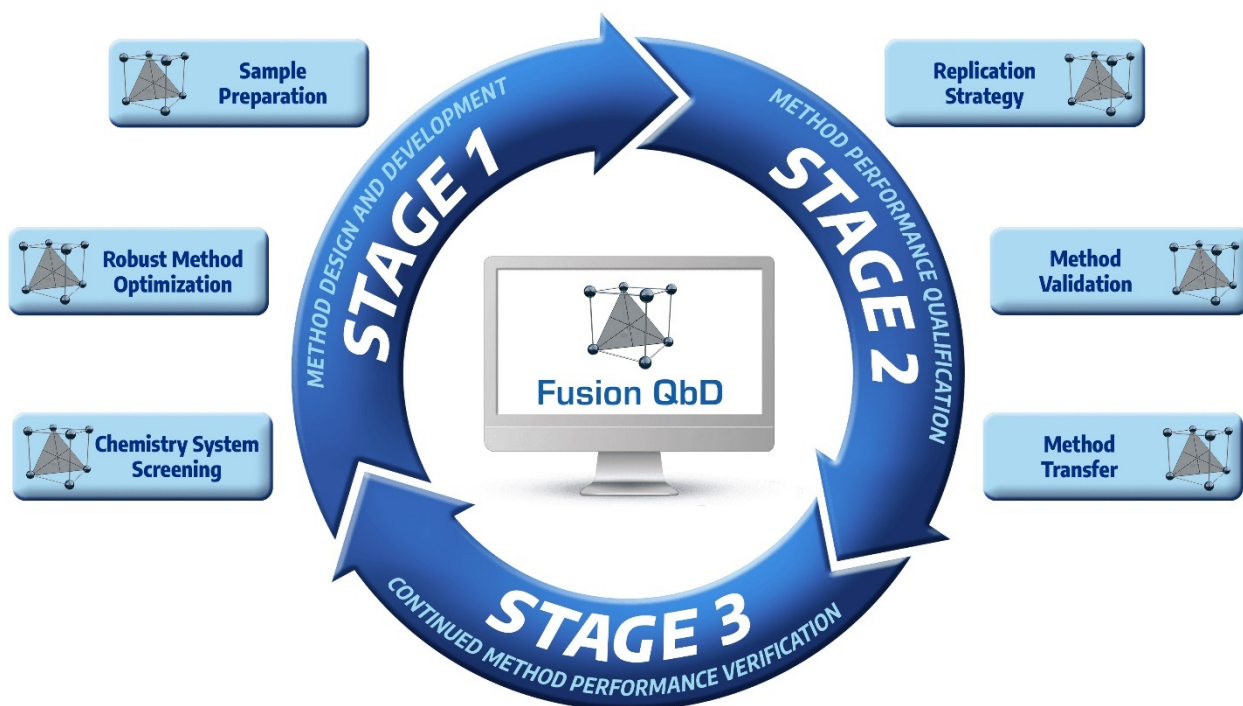


NEW FEATURES – VERSION 9.9.2



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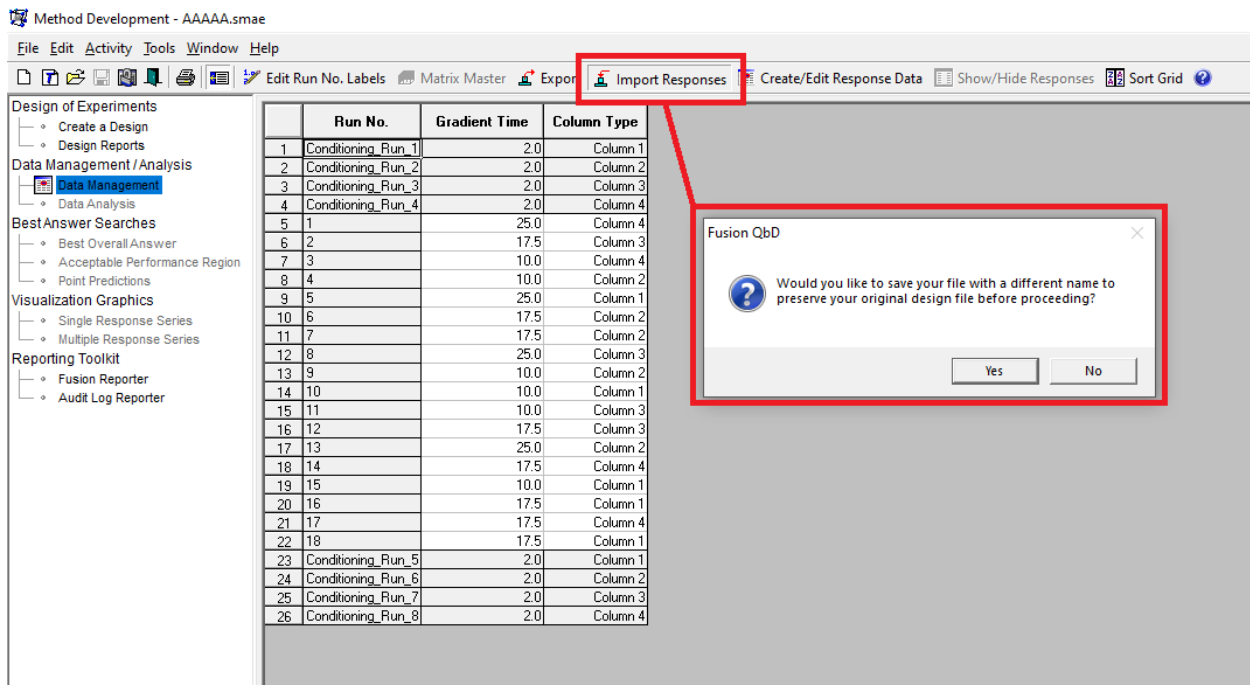
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### **Instrument Drivers/Configurations – Increased Data Integrity**

Fusion Administrator application (FA) instrument and device drivers, and instrument configurations for Named Instrument Systems generated in Fusion Administrator, are now integrated within an encrypted FA database for greater security and integrity. This data security enhancement eliminates the possibility of driver/configuration corruption and facilitates the FA database Backup and Restore operations.

# Response Data Import – Rename File Support

Initiating the Import Responses operation now prompts the user to rename the file prior to proceeding with data import. This enables the user to preserve the original design file in case the user wishes to start over after importing results, analyzing data, etc. S-Matrix implemented this feature in response to a large number of support inquiries over the years in which the user wanted to know how to return to a “clean slate” starting point but no longer had access to their original design file.



# Best Overall Answer Math Engine – Efficiency Enhancement

The mathematics underlying the Best Overall Answer (BOA) search routine has been upgraded to accelerate the search operation. A more efficient integrated search operation has now replaced the three-search-cycle operation in previous releases. As a result, users will now typically experience a 3x–5-x increase in speed associated with each search. For example, a search which previously took three minutes should now take a maximum of one minute.

Best Answer Search - Response Goal Settings
✕

Report Name  
 Numerical Search 2

Model Prediction Error C.I. for Report ± 2 Sigma

**Response Settings**

**Maximize**  
 Maximize means a larger number is better.

**Lower Bound:** any answer  $\leq$  this value is equally unacceptable. (Desirability = 0.0000).  
 Recommended Setting: the value at the threshold of unacceptable performance

**Upper Bound:** any answer  $\geq$  this value is equally acceptable. (Desirability = 1.0000).  
 Recommended Setting: the value at or above the threshold of acceptable performance.

[ Desirability: Absolute Scale = Zero (0.0000) to One (+1.0000). ]

Best Overall Answer: Goal = Maximize

Example Response: Lower Bound = 60

Enabled	Response	Goal	Lower Bound	Target	Upper Bound	Relative Rank
<input checked="" type="checkbox"/>	F - Rs-Map USP Resolution	Maximize	2.000		3.000	1.0
<input checked="" type="checkbox"/>	A - Rs-Map USP Resolution	Maximize	2.000		3.000	1.0
<input checked="" type="checkbox"/>	API - Rs-Map USP Resolution	Maximize	2.000		3.000	1.0
<input checked="" type="checkbox"/>	D-Deg - Rs-Map USP Resolution	Maximize	2.000		3.000	1.0
<input checked="" type="checkbox"/>	E - Rs-Map USP Resolution	Maximize	2.000		3.000	1.0
<input checked="" type="checkbox"/>	B - RetentionTime	Maximize	1.000		2.000	1.0
<input checked="" type="checkbox"/>	API - USPTailing	Minimize	1.000		1.500	1.0
<input checked="" type="checkbox"/>	B - KPrime	Maximize	2.000		3.000	1.0

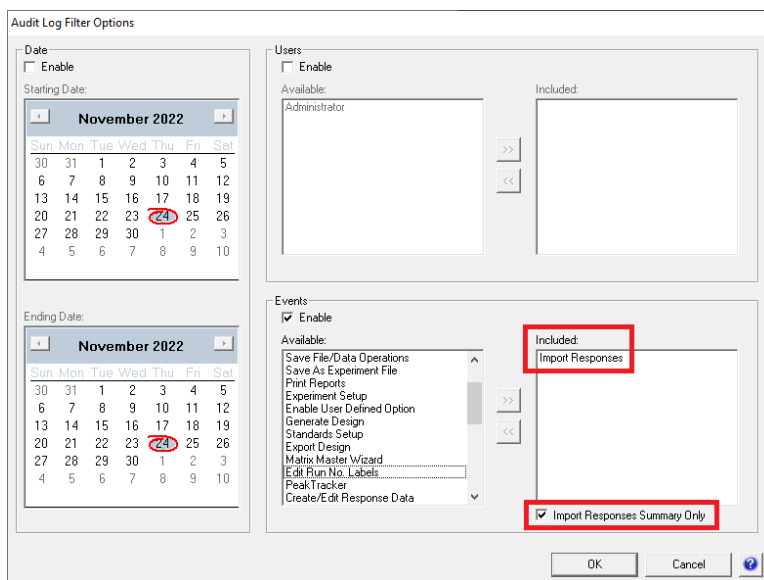
Select All
Select None
Response Ranges
Add Named Peak Rs Responses...

✔ The settings are valid.

Modify Search Region
Finish
Cancel

# Audit Log Report – Import Responses Summary

Report generation can require a significant amount of time in cases in which the user has imported a large amount of response data. This is especially true in cases in which the imported results include MS spectra data imported to support PeakTracker. Therefore, as shown in the top image below, the Audit Log Report wizard now includes an “Import Responses Summary Only” checkbox option which is enabled when the user includes the Import Responses auditable operation. When the checkbox is checked, the Audit Log Report will only contain the metadata associated with the Import Responses operation and not all the imported response data.



## Audit Log

20 JUN 2021 10:13:51 PDT [UTC-07:00] - Administrator

Event Type: Import Responses

## Import Response Settings

Setting	Value
Target CDS	EMPOWER
Empower Version	Empower 3 Software Build 3471 SPs Installed: Service Release 3 DB ID: 2484307300
Empower Database	(local)
Empower User	system
Project Name	RD2 - Optimization - 9_9_0
Result Set(ID)	RD2 Optimization (9001)
Processed Channel	PDA, Ch1 225nm@4.8nm, Time offset by 0.020 mins.
Activate PeakTracker	Checked
Raw PDA Channel	Unchecked
Raw MS Channel	QDa Positive Scan
MS Time Offset(min)	0.02
MS Intensity Threshold	100000
Processed MS Channel	QDa Positive Scan MS TIC, Smoothed by 59 point Savitzky-Golay Filter. (QDa Positive+) Scan (100.00-1250.00)Da, Centroid, CV=15)
Track Non-absorbing Peaks	Checked
Auto-imported Response(s)	Height, RetentionTime, WidthAt50Pct, USPTailing, WidthAtTangentUSPResolution, Area
Import Chromatogram Trace Data	Checked
Import Prediction Chromatogram Data	Checked
Total Import Time	00:06:42
Locale	English (United States)

## User Access Passwords – Complexity Enhancements

The following password requirement setting options have been added to the current requirement that the password “Must contain at least one digit” to enhance password complexity:

- Must contain at least one upper case and one lower case letter
- Must contain at least one of the following special characters:

~ ! @ # \$ % ^ & \* ( ) \_ - + = ` | \ ( ) { } [ ] : ; < > , . ? /

Change Password Settings for: analyst

User must change password at next login

Prevent duplicate passwords

Password never expires Expiration interval  days

Minimum password length

Must contain at least one digit

Must contain at least one upper case and one lower case letter

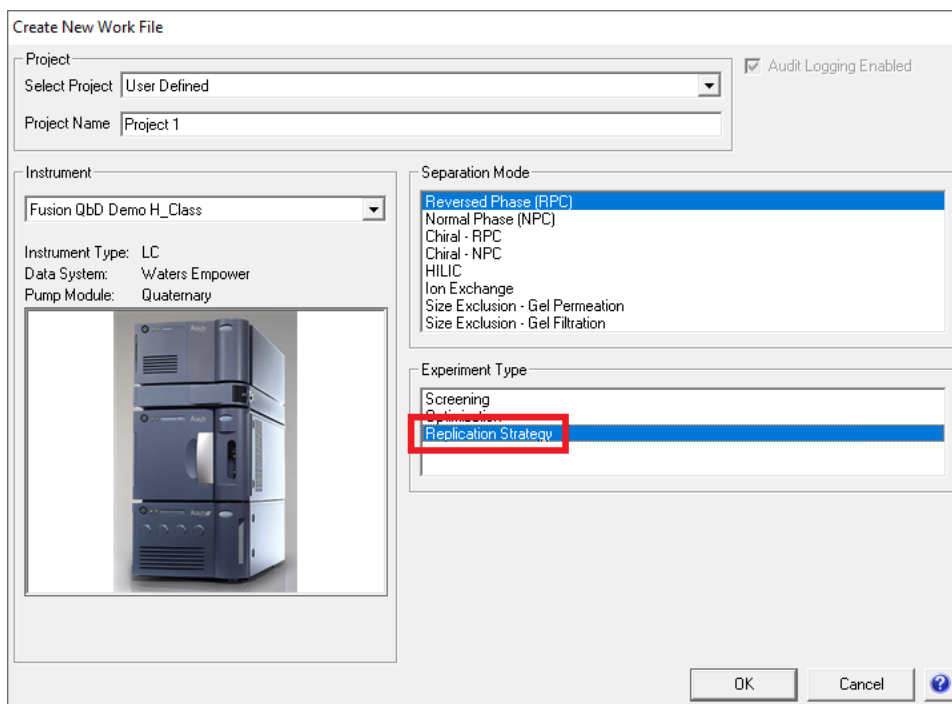
Must contain at least one of the following special characters:  
~ ! @ # \$ % ^ & \* ( ) \_ - + = ` | \ ( ) { } [ ] : ; < > , . ? /

OK Cancel

## Replication Strategy Experiment

**Replication Strategy** is described in the new ICH Q14 and USP <1220> guidances on Analytical Procedure Lifecycle Management (APLM). The optimal **Replication Strategy** for the method is determined during development and becomes part of the final method SOP.

The Fusion Method Development application module (FMD) now includes a **Replication Strategy** experiment. A **Replication Strategy** is a combination of Sample Preparation and Sample Injection repeats (*preparation x injection*). The result obtained from averaging these repeated measures is the **Reportable Value** (or Reportable Result) for each critical method performance characteristic.





The **Replication Strategy** experiment in FMD has the following capabilities:

- Quantifies the relative contribution of Sample Preparation error and Sample Injection error to the Total Analytical Error (TAE), which includes both accuracy (bias) and precision limits.
- Incorporates the USP <1210> Interval metric calculations which combine accuracy and precision into a single criterion which can be used to simultaneously evaluate both accuracy and precision for each measured critical method performance characteristic.
- Determines the TAE and the specified USP <1210> Interval metric associated with all replication strategies from 1x1 to 10x10.
- Identifies all replication strategies which generate reportable values meeting the method precision requirement specified in your Analytical Target Profile (ATP) for each critical method performance characteristic.

# Gradient Time Settings Control

The Experiment Setup activity within FMD now has a flexible settings control for the Gradient Time study factor. Users can now specify the exact number of levels which should be included in the experiment design. Users can also enter the target levels as either slope or time. The control will automatically convert user-entered slope levels as the corresponding time levels which will be used in design generation.

Pump Program

No. of Gradient Steps: 1  Time Precision

No.	Step Name	Time State	Time - Lower Bound	Time - Upper Bound	% Strong Solvent
<input checked="" type="checkbox"/>	1 Equilibration	Constant	3.0	---	5.0
<input checked="" type="checkbox"/>	2 Initial Hold	Constant	1.0	---	5.0
<input checked="" type="checkbox"/>	3 Gradient	Variable	10.0	25.0	---
<input checked="" type="checkbox"/>	4 Final Hold	Constant	1.0	---	95.0
<input checked="" type="checkbox"/>	5 Ramp Up to Wash	Constant	0.5	---	---
<input checked="" type="checkbox"/>	6 Column Wash	Constant	4.0	---	99.0
<input checked="" type="checkbox"/>	7 Ramp Down from Wash	Constant	0.5	---	---
<input checked="" type="checkbox"/>	8 Re-equilibration	Constant	3.0	---	5.0

Program duration: Min = 23.0 minutes, Max = 30.5 minutes

Gradient Study Factor: Gradient Time

Setting Mode  
 Time  
 Slope

**Gradient**

No. of Levels: 3

Time(min)	Slope(%/min)
10.0	9.0
17.5	5.1
25.0	3.6

## Combining Gradient Time and Gradient Slope

As shown in the images below, Fusion QbD now enables the user to create method development and robustness studies which include both Gradient Time and Gradient Slope study factors. In the case of the Gradient Slope study factor, the user can specify varying the starting point or the endpoint % strong solvent. Studies have shown that these factors can have strong interaction effects on shape and selectivity. Therefore, in many cases combining them in a study can provide important method development results.

Pump Program

No. of Gradient Steps:  Time Precision:

No.	Step Name	Time State	Time - Lower Bound	Time - Upper Bound	% Strong Solvent
<input checked="" type="checkbox"/>	1 Equilibration	Constant	3.0	---	10.0-30.0
<input type="checkbox"/>	2 Initial Hold	Constant	1.0	---	10.0-30.0
<input type="checkbox"/>	3 Gradient	Variable	10.0	25.0	---
<input type="checkbox"/>	4 Final Hold	Constant	1.0	---	95.0
<input type="checkbox"/>	5 Ramp Up to Wash	Constant	0.5	---	---
<input checked="" type="checkbox"/>	6 Column Wash	Constant	4.0	---	99.0
<input type="checkbox"/>	7 Ramp Down from Wash	Constant	0.5	---	10.0-30.0
<input checked="" type="checkbox"/>	8 Re-equilibration	Constant	3.0	---	10.0-30.0

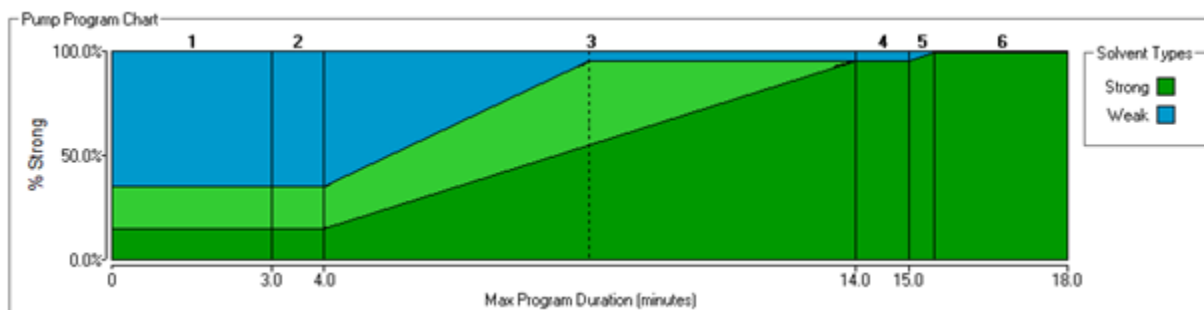
Program duration: Min = 23.0 minutes, Max = 38.0 minutes

Gradient Study Factor: Gradient Slope

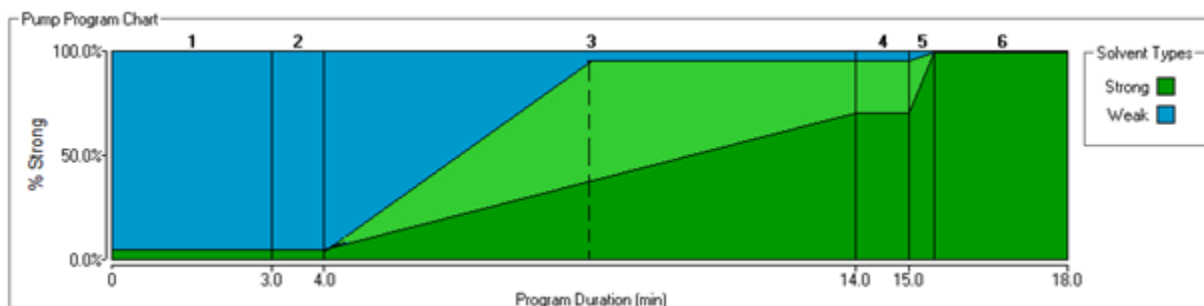
Vary starting point  
 Vary end point

Solvent Type	Initial % Lower	Initial % Upper	Final %
Strong (Organic)	10.0	30.0	95.0
Weak (Aqueous)	90.0	70.0	5.0

### Gradient Time + Gradient Slope – Vary Starting Point % Strong Solvent



### Gradient Time + Gradient Slope – Vary End Point % Strong Solvent



# PeakTracker – New Features

## Global Tracking Method Optimization

Two new simple operations have been added to the PeakTracker popup menu to optimize the Global Tracking Method (GTM) used in peak tracking:

- Add Peak to Global Tracking Method

This option is used when a peak is not visible in the chromatogram on which the GTM is based – for example due to peak co-elution, but which is at least partially separated in another run, and so visible in the run. In this case users can select this option to add the peak to the GTM. This option assures that all sample peaks are included in the GTM prior to tracking.

- Ignore/Track Peak

This option is used when the chromatogram for the run on which the GTM is based contains an integrated peak which the user does not want to track. In this case the user can exclude the peak from the GTM prior to tracking. Alternatively, if a peak was incorrectly excluded, then the option can toggle to include the previously excluded peak, in which case the peak will again be present in the GTM.

The screenshot displays the PeakTracker software interface. It features two chromatograms at the top. The first is a Total Ion Chromatogram (TIC) for Run No. 15, showing peaks at retention times 262.3, 193.1, 336.8, 274.2, 332.2, 288.1, 304.1, and 360.2. The second is a Mass Spectrometry (MS) chromatogram for the same run, showing peaks at 262.2, 193.1, 144.2, 336.8, 274.2, 332.2, 288.1, 304.1, and 360.2. Below the chromatograms is a 'Peak Table' for Run No. 15, which lists peak names, retention times (RT), base peaks, heights, and areas. A red box highlights the 'Add Peak to Global Tracking Method' option in the popup menu. To the right, the 'Global Tracking Method (GTM)' section shows a table of tracked peaks with columns for Run #, Component Name, RT, Area, and Expected Mass values.

Name	RT (min)	Base Peak (m/z)	Height (a.u.)	Area
1	1.037	262.3	973.202	110.123
2			296.881	397.548
3			1,247.109	288.592
4			809.241	332.730
5				
6				
7				
8				

Run #	Component Name	RT	Area	Expected Mass 1	Expected Mass 2	Expected Mass 3	Expected Mass 4	
1	15	262.3	1,037	973.202.2	262.3	263.2	279.1	160.
2	15	193.1	3,061	110.123.2	193.1	215.1	132.1	279.
3	15*	144.2	3,958	17,435.187.9	144.2	190.2	145.3	126.
4	15	336.8	4,656	296.880.8	336.8	672.4	673.3	279.
5	15	274.2	4,926	397.548.5	274.2	275.2	279.0	296.
6	15	288.1	5,122	1,247.108.7	288.1	289.1	126.0	160.
7	15	332.2	5,344	288.591.8	332.2	344.8	126.0	279.
8	15	304.1	5,633	809.240.9	304.1	305.2	326.1	607.
9	15	360.2	7,171	332.729.9	360.2	361.2	279.1	126.

## m/z Filtering for Baseline & Interfering Compounds

Filters can now be added to PeakTracker to eliminate specific m/z values from the imported mass spectra data used for peak tracking. Filter values can be entered for extraneous (background noise) compounds such as mobile phase solvents and their associated adducts which may compromise the mass spectra of compounds of interest, especially in the case of small peaks with low mass signal. The filters enable you to specify the expected compound mass and the possible presence of three common ions: H<sup>+</sup>, Na<sup>+</sup>, and K<sup>+</sup>. PeakTracker will automatically eliminate these masses from the mass spectra data for the Global Tracking Method compounds prior to tracking.

The screenshot displays the PeakTracker software interface. On the left is a vertical list of run numbers from 1 to 30. The main area is divided into three sections:

- Top Section:** A chromatogram plot showing intensity versus time (0.00 to 19.00 minutes). Peaks are labeled with letters B, G, H<sup>+</sup>, API, D-Dep, E, and D.
- Middle Section:** A mass spectrum plot showing intensity versus m/z (0.00 to 19.00). Peaks are labeled with m/z values: 262.2, 198.1, 144.2, 336.8, 274.1, 288.1, 304.1, 330, and 360.2.
- Bottom Section:** A table titled "Peak Table - FDA Ch1 225nm@4.8nm - Run No. 1" and a "Global Tracking Method (GTM) Generated from run 15" configuration panel.

Name	RT (min)	Base Peak (m/z)	Height (µV)	Area
1 B	0.913	262.2	543.625	956.268
2 G	1.949	193.1	237.67	68.671
3 H <sup>+</sup>	3.561	144.1	297.562	19796.498
4 F	4.688	336.8	140.977	293.343
5 A	5.008	274.1	191.463	395.600
6 API	5.261	288.1	565.795	1,227.862
7 D-Dep	5.820	332.1	132.230	259.121
8 E	5.998	304.1	267.964	608.858
9 D	7.908	360.2	157.921	331.059

The "Global Tracking Method (GTM)" configuration panel includes the following settings:

- Number of Masses: 3
- M/Z Precision Limit (+/-): 0.5
- Mass Filters table:

Mass Value (m/z)	Include H <sup>+</sup>	Include Na <sup>+</sup>	Include K <sup>+</sup>
1 41	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
2 82	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>
3 144	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>

Intensity Threshold: 10,000  
[Intensity threshold for MS spectra data import.]

## Tracking Algorithm Enhancements

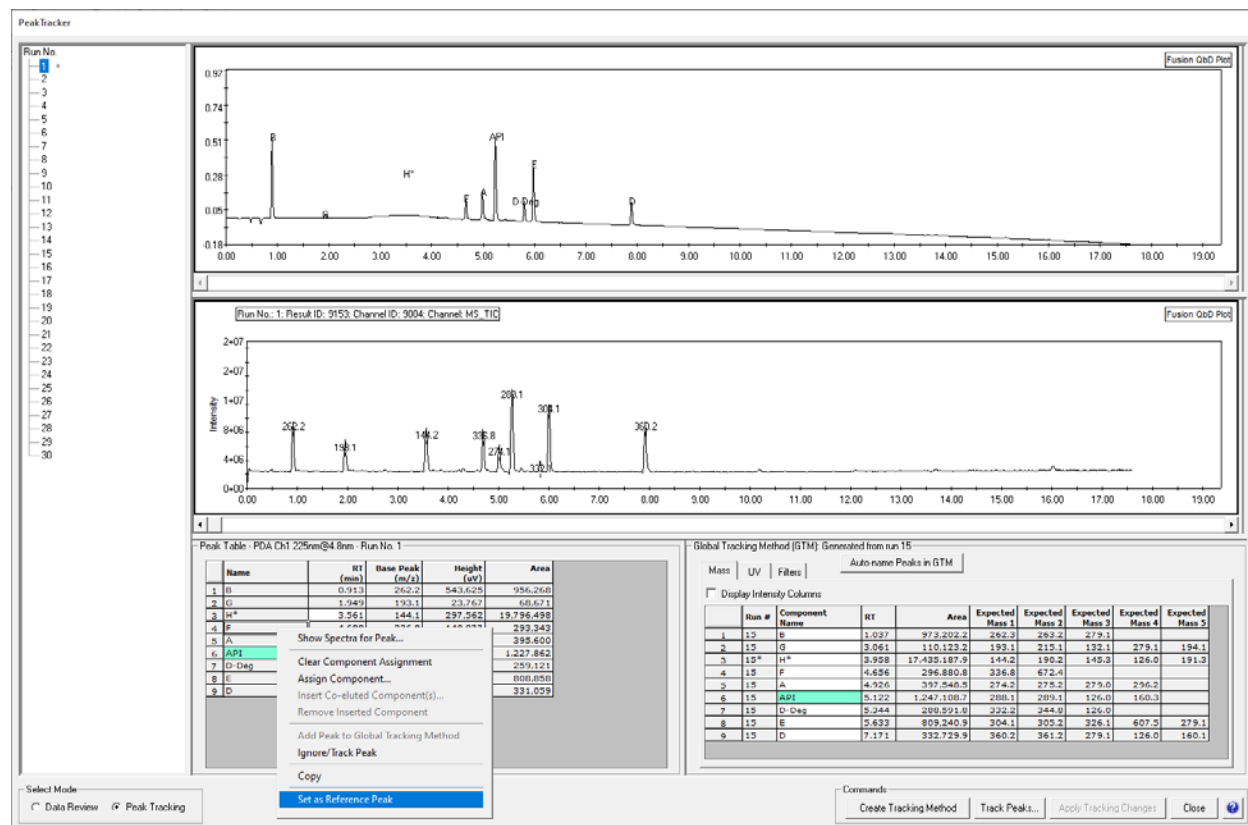
S-Matrix has developed powerful advancements to its peak tracking algorithms which support the following cases:

- Peak results data do not include MS spectra data.
- One or more sample compounds do not ionize.
- Forced Degradation Studies.
- Peptide Mapping studies.

## Reference Peak Designation

In cases such as Peptide Mapping studies there is normally no single, large API peak present in the sample. In such cases it is best if the user can spike the sample with a ‘Reference Peak’ prior to running the experiment. The spiked peak should 1) be substantially larger than all other peaks, and 2) elute in a region of the chromatogram which results in it being always well separated from all other sample compounds. When this is not possible, PeakTracker now enables the user to define an alternate ‘Reference Peak’ to support corrections needed to the tracking for individual chromatograms.

As shown in the image below, the initial tracking operation has defined the API component as the ‘Reference Peak’ – as indicated by the blue background in the corresponding ‘Component Name’ cell within the Global Tracking Method (GTM) grid. However, a new “Set as Reference Peak” function has been added to the popup menu in the ‘Peak Table’ panel whenever a peak other than the current reference peak has the focus. This enables the user to easily designate another peak as the ‘Reference Peak’ and automatically retrack the peaks in the current run.



## **Robustness Simulator – New Features**

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### Mobile Phase Composition (MPC) Variation

Gradient slope variation during method execution is an expression of moment-to-moment Mobile Phase Composition (MPC) variation due to pump precision limits. Gradient Time and Gradient Slope study factors both affect the slope of the gradient. For example, Gradient Time varies the time at constant initial and final % strong solvent. The different time level settings therefore directly equal changes in slope. And Gradient Slope directly varies either the starting point % or endpoint % strong solvent. Therefore, MPC variation is the correct input into robustness simulation to represent slope variation occurring during method execution for Gradient Time and Gradient Slope study factors included in an experiment design.

Users have always been able to directly input the desired MPC variation, for example  $\pm 2.0\%$ , into the Robustness Simulator wizard for each Gradient Slope study factor. However, prior to Version 9.9.2 the user was required to carry out a 2-step calculation procedure for each Gradient Time study factor to convert the desired MPC variation setting into the corresponding time variation for input into the wizard. As shown in the image below, with Version 9.9.2 users can now directly input the desired MPC variation as a single global entry into the Robustness Simulator wizard. For Gradient Time study factors the software will automatically convert the desired MPC variation setting into the corresponding time variation for the simulation and then associate the single input with each Gradient Time and Gradient Slope study factor in the design.



**Robustness Simulator**

**Maximum Expected Variation ( $\pm 3\sigma$ ):**

The  $\pm 3\sigma$  value defines the "total" setpoint error. This is the maximum variation around a given setpoint expected during ongoing use over time due to random error.

**Maximum Expected Variation Around Setpoint for Each Variable**

**IMPORTANT:** Use manufacturer's specs for the setpoint Control Limit value or extend it based on the least-capable system in use.

---

**Variable Settings**

Enabled	Experiment Variable	Units	Maximum Expected Variation ( $\pm 3\sigma$ Value)
<input checked="" type="checkbox"/>	Pump Flow Rate	mL/min	0.010
<input checked="" type="checkbox"/>	Oven Temperature	$^{\circ}\text{C}$	2.0
<input checked="" type="checkbox"/>	pH	*	0.10
<input checked="" type="checkbox"/>	Mobile Phase Composition (MPC)*	%	2.0

\* MPC variation is composition (blend) variation due to pump precision limits. A commonly used  $\pm 3\sigma$  value =  $\pm 2.0\%$ .  
 The value you enter will be applied to all Gradient Slope factors (e.g., Time, Slope, and Ramp Steps) in the experiment design.

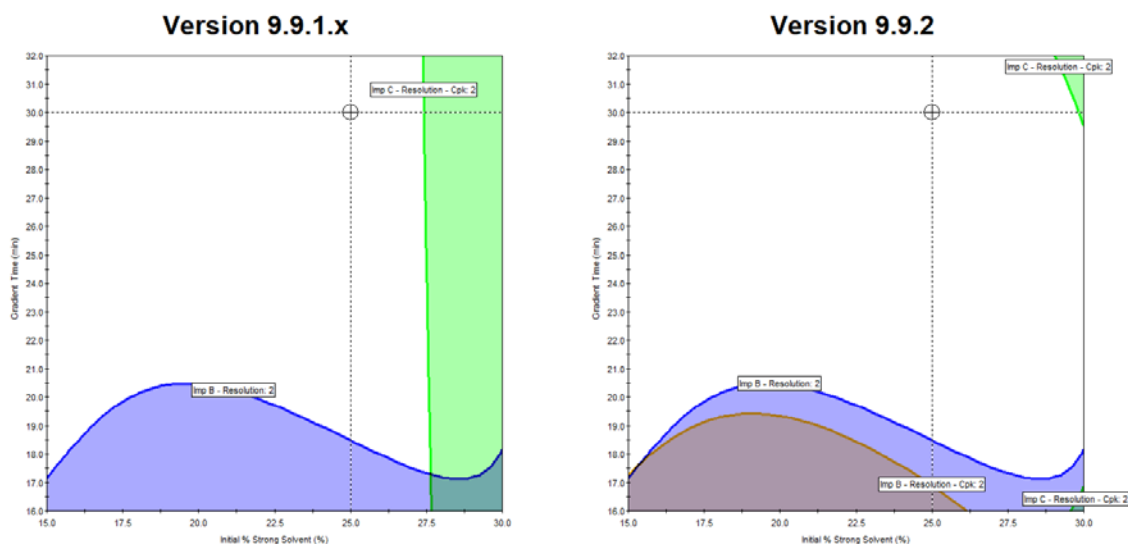
Use MPC Mode

The settings are valid.

## Modeling Advancement – Resolution Robustness

S-Matrix has adapted its hyper-precise resolution modeling capabilities to its Robustness Simulator for robustness simulation of the Rs-Map Resolution response and of individual peak resolutions. This has resulted in a powerful advancement to the precision associated with resolution robustness predictions – especially in experimental regions corresponding to methods which yield results close to edges of failure for one or more peak resolutions.

The two graphs below show the mean (average) resolution and the corresponding resolution robustness of two critical peak pairs (B–A and C–E) obtained from Version 9.9.1.x (left graph) and from Version 9.9.2 (right graph). In both graphs the resolution performance requirement for each critical pair was set to a mean (average) resolution of  $\geq 2.00$  and a minimum acceptable resolution threshold for individual injections of  $\geq 1.50$ . A comparison of the two graphs shows that Version 9.9.1.x (left graph) over predicted the resolution robustness of the B–A peak pair at the lower end of the Gradient Time study range (no orange shaded region). This is evidenced by the fact that the orange robustness failure region for the B–A peak pair, which is present in the right graph, is more closely aligned with the corresponding mean performance failure region (blue shaded region). The two graphs also show that Version 9.9.1.x under-predicted the resolution robustness of the C–E peak pair at the upper end of the Initial % Strong Solvent study range. This is evidenced by the large robustness performance failure region for the C–E peak pair in the left graph (green shaded region) and reinforced by the fact that the mean resolution of the C–E peak pair is  $> 2.00$  throughout the graphed region (no red shaded regions in either graph).



# Verification Runs – Full Automation and Reporting Support

Fusion QbD now provides full closed-loop CDS automation and reporting support for experiment verification runs. As shown in the top image below, users can now select an Acceptable Performance Region report containing verification runs and generate a report containing predicted results and graphs for these runs. Users can then export them directly to the CDS as a ready-to-run Prediction sequence and methods. As shown in the bottom image below, when the user runs the sequence and processes the chromatograms in the CDS, Fusion QbD can then import the verification run chromatograms and data and integrate them into the report.

Point Predictions Wizard

Report Name: Verification Runs Report

Starting Point Options:

User Defined

No. of Prediction Points: 1

Acceptable Performance Region Verification Runs

Reports: Verification Runs

Include	Verification Run
<input checked="" type="checkbox"/>	APR_2_1
<input checked="" type="checkbox"/>	APR_2_2
<input checked="" type="checkbox"/>	APR_2_3
<input checked="" type="checkbox"/>	APR_2_4
<input checked="" type="checkbox"/>	APR_2_5

Select All | Select None

Included Responses

Prediction Confidence Limits: ±2 Sigma

Include	Response Name
<input type="checkbox"/>	Rs-Map Response
<input type="checkbox"/>	B - USP Resolution
<input type="checkbox"/>	G - USP Resolution
<input type="checkbox"/>	H* - USP Resolution
<input checked="" type="checkbox"/>	F - USP Resolution
<input checked="" type="checkbox"/>	A - USP Resolution
<input checked="" type="checkbox"/>	API - USP Resolution
<input checked="" type="checkbox"/>	D-Deg - USP Resolution
<input checked="" type="checkbox"/>	E - USP Resolution
<input type="checkbox"/>	D - USP Resolution
<input checked="" type="checkbox"/>	API - USPTailing
<input checked="" type="checkbox"/>	B - KPrime

Select All | Select None

#	Run No.	Pump Flow Rate	Gradient Time	Oven Temperature	pH
1	APR_2_1	0.450	12.00	48.00	3.700
2	APR_2_2	0.450	12.00	48.00	3.900
3	APR_2_3	0.450	12.00	42.00	3.700
4	APR_2_4	0.450	12.00	42.00	3.900
5	APR_2_5	0.450	12.00	45.00	3.800

Validation Status: Your settings are valid.

Include Observed Values  Include Prediction Chromatograms

Add Named Peak Rs Responses... | Finish | Cancel

Method Development - Optimization - Part 1 - Verification Runs.mae

File Edit Activity Tools Window Help

Generate Predictions Delete Report **Export** Import Responses

Point Predictions Reports

Verification Runs Report | PP 2 | Report Chromatograms...

Name: Administrator  
Company: S-Matrix Corporation  
Project: Project 1  
Date: 24 NOV 2022 16:13:47 PST [UTC-08:00]

**Point Predictions - Verification Runs Report**

**Predicted Point - APR\_2\_1**

**Variable Settings**

Name	Level Setting	Units
Pump Flow Rate	0.450	mL/min
Gradient Time	12.00	min
Oven Temperature	48.0	°C
pH	3.70	°

## Intermediate Precision and Reproducibility (IP&R) Advancements

Prior to Version 9.9.2, the Validation Acceptance Criteria (VAC) settings for IP&R experiments were located on the main Experiment Setup display, and these settings were global – meaning the same settings were used for all compounds. As shown in the image below, the analysis wizard now contains the VAC settings, and the settings are now compound specific – meaning that users can now set independent VAC criteria for each compound included in the analysis.

The screenshot displays the 'Small Molecule Data Analysis' window. At the top, a dropdown menu labeled 'Select Response for Analysis' is set to 'API - Amount'. Below this, the 'Perform Data Analysis' section is checked. Underneath, the 'Validation Acceptance Criteria' section is expanded, showing several options: 'Intermediate Precision (Std. Dev. <=)' is unchecked; 'Intermediate Precision (% RSD <=)' is checked with a value of 2.00; 'Repeatability (Std. Dev. <=)' is unchecked; 'Repeatability (% RSD <=)' is checked with a value of 5.00; 'Reproducibility (% RSD <=)' is checked with a value of 2.00; and 'USP Ruggedness (% Effect <=)' is checked with a value of 10.00. The 'Confidence Interval and Max. Allowable Limit Settings' section shows '% C.I. for Mean' and '% C.I. for Std. Dev.' both set to 95.00, and 'Maximum Limit' checked with a value of 0.08. A 'Set Defaults' button is located at the bottom left of the settings area. A status bar at the bottom indicates 'The settings are valid.' and navigation buttons for 'Back', 'Finish', and 'Cancel' are at the bottom right.

In addition, as shown in the image above, the IP&R analysis wizard now also contains Repeatability VAC settings. When the user enters VAC values, Fusion QbD automatically performs a full Repeatability analysis, and the report will contain the Repeatability analysis results within the Intermediate Precision and Repeatability Results table shown below.

**Intermediate Precision and Repeatability Results**

<b>Name</b>	<b>Value</b>	<b>Pass/Fail</b>
Intermediate Precision Variance	0.003	
Intermediate Precision Std. Dev.	0.054	---
Intermediate Precision Upper 95% C.I.	0.078	
Intermediate Precision Lower 95% C.I.	0.042	
Intermediate Precision % RSD	1.06	Pass
Repeatability Variance	0.001	
Repeatability Std. Dev.	0.027	---
Repeatability Upper 95% C.I.	0.045	
Repeatability Lower 95% C.I.	0.019	
Repeatability % RSD	0.52	Pass

**Acceptance Criterion: Intermediate Precision % RSD <= 2**

**Acceptance Criterion: Repeatability % RSD <= 5**

# New Features in Fusion Inhaler Testing (FIT) – 9.9.2

## Product Testing Configuration – Automated LOQ Calculations

Prior to Version 9.9.2, users had to manually calculate the individual apparatus stage LOQ values for each compound manually and enter the values into the LOQ column within the “Impactor Sample Properties” grid. Now Fusion Inhaler Testing will automatically calculate the individual apparatus stage LOQ values for each compound based on 1) the Compound LOQ value, and 2) “Dilution Factor” value associated with the stage.

The screenshot displays the 'Product Testing Configuration' window. It is divided into several sections:

- General Settings:** Includes 'Configuration Name' (Default Config\_USP5), 'Sampling Flow Rate' (60.00 L/min), 'Dose Delivery Mode' (Oral), and 'Mass Balance Calculation Method' (Uniformity).
- Data Treatment Settings:** Includes 'Missing Peaks' (Use Zero) and 'Data Below LOQ' (Use Zero).
- Compound Data Settings:** Shows 'Number of Compounds' (2) and a table with columns for Compound Name, Unit, LOQ, and Uniformity. The LOQ column is highlighted in blue.
- Impactor Sample Properties:** A table with columns for Stage Name, Stage Type, Dilution Factor, LOQ - API 1, LOQ - API 2, and LOQ Precision. The LOQ - API 1 and LOQ - API 2 columns are highlighted in blue.

Compound Name	Unit	LOQ	Uniformity
API 1	µg	0.175	35.000
API 2	µg	0.175	12.500

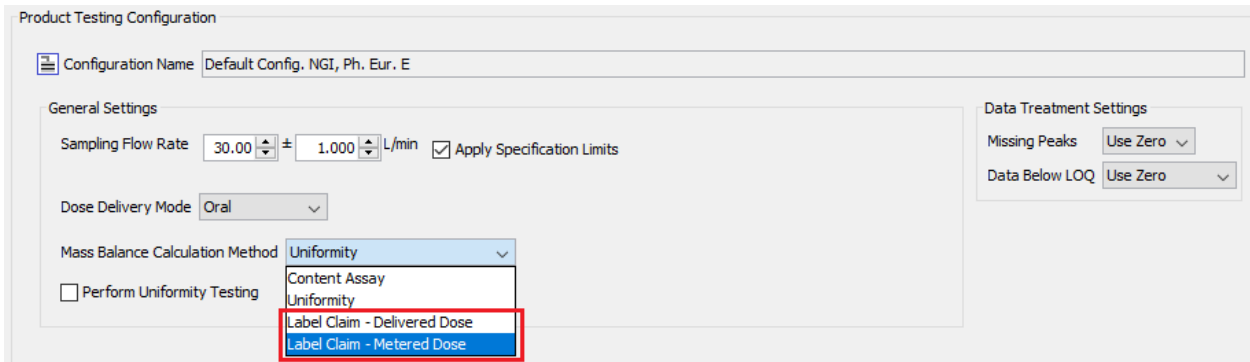
  

Stage Name	Stage Type	Dilution Factor	LOQ - API 1	LOQ - API 2	LOQ Precision
Device	Device	1.000	0.175	0.175	0.180
Throat	Apparatus	3.000	0.175	0.175	0.180
Preseparator	Apparatus	3.000	0.175	0.175	0.180
Stage 1	Apparatus	2.000	0.175	0.175	0.125
Stage 2	Apparatus	2.000	0.175	0.175	0.125
Stage 3	Apparatus	2.000	0.175	0.175	0.125
Stage 4	Apparatus	2.000	0.175	0.175	0.125
Stage 5	Apparatus	2.000	0.175	0.175	0.125
Stage 6	Apparatus	2.000	0.175	0.175	0.125
Stage 7	Apparatus	2.000	0.175	0.175	0.125
NDC	Apparatus	1.000	0.175	0.175	0.063

# New Mass Balance Calculation Method Options

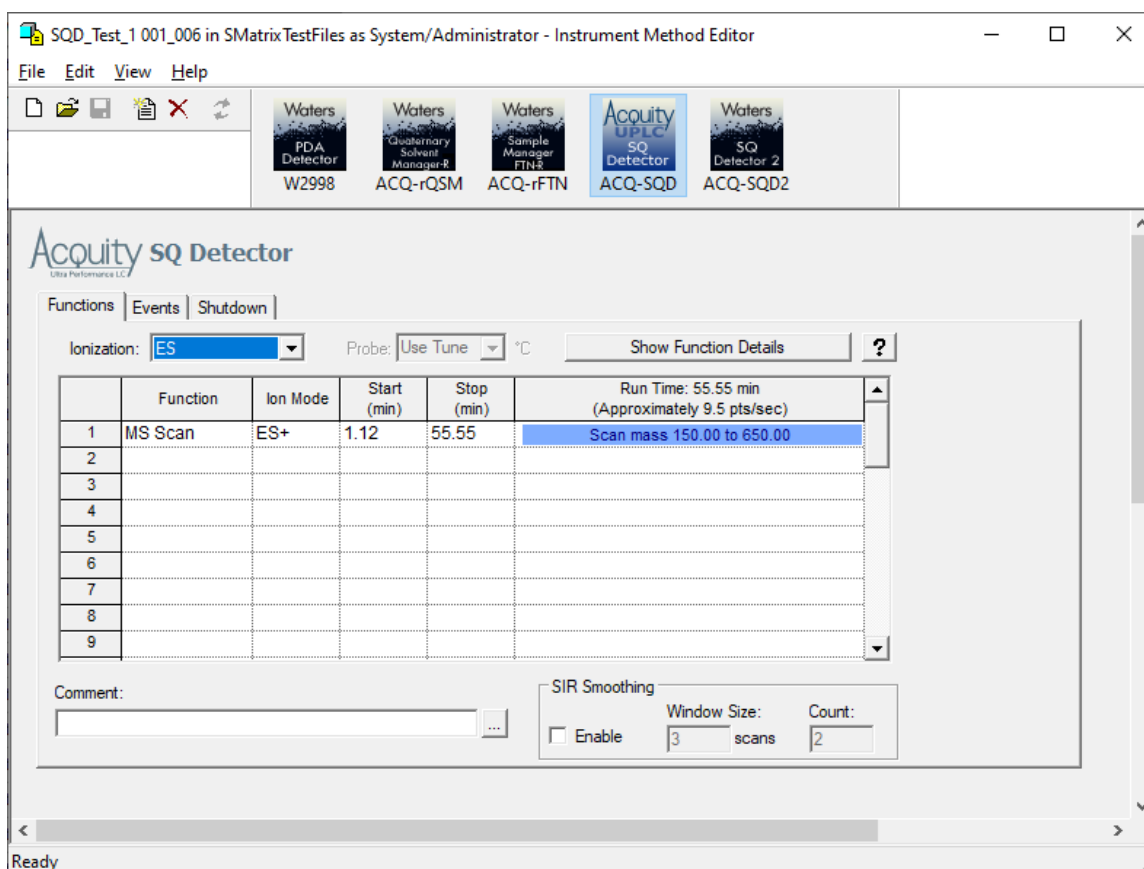
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In Version 9.9.2 the main Product Testing Configuration setup display contains two new mass balance calculation options: **Label Claim – Metered Dose** and **Label Claim – Delivered Dose**. Fusion Inhaler Testing calculations and reporting operations now include support for these new mass balance calculation options.



## Empower CDS – SQD and SQD2 Support

Fusion QbD now automatically updates the “**Start**” and “**Stop**” time settings in the Functions tab grid within Empower instrument methods for both the **SQD** and **SQD2** Mass Detectors supported by Empower to those required by the individual experiment runs based on the pump program settings within Experiment Setup. This assures that MS detection is activated, and coordinated with UV detection, to support MS spectra based peak tracking in Fusion QbD.





## Chromleon CDS – External Solvent Selection Valve Support

Fusion QbD now supports the flexible configuration (2-position to 15-position) solvent selection valve drive (Dionex-Ext-SSV). As shown in the image below, users can now easily configure the specific valve configuration on their LC system within Fusion Administrator.

