



Byosphere Software Release Notes

October 2025

5.11

Protein Metrics LLC, Boston, Massachusetts, USA

Contents

- Protein Metrics Byosphere Software Release Notes3
 - Release 2025-10 (v5.11)3
 - Byosphere Web3
 - Deep Query4
 - Web Analysis6
 - Release 2025-07 (v5.10)18
 - Byosphere Desktop Client18
 - Deep Query Dashboards Usability Enhancements18
 - Additional Deep Query improvements22
 - Web Analysis23
 - Release 2025-04 (v5.9)25
 - Byosphere25
 - Virtual Client, Byosphere26
 - Web Analysis, Byosphere27
 - Deep Query, Byosphere31

Protein Metrics Byosphere Software Release Notes

Byosphere®, Byos®, MS/MS Analysis (Byonic™), Peptide Analysis (Byologic®), Chromatogram Analysis (Byomap™), Intact Analysis (Intact Mass™), Supernovo™, Footprint™, and Preview™.

For new features in the Byos application, see **Byos 01 Software Release Notes.pdf**.

Release 2025-10 (v5.11)

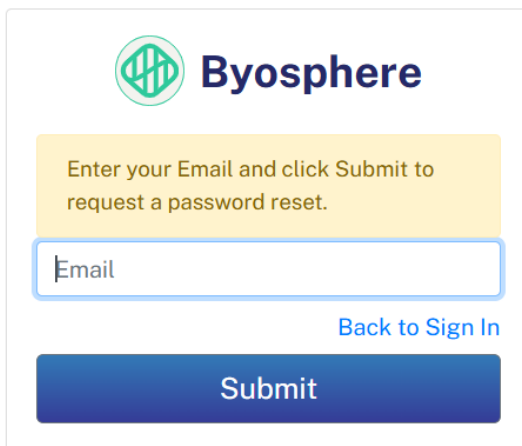
Byosphere Web

- **New minimum password length of 16 characters**

New user passwords must consist of a minimum of 16 characters for enhanced security.

- **Update to password reset form**

The password reset form now requires users to enter their email address in addition to the new password. Password reset links sent to users will now also expire after 15 minutes.



- **The Acquired On metadata field is now mapped for additional vendors**

The Acquired On metadata field now maps to corresponding values from the following vendors:

Byosphere metadata filed	Vendor metadata filed from which we get the value	Vendor
"Acquired On"	"Run date"	Thermo, Sciex, Sciex2
"Acquired On"	"Run date" + "Lynx.ACQUIRED_TIME"	Waters

- **Publishing a Web Analysis now triggers a Deep Query import job**

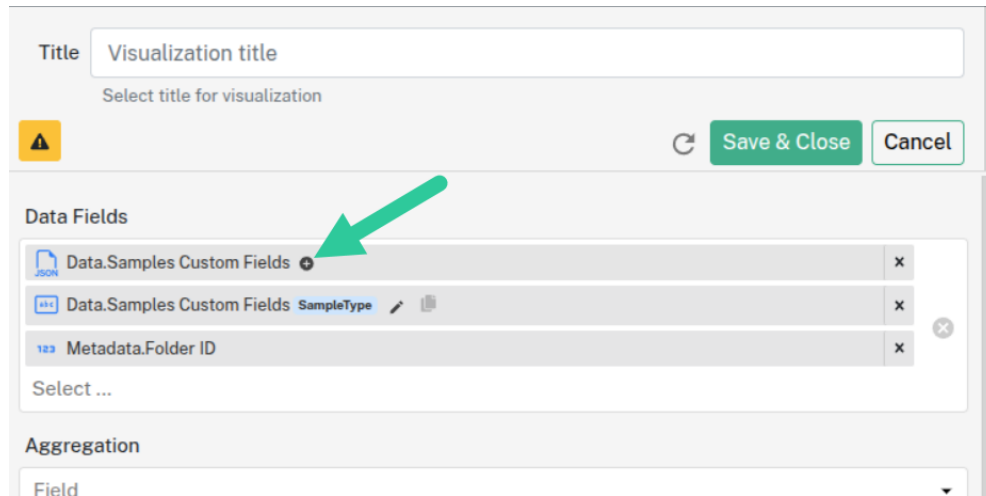
Publishing a Web Analysis will now generate a Deep Query Import job associated with the analysis that can be seen within the Jobs page.

👁	3779	doc_7770_1_test.wa	Completed	DQ Import
⋮	3774	Sample Test 1	Failed	Analysis

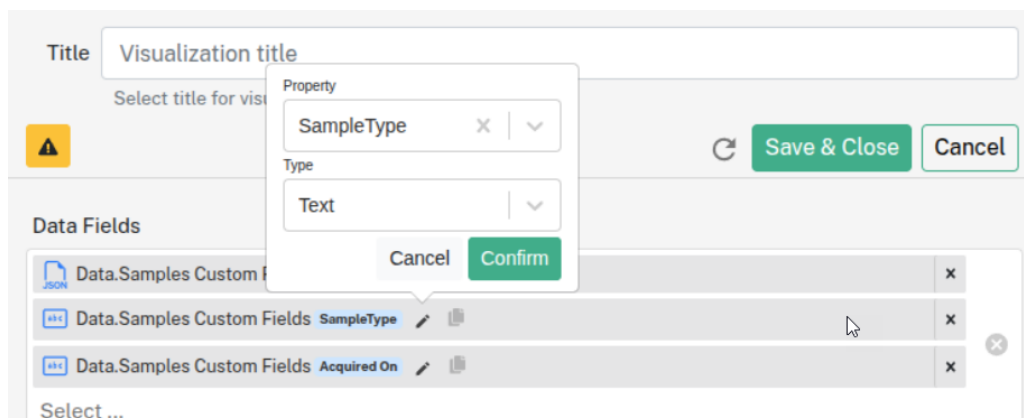
Deep Query

- **Users can now parse individual fields from “Custom Fields” to use in querying, filtering, visualization, and calculations.**

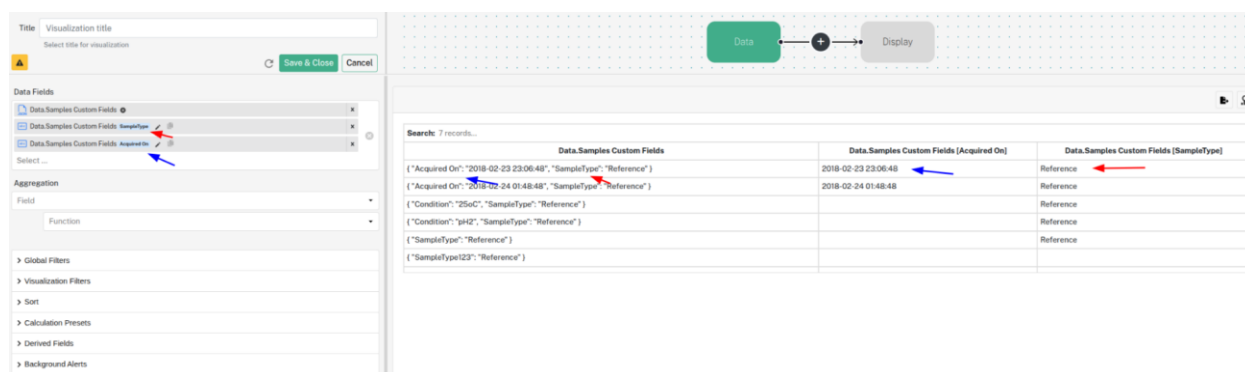
Users can parse individual fields from “Data.Samples Custom Fields” to use in querying, filtering, visualization, and calculations. A plus sign icon displayed next to this field indicates the ability to parse.



Clicking on this icon will open a dialog box. Within this dialog box, users can designate the property (the metadata value to parse out, based on which are available in the field) and type (Text, Date, Numeric).



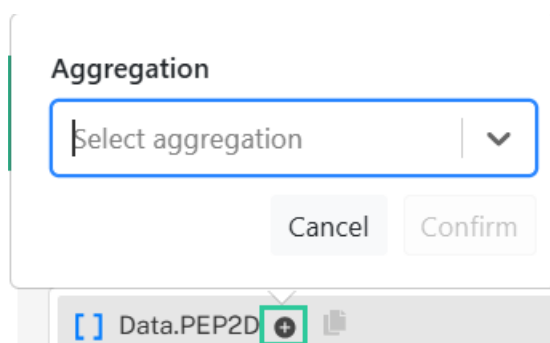
The image below shows the mapping between parsed fields and fields available within Data.Samples Custom Fields and their subsequent parsing as individual fields as the last two columns in the table.



Once a field has been created, it will remain present as a field option in the dropdown for that Visualization.

- **Users can now select different types of aggregation for numerical data fields**

When applicable, users can select an aggregation type for their numerical list field. Aggregation options include Min, Max, Average, and Sum.



Once an aggregation is selected, it is listed next to the field in brackets.

ame List	Data.Delta Score [MAX]	Data.Optimal Score [MIN]	Data.PEP1D [AVG]	Data.PEP2D [SUM]
	290.14224948806	270.231268112686	0.0034364599059979	0.0024349652893702

- **Three additional fields have been added to the Biophysical Data Source**

Three additional fields have been added to the Biophysical Data Source. These fields were originally present in other data sources:

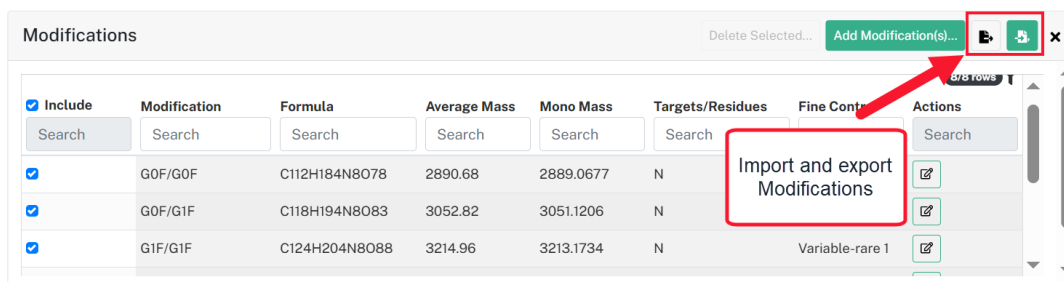
- Peptide Samples Custom Fields (from Peptide projects)
- Intact Samples Custom Fields (from Intact projects)
- Chromatogram Samples Custom Fields (from Chromatogram)







- **Two additional fields have been added to the Combined Data Source**
 - The data field **Peak Label** has been added to the Combined Data Source so that users can query using peak numbering that matches the peak numbering present in Byos.
 - The data field **Samples Custom Fields** has been added to the Combined Data Source so that users can query off of custom fields originating from Intact, Peptide, and Chromatogram projects within the Combined Data Source.
- **A new field has been added to the Intact Data Source**
The field **Protein Alias Name** has been added to the Intact Data Source.
- **Three additional fields derived from parsed out Glycan data are now available in the Combined Analysis Data Source**
Three additional fields containing parsed out Glycan data are now available in the Combined Analysis Data Source, including the following:
 - **Glycan Label**
 - **Glycan Alias**
 - **Glycan Adduct**


Note that these fields were previously only available within the Chromatogram Data Source.

Web Analysis

- **The contents of the Modifications widget are now importable/exportable as a CSV file**
Users can now export the values within the Modifications table as a CSV file.



Include	Modification	Formula	Average Mass	Mono Mass	Targets/Residues	Fine Cont	Actions
<input checked="" type="checkbox"/>	G0F/G0F	C112H184N8O78	2890.68	2889.0677	N		 
<input checked="" type="checkbox"/>	G0F/G1F	C118H194N8O83	3052.82	3051.1206	N		 
<input checked="" type="checkbox"/>	G1F/G1F	C124H204N8O88	3214.96	3213.1734	N	Variable-rare 1	 

Clicking on  will open a dialog allowing the user to specify a folder within the Byosphere server where they wish to export a CSV file containing the currently populated values within the Modifications table.

Select folder and file name



Select modification file to import

<input type="checkbox"/>	ID	File Alias	File Name
<input type="checkbox"/>	8765	CSV modf	CSV modf.csv

Modifications (*.csv)

Select Modification

Cancel

- **Updates to the Iso-Resolved template**

The **Iso-Resolved** Web Analysis template has been updated with the following changes:

- Expected Mono Mass has been added to the **Expected Mass-Mass Accuracy (Da)** Visualization in Charts and Tables
- Additional fields have been added to the Visualization, including: Mono Mass, Expected Mono Mass, Delta Mono Mass, Delta Mono Mass (PPM), and Average Mass
- Expected Mono Mass has been added to the **All Mass- Intensity** Visualization in Charts and Tables
- Additional fields have been added to the Visualization, including Mono Mass and Expected Mono Mass. Additionally, Expected Average Mass was removed.

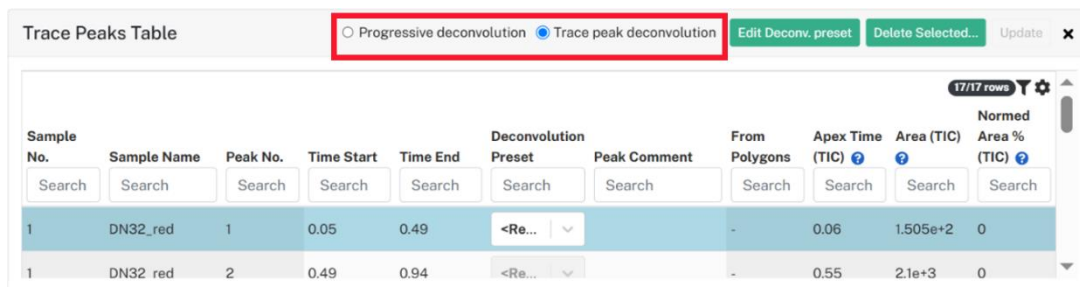
- **New Progressive Deconvolution mode in Web Analysis**

Progressive Deconvolution mode is now available as an alternative data processing pathway for Mass Deconvolution.

Using Progressive Deconvolution mode, users can:

- Monitor the separation of proteoforms by retention time that are not separated by mass (e.g., Glycoforms)
- Identify low level contaminants that are not otherwise visible
- Utilize enhanced capabilities for visualizing co-eluting proteoforms
- Allow quantitation via Neutral/Deconvolved Mass XIC AUC

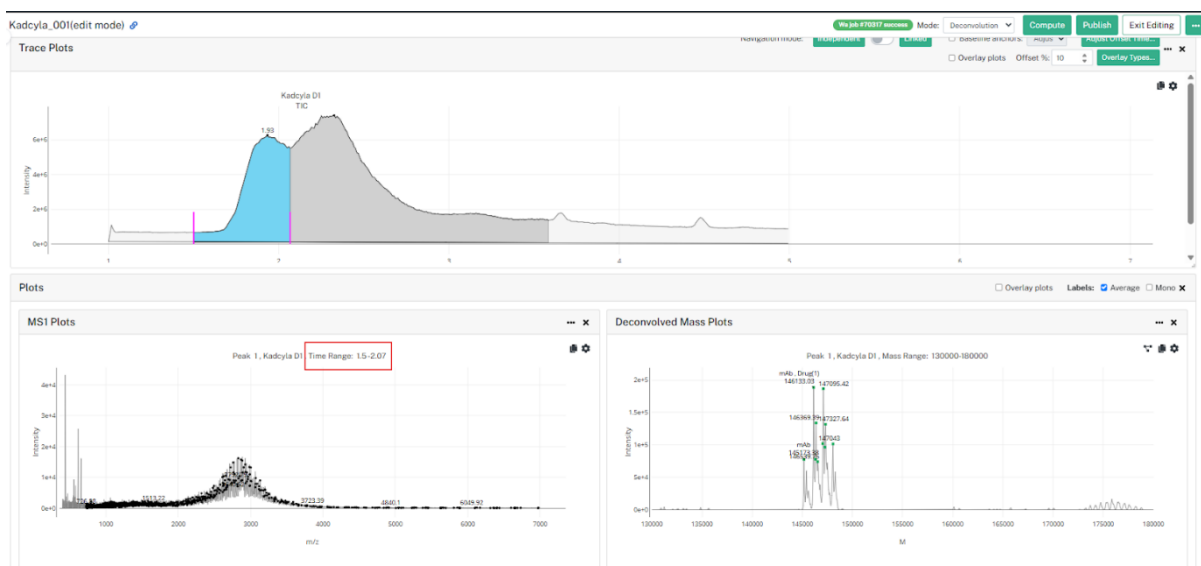
Progressive Deconvolution mode can be toggled by the user from a radio button within the header of the Trace Peaks table. Users have the option to perform either Progressive Deconvolution or Trace Peak deconvolution (the default mode up until this release). If the user selects either mode of deconvolution, this setting will persist in saved projects and templates. The new **Progressive Deconvolution** template will utilize this mode by default.



The screenshot shows the 'Trace Peaks Table' interface. At the top, there are two radio buttons: 'Progressive deconvolution' (unselected) and 'Trace peak deconvolution' (selected). To the right of these buttons are three buttons: 'Edit Deconv. preset', 'Delete Selected...', and 'Update'. Below the buttons is a table with the following columns: Sample No., Sample Name, Peak No., Time Start, Time End, Deconvolution Preset, Peak Comment, From Polygons, Apex Time (TIC), Area (TIC), and Normed Area % (TIC). The table contains two rows of data. The first row is highlighted in blue and corresponds to peak 1 of sample DN32_red, with a time range of 0.05 to 0.49 minutes. The second row is grey and corresponds to peak 2 of sample DN32 red, with a time range of 0.49 to 0.94 minutes.

Sample No.	Sample Name	Peak No.	Time Start	Time End	Deconvolution Preset	Peak Comment	From Polygons	Apex Time (TIC)	Area (TIC)	Normed Area % (TIC)
1	DN32_red	1	0.05	0.49	<Re...		-	0.06	1.505e+2	0
1	DN32 red	2	0.49	0.94	<Re...		-	0.55	2.1e+3	0

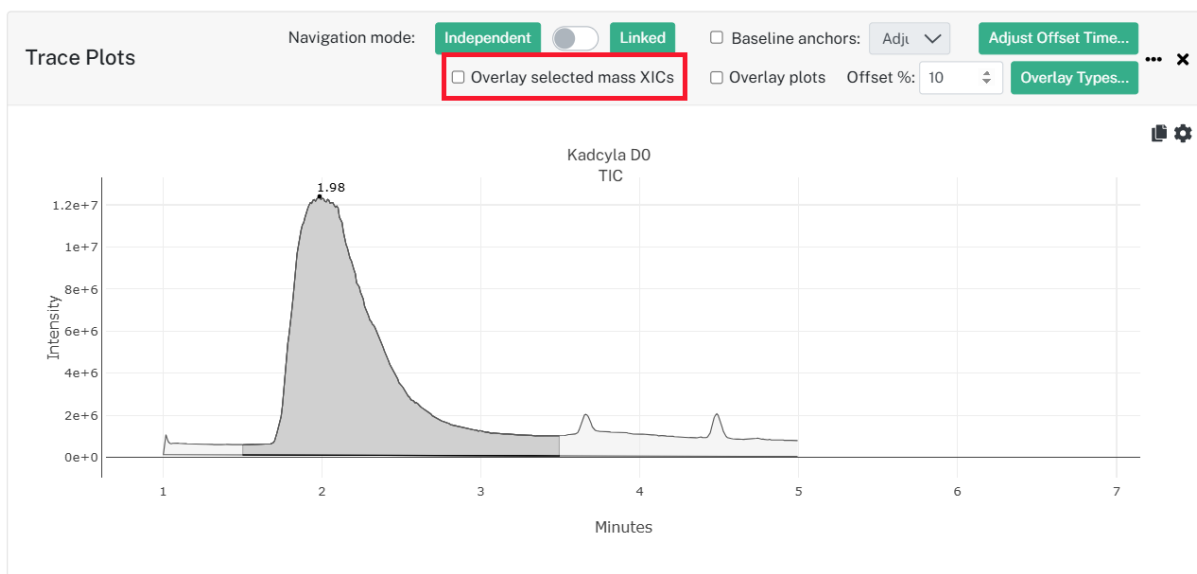
For example, when a user selects **Trace Peak Deconvolution**, the range used for deconvolution is directly associated with the range from trace peak integration. The figure below shows the range for the MS1 plot corresponds with the highlighted peak, where the time range is 1.5-2.07 minutes.



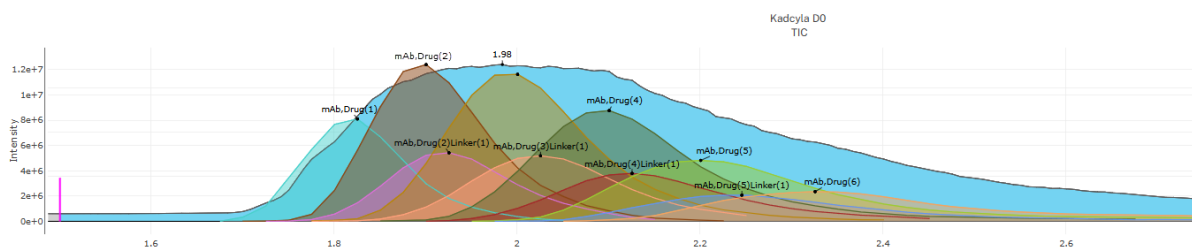
When a user selects **Progressive Deconvolution**, deconvolution is no longer restricted to the integrated trace peaks. Instead, a user may specify windows to produce multiple slices for deconvolution. They may also specify an overlap between these windows. In this way, Deconvolution is no longer restricted to integrated trace peaks and may be applied across an entire trace. These settings may be accessed via the Deconvolution Presets in the inspection room, or by using the new Progressive Template available as a system resource default template in Web Analysis.

Progressive Deconvolution mode utilizes the **sliding window deconvolution** approach, which creates narrow sliding overlapping time windows and performs deconvolution iteratively on sequential time ranges. Masses observed across stretches of consecutive slices are grouped together to identify mass features. Isomers are distinguished based on the differential elution profiles and reported separately. **Mass XICs** (Extracted Ion Chromatograms) are available to display on the trace plot. Either the AUC (Area Under the Curve) or apex intensity for each Mass XIC may be for feature quantitation.

Users can overlay selected mass XICs on the corresponding traces so that they can be compared by checking the “Overlay selected mass XICs” box in the Trace Plots header.



Result:



Settings to generate slices may be applied over the entire time range or be restricted to a time of interest as set in the Trace Peak Integration Settings in the Samples Room.

The **Progressive Deconvolution** tab within the Deconvolution Parameters is outlined below:

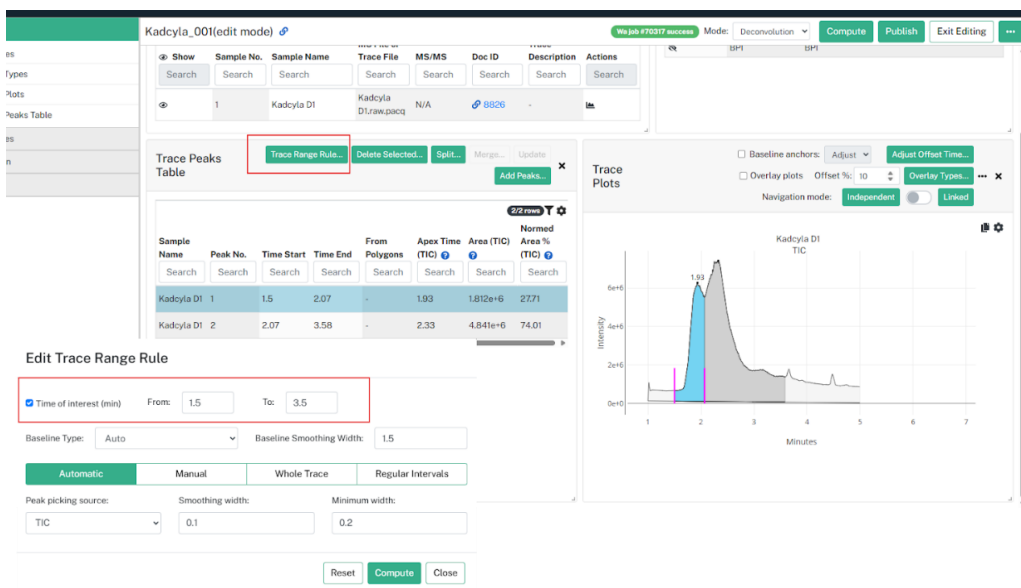
Deconvolution

Parameters applied to the deconvolved spectra.

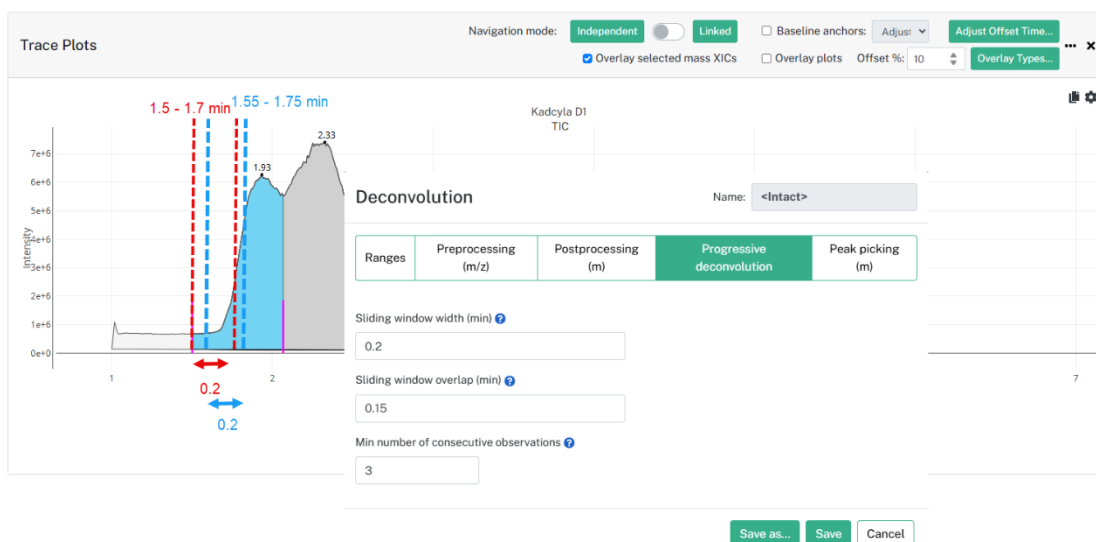
Ranges	Preprocessing (m/z)	Postprocessing (m)	Progressive deconvolution	Peak picking (m)
<p>Sliding window width (min) <input type="text" value="1"/></p> <p>Sliding window overlap (min) <input type="text" value="0.5"/></p> <p>Min number of consecutive observations <input type="text" value="3"/></p>				
<p><input type="button" value="Save as..."/> <input type="button" value="Save"/> <input type="button" value="Cancel"/></p>				

- **Sliding window width:** Width of the deconvolution sliding window applied across time range to perform progressive deconvolution. This will be the width of each deconvolution slice.
- **Sliding window overlap:** Time overlaps between consecutive deconvolution slices (windows) for progressive deconvolution.
- **Min number of consecutive observations:** Minimum number of same mass observations to generate deconvolved mass feature. For example, if this value is set to 3, then the same mass must be observed in 3 consecutive windows/slices. The aim of this is to reduce noise. It is suggested that the number is decreased if the sliding window overlap results in < 3 slices generated across the time range of trace peaks.

The example below outlines the result of these settings being configured. In the example below, a time range of interest from 1.5-3.5 minutes was specified, and Trace Peak integration was performed, resulting in two integrated peaks from the TIC trace:



The next figure outlines how the first two slices are calculated and applied when using the default settings in the progressive deconvolution template:



Each slice window in this example is **0.2**. Since the Time Range of interest was set at **1.5-3 minutes**, the first slice will start at **1.50** and end at **1.70** ($1.50 + 0.2 = 1.70$). The overlap was set to **0.15**, so the second slice will overlap the previous slice by **0.15 minutes**, starting at **1.55 minutes** (this is calculated by subtracting the overlap value from the end time of the slice, in this case, $1.70 - 0.15 = 1.55$ minutes).

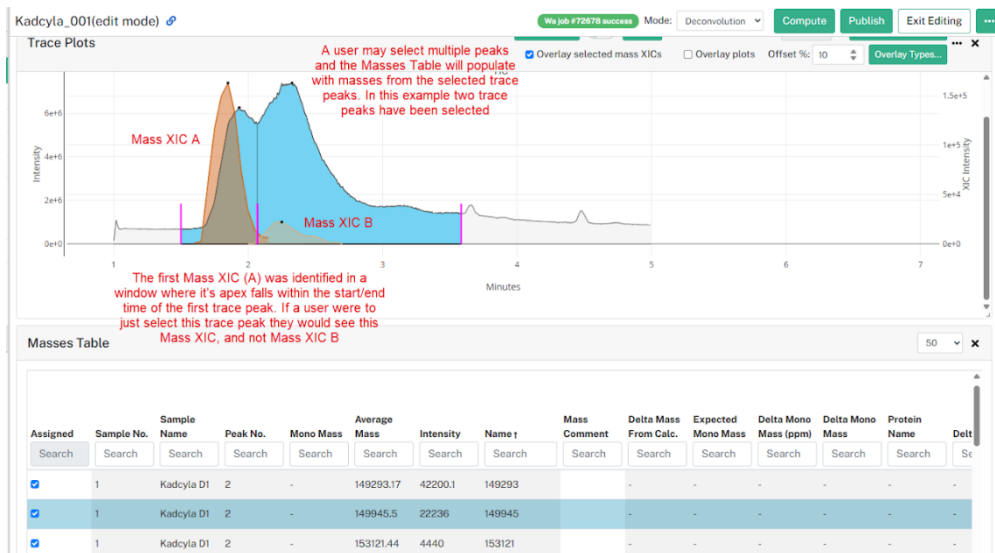
Again, as the window is set to 0.2, the second slice will end at **1.75**, making the time range of the second slice **1.55 - 1.75 minutes** ($1.55 + 0.2 = 1.75$). Deconvolution will be performed on *each* slice using the deconvolution parameters specified in the preset tab. The table below shows all the slices that would be generated in this example:

Slice Start Time	Slice End Time
1.50	1.70
1.55	1.75
1.60	1.80
1.65	1.85
1.70	1.90
1.75	1.95
1.80	2.00
1.85	2.05
1.90	2.10
1.95	2.15
2.00	2.20
2.05	2.25
2.10	2.30
2.15	2.35
2.20	2.40
2.25	2.45
2.30	2.50
2.35	2.55
2.40	2.60
2.45	2.65
2.50	2.70
2.55	2.75
2.60	2.80
2.65	2.85
2.70	2.90
2.75	2.95
2.80	3.00

As a rule, the default parameters in the Progressive Deconvolution Template are a good starting point for fully intact mAb data.

To view the masses identified and spectra associated with slices from performing Progressive Deconvolution, a trace peak(s) from the trace peaks table must be selected. This will populate the masses table with all masses that were identified and have generated a mass XIC (Extracted Ion Chromatogram) where the apex of that XIC is within the boundaries of that trace peak.

Users can select more than one trace peak at a time and the Masses table will populate with masses from all selected peaks. The mass value reported is an aggregation of masses for that Mass ID from all slices that fall within the time range of the trace peak.

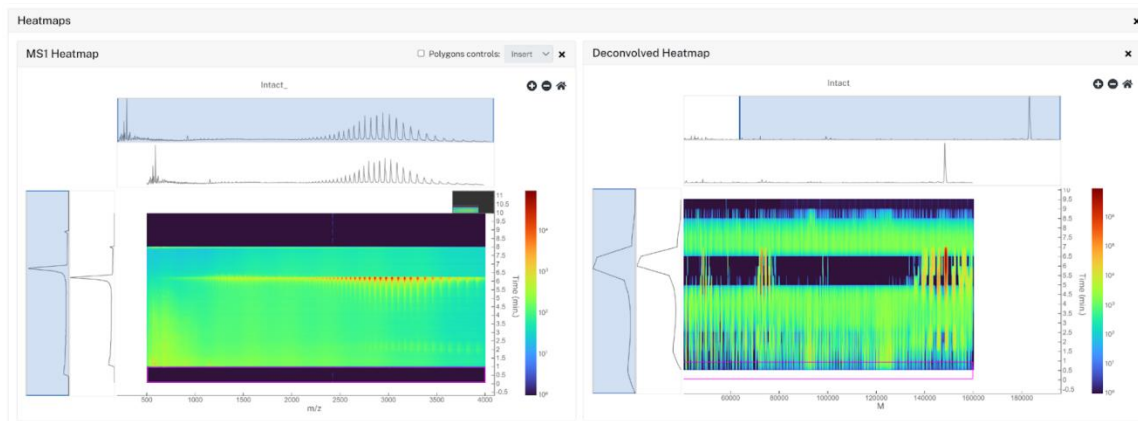


When a user selects a mass from the Masses Table, the MS1 and Deconvolution plots displayed are taken from this slice:

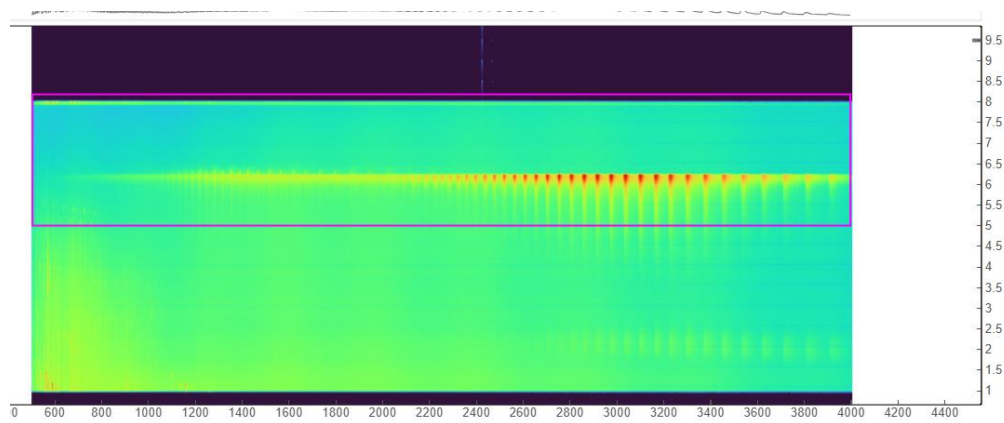


- **New Heatmap Widget now available within Deconvolution Web Analysis**

This release introduces the capability to generate interactive Heatmaps to visualize MS1 and Deconvolved Mass data. This enhancement allows users to visualize data trends and patterns more effectively, facilitating better decision-making based on the analysis results. Heatmaps are present in the Inspection and Report rooms. Note that the Deconvolved Heatmap is only generated if the user processes their data using **Progressive Deconvolution**.



Heatmaps visualize m/z vs time (MS1 Heatmap) and M vs time (Deconvolved Heatmap). When a trace peak row is selected, the corresponding area is highlighted with a red box on the heatmap.

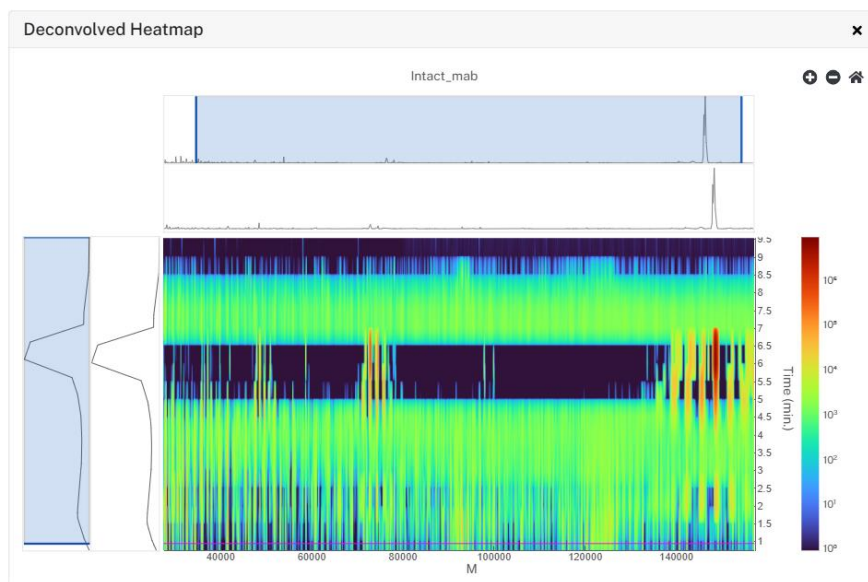


If multiple rows are selected in the trace peaks table, multiple regions will be highlighted on the heatmap. Heatmaps are generated for each input sample. For a sample's heatmap to be displayed, a trace peak from that sample must be selected.

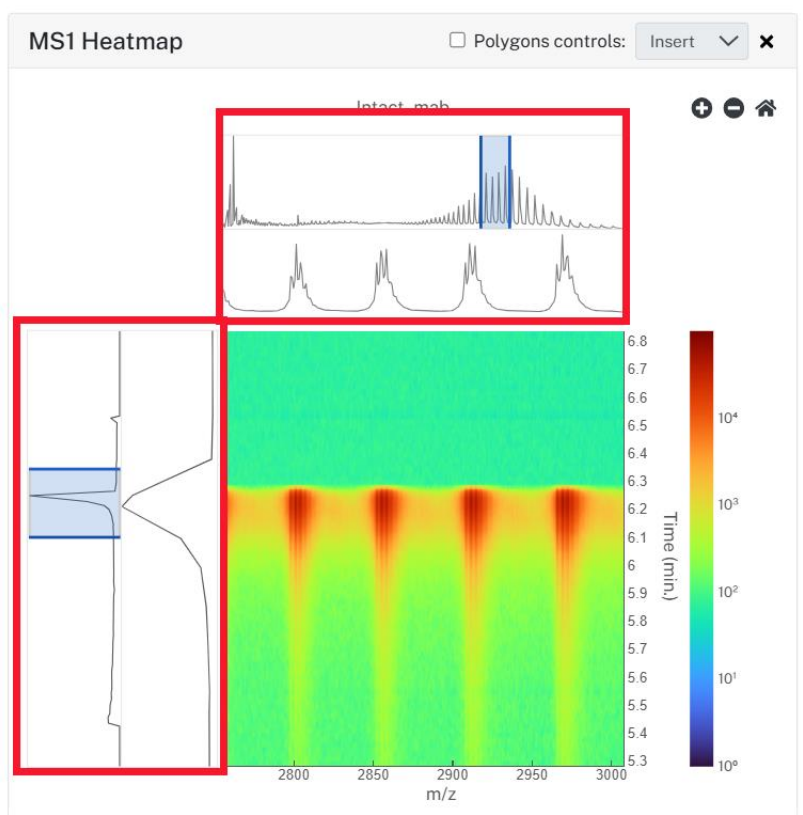
The heatmaps have the following dynamic zoom controls:

- Users can zoom in and out on the heatmap as well as return to home position (Home icon)
- Zoom in with + icon or left clicking the heatmap
- Mouse scroll to zoom in/out while hovering over the heatmap

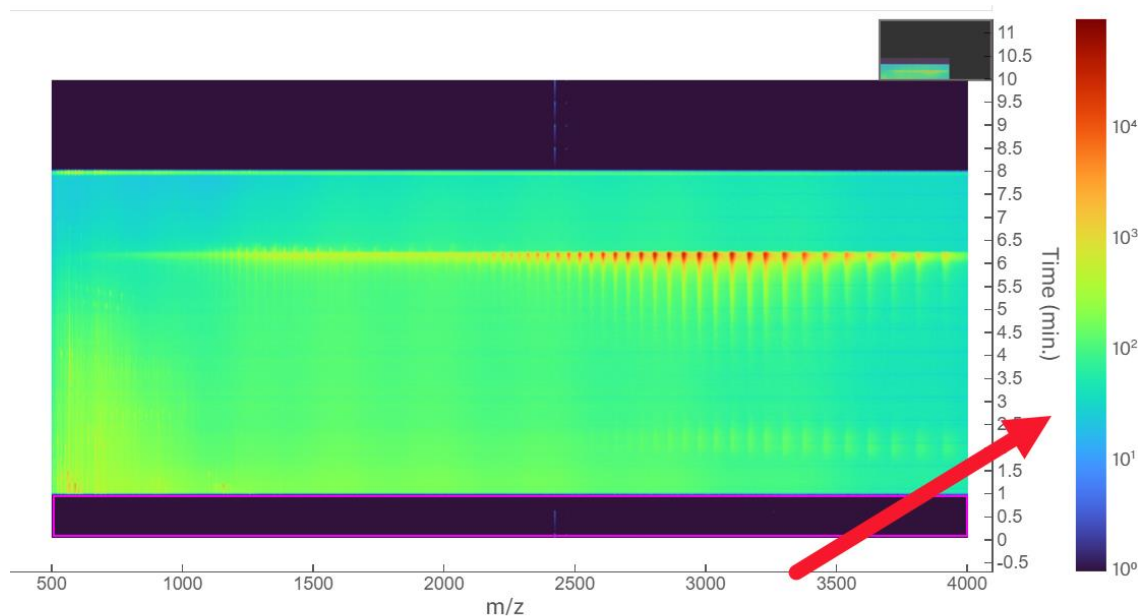
When a user selects **Progressive Deconvolution** mode, deconvolution is no longer restricted to the integrated trace peaks. Instead, a user may specify windows to produce multiple slices for deconvolution. As a part of selecting Progressive Deconvolution, an additional Deconvolved heatmap is created which provides the same level of granularity as the progressive deconvolution.



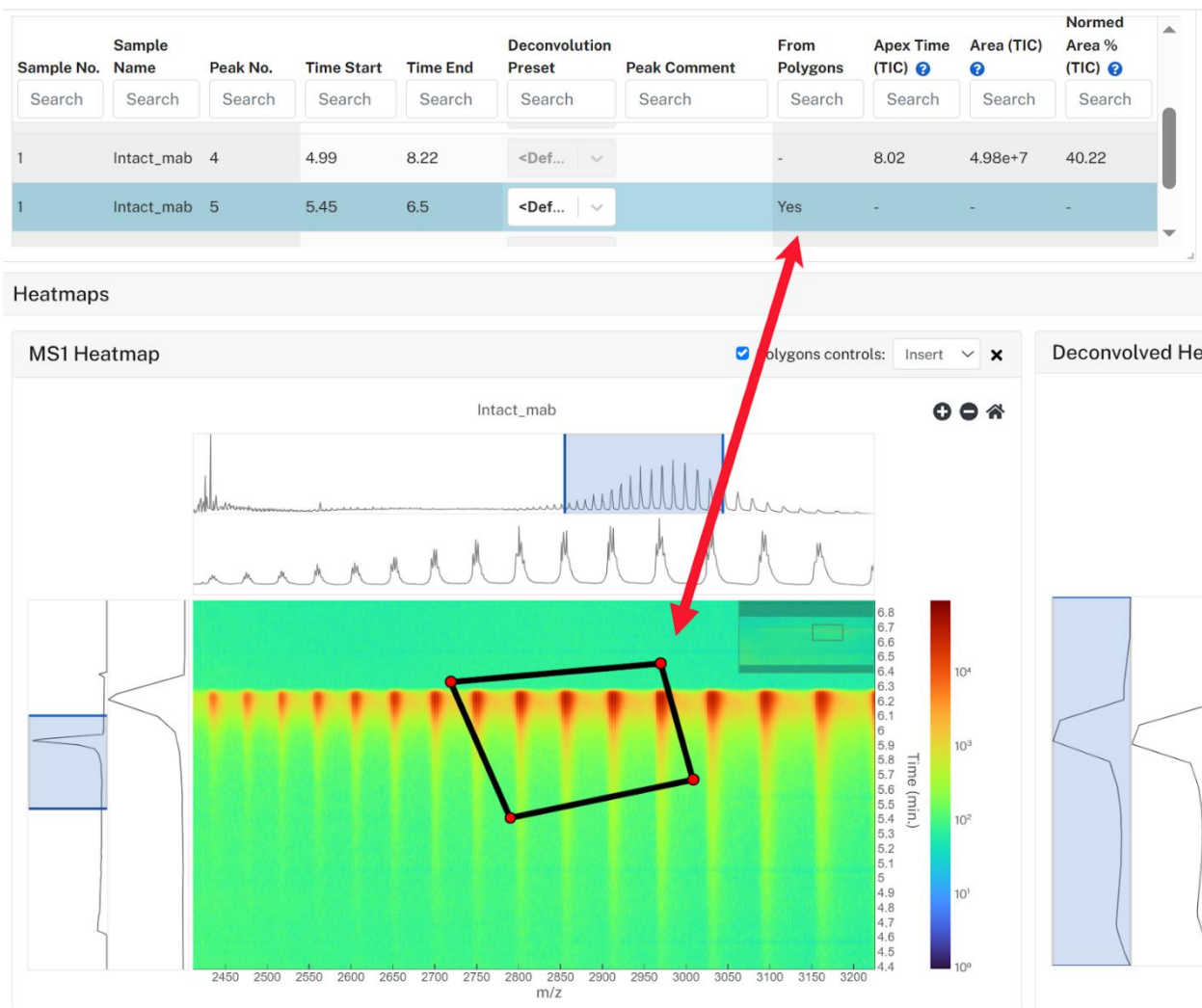
Alongside each heatmap are **margin plots** which display the corresponding trace plot and the m/z or M spectra, respectively. Each margin plot contains two stacked instances of the same data – the bottom trace will change boundaries as the user zooms into areas of the heatmap. The top trace will remain at full zoom and show vertical bars representing the zoom level of the trace below.



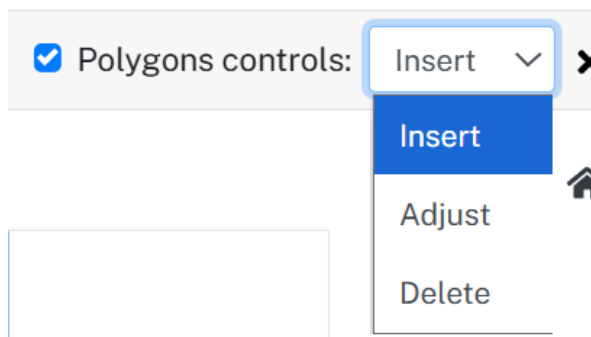
A color scale on the right side of the Heatmap denotes the relationship between pixel colors and signal intensity.



An additional feature available in the MS1 Heatmap is **MS1 polygon filtering**. Using the new polygon drawing tools, users can draw a polygon around a region of interest within the heatmap and the polygon selection will be saved to the Trace Peaks table. After computing, a summed MS1 and Deconvolved spectrum will be generated in that input m/z and time range.



When Polygon controls are enabled, users can select to **Insert**, **Adjust**, or **Delete** anchor points in the Polygon. If the user wishes to delete the Polygon entirely, this can be done by deleting the resultant Trace Peak row created by the bounded polygon.

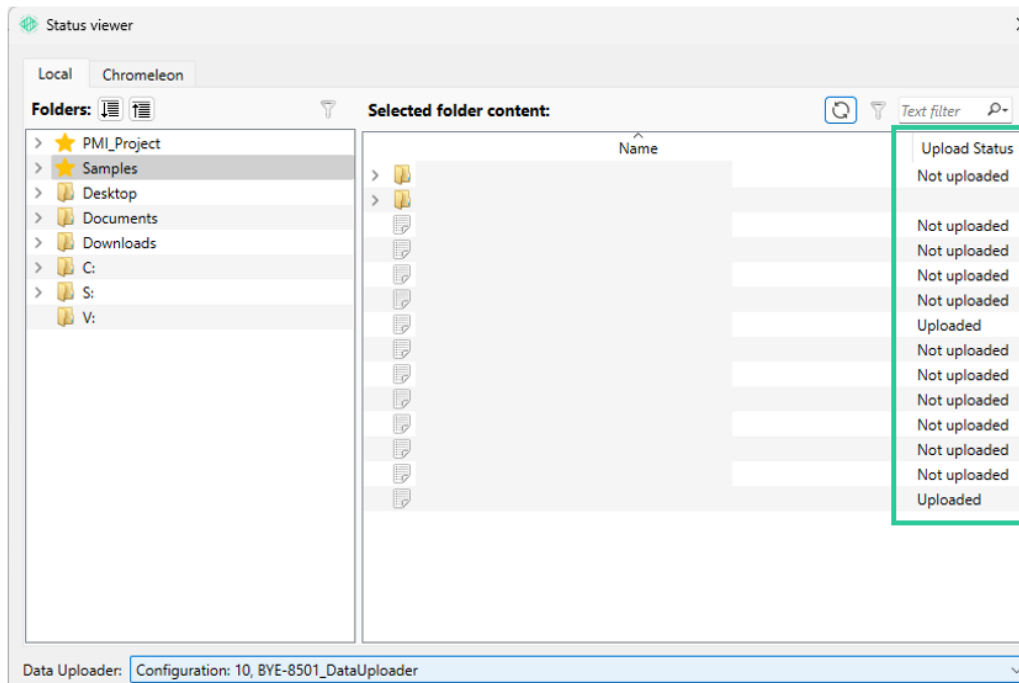


Release 2025-07 (v5.10)

Byosphere Desktop Client

- **New Data Upload Status Viewer available in Byosphere Desktop Client**

A new **Status Viewer** dialog is available in Byosphere Desktop Client which allows the user to see which files have already been uploaded to the Byosphere server to a specific folder (or any of its subfolders) specified in the selected Data Uploader configuration. **Note: This feature does not extend to the Byosphere Web Client in this release.**



Deep Query Dashboards Usability Enhancements

Several changes have been made to Deep Query Dashboards to improve the user experience.

- **Visualization Selection has been added to Display Settings**

The **Select Visualization Type** option has been added to the **Display Settings** within the Visualization editor. The purpose of this change was to allow the user to perform any data transformations and adjustments prior to having to select a specific method of visualization and corresponding settings.



Once the user adds any fields within the Data Settings a Data Grid Visualization will be generated as default. Changes made to the data can be assessed within the Data Grid prior to the selection of a different Visualization type from within the Display Settings and available data results can be consistently assessed via the new **Data Preview** panel outlined below.

- **New Data Preview panel in the Visualization Editor**

The new **Data Preview** pane provides the user with a data grid containing the underlying data being used to generate the Visualization. Updates to the Data Preview occur in sync with any updates made to the data used to build the Visualization, excluding any numerical display changes applied to the Visualization (since these only affect the visualization of the data rather than the underlying values themselves).

Data Preview			
Data.MS Alias Name	Glycan Short Name	SUM(Relative Glycan Quant)	
09315_E_SN_NIST_Guanidine_CTrypsin	G2F NA	0.507553603609197	
09315_E_SN_NIST_Guanidine_CTrypsin	GlcNAc	0.09663941557671231	
09315_E_SN_NIST_Guanidine_CTrypsin	Man3	0.12819015909568296	
09315_E_SN_NIST_Guanidine_CTrypsin	Man3 + GlcNAc	0.17689039263642065	
09315_E_SN_NIST_Guanidine_CTrypsin	Man3F	0.40373345402184335	
09315_E_SN_NIST_Guanidine_CTrypsin	Man4	0.038639133949044516	
09315_E_SN_NIST_Guanidine_CTrypsin	Man5	0.3014283145592117	
09315_E_SN_NIST_Guanidine_CTrypsin	other	0.6898753533623342	
09315_E_SN_NIST_Guanidine_LysC	AGly	0.508788440069641	
09315_E_SN_NIST_Guanidine_LysC	G0F	31.044163819321696	
09315_E_SN_NIST_Guanidine_LysC	G0F - GlcNAc	1.7223853112500473	
09315_E_SN_NIST_Guanidine_LysC	G1 - GlcNAc	0.011072569350648919	
09315_E_SN_NIST_Guanidine_LysC	G1F	52.70200958451611	


Note: All of the outlined changes above apply to **Charts and Tables** within **Web Analysis**.

- **Visualization Editor Actions have been updated**

New action buttons have been added to the Visualization Editor in Deep Query, replacing the previous Apply/Cancel/Close controls. The controls and their behavior are now as follows:

Title ×

Select title for visualization

 **Save & Close** **Cancel**


Data Fields

123	Data.Mass	x
abc	Data.Oligonucleotide Name	x
abc	Data.Delta Mass Name	x

Refresh button: Updates the Visualization and Data Preview panes with any changes made by the user since the last refresh/opening.

Title ×

Select title for visualization

 **Save & Close** **Cancel**


Data Fields

123	Data.Mass	x
abc	Data.Oligonucleotide Name	x
abc	Data.Delta Mass Name	x

Save & Close: Performs one additional refresh and saves all changes made to the Visualization, returning the user to the main Dashboard screen

Title ×

Select title for visualization

 **Save & Close** **Cancel**

Data Fields


123	Data.Mass	x
abc	Data.Oligonucleotide Name	x
abc	Data.Delta Mass Name	x

Cancel: Reverts all changes made since the Visualization was opened and returns the user to the main Dashboard screen.

Additionally, the section that is shared across different options (title + action buttons) has been moved to the top left of the Visualization Editor page, and this section will persist across all both Display and Data settings panels.

Most Display settings will now update live/automatically whenever a user modifies

Data and Transformation settings will now trigger a banner as shown below that can be clicked to trigger a refresh:

As detailed above, the user can also perform a refresh at any time by clicking on the **Refresh** icon .

- **Updated logic for Advanced Functions**

Upon adding the Linear Regression Advanced Function, the user will need to add the Independent and Dependent Variables from the fields provided in the dropdown. This change provides users with more flexibility in defining Linear Regression inputs.

Advanced Functions

Revert
Create

Function ⓘ

Linear Regression

Independent Variable ⓘ

SUM(Data.Delta Monoisotop

Dependent Variable ⓘ

SUM(Data.Delta Monoisotop

- Improved Legend controls**

The following controls have been added to Legends to improve customization:

- Legend font size
- Truncation of legend
- Word wrapping of legend

- Numerical Display options are now available for Line Charts, Bar Charts, Stacked Bar Charts, and Scatter Plots**

Numerical Display options have been added to additional Visualization types, including Line Charts, Stacked Bar Charts, and Scatter Plots.

Additionally, numerical display adjustments previously available as a function of tooltips have been removed—previous instances of numerical display in tooltips will be migrated to scientific notation.

Additional Deep Query improvements

- New derived field for Acquired Time**

A new derived field is now available upon request for parsing out the datetime information for Acquired On. This value is available from the Samples Custom Fields, which must be included in the analysis project during data processing. This allows users to query on this information within their Dashboard Visualizations. Please contact support@proteinmetrics.com for more information.

Search: 2 records...	
Data.MS Alias Name	Data.Samples Custom Fields
NISTmAb_Control_MS2	{ "Acquired On": "2018-02-23 23:06:48", "SampleType": "Reference" }
NISTmAb_Stressed_MS2	{ "Acquired On": "2018-02-24 01:48:48", "SampleType": "Reference" }

- Additional field added to Combined Data Source to capture Sequence values from Chromatogram projects**

Added field "Chromatogram Sequence" to the Combined Data Source.

Intact Analysis	
Combined Analysis	
Chromatogram Analysis	
Biophysical Analysis	

Field Name	Type	Description
Analysis Type	string	Type of analysis (e.g. intact, peptide, chromatogram)
Apex Time	number	Apex time associated with the peak
Charge	number	Charge
Chromatogram Sequence	string	Peptide sequence or released glycan information
Delta Mass Name	string	The name of the delta mass
Document ID	number	The ID of the source document in the Byosphere file system
Glycan Adduct	string	Glycan adduct e.g. "Cation:Na", "Ammonium" specified in analysis glycan option

- **Added the "Oligo Candidate" field for sequence information within Oligonucleotide Analysis**

The "Oligo Candidate" field represents the candidate assignment for a deconvolved mass which could be either a sequence or a mass. This field is also present in the Intact Oligo Dashboard template.

Select a Data Source

Peptide Analysis	<p>Description</p> <p>A data source containing data from multiple Oligonucleotide Projects involving Charge State Deconvolution.</p> <table> <tr> <th>Field Name</th><th>Type</th><th>Description</th></tr> <tr> <td>Oligonucleotide Candidate</td><td>string</td><td>Candidate assignment for a deconvolved mass which could be either a sequence or a mass</td></tr> <tr> <td>Oligonucleotide Custom Fields</td><td>string</td><td>Legacy user defined oligonucleotide sequences custom fields</td></tr> </table>	Field Name	Type	Description	Oligonucleotide Candidate	string	Candidate assignment for a deconvolved mass which could be either a sequence or a mass	Oligonucleotide Custom Fields	string	Legacy user defined oligonucleotide sequences custom fields
Field Name		Type	Description							
Oligonucleotide Candidate		string	Candidate assignment for a deconvolved mass which could be either a sequence or a mass							
Oligonucleotide Custom Fields		string	Legacy user defined oligonucleotide sequences custom fields							
Oligonucleotide Analysis										
Intact Analysis										
Combined Analysis										
Chromatogram Analysis										

Biophysical Analysis

Web Analysis

- **Updated file formats for Web Analysis templates and projects**

The file formats used for Web Analysis projects have been updated. Web Analysis **projects**, which previously had the extension `*.bproj`, will now have the extension `*.wa`. Projects created prior to v5.10 will be maintained and still have the extension `*.bproj`.

Web Analysis **templates** created in v5.10, which previously had the extension `*.bproj.t`, will now have the extension `*.wat`.

If users created custom templates or analyses from these templates prior to version 5.10, they must open an old analysis and resave it as a template within Byosphere v5.10 and it will be saved as a usable `*.wat` file.

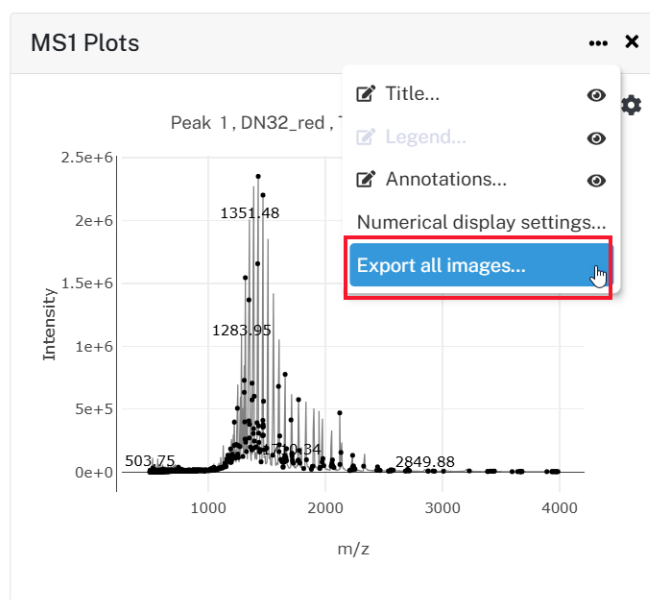
- **New column in the Sequences table, "Molecule Type"**

A new column, **Molecule Type**, has been added to the Sequences table in Web Analysis. This column allows the user to specify whether a molecule is a protein or an oligonucleotide. The default value is **Protein**.

Sequences				
Code	Name	Sequence	Molecule Type	Average Mass
Search	Search	Search	Search	Search
F	WATERS_MASSCHECK_LC	DVLMTQTPLSLPVSLODQ...	Protein	24197.8099267
E	WATERS_MASSCHECK_HC	QVQLKESGPGLVAPSQLS...	Protein	48501.638122
D	Test		Oligonucleotide	135570.93
C	Large	EVKLEESGGGLVQPGGSM...	Protein	49544.5050693
B	Small2	EEQYNSTYR	Protein	1189.1950453
A	Small1	TKPREEQYNSTYR	Protein	1671.7748154

- **Export all stacked plots feature added to Web Analysis**

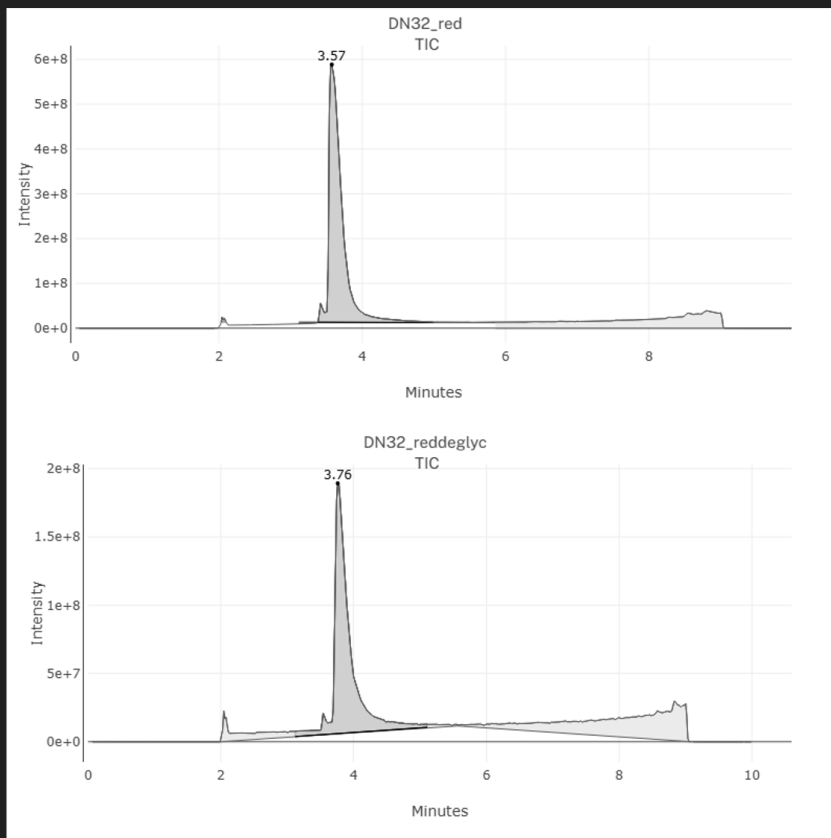
Users can now export an image including all stacked plots within a widget in WA. This feature is available from the three-dot icon in the header of each plot widget.



Clicking on **Export all images** launches a dialog allowing users to select the image format (PNG, JPEG, SVG), the dimensions of each plot within the image, and the option of fix the aspect ratio when adjusting dimensions.

The figure shows a dialog box titled 'Export All Images'. It contains three radio buttons for image format: 'PNG' (selected), 'JPEG', and 'SVG'. Below these are two input fields: 'Width (px)' with a value of 800 and 'Height (px)' with a value of 400. There is a checked checkbox labeled 'Fix Aspect Ratio' with an information icon to its right. At the bottom of the dialog are two buttons: 'Download' and 'Cancel'.

The resultant image contains all plots visible within the widget at the time of export:



- **Improvements to Deconvolved Mass Plot labelling**

Users can now select to view Mono, Average, or *both* types via checkbox to annotate their plot.

Release 2025-04 (v5.9)

Byosphere

- **Metadata from MS files is now added to pacq metadata when creating it**

Vendor MS metadata is now present within the pacq metadata after adding an MS sample to pacq.

- **New reserved metadata field “Acquired On”**

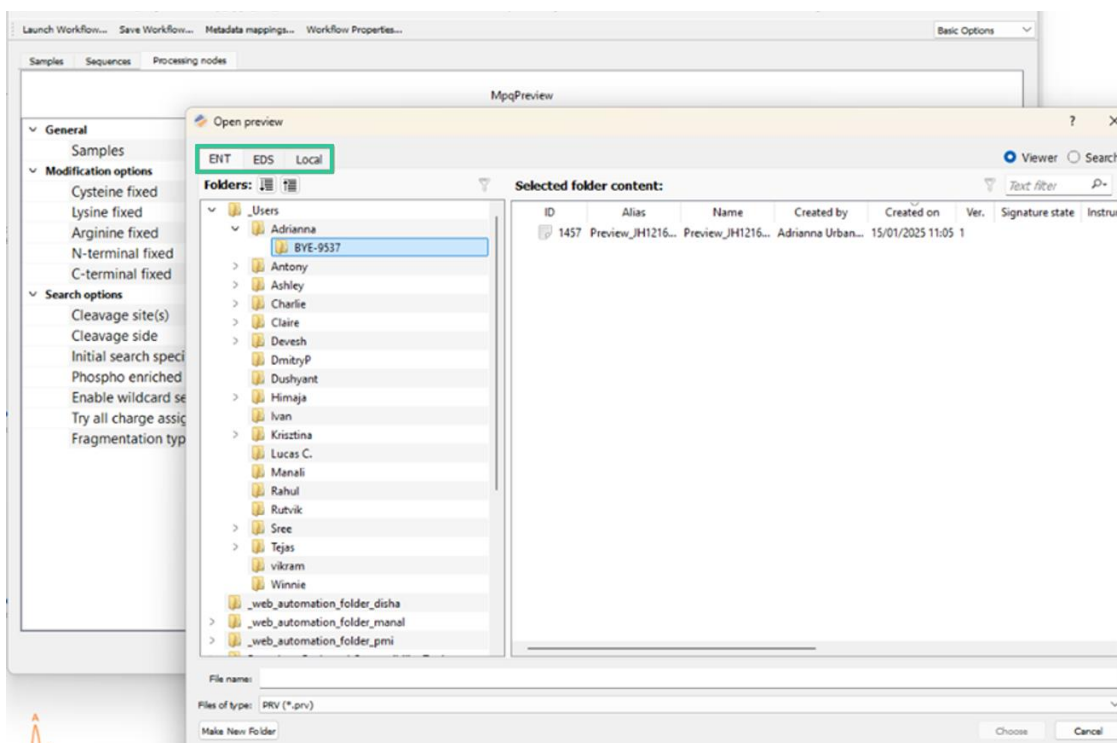
A new reserved metadata field exists in Byosphere called “Acquired on”, which includes the date and time of acquisition of a raw data file if available. This field has the format YYYY-MM-DD HH:mm:ss.SS.

te	Acquired On
	2024-08-28T20:33:18.000Z

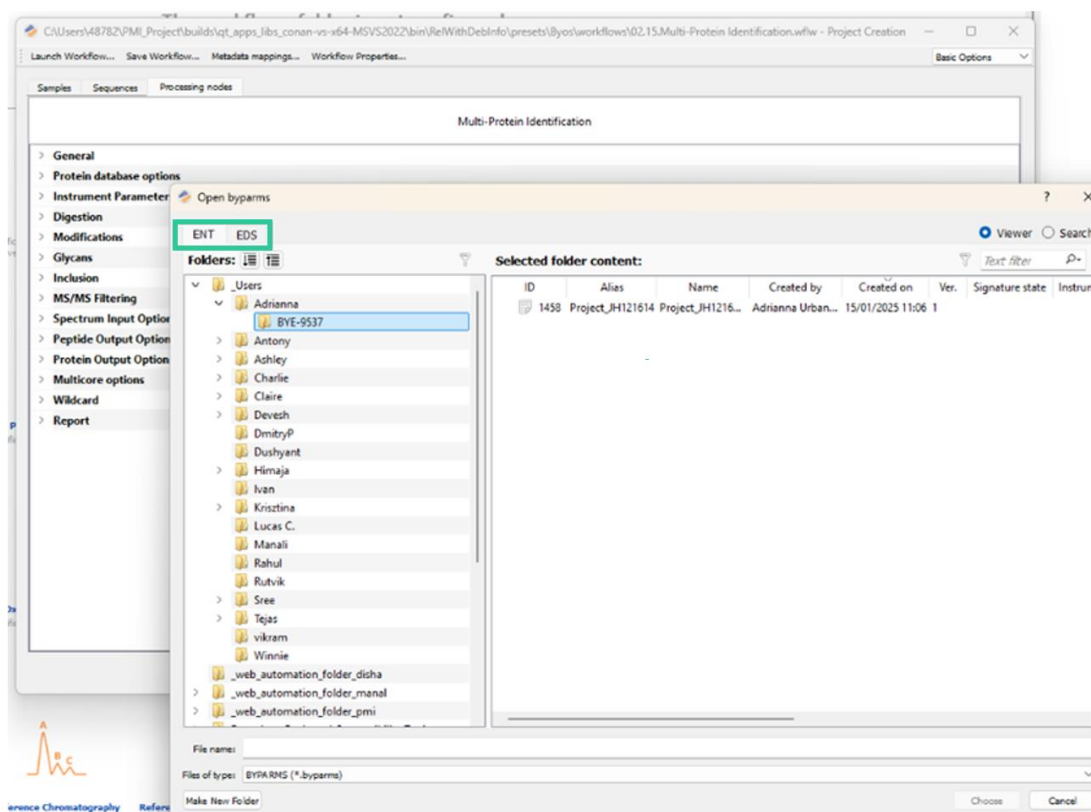
Virtual Client, Byosphere

- Users can now load .byparms files from the Enterprise file server

The File Chooser dialog for selecting byparms/prv files in Byosphere Desktop/Virtual Client now includes options for file selection from EN, EDS, and Local Servers.



The **Virtual Client** provides access to ENT and EDS servers:



Web Analysis, Byosphere

- **Web Analysis templates now open directly within Edit mode**

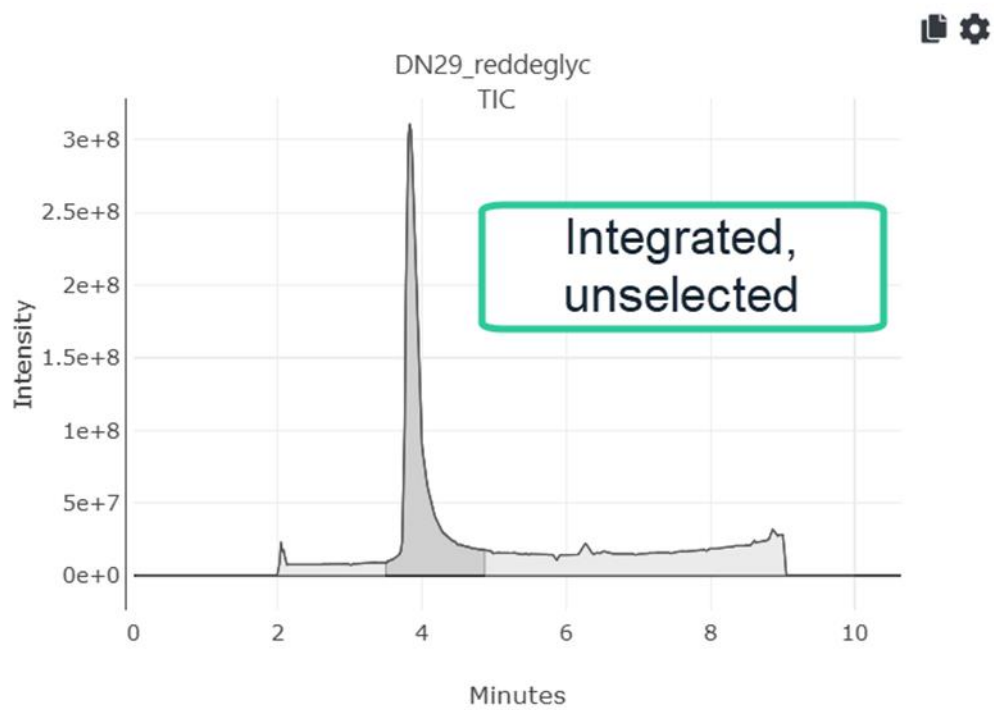
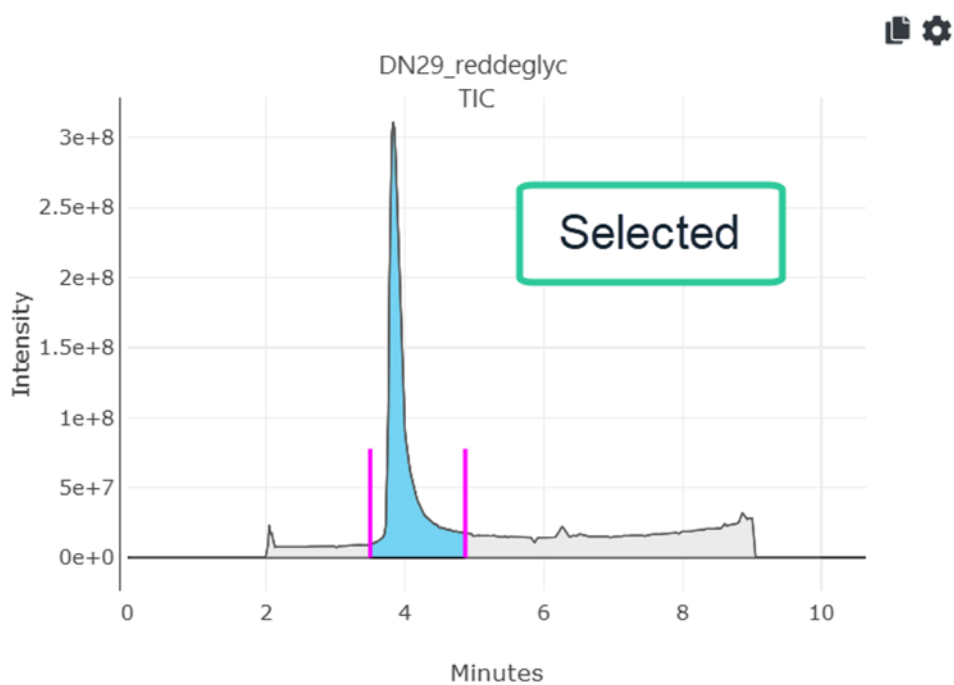
When users use Web Analysis templates to create a new analysis, they are now immediately greeted with their Analysis in Edit Mode for ease of use.

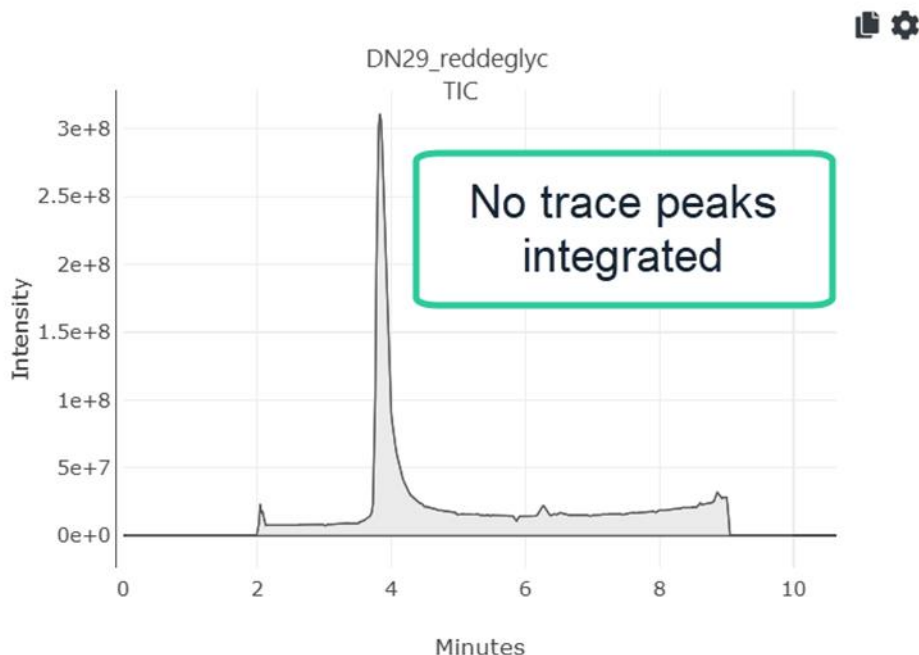
- **Improved behavior for annotations in Trace Plots**

Trace Plot annotations will now always be shown, not just when the corresponding row for the Trace has been selected.

- **Improved Trace Peak integration**

New colors have been introduced to differentiate non-integrated peaks (light gray), integrated peaks (dark gray), and the selected peak (blue), to provide greater visual cues for result inspection within the Trace Peaks plots.





- **Improvements in forming associations with Combinations in Web Analysis for defined data processing**

Users can now associate sequence combinations with both specific Samples and with custom fields in order to use a specific combination for mass matching during processing.

Combinations are associated with all samples by default, as represented in the new **Sample associations** column:

Combinations 50 Digestion Parameters... Delete Selected... Add Combination... x

Name	Alias	Composition	Disulfides	Average Mass	Monoisotopic Mass	Expected Type	Actions	Sample associations
DN29 HC	-	A(1)	Reduced	49675.9	49644.45	Desired		1 - DN29...
DN29 LC	-	B(1)	Reduced	23082.6	23068.32	Desired		All samples

Reference Mass Modifications

☒ Change N-terminal Q to pyroGlu ☒ Clip off C-terminal K ☐ N-glycans removed by PNGase F (N-X-S/T → D)

Clicking on the dropdown within a row opens the **Sample Associations** dialog, which lists all current associations and provides all available fields, including Samples, to form associations on.

In the following example, associations can be made based upon Sample or the custom field "Glycosylation". The Glycosylation option is set within the Samples table:

Samples

Manage Custom Fields...

Import Samples-Sequence Data...

Lock Mass...

Delete Selected...

Add Samples...

X

Show	Sample		MS File or Trace File	MS/MS	Doc ID	Trace Description	Actions	Glycosylation (string)
	No.	Sample Name						
Search	Search	Search	Search	Search	Search	Search	Search	Search
	1	DN29_red	DN29_red.raw.pacq	N/A	1012	-		
	2	DN29_reddeglyc	DN29_reddeglyc.raw.pacq	N/A	1013	-		Degly
	3	DN32_red	DN32_red.raw.pacq	N/A	1014	-		
	4	DN32_reddeglyc	DN32_reddeglyc.raw.pacq	N/A	231	-		Degly

Both Samples and Glycosylation are present as options within the Sample Associations dialog:

Sample Associations

1 - DN29_red X
(Glycosylation) Degly X
X

All samples ☐

Or

Sample number ▼

Search...

☐ Select all present below

☒ 1 - DN29_red
☐ 2 - DN29_reddeglyc
☐ 3 - DN32_red
☐ 4 - DN32_reddeglyc

Sample Associations

1 - DN29_red X
(Glycosylation) Degly X
X

All samples ☐

Or

Sample number ▼

Glycosylation ▼

Search...

☐ Select all present below

☐ null
☒ Degly

In this example, the combination has been associated with both Sample 1 (DN29_red) and all Samples with the value of “Degly” for the custom field “Glycosylation”.

DN29 HC	-	A(1)	Reduced	49675.9	49644.45	Desired		1 - DN29_red (Glycosylation) D...
---------	---	------	---------	---------	----------	---------	--	---------------------------------------

As a result, DN29_red, DN29_reddeglyc, and DN32_reddeglyc will be matched against the combination DN29 HC.

Toggling **All samples** to on will automatically associate the Combination to All samples, including those added after the associations are set.

Deep Query, Byosphere

- A new interactive **Visualization Builder** is now available in Deep Query

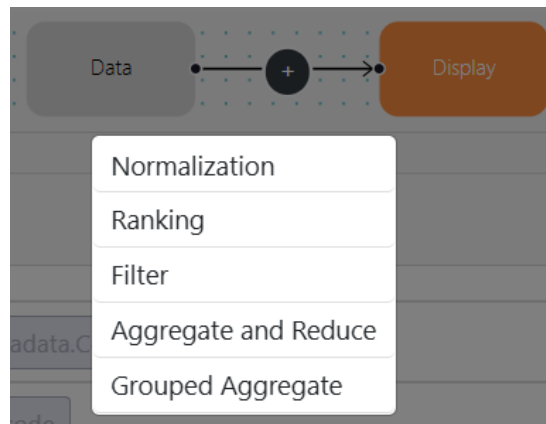
Deep Query Dashboards has been updated with the new Deep Query **Visualization Builder**. This flowchart tool enables users to visualize the flow of all changes that occur on their dataset, from project data ingestion to Visualization generation and display.

By default, the **Visualization Builder** will start with **Data** and **Display** sections. Clicking on these interactive buttons will provide access to Data and Display controls, respectively, which were previously accessed via tabs.

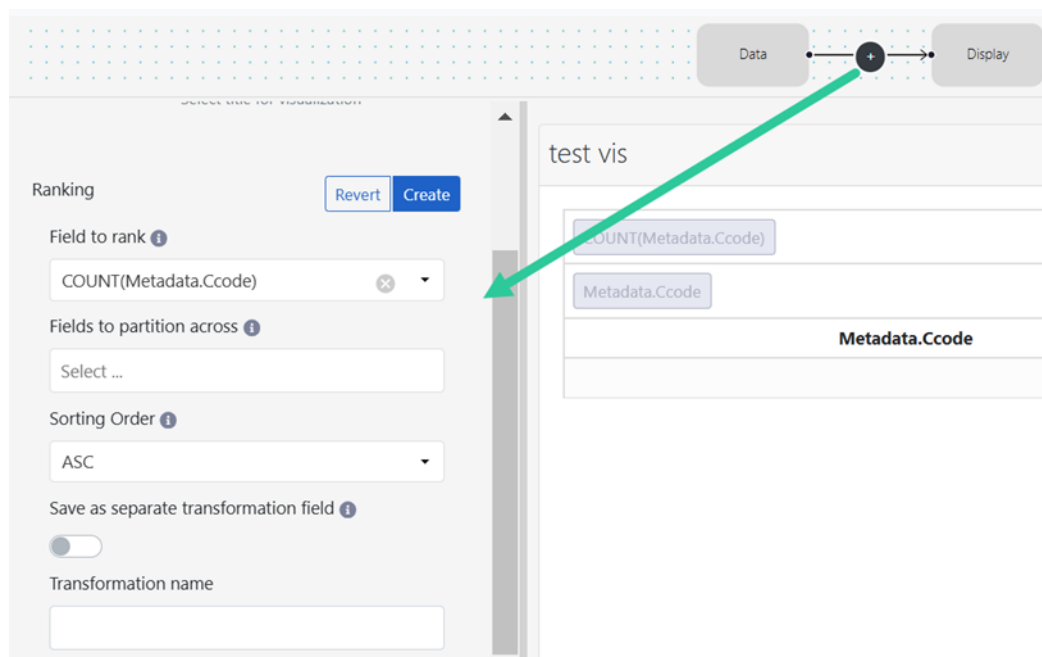
The screenshot displays the Deep Query Visualization Builder interface. At the top, a flowchart shows a sequence: Data (orange box) → + (black circle with a plus sign) → Display (grey box). Below this, the interface is divided into several panels. On the left, the 'Data Settings' panel is active, showing options for 'Select Visualization Type' (Pivot Table), 'Chart type' (Select ...), 'Rows' (Select ...), 'Columns' (Select ...), 'Data' (Field), and 'Aggregation' (Aggregation). A green box highlights the 'v5.8' version number. In the center, the 'Transformations' panel is visible, showing a 'v5.9' version number and a 'Select Visualization Type' dropdown. On the right, the 'Display Settings' panel is active, showing a 'test vis' title and a 'Metadata.Code' field. A green arrow points from the 'Display' button in the flowchart to the 'Display Settings' panel. Another green arrow points from the 'v5.9' version number in the Transformations panel to the 'v5.8' version number in the Data Settings panel. A table of data is visible in the background, with columns for 'Data.Average PPM', 'Data.Apex PPM Time', and 'Data.Document ID'.

Data.Average PPM	Data.Apex PPM Time	Data.Document ID
-13.3449	43.13	951
-13.2250	1.08	951
-12.2580	43.18	951
-12.1027	43.38	951
-11.8201	11.54	951
-11.9152	56.97	951
-11.5099	43.17	951
-11.0297	11.55	951
-10.5090	11.53	951
-10.3676	44.68	951

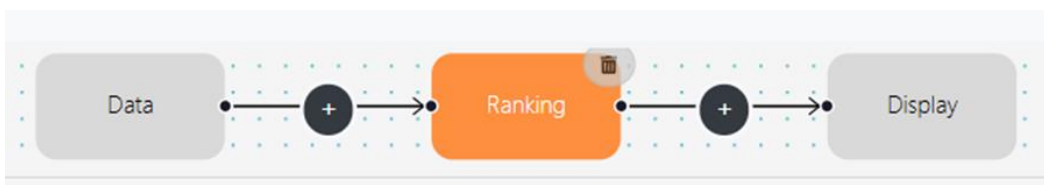
Transformations can be added by clicking on the **+** icon within the flow. Users will be prompted with all available Transformation options for their selected Visualization. Once selected, the lefthand sidebar will populate with options to configure the Transformation and once added, the Transformation will be performed in sequence with all steps within the Flowchart.



For example, if **Ranking** is selected, the left panel will populate with the settings needed to build a Ranking transformation:



Once the user clicks **Create**, Ranking will be added as a step within the Flowchart. The Transformation can then be deleted from the trash icon within the Flowchart.

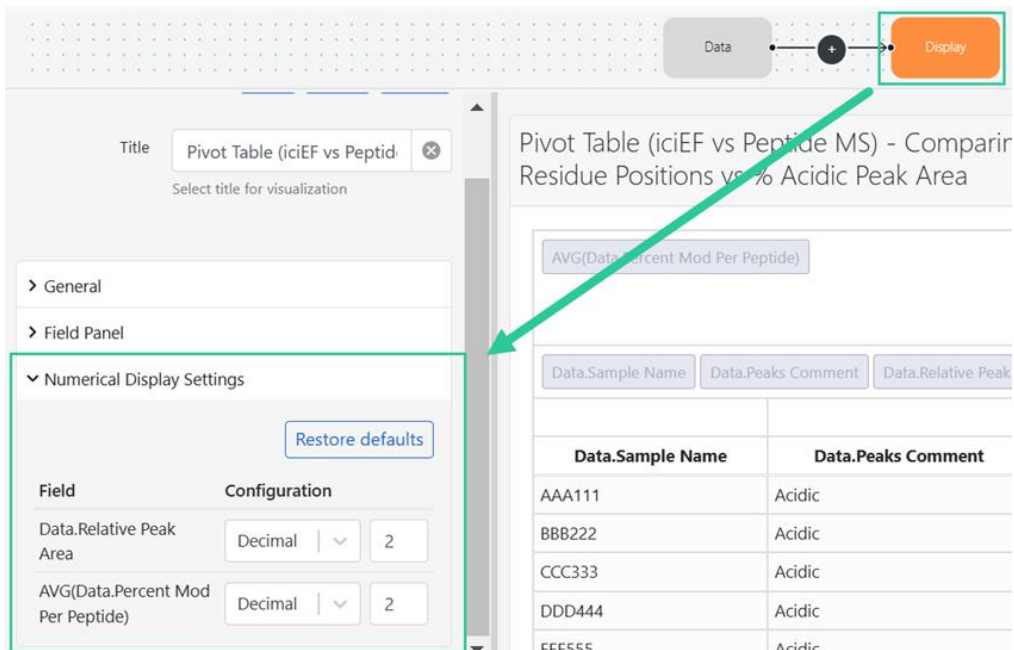


Note that Data and Display are fundamental steps and cannot be deleted.

- **New tools are available in Deep Query to adjust numerical display settings**

Numerical displays settings such as **format** and **number of decimal places** are now available for Pivot tables and Data Grid Visualizations in Deep Query Dashboards. Numerical display

settings can be accessed from the **Display** settings section of the Visualization Editor, which is now available via the new Visualization Builder described above.



Configurations include **Decimal**, **Scientific**, and **Percentage**. The user can also determine how many decimal places they wish to have displayed in the resultant configuration.

Note: Due to how we pre-compute percentage values in the database, some numerical displays were set to decimals to avoid double computation. For instance, for a number that would be 0.1, or 10% may have been stored as 10 already, so if percentage formatting is applied, it will display as '1000%'. In this case, the value should be kept in decimal format.

These tools are also available in **Web Analysis Charts and Tables**.

- **XIC Area Summed IsoX Normalized field added to the Biophysical Datasource**

The Biophysical Data Source now contains the data field **XIC Area Summed Isox Normalized** for Peptide data. This field can be used within Visualizations for correlation between analyses for the same samples vs Biophysical data values as well as in other calculations.

- **Any unapplied changes in the Visualization Editor will now be preserved if users navigate to other tabs in Byosphere**

Change made within the Visualization Editor are now preserved when making changes in Deep Query and then moving to another part of Byosphere web client (such as Job Queue, Search, or Web Analysis) even if the user has not clicked Apply. However, for the final Visualization edits to be made permanent, the user will need to click on Apply and Publish the Dashboard. The preservation has been introduced for ease of use so users would not lose their changes.

- **Users will now have the option to set the x-axis to be treated as a numerical value**

A new option is now available under the **Group By Axis** tab of the **Display** settings to enable a **numeric x-axis** for Line Chart and Scatter Plot Visualizations. If enabled, labels and spacing will be provided numerically following the real numerical value of the datapoints.

▼ Group By Axis

Label

Label for x-axis. Defaults to group-by field

Label Visible



Whether to display label

Axis Position

Bottom



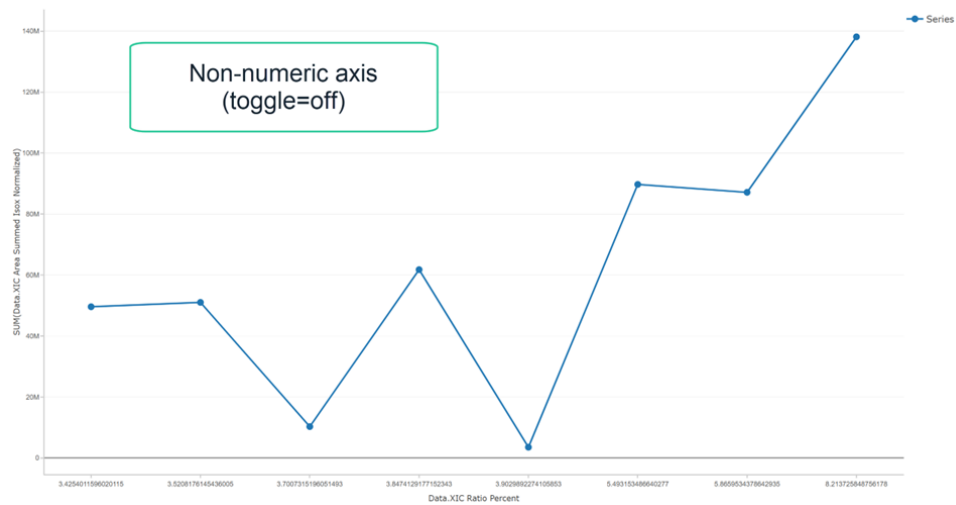
Chart position of X axis

Numeric x-axis

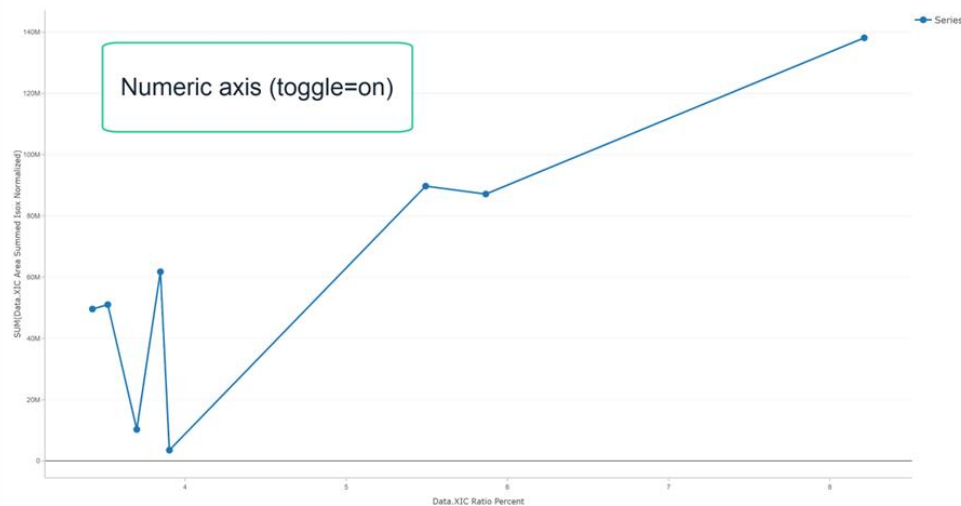


Set x-axis spacing and labels to numeric values

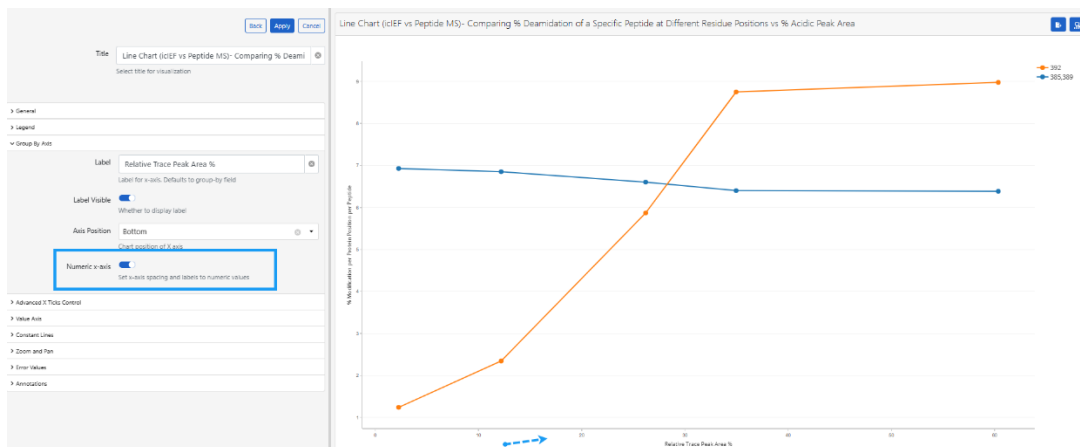
Line Chart Example for numeric X axis



Line Chart Example for numeric X axis



- The Biophysical Dashboard template has been updated to display the numeric x axis for Line Chart Visualizations that have numeric values

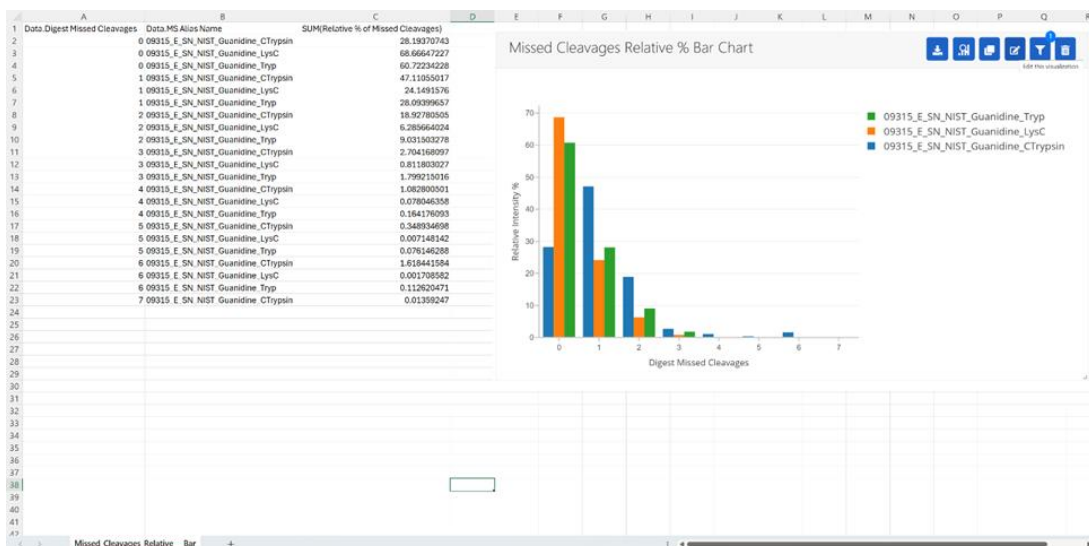


- Users can now export XY data from all Visualizations

An "Export to CSV" option is now available on *all* Visualizations. This will export the underlying XY data that is used to build the Visualization.



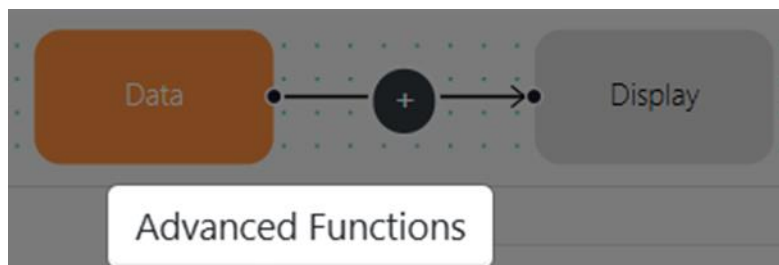
Example output with Visualization on the right for comparison:



This tool is also available in **Web Analysis Charts and Tables**.

- **New Advanced Function for adding Linear Regression, R^2 and Pearson Correlation**

If a user has selected either a Line Chart or Scatter Plot Visualization, a plus sign icon will appear within the new Visualization Builder which allows the user to add an **Advanced Function** which can be applied to their data.



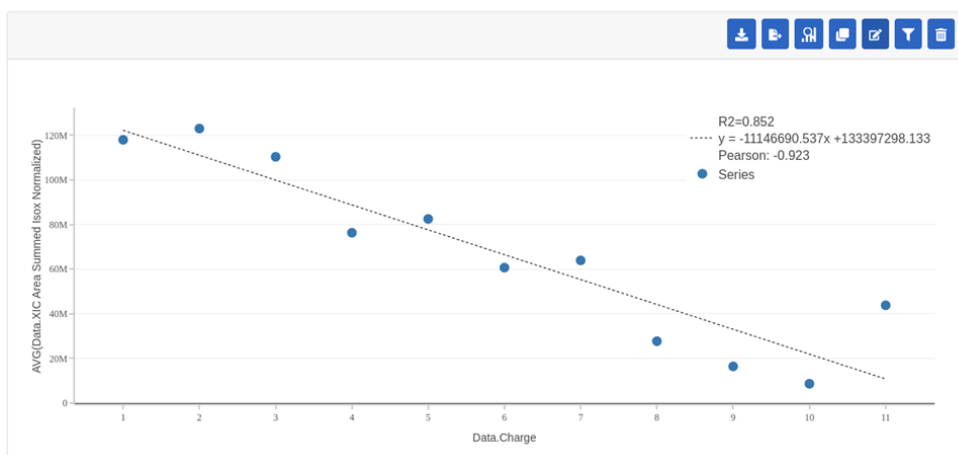
The first Advanced Function introduced in Byosphere v5.9 is **Linear Regression**. Adding Linear Regression will calculate the equation for the line of best fit, the Pearson Correlation, and the R^2 value.

The screenshot shows the 'Advanced Functions' configuration panel. At the top right are 'Revert' and 'Update' buttons. The 'Function' dropdown is set to 'Linear Regression'. The 'Independent Variable' field contains 'Data.Charge'. The 'Dependent Variable' field contains 'AVG(Data.XIC Area Summed Isox Normalized)'. Information icons are present next to the function and variable labels.

Display of these values within the Visualization can be toggled from **General > Display** settings, but when first adding this correlation under Advanced Functions it will be automatically enabled.

The screenshot shows a toggle switch for 'Display R^2 , Slope, Intercept and Pearson's Correlation'. The toggle is currently turned on (blue).

The results from this advanced function, when enabled for display, can be seen in the top right-hand corner of the Visualization.



- **The Multi-Protein Quantitation template has been updated with two new Visualizations**

The **Multi-Protein Quantitation** template has been updated to include the following Visualizations:

- **Pivot Table: Protein ppm Concentration - Relative to mAb:** This pivot table provides the average protein ppm concentration based upon the mAb across different replicates and conditions.
- **Stacked Bar Chart: Stacked Bar Chart - Protein ppm Concentration:** This bar chart is to visualize the relationship outlined above.

- **Alignment in naming convention for Custom Fields between Peptide and Intact data sources**

The display name for custom field values coming from Byos projects is now "Data.Samples Custom Fields" for both **Intact** and **Peptide** data sources.

Data.Samples Custom Fields
{ "SampleType": "Reference" }
{ "SampleType": "Reference" }
{ "SampleType": "Reference" }
{ "SampleType": "Reference" }
{ "SampleType": "Reference" }