UnknownProcessor

By Leoson

niels@waleson.eu

1. Batch creation

2. Windows and tables overview

3. Alkanes processing

4. Data Reviewing

5. Quantitation

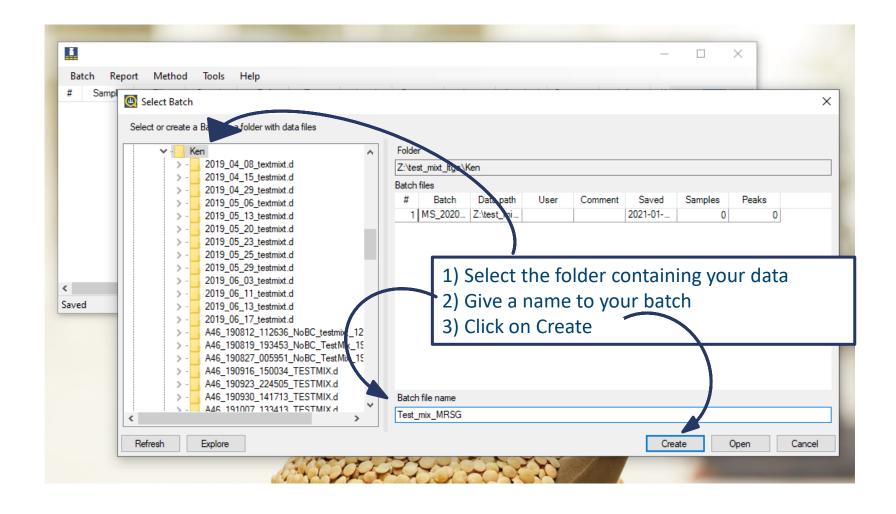
6. Report

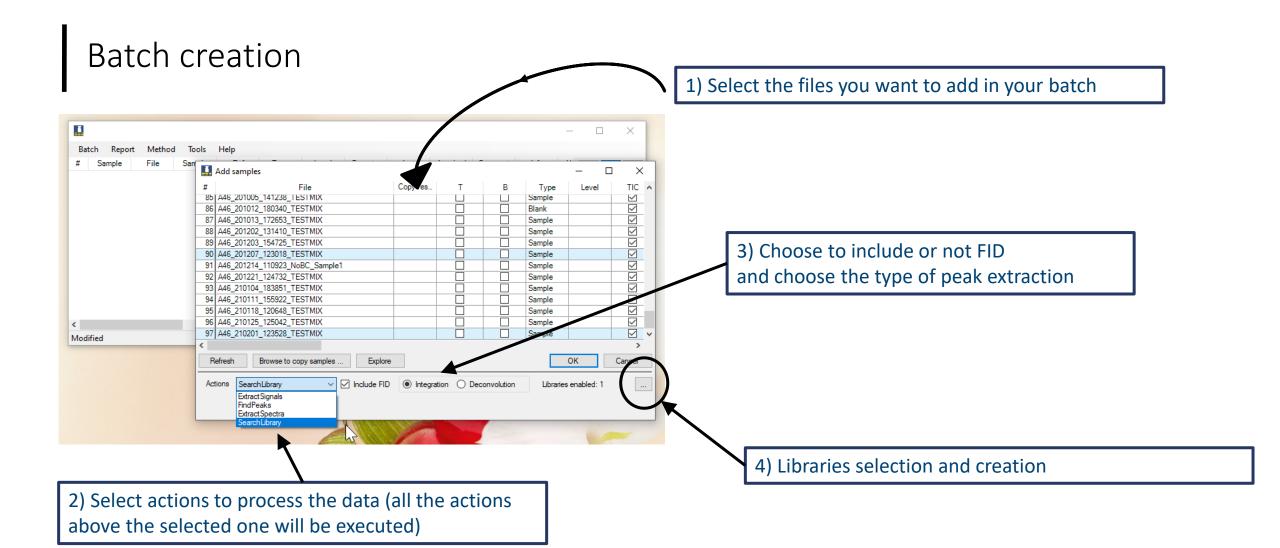
01 Batch creation

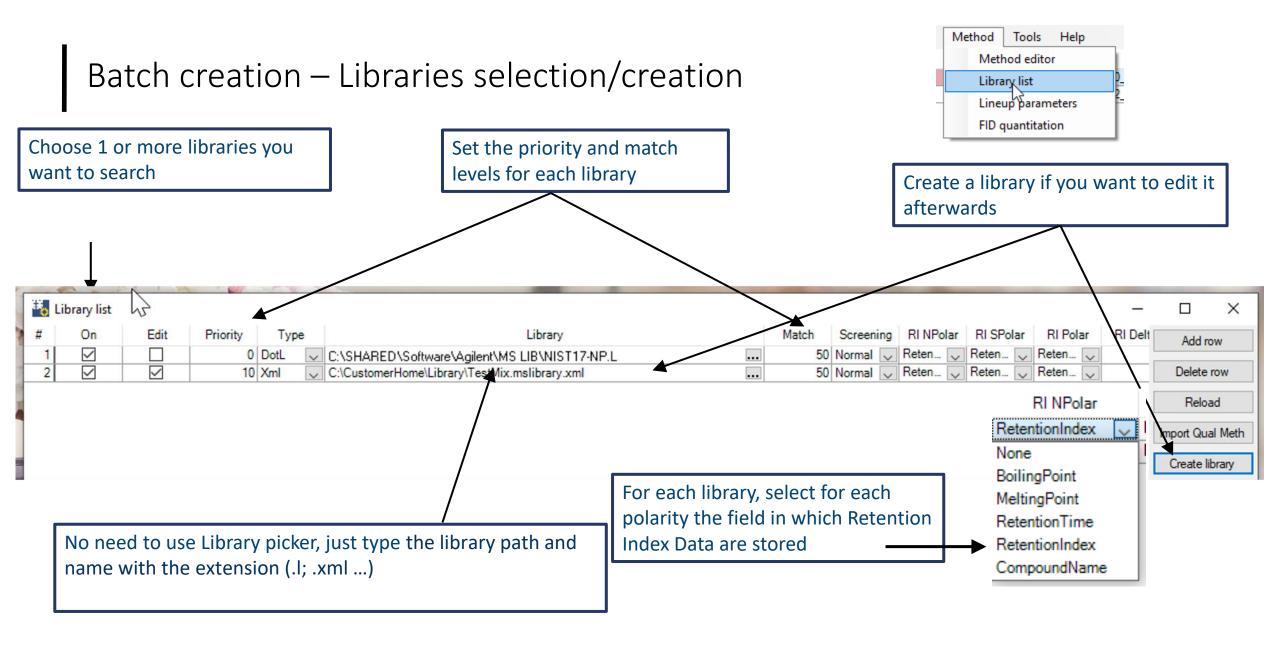
Batch creation

 Open UnknownProcessor: the Select Batch window automatically opens

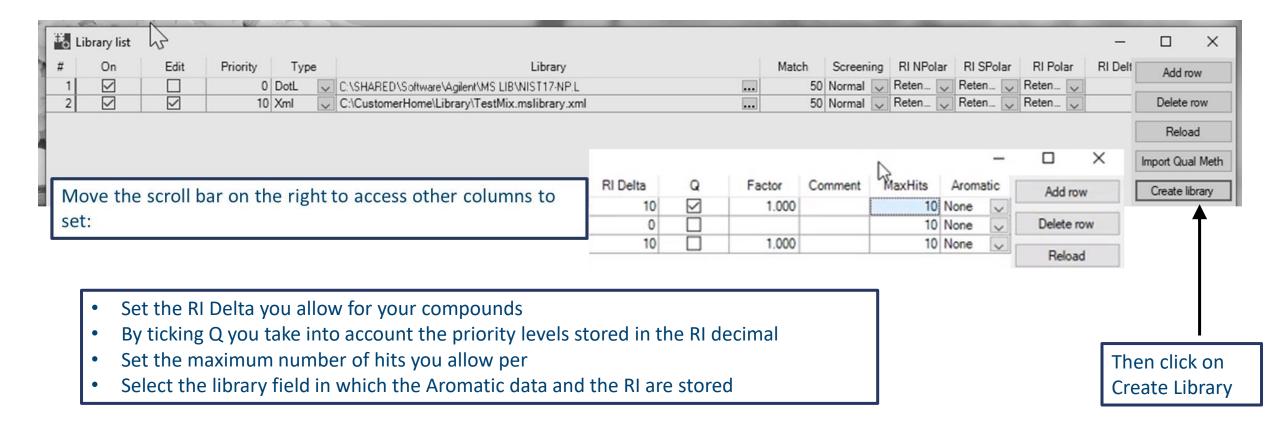


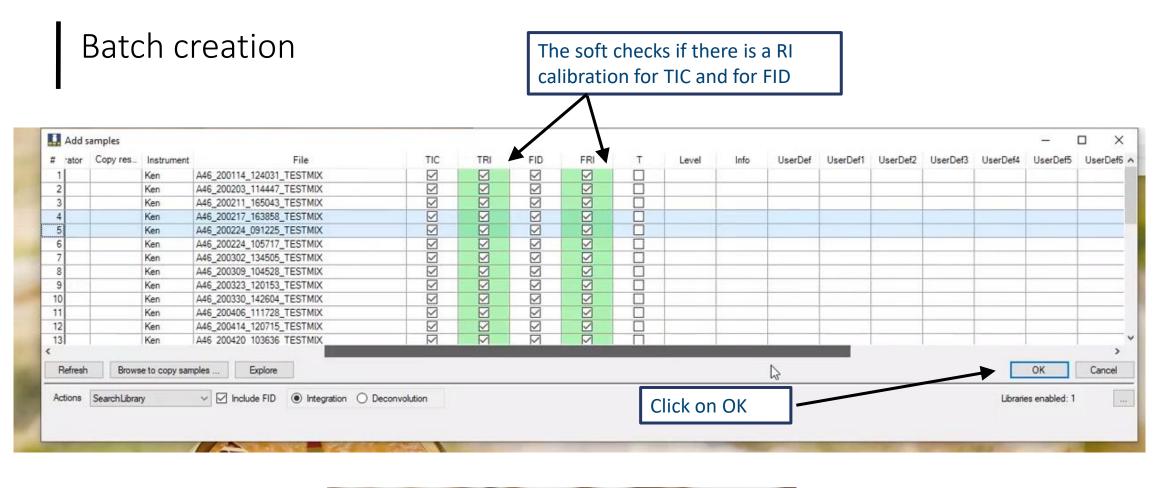


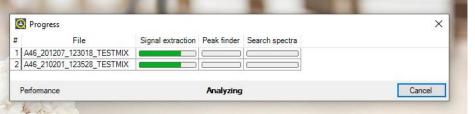




Batch creation - Libraries selection/creation

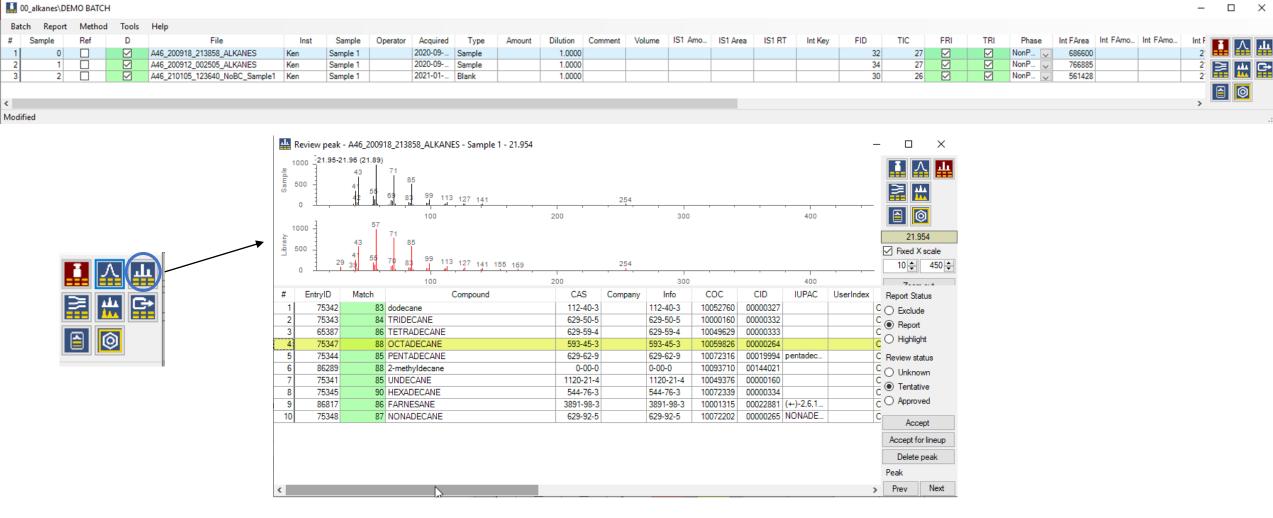




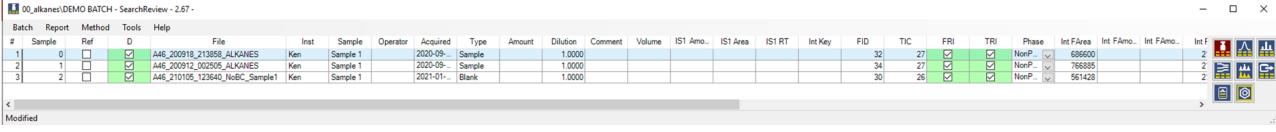


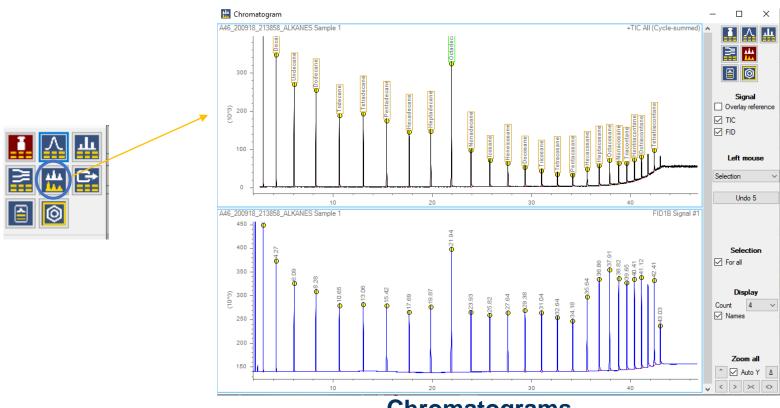
Data loading ...

02 Windows and tables

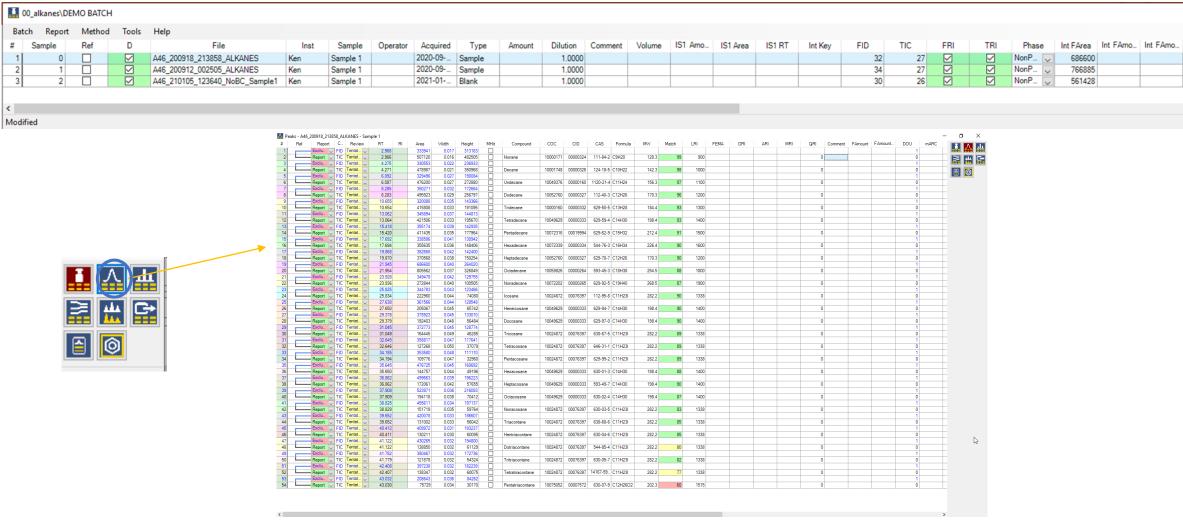


MS spectra





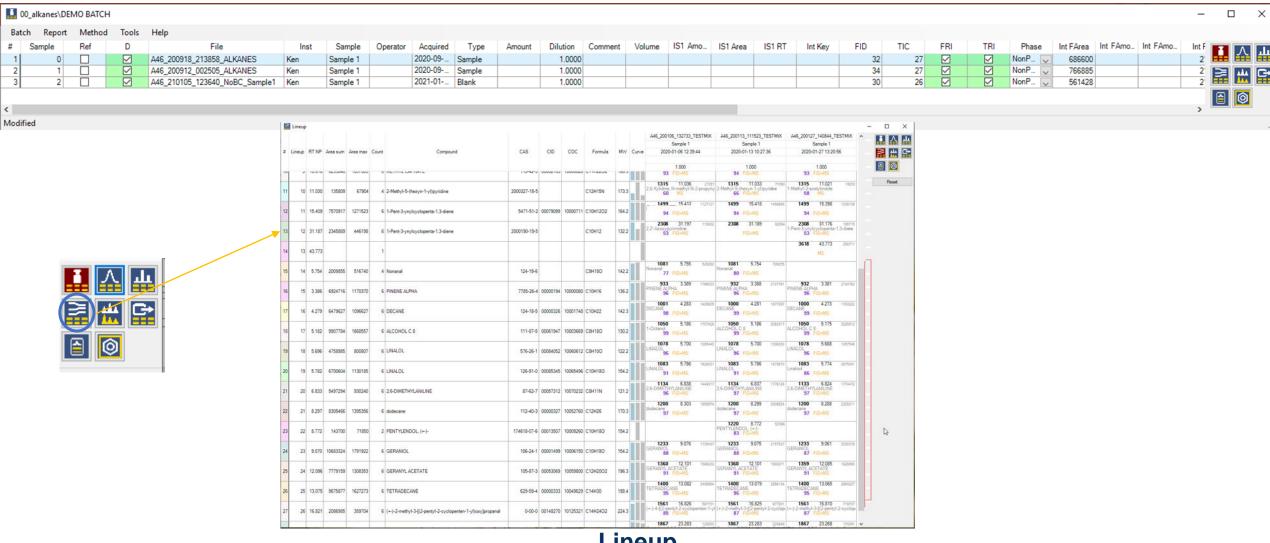
Chromatograms



2 2 2

A

Compound list of selected sample

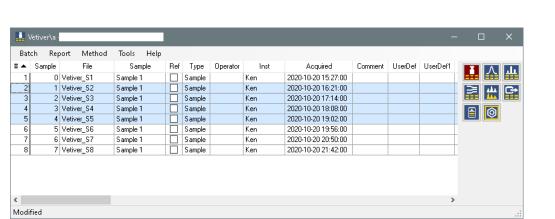


Lineup

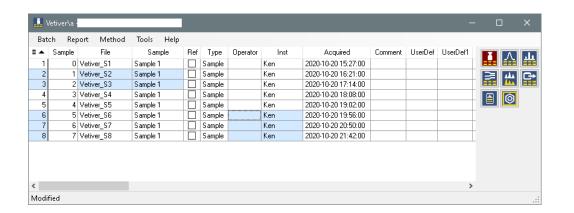
User Interface, tables: selecting and moving rows

The tables have common feature, the sample table is used as example:

- First column cell **turn blue** if any cell in the row is selected
- Click on first column cell to select all row cells
- Drag mouse down to select multiple rows
- Click on a blue first column cell and drag up or down to move rows

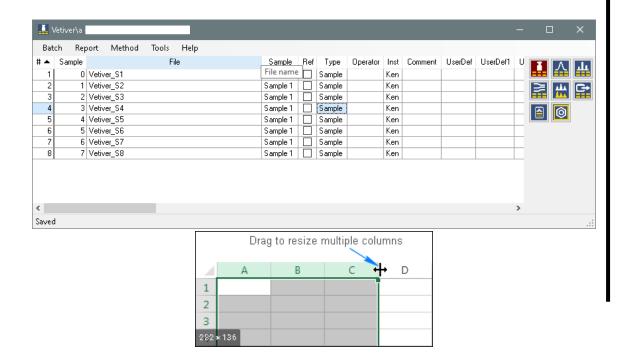


- Use shift and ctrl keys with mouse click to select multiple cells
- Use shift and ctrl keys with **cursus keys** (up, down, left, right)
- Click top left cell '#' to select all cells
- Click top cell 'column header' to select all cells in the column

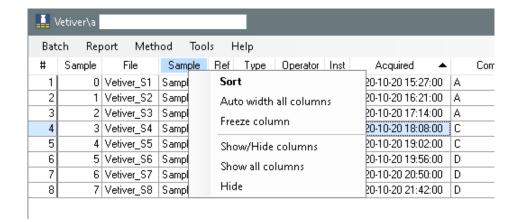


Tables, columns moving and width

- Click and drag column header to move columns
- Click and drag between column headers to adjust the width
- Double click between column headers to auto width
- Ctrl and double click between columns headers to auto width all

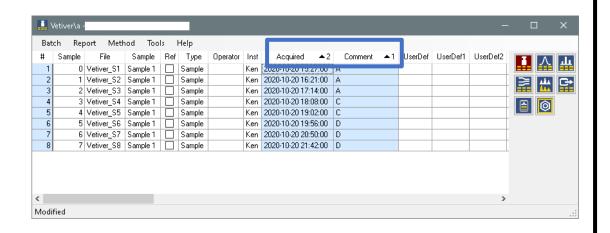


- Double click on a column header to sort
- Ctrl double click another column to add an additional sort
- Column width and sorting is stored in the user profile

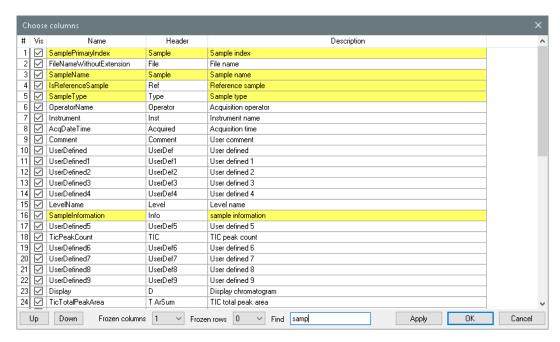


Tables, sorting rows, column header menu

- Double click on a column header to sort
- Ctrl double click another column to add an additional sort
- Column width and sorting is stored in the user profile

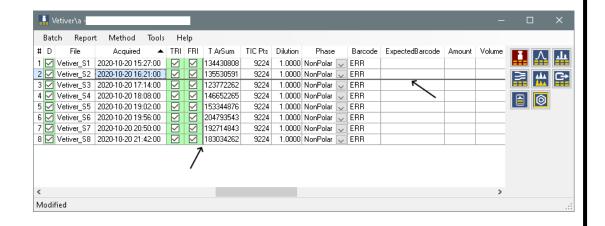


- Right click on a column header to show the column menu
- Show/Hide columns to open a column editor
- Show/Hide columns dialog
- Use the Find text box to search
- Move multiple rows up and down

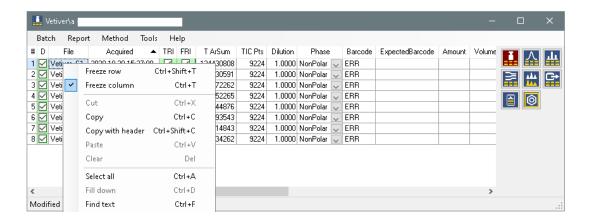


Tables, freeze columns, rows and body menu

- Right click column and toggle Freeze
- Here 5 important columns are frozen add the left side of the table
- And 2 important rows are frozen ad the top of the table
- Frozen column and row count are stored in the user profile

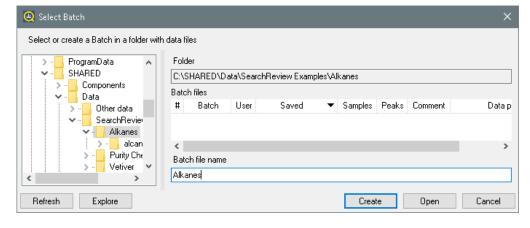


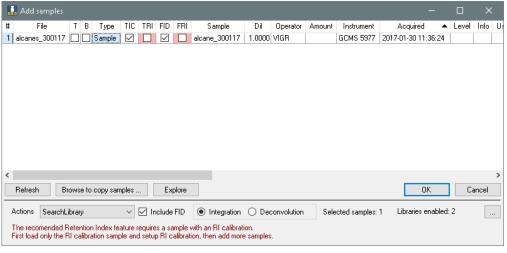
- Right click on a cell: table body menu (combined with context menu)
- Note: Keyboard shortcuts, Copy with header, Fill down, Find text



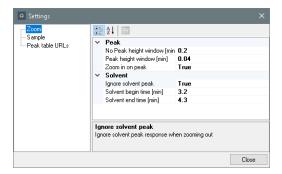
03 Alkanes processing

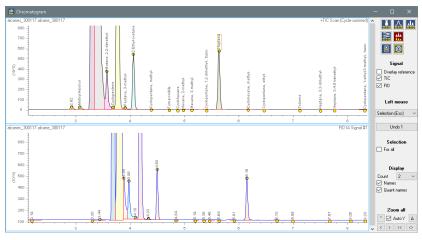
- Create batch in the folder with data files
- Add n-Alkane series sample
- TRI and FRI show invalid RI calibration files





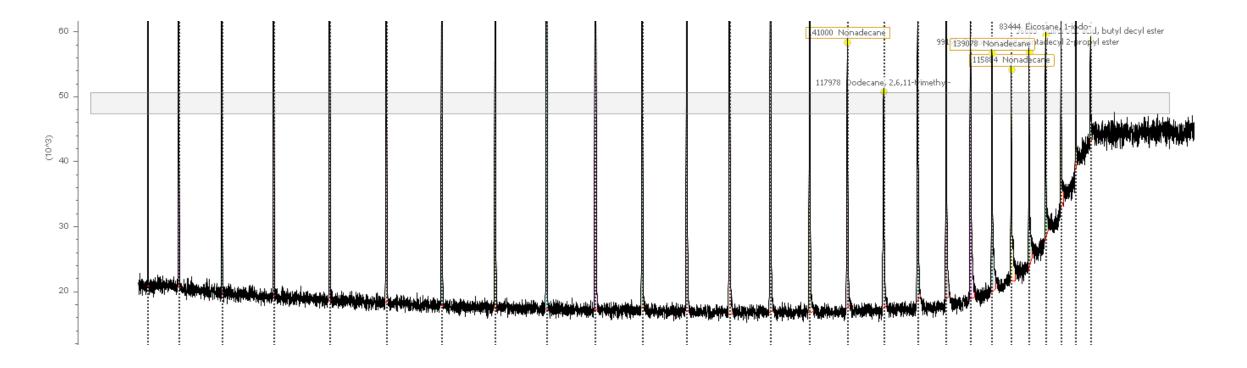
- Tools Settings
- Zoom, ignore solvent
- In the chromatogram window, Zoom FID and TIC to show n-Hexane



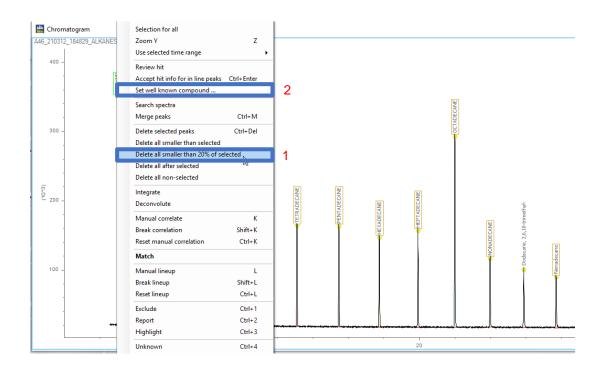


The Shift + Left Drag combination is kind of magic.

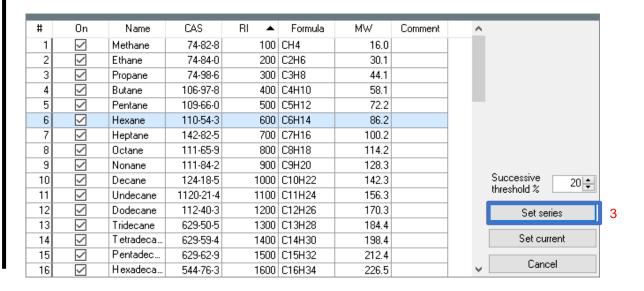
It selects peaks that are **intersected** (see screenshot) and also peaks that are **fully contained** in the selection. Now you can select large peaks (or small peaks). This is useful for n-Alkanes. Right click and 'Delete all non-selected'



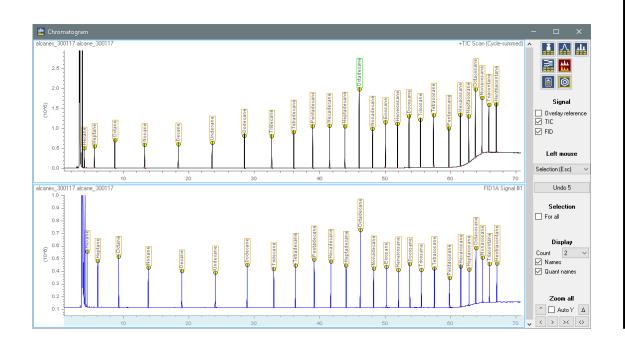
- Click on the n-Hexane peak, right click: Delete all smaller than 20%
- Select and delete all non n-Alkane peaks



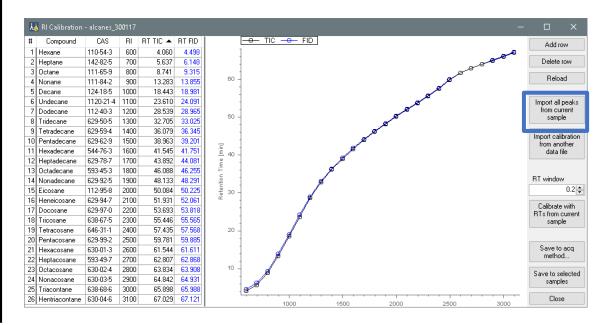
- Click on the n-Hexane peak, right click Set well known compound
- Select n-Hexane and click Set series, for both FID and TIC signals



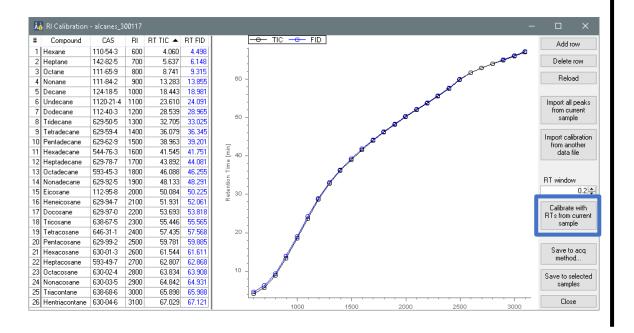
All n-Alkanes are labeled



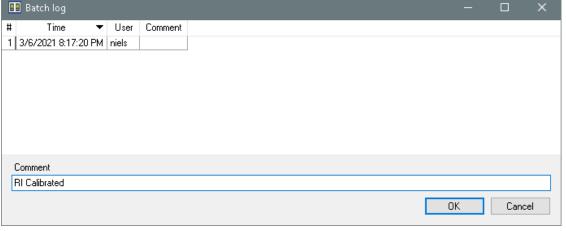
- Tools RI Calibration
- Select all rows and press Delete row button
- Import All peaks from current sample, and Save to selected samples



- Next RI re-calibration is just one click
- Calibrate with RTs from current sample
- The RT of largest peak within the RT window will be used



- Save batch
- Enter meaningful text to the logbook

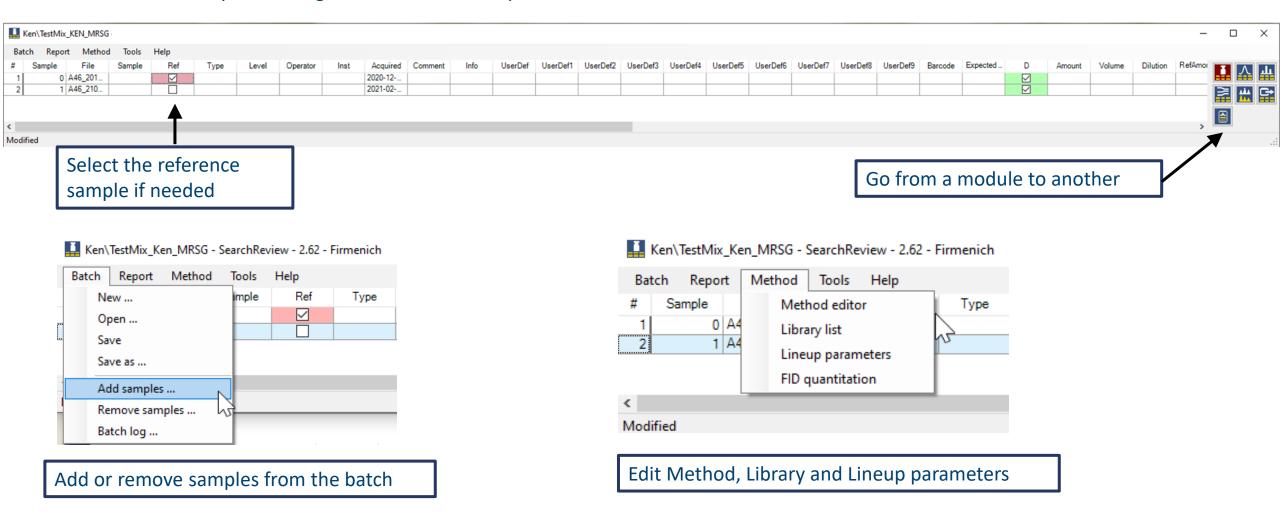


04 Data Reviewing

Data Reviewing – Main Window (samples)



This module allows you to navigate between the samples



Data Reviewing – Peaks Window

Selected sample



Right click on a column to access these actions

Freeze column

Hide

Show all columns

Show/Hide columns

Sort

Auto width all columns

Left click on a column and move it to right or left

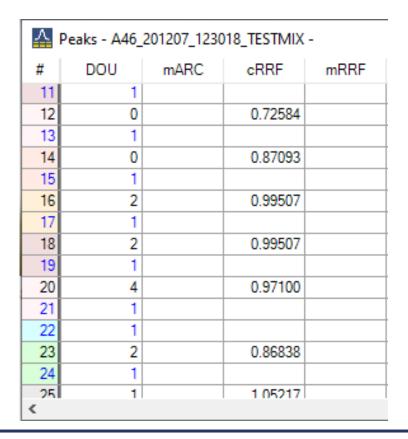
A Peaks - A46_201207_123018_TESTMIX -

#	Rel	Chrom	RT 🔺	RI	Compou	Formula	MW	CAS	FEMA	COC	CID	Area l ∔	••ghtr√idth	Height	Dec	Report	MReport	Review
8		TIC	3.405	932	PINENE	C10H16	136.2	7785-26-4	2902	10000080	00000194	3165606	0.019	2563888		Report 🔍		Tentat
9		FID .	3.412	932								2621251	0.019	2130076		Exclu		Tentat
10		TIC	3.580	945	CAMPHE	C10H16	136.2	79-92-5	2229	10000223	00000461	37018	0.020	27442		Report 🔍		Tentat
11		FID	3.585	945								30464	0.020	23853		Exclu		Unkno
12		TIC	4.306	1000	DECANE	C10H22	142.3	124-18-5		10001748	00000326	3118323	0.023	2128648		Report 🔍		Tentat
13		FID	4.308	1000								2762747	0.023	1894686		Exclu		Tentat
14		TIC	5.216	1050	ALCOHO	C8H18O	130.2	111-87-5	2800	10003669	00061947	4223225	0.028	2345405		Report 🔍		Tentat
15	4-	FID .	5.218	1050								3824302	0.028	2130573		Exclu		Tentat
16		TIC	5.328	1056	CIS-LINA	C10H18O2	170.2	5989-33-3	3746	10063894	00069640	102311	0.025	57983		Report 🔍		Appro
17		FID	5.332	1056								69653	0.024	44523		Exclu		Unknown
18		TIC	5.586	1070	CIS-LINA	C10H18O2	170.2	5989-33-3	3746	10063894	00069640	68236	0.028	38155		Report 🔍		Tentative
19		FID	5.592	1070								59473	0.027	34301		Exclu		Approved
20		TIC	5.727	1078	CIS-LINA	C8H10O	122.2	576-26-1	3249	10060612	00084052	2323865	0.028	1321236		Report 🔍		Tentat
21		FID	5.728	1078								1998719	0.028	1123396		Exclu		Te at
		1										1005700	0.000	CCETOO				7

Visual correlation between TIC and FID

Compound status

Data Reviewing – Peaks Window



The library can contain the RRF

If you work with another library without RRF data, it can be adjusted by filling in the mARC: manual Aromatic Ring Count, with help of DOU: Degree Of Unsaturation



Fields related to internal standard: possibility to quantitate

$^{\lambda}$	Peaks - A46	201207	123018	TESTMIX -
	reaks Arro		123010	TES HVIIIX

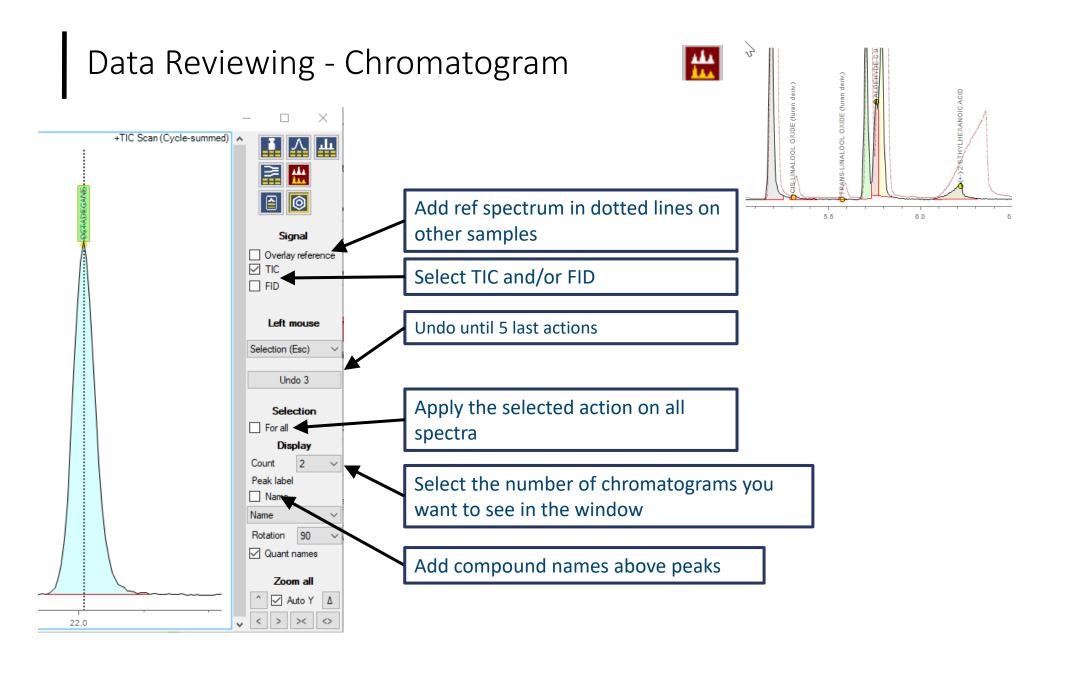
#	IRRF	IConc	mlConc	ISTD	Isl
- 1					
2					
3					
4					
5					
6					
7					
8					
9					
10					
11					

Data Reviewing – Peaks Window

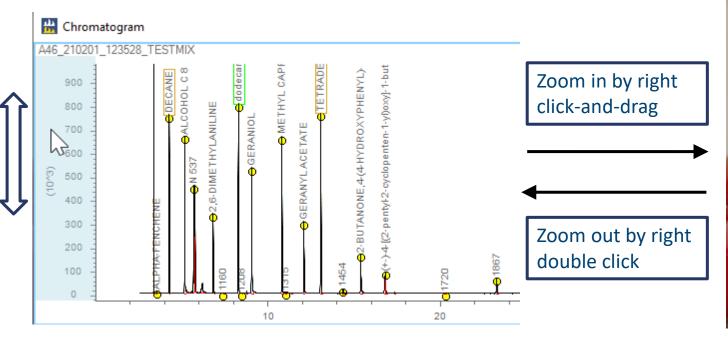


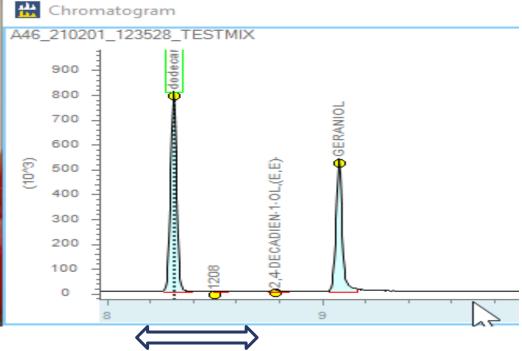
#	Rel	46_201207_1230 Chrom	RT 🔺	Freeze row	Ctrl+Shift+T
8		TIC	3.405	Freeze column	Ctrl+T
9		- FID	3.412	Total outside the and so that	202000000
10		TIC TIC	3.580	Cut	Ctrl+X
11		- FID	3.585	Сору	Ctrl+C
				Copy with header	Ctrl+Shift+C
				Paste	Ctrl+V
				Clear	Del
				Select all	Ctrl+A
				Fill down	Ctrl+D
				Find text	Ctrl+F
				Search spectra	
				Review hit	
				Merge peaks	Ctrl+M

Delete selected peaks	Ctrl+Del						
Delete all smaller than selected Delete all smaller than 20% of selected Delete all after selected							
						Manual correlate	K
						Break correlation	Shift+K
Reset manual correlation	Ctrl+K						
Add (approved and selected) to library						
Exclude	Ctrl+1						
Report	Ctrl+2						
Highlight	Ctrl+3						
Unknown	Ctrl+4						
Tentative	Ctrl+5						
Approved	Ctrl+6						







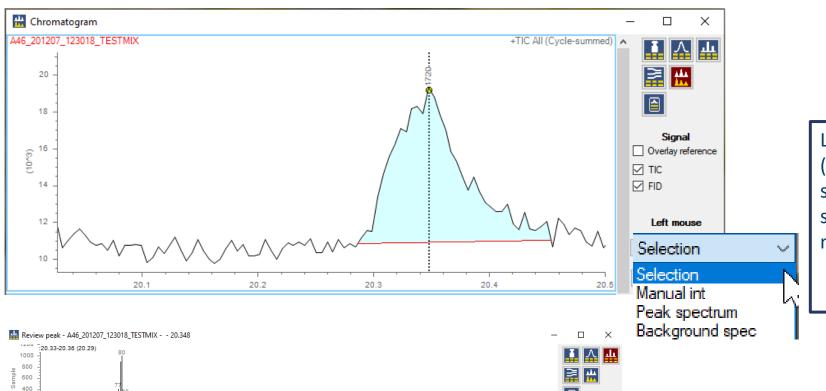




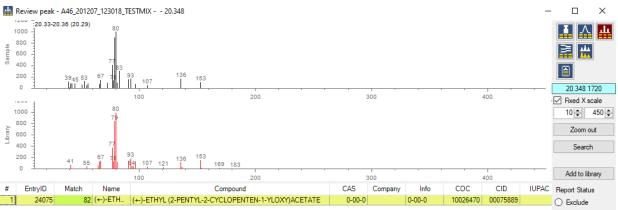
Other zoom and navigation panel

- Left click on x/y axis and move from left to right / up to down by dragging the mouse or with keyboard arrows
- Double click to zoom out
- Right click and move to zoom in / out on the selected axis

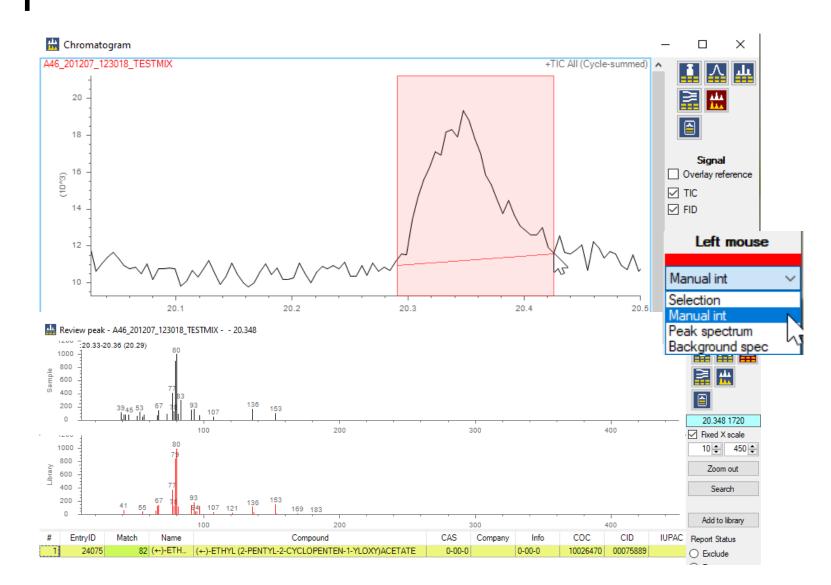




Left mouse in Selection Mode (Keyboard shortcut: Esc.): select a peak and display its spectrum in Review peak module

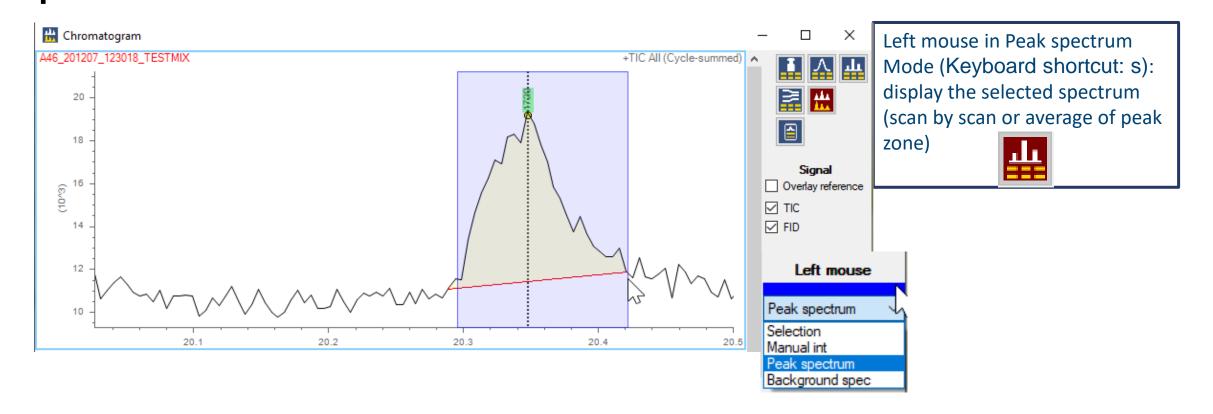






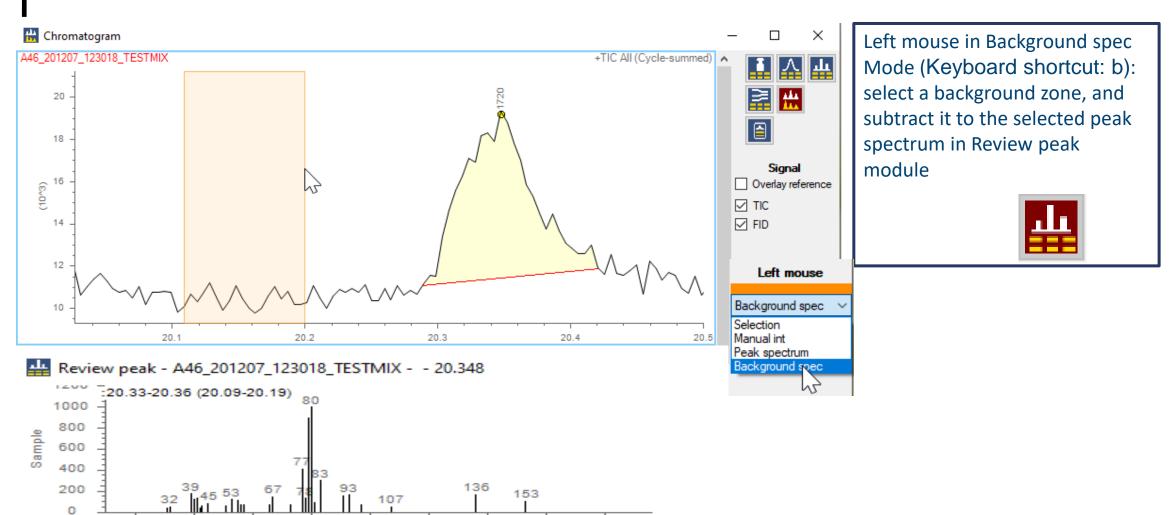
Left mouse in Manual int Mode (Keyboard shortcut: m): integrate a peak and display its spectrum in Review peak module

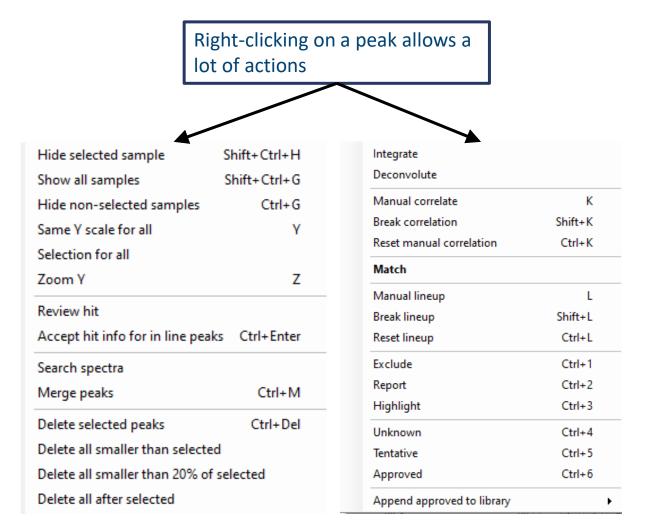




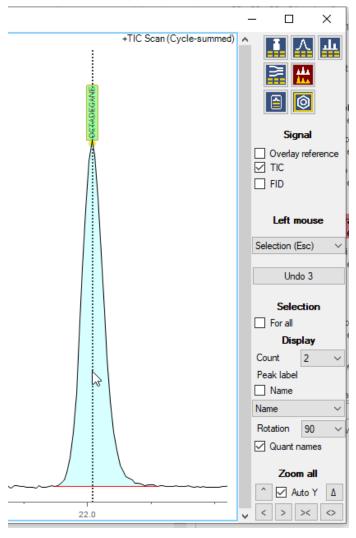
100





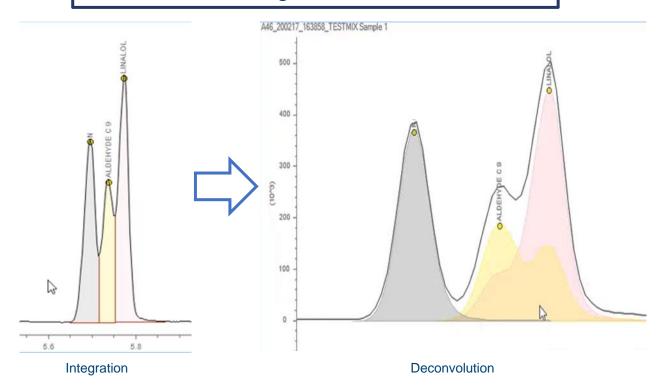


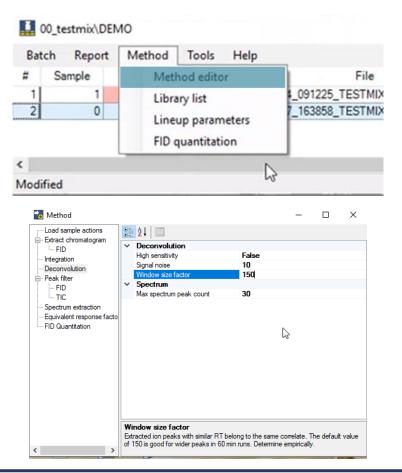






Local deconvolution: right click → deconvolute

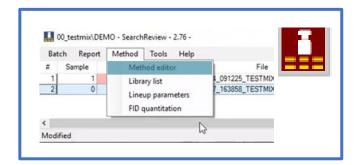




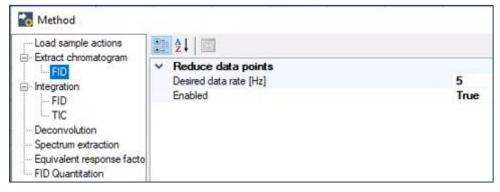
Adjust deconvolution parameters: in the main window, click on Method → Method editor → Deconvolution Tab

Data Reviewing – Chromatogram

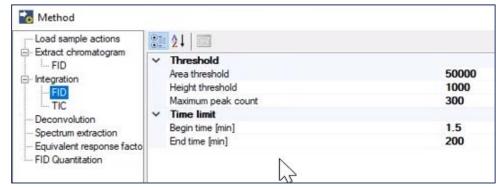




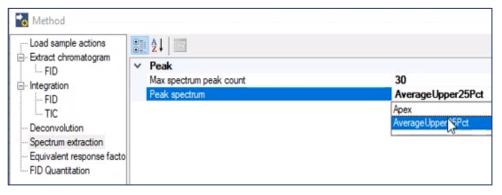
Several other parameters can be adjusted through the Main window:



FID: desired data rate for extraction and do we went to extract FID or not



Integration parameters :Area threshold and height threshold for peak exclusion and time range for integration to be on or off



Spectrum extraction type: 1 scan from the apex or average scan for scan upper of 25% peak hight



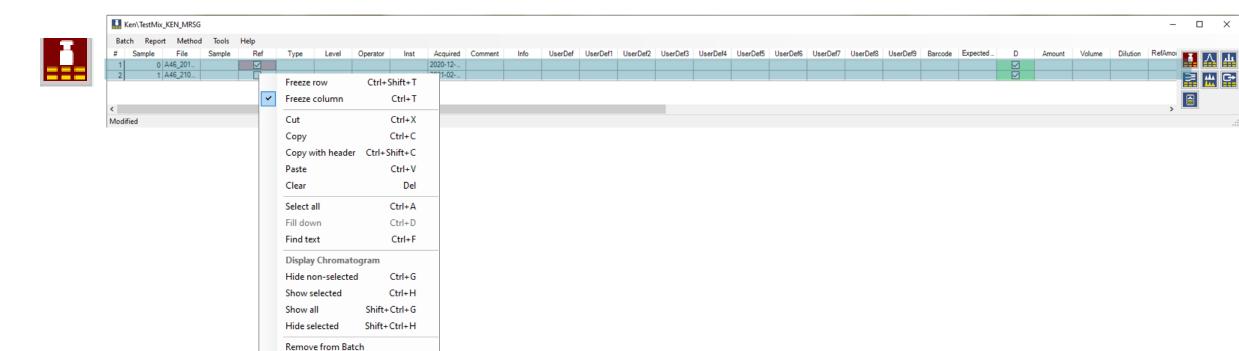
FID quantification: Default RRF used if no rrf could be caculated or extract from Librarie

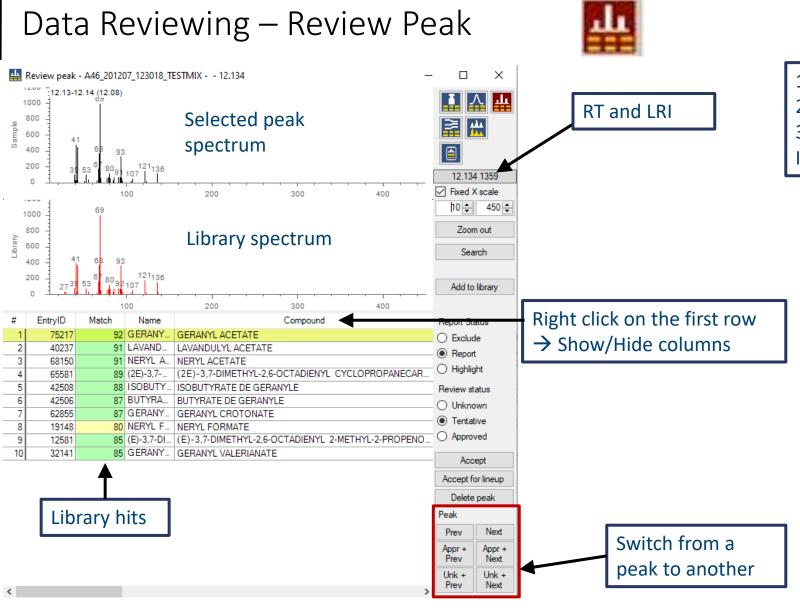
Data Reviewing – Chromatogram

Explore Integrate FID Integrate TIC Deconvolute Search spectra

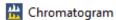


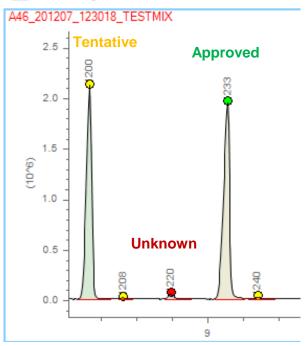
When you modify any method or library parameter, right click on the samples and select «Integrate», «Deconvolute» or «Search spectra» according to the modification you made to reintegrate data.





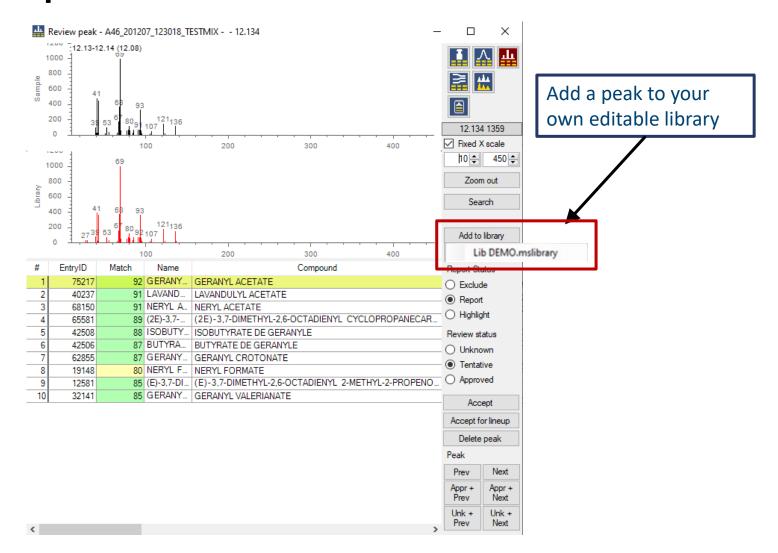
- 1) Select the best hit, if available
- 2) Select the status
- 3) Click on accept
 It updates the chromatogram colors

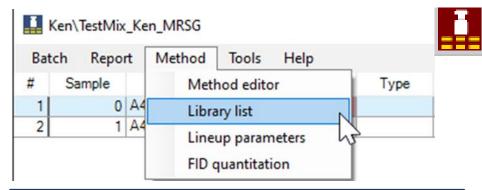




Data Reviewing – Review Peak







Access libraries parameters at any time via the Main Window

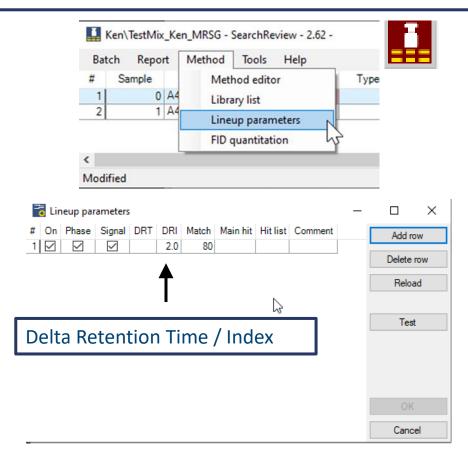
Data Reviewing – Lineup



\equiv	Lineup						-	-		×
					A46_201207_123018_TESTMIX	A46_210201_123528_TESTMIX	^		IΛ	ıШ
#	Compound	Formula	MW	Curve	2020-12-07 12:30:03	2021-02-01 12:35:12		Ē	a	G.
					0.000	0.000		(
54	PINENE ALPHA	C10H16	136.2		PINENE ALPHA 96 FID+MS 0	PINENE ALPHA 96 FID+MS -63			Reset	
55	CAMPHENE	C10H16	136.2		945 3.580 37018 CAMPHENE 94 FID+MS 0	945 3.570 11227 CAMPHENE 89 FID+MS 64			Lineup	
56	DECANE	C10H22	142.3		1000 4.306 3118323 DECANE 98 FID+MS 0	1000 4.291 1087162 DECANE 99 FID+MS 65				
57	ALCOHOL C 8	C8H18O	130.2		1050 5.216 4223225 ALCOHOL C 8 99 FID+MS 0	1050 5.192 1014907 ALCOHOL C 8 99 FID+MS 67				
58	CIS-LINALOOL OXIDE (furan deriv.)	C10H18O2	170.2			1056 5.309 41365 CIS-LINALOOL OXIDE (furan deriv 80 FID+MS				
59	ALDEHYDE	C8H10O	122.2		N 96 FID+MS 0	N 96 FID+MS -67 5.703 694173	l			
60	ALDEHYDE C 9	C9H18O	142.2		1081 5.781 1191547 ALDEHYDE C 9 91 FID+MS 0	1081 5.761 384733 ALDEHYDE C 9 95 FID+MS -68				
61	LINALOL	C10H18O	154.2		1083 5.815 2550477 LINALOL 90 FID+MS 0	1083 5.791 743643 LINALOL 90 FID+MS 65				
62	(+-)-2-ETHYLHEXANOIC ACID	C8H16O2	144.2		1110 6.355 1847979 (+-)-2-ETHYLHEXANOIC ACID 96 FID+MS 0	1105 6.219 187255 (+-)-2-ETHYLHEXANOIC ACID 95 FID+MS 67				
63	2,6-DIMETHYLANILINE	C8H11N	121.2		1133 6.862 1915248 2,6-DIMETHYLANILINE 96 FID+MS 0	1133 6.842 599869 2,6-DIMETHYLANILINE 96 FID+MS -67				
64	dodecane	C12H26	170.3		1200 8.337 4589974 dodecane 97 FID+MS 0	1200 8.312 1610934 dodecane 97 FID+MS -66				
65	PENTYLENDOL, (+-)-	C10H18O	154.2		-	1220 8.785 20221 PENTYLENDOL. (+-)- 80 FID+MS				
66	GERANIOL	C10H18O	154.2		1233 9.116 4548783 GERANIOL 89 FID+MS 0	1233 9.082 1077472 GERANIOL 83 FID+MS 67				
		1			1306 10.864 4461957 MFTHYI CAPRATE	1306 10.834 1452602 METHYL CAPRATE	~			

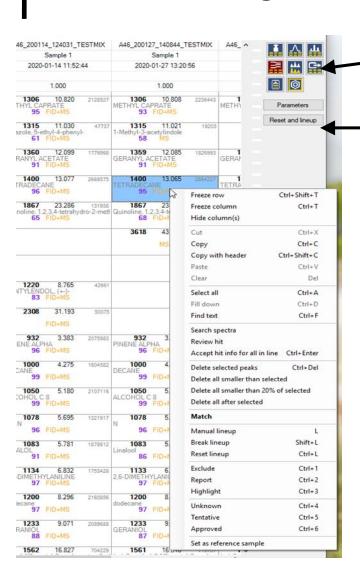
Peaks lineup/comparison between chromatograms

Parameters can be adjusted by clicking on Method -> Lineup parameters in the main window



Data Reviewing – Lineup





Export: Export lineup window to excel file

Reset and Lineup: remove all the lineups and "refresh" with latest parameters

Manual lineup or break lineup:

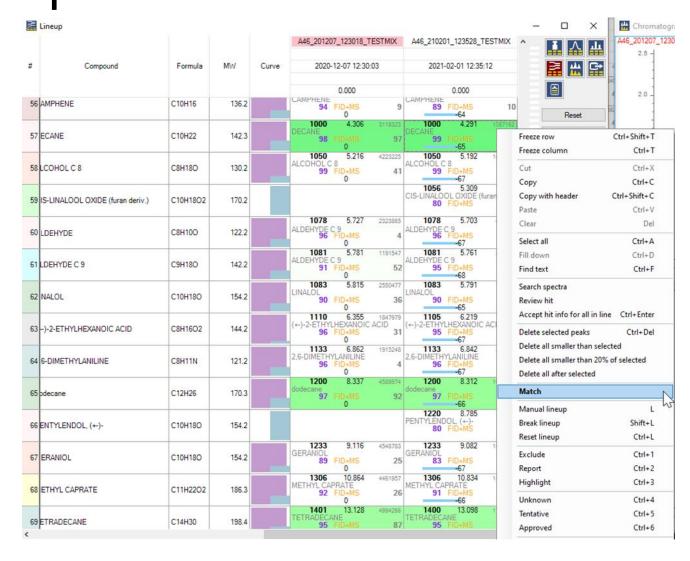
Select the compounds you want to lineup or reset lineup (Ctrl + left click)

Press "L" → Manual Lineup

Press shift +"L" → Break Lineup

Data Reviewing – Lineup

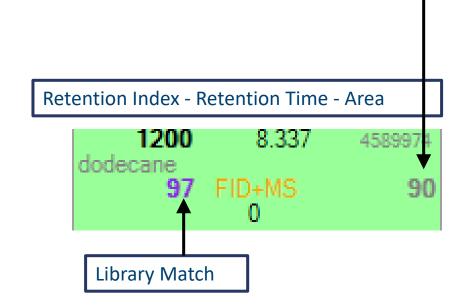




Spectrum Match:

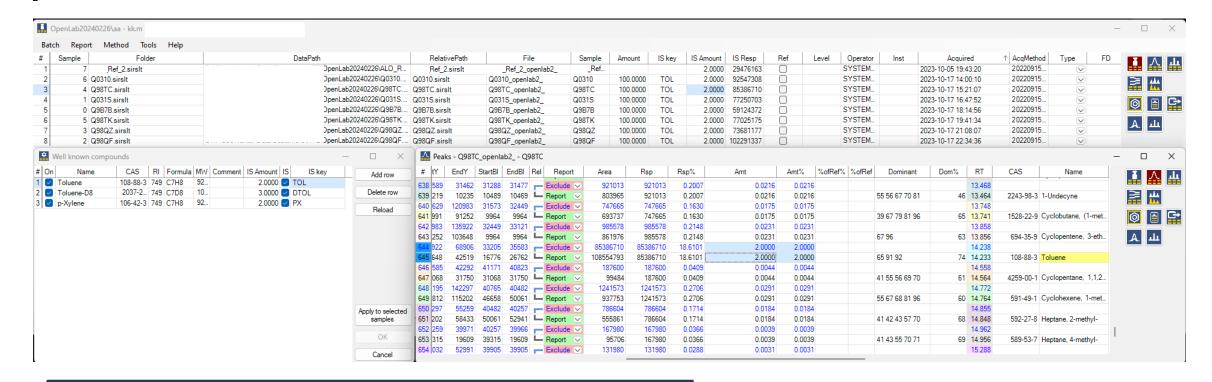
Select a compound Left double click: All the compounds with a close spectrum highlight in green.

ie: If DECANE is selected, DODECANE has a match of 90



05 Quantitation

Quantitation



Quantitation:

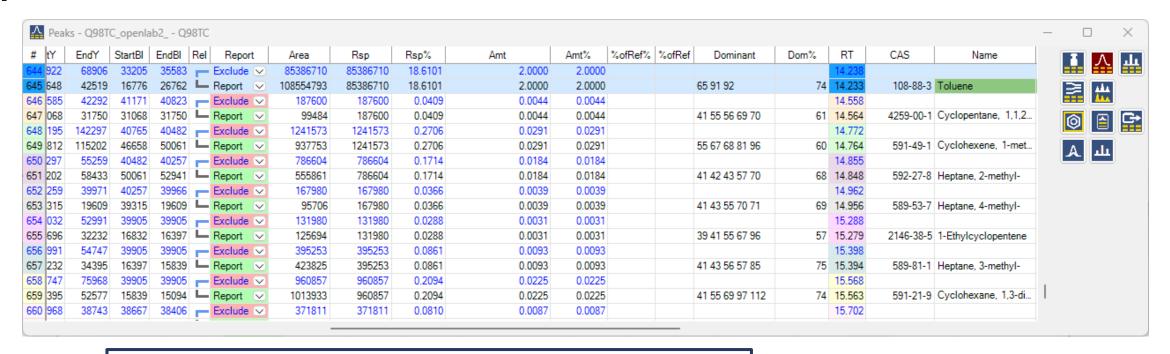
Example: Toluene equivalent base on FID response

Add rows to the Well known compound table

The default IS Amount can be overridden per sample

The sample IS key should correspond with the Well known compound

Quantitation



Quantitation:

Area is the integrated peak area

Response (Rsp) is the area of the correlated FID peak. If 2 MS peaks are correlated with 1 FID, the FID area is divided per MS area.

If there is no correlated FID peak, the response is just the MS area.

Rsp% is the normalized Response

Amt is calculated with the Well known response factor

Amt% is (peak Amount / sample Amount) * 100%

06 Report

Export Data



Available for:



Samples (Main Window)



Peaks



Lineup

Exports Data to an Excel File in the batch folder

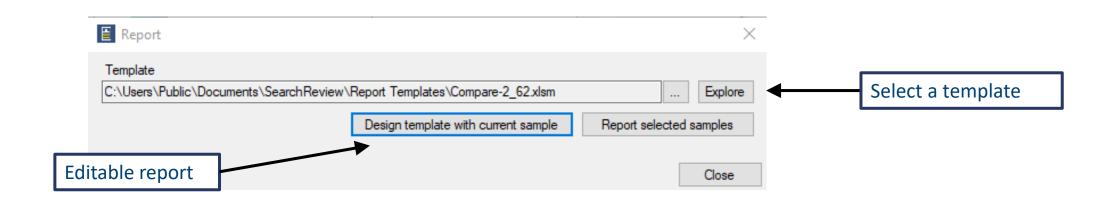
- TestMix_Ken_MRSG_Lineup_20210210095501
- TestMix_KEN_MRSG_Samples_20210203134944
- TestMix_Ken_MRSG_A46_210201_123528_TESTMIX_Peaks_202102101016

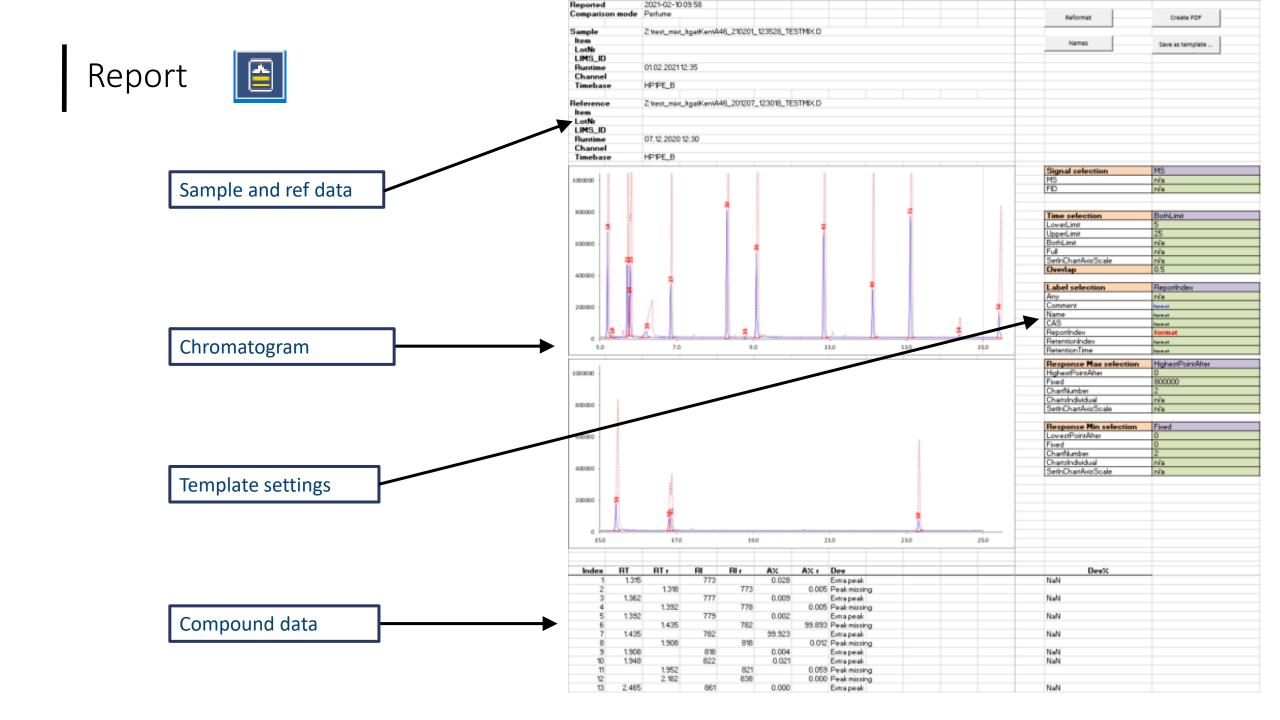
Report





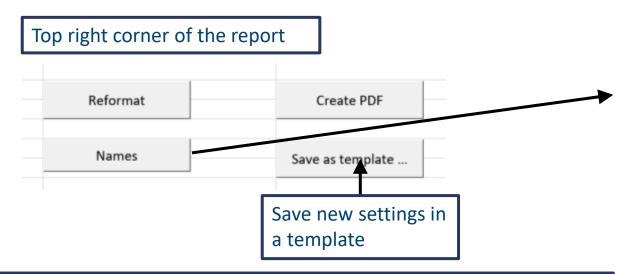
Mind to tick the reference and to select the sample to compare (highlighted line)



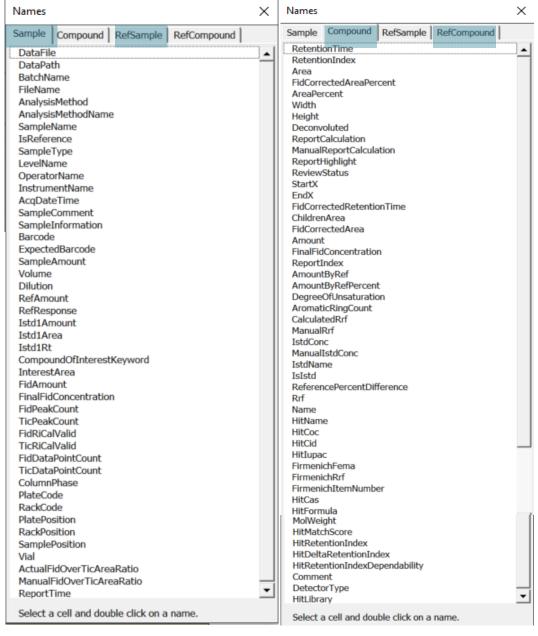


Report





- 1) Select a cell in the report where you want to add a new field
- 2) Click on Name: a table with fields concerning the **sample**, the **reference sample** or **compounds found in the sample or in the reference** opens
- 3) Select the desired field by double clicking
- 4) Click on «Save as template» and give it a name
- 5) Re open the report by selecting the new Template





n/a n/a BothLimit 5 25 n/a		play]
n/a n/a 0.5			
ReportIndex n/a format format format format format format format	Any Comment Name CAS ReportIndex RetentionIndex RetentionTime	Chromatogram labelling options	Reformat
HighestPointAfter 0 800000 2 n/a n/a SetInChartAxisScale 0 0 2 n/a	HighestPointAfter Fixed ChartNumber ChartsIndividual SetInChartAxisScale LowestPointAfter Fixed ChartNumber ChartsIndividual	Scaling options for y axis	Click on reformat to apply the new settings
	n/a BothLimit 5 25 n/a n/a n/a 0.5 ReportIndex n/a format format format format format format format SetInChartAxisScale 0 0 2 n/a n/a	n/a n/a BothLimit LowerLimit UpperLimit UpperLimit In/a n/a N/a N/a N/a O.5 SetInChartAxisScale ReportIndex Name format format format format format format HighestPointAfter O 800000 Phished ChartNumber ChartAxisScale SetInChartAxisScale LowestPointAfter O SetInChartAxisScale LowestPointAfter O SetInChartAxisScale LowestPointAfter O ChartNumber ChartSIndividual	BothLimit Solution BothLimit Solution Solution BothLimit Solution Sol