Table improved setting of filters
- As more and more settings are added to the filters the toolbar took too much space and is wrapped if the view is too narrow
- Filter toolbar icon opens a dialog
- Selected filters are shown in the top left corner of view

Statistic Table ×

Active filters: Level | Sample Type

	Sample Type	Level	Property	ΔRT [min]	Δm/z [mDa]	mSigma
1	CALIBRANT	6	nrDatapoints	15	15	15
2	CALIBRANT	6	mean	-0.0008	0.0554	63.5
3	CALIBRANT	6			0.0898	65.4
4	CALIBRANT	6			0.220	7.54
5	CALIBRANT	6			-0.4662	46.2
6	CALIBRANT	6			0.377	73.7
7	CALIBRANT	6			397	11.9
8	CALIBRANT	5			15	15
9	CALIBRANT	5			-0.1218	61.8
10	CALIBRANT	5			-0.1712	60.4
11	CALIBRANT	5			0.149	10.5
12	CALIBRANT	5			-0.2936	34.3
13	CALIBRANT	5			0.129	76.1
14	CALIBRANT	5			-122.6596	17.0
15	CALIBRANT	4			15	15
16	CALIBRANT	4			0.00422	55.2
17	CALIBRANT	4			0.0738	59.2
18	CALIBRANT	4			0.186	12.1
19	CALIBRANT	4			-0.4450	26.9
20	CALIBRANT	4			0.274	72.6
21	CALIBRANT	4			4410	22.0
22	CALIBRANT	3			15	15
23	CALIBRANT	3			-0.0276	47.3
24	CALIBRANT	3			0.0251	51.3
25	CALIBRANT	3			0.222	17.2
26	CALIBRANT	3			-0.5693	10.6
27	CALIBRANT	3	maximum	0.00570	0.187	71.8

ASQ Select filters ×

ON Sample Type

OFF Sample Subtype

ON Level

OFF Analyte Name

OFF Data Set

OFF Sample

OFF Score

OFF IS

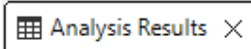
OFF Analyte Tag

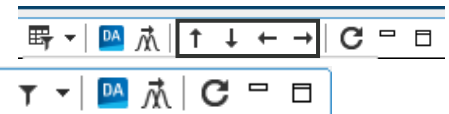
? OK Cancel

TASQ 2025b: Statistic Table, Statistic Graph, Batch Statistic Graph, RSD Statistic Graph

- All views shows the same set of numerical properties presented in the result tables
- All properties have the same label as known from result tables

TASQ 2025b: Miscellaneous

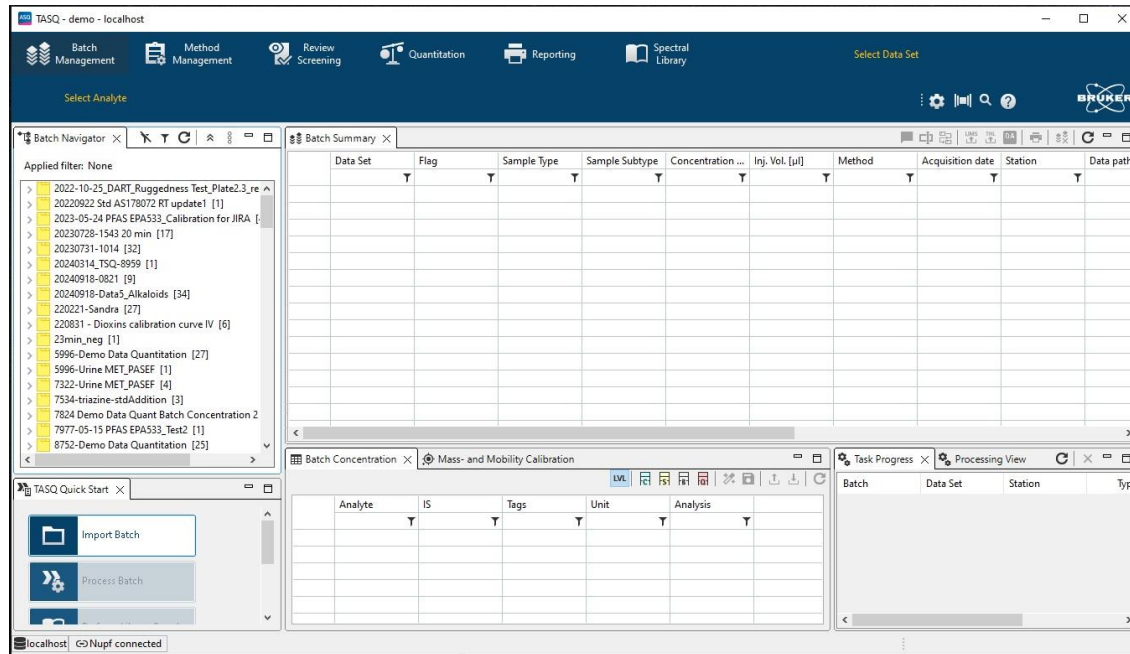
- Improvements on the presented tables in TASQ client
 - Tables does not jump on changes of data that often
 - Rearranged Filter options and improved presentation in UI
 - Open filter options dialog with [ALT]-F
- Clearer appearance of toolbars of result views
 - Removed arrow key to select next | previous determination or data set
 - Use arrow keys of keyboard instead 
 - If a row is selected do not hide background colors



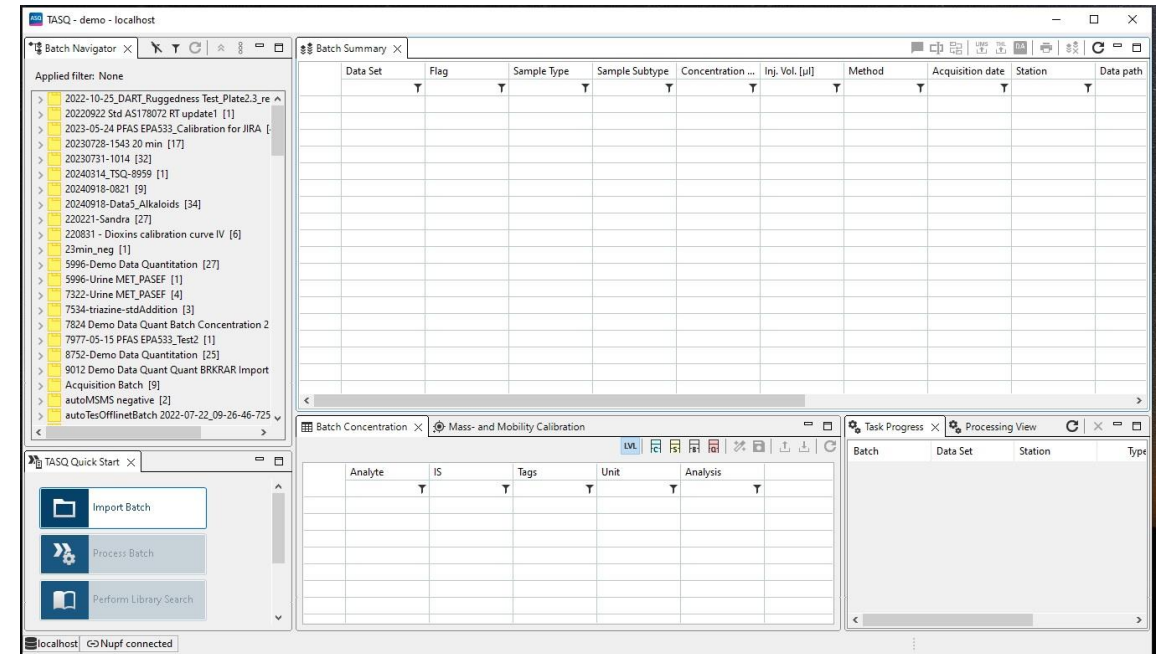
	Analyte Name	Quantity [ng/...	Score	Rule: RLE	RT Score	ΔRT [min]	RT expected [...	Ions Score	Exp.Diag.Ions	Found.Diag.Ions	Rule: Min R ^
1	Acetochlor	1.7	+++		++	-0.06	9.56	++	1	1	
2	Acibenzolar-S-...	4.5	+++		++	0.00	9.97	++	1	1	
3	Aclonifen	7.4	---		++	0.00	15.12	---	1	1	
4	Acrinathrin	19.1	+++		++	-0.09	20.30	++	1	1	
5	Alachlor	19.1	+++		++	-0.02	9.75	++	1	1	
6	Aldrin	18.6	+++		++	-0.08	10.92	++	1	1	
7	Allethrin I + II	n.a.	---		++	-0.09	12.15	---	1	1	

TASQ 2025b: Miscellaneous

- Toggle visibility of Bruker Ribbon on / off to save space by pressing F11 key, like internet browsers
 - Small devices with large display settings -> Bruker Ribbon will be shown in two or more lines as Icons have no space within one line

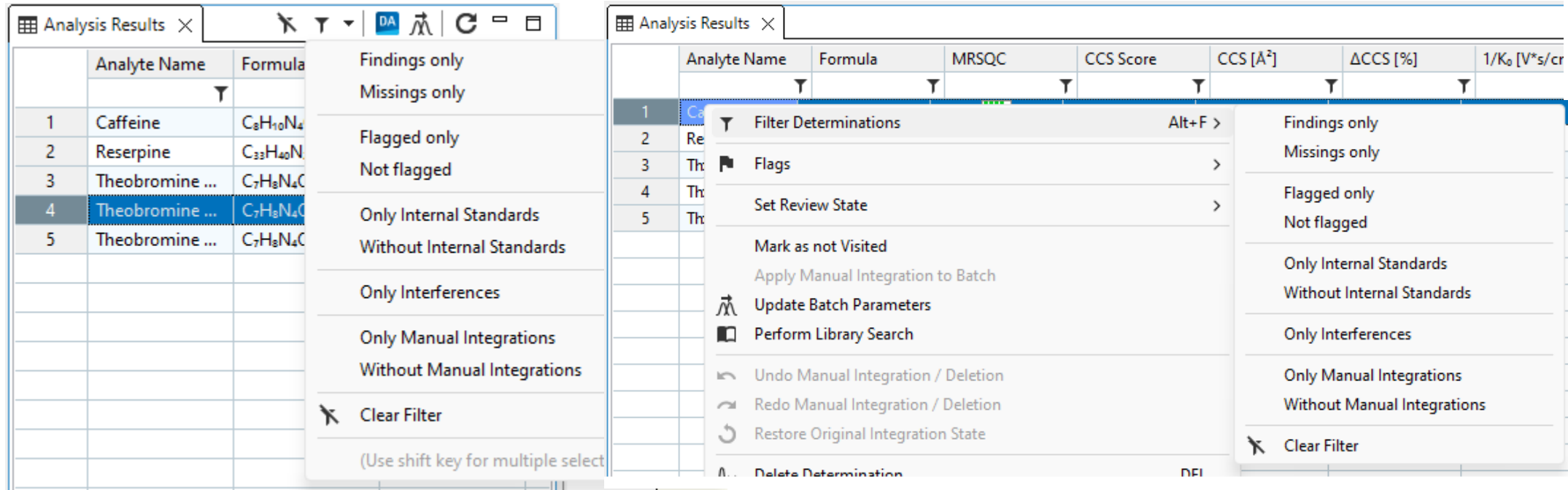


The screenshot shows the TASQ software interface with the Bruker Ribbon visible. The ribbon contains several tabs: Batch Management, Method Management, Review Screening, Quantitation, Reporting, and Spectral Library. Below the ribbon, there are several panels: Batch Navigator (showing a list of data sets), Batch Summary (a table with columns: Data Set, Flag, Sample Type, Sample Subtype, Concentration, Inj. Vol. [µl], Method, Acquisition date, Station, Data path), Batch Concentration (a table with columns: Analyte, IS, Tags, Unit, Analysis), and Task Progress / Processing View.



The screenshot shows the TASQ software interface with the Bruker Ribbon hidden. The interface is more compact, with the Batch Navigator and Batch Summary panels visible. The Batch Summary table has columns: Data Set, Flag, Sample Type, Sample Subtype, Concentration, Inj. Vol. [µl], Method, Acquisition date, Station, Data path. The Batch Concentration panel is also visible with columns: Analyte, IS, Tags, Unit, Analysis. The Task Progress / Processing View panel is also visible.

TASQ 2025b: Improved Filters for Analysis Results View

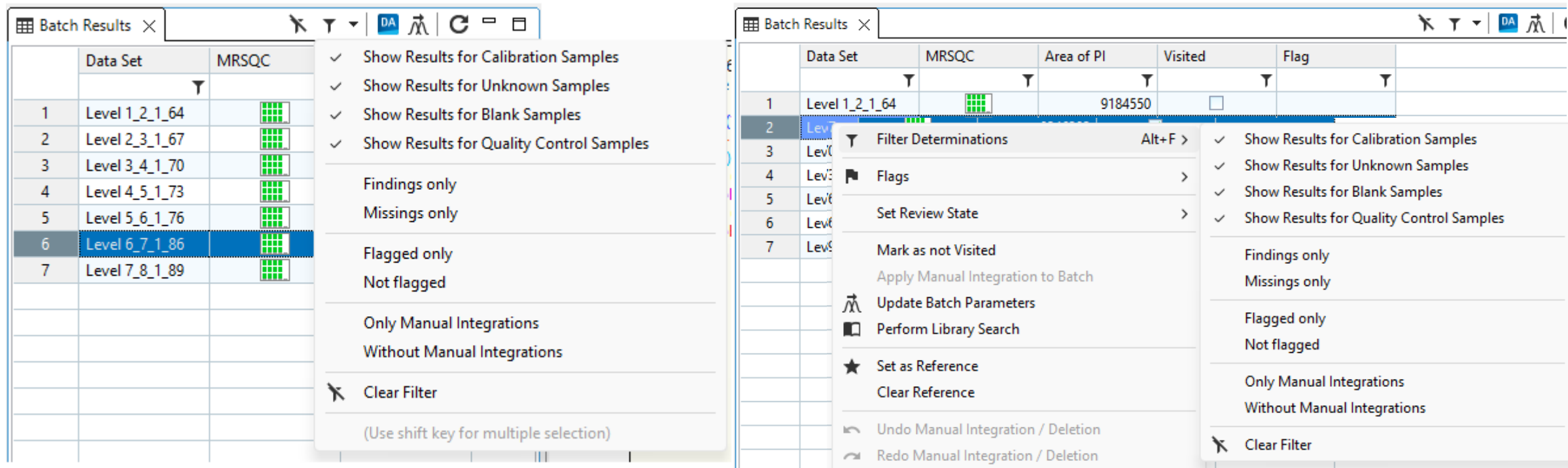


The screenshot displays two side-by-side windows of the 'Analysis Results' view. The left window shows a table with columns for 'Analyte Name' and 'Formula'. A context menu is open over the table, listing various filter options: Findings only, Missings only, Flagged only, Not flagged, Only Internal Standards, Without Internal Standards, Only Interferences, Only Manual Integrations, Without Manual Integrations, and Clear Filter. A note at the bottom of the menu says '(Use shift key for multiple select)'. The right window shows a more detailed table with columns: 'Analyte Name', 'Formula', 'MRSQC', 'CCS Score', 'CCS [Å²]', 'ΔCCS [%]', and '1/K₀ [V*s/cr]'. A context menu is open over this table, listing actions: Filter Determinations (Alt+F >), Flags (>), Set Review State (>), Mark as not Visited, Apply Manual Integration to Batch, Update Batch Parameters (with a magnifying glass icon), Perform Library Search (with a magnifying glass icon), Undo Manual Integration / Deletion, Redo Manual Integration / Deletion, Restore Original Integration State, and Delete Determination (DEFI).

	Analyte Name	Formula
1	Caffeine	C ₈ H ₁₀ N ₄
2	Reserpine	C ₃₃ H ₄₀ N ₂
3	Theobromine ...	C ₇ H ₈ N ₄ O
4	Theobromine ...	C ₇ H ₈ N ₄ O
5	Theobromine ...	C ₇ H ₈ N ₄ O

	Analyte Name	Formula	MRSQC	CCS Score	CCS [Å ²]	ΔCCS [%]	1/K ₀ [V*s/cr]
1	Caffeine						
2	Reserpine						
3	Theobromine ...						
4	Theobromine ...						
5	Theobromine ...						

TASQ 2025b: Improved Filters for Batch Results View



Left Screenshot: Filter Menu

	Data Set	MRSQC
1	Level 1_2_1_64	
2	Level 2_3_1_67	
3	Level 3_4_1_70	
4	Level 4_5_1_73	
5	Level 5_6_1_76	
6	Level 6_7_1_86	
7	Level 7_8_1_89	

- ✓ Show Results for Calibration Samples
- ✓ Show Results for Unknown Samples
- ✓ Show Results for Blank Samples
- ✓ Show Results for Quality Control Samples
- Findings only
- Missings only
- Flagged only
- Not flagged
- Only Manual Integrations
- Without Manual Integrations
- ✎ Clear Filter

(Use shift key for multiple selection)

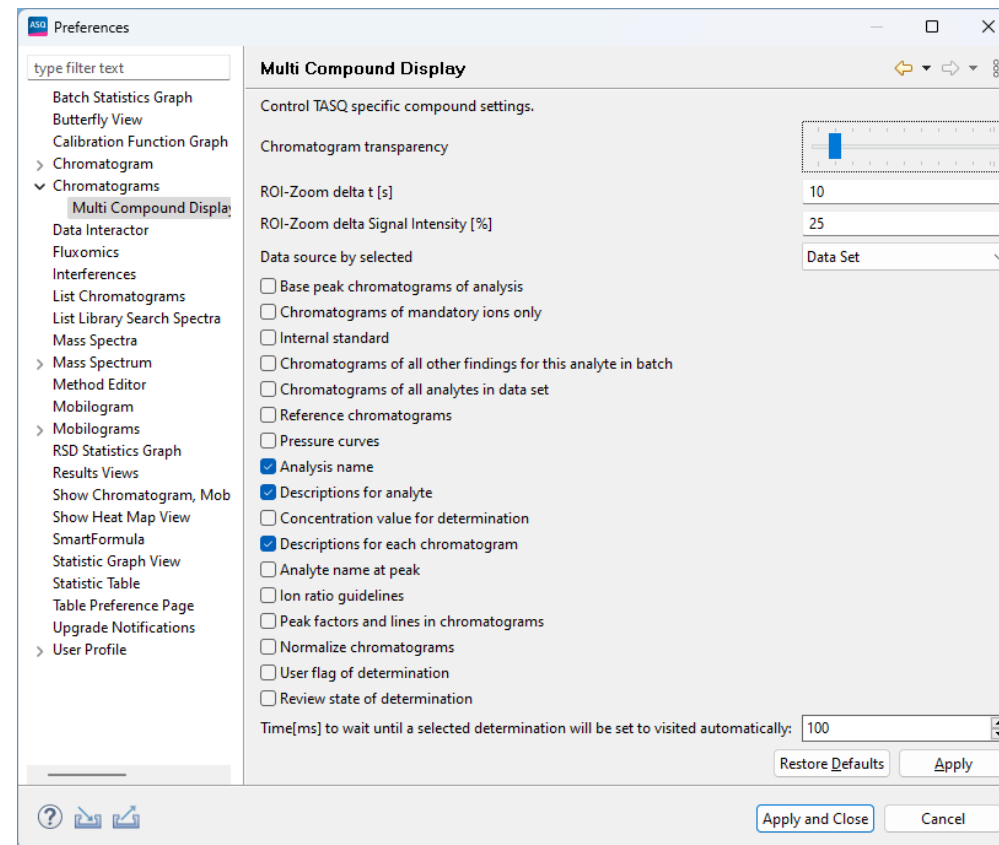
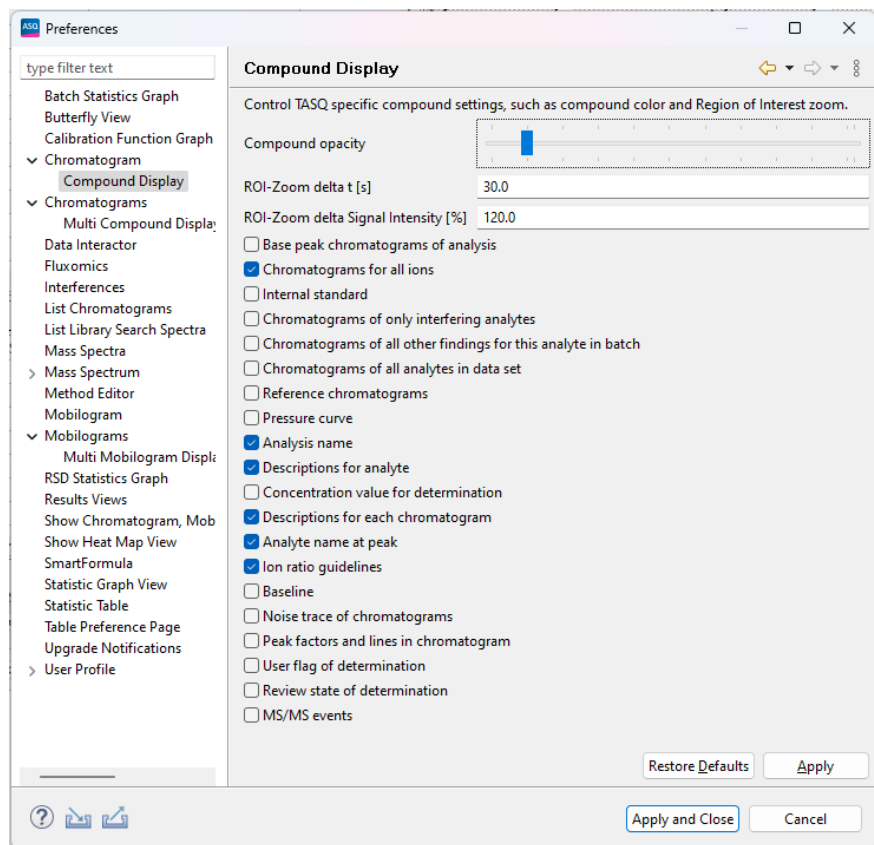
Right Screenshot: Filter Menu

	Data Set	MRSQC	Area of PI	Visited	Flag
1	Level 1_2_1_64		9184550	<input type="checkbox"/>	
2	Level 2_3_1_67				
3	Level 3_4_1_70				
4	Level 4_5_1_73				
5	Level 5_6_1_76				
6	Level 6_7_1_86				
7	Level 7_8_1_89				

- Filter Determinations Alt+F >
- Flags >
- Set Review State >
- Mark as not Visited
- Apply Manual Integration to Batch
- Update Batch Parameters
- Perform Library Search
- Set as Reference
- Clear Reference
- Undo Manual Integration / Deletion
- Redo Manual Integration / Deletion
- ✓ Show Results for Calibration Samples
- ✓ Show Results for Unknown Samples
- ✓ Show Results for Blank Samples
- ✓ Show Results for Quality Control Samples
- Findings only
- Missings only
- Flagged only
- Not flagged
- Only Manual Integrations
- Without Manual Integrations
- ✎ Clear Filter

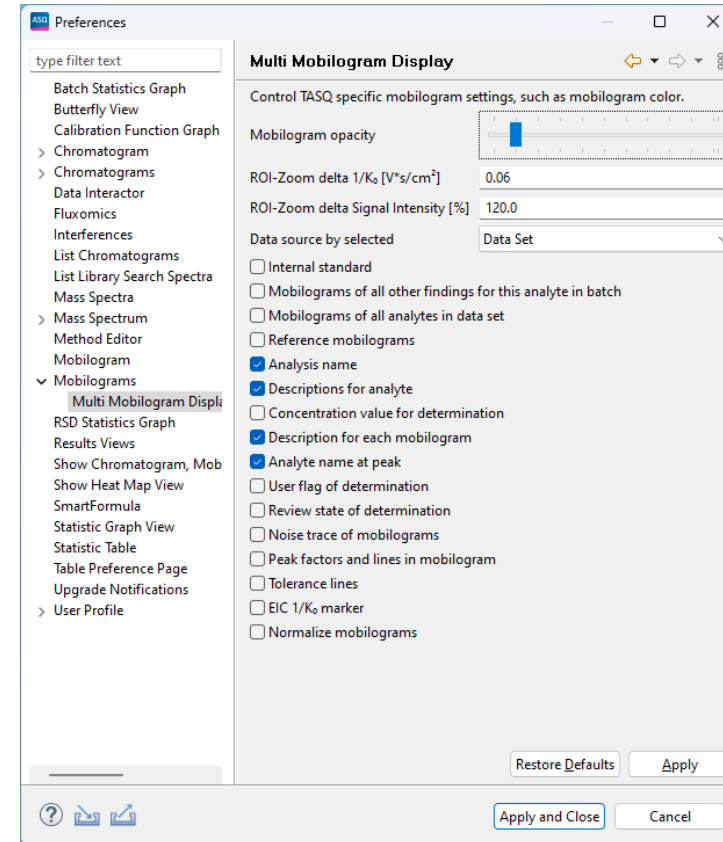
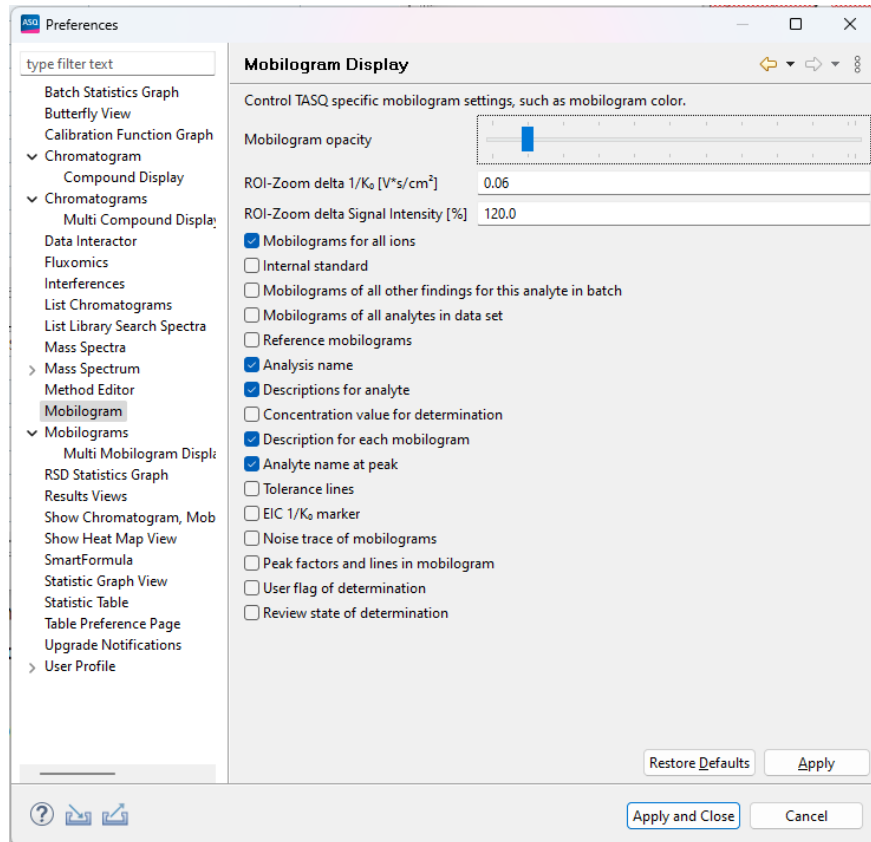
TASQ 2025b: Miscellaneous

- Improved text and order of properties pages for Chromatogram, Chromatograms, Mobilogram, Mobilograms view



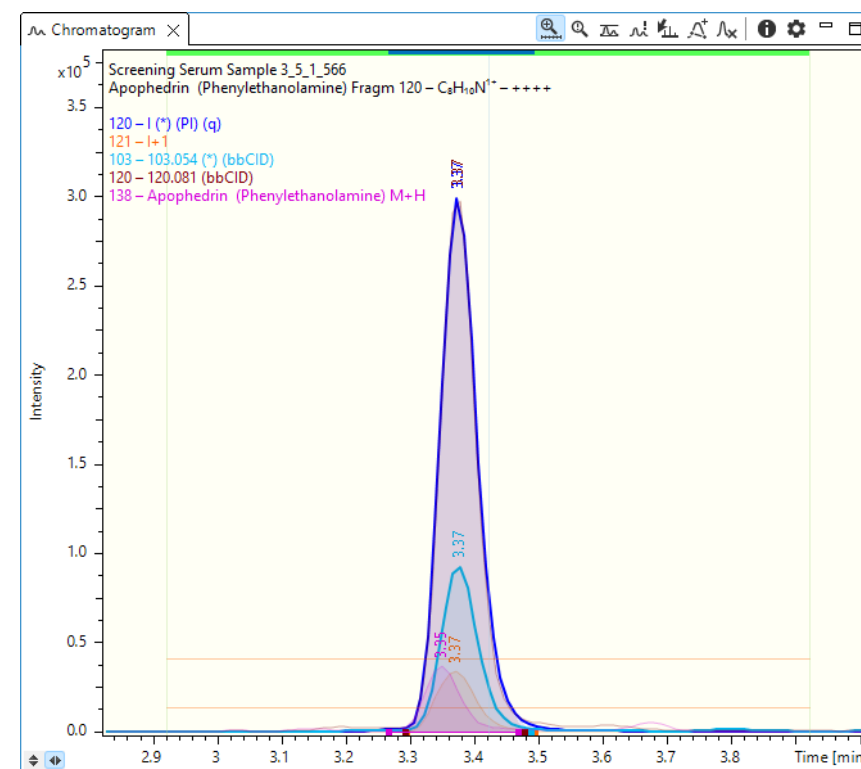
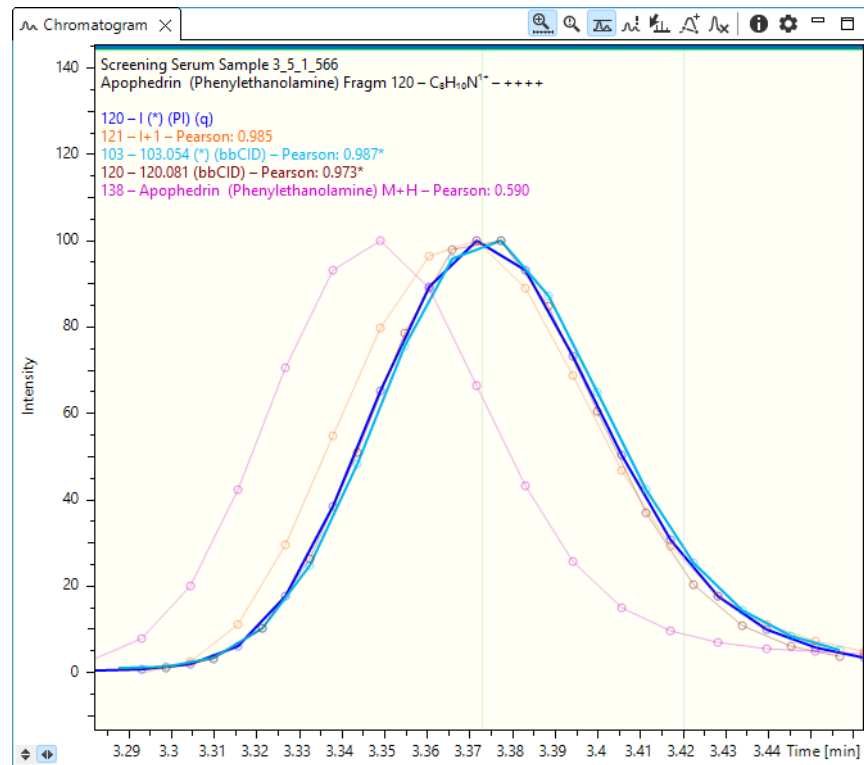
TASQ 2025b: Miscellaneous

- Improved text and order of properties pages for Chromatogram, Chromatograms, Mobilogram, Mobilograms view



TASQ 2025b: Miscellaneous

- Calculate Pearson correlation of chromatographic traces in Chromatogram view when normalizing chromatograms – does the different ions belong together or is this potentially a false positive?
- The traces are compared to the trace of the principle ion (PI), the correlation coefficient is added to the trace label

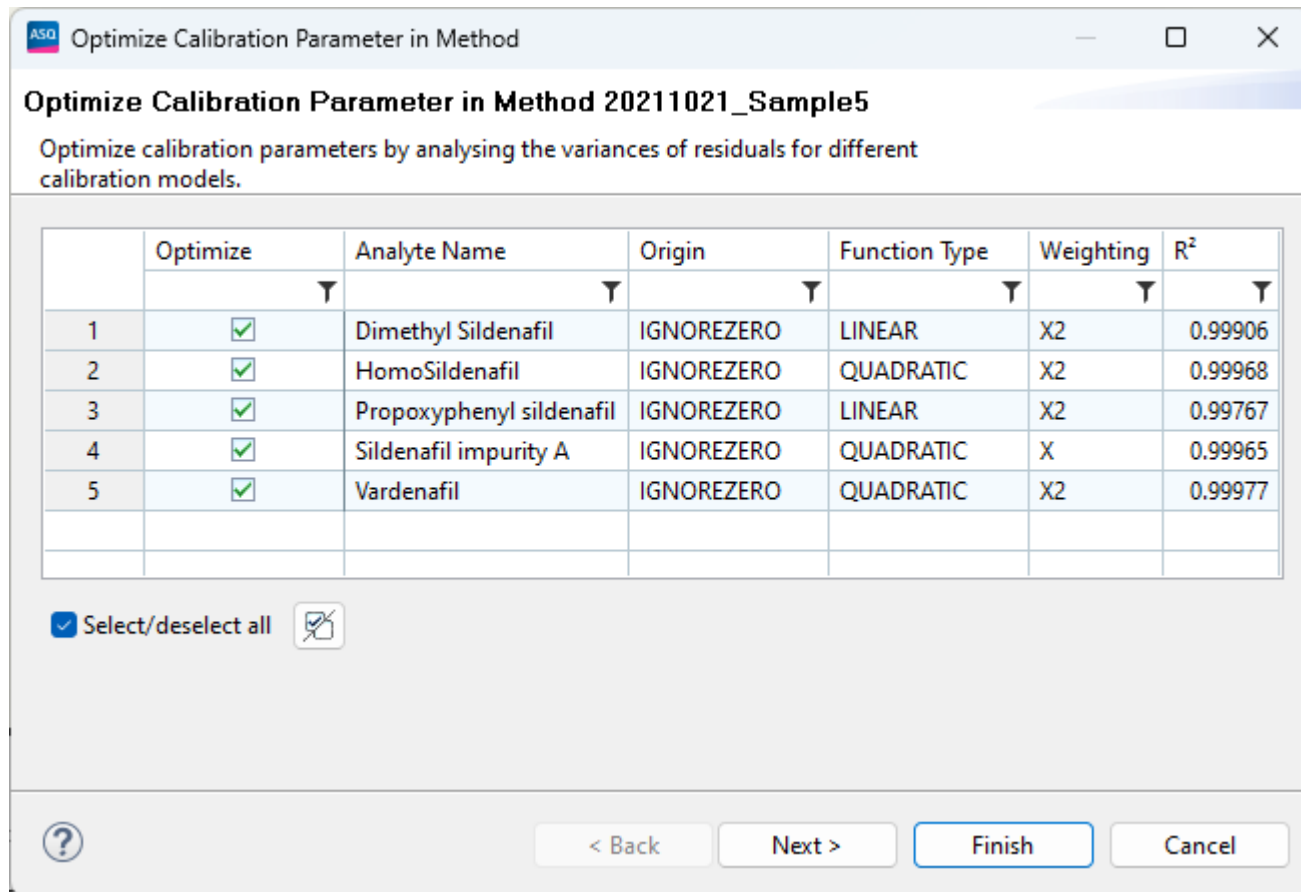


TASQ 2025b: Quantification

- New preference options for Calibration Function Graph view
 - Do not calculate automatically a calibration function for the selected analyte if the batch has not been quantified previously
 - Set the option for the regression calculation as specified in the TASQ method if calibration function has not been calculated previously
 - Use method settings for automatic generation of calibration functions in calibration function graph view if no calibration function is available
- Hint: If you want to know which is the best possible calibration function for the given data use Optimize Calibration Function to get the parameter settings for calculating the optimal calibration function
- Added command to set review state in Calibration Data Point view

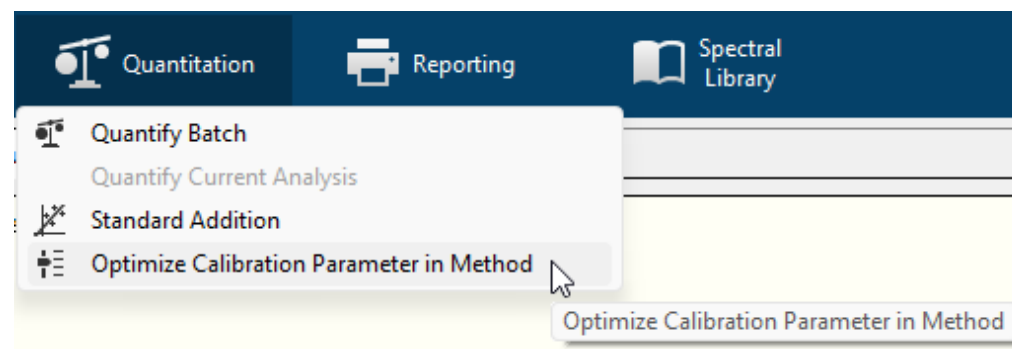
- Improvements to the Batch Concentrations view

TASQ 2025b: Hint Optimize Calibration Parameter in Method



	Optimize	Analyte Name	Origin	Function Type	Weighting	R ²
1	<input checked="" type="checkbox"/>	Dimethyl Sildenafil	IGNOREZERO	LINEAR	X2	0.99906
2	<input checked="" type="checkbox"/>	HomoSildenafil	IGNOREZERO	QUADRATIC	X2	0.99968
3	<input checked="" type="checkbox"/>	Propoxyphenyl sildenafil	IGNOREZERO	LINEAR	X2	0.99767
4	<input checked="" type="checkbox"/>	Sildenafil impurity A	IGNOREZERO	QUADRATIC	X	0.99965
5	<input checked="" type="checkbox"/>	Vardenafil	IGNOREZERO	QUADRATIC	X2	0.99977

- Calculate the set of optimized parameters
- Check for heteroscedasticity
- Check which weighting / function type is best
- Transfer parameter sets to TASQ method
- Available from Quantitation menu



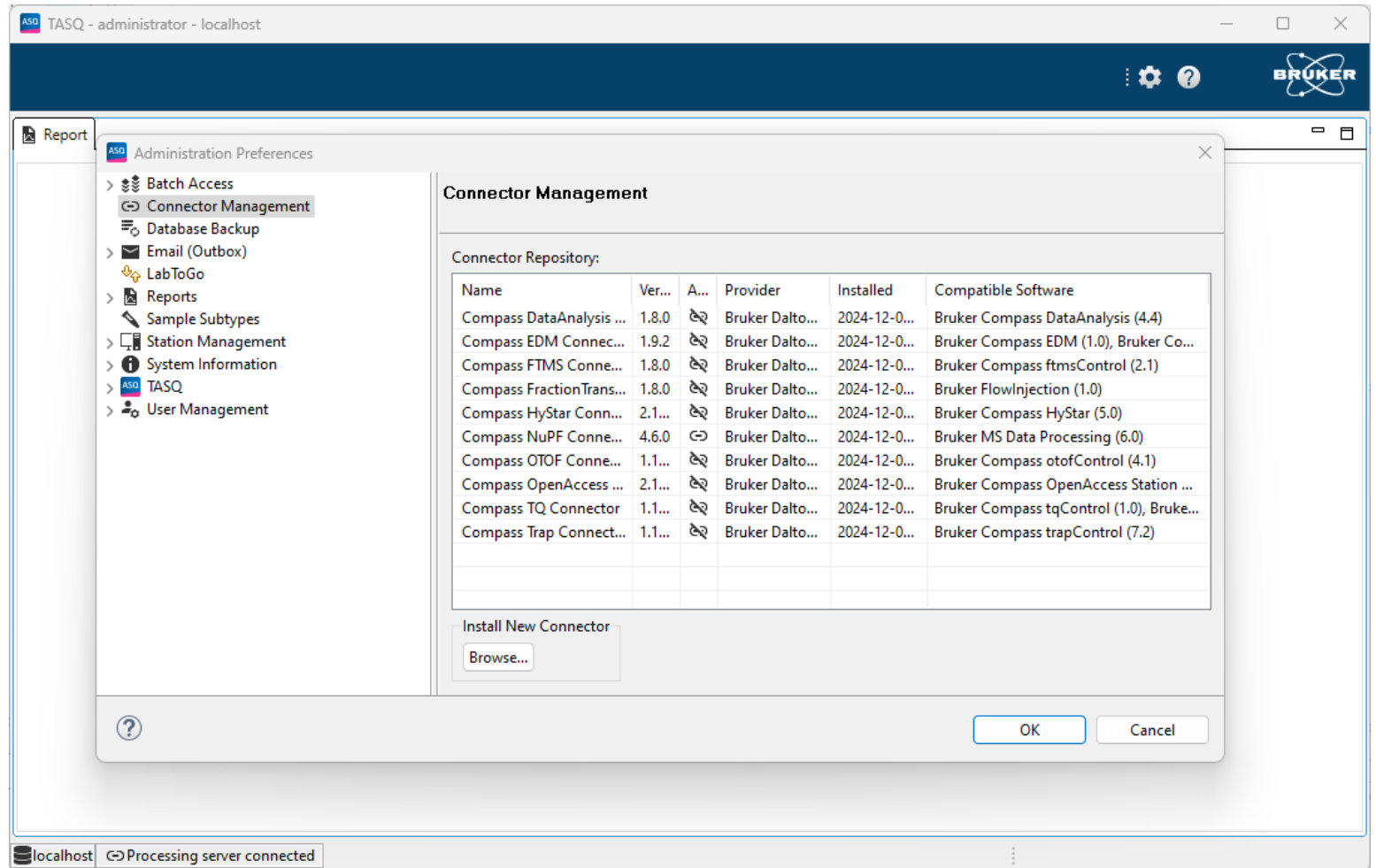
TASQ 2025b: Miscellaneous

- Support generation mobilograms for data sets with segments having different mobility ranges
- Enable manual integration with SHIFT LMB in mobilogram view, fix chromatogram view
- Improved Add Multiple Ions wizard: disable Finish button if not all mandatory properties are set (Spectrum type, charge state...)
- Reminder: In Butterfly view copy peak list of measured MS/MS spectrum or of library spectrum to clipboard
Open Add Multiple Ions wizard in TASQ method editor to add multiple ions from peak list in clipboard to selected analyte

- Performance of installation of client and server components improved

TASQ 2025b: Connector Management Available in TASQ Administration Preferences

- If a user wants to import a brkrar file containing TQ methods into a TASQ only system EDM and TQ connectors have to be activated
- This can be done in connector management in Administration client or now in TASQ administration preferences



ASQ TASQ - administrator - localhost

Administration Preferences

Connector Management

Connector Repository:

Name	Ver...	A...	Provider	Installed	Compatible Software
Compass DataAnalysis ...	1.8.0	64	Bruker Dalto...	2024-12-0...	Bruker Compass DataAnalysis (4.4)
Compass EDM Conne...	1.9.2	64	Bruker Dalto...	2024-12-0...	Bruker Compass EDM (1.0), Bruker Co...
Compass FTMS Conne...	1.8.0	64	Bruker Dalto...	2024-12-0...	Bruker Compass ftmsControl (2.1)
Compass FractionTrans...	1.8.0	64	Bruker Dalto...	2024-12-0...	Bruker FlowInjection (1.0)
Compass HyStar Conn...	2.1...	64	Bruker Dalto...	2024-12-0...	Bruker Compass HyStar (5.0)
Compass NuPF Conne...	4.6.0	64	Bruker Dalto...	2024-12-0...	Bruker MS Data Processing (6.0)
Compass OTOF Conne...	1.1...	64	Bruker Dalto...	2024-12-0...	Bruker Compass otofControl (4.1)
Compass OpenAccess ...	2.1...	64	Bruker Dalto...	2024-12-0...	Bruker Compass OpenAccess Station ...
Compass TQ Connector	1.1...	64	Bruker Dalto...	2024-12-0...	Bruker Compass tqControl (1.0), Bruke...
Compass Trap Connect...	1.1...	64	Bruker Dalto...	2024-12-0...	Bruker Compass trapControl (7.2)

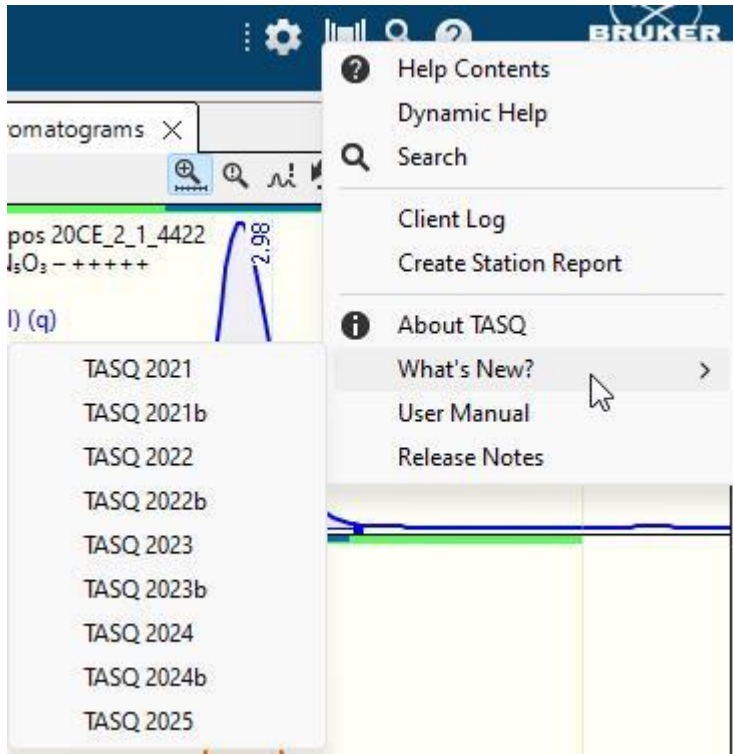
Install New Connector

Browse...

OK Cancel

localhost Processing server connected

TASQ 2025b: Offer User Documentation within TASQ Help Menu

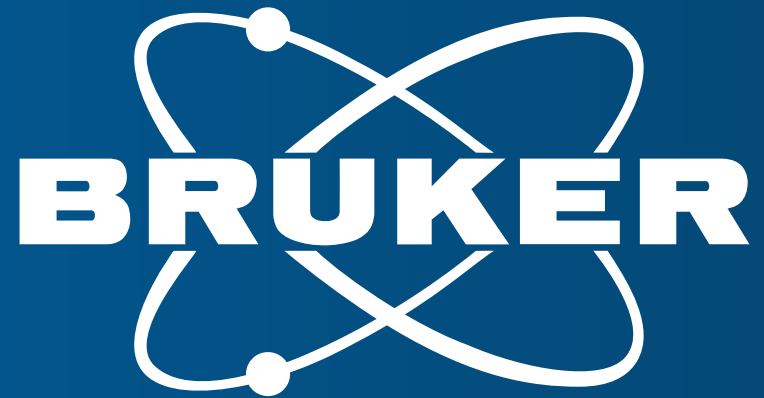


TASQ 2025b: Discontinued Feature

- Purity plot is no longer supported for Chromatogram/s, Mobilogram/s view

TASQ 2025b and older: Known Issues

- TSF data of autoMSMS data can't be processed by TASQ – no chromatograms can be created
 - TASQ is not able to retrieve the MS fullscan data
- This has been fixed in TASQ 2025b
- TASQ 2025: importing and processing of batches will show current date time of processing but the actual acquisition date in acquisition date column – fixed in TASQ 2025b
- On segment borders TQ instruments may store data which is non monotone – TASQ sorts data points by RT if it detects that time axis is not monotone



Innovation with Integrity