



Byosphere Software Release Notes

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5.12

Protein Metrics LLC, Boston, Massachusetts, USA

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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**.

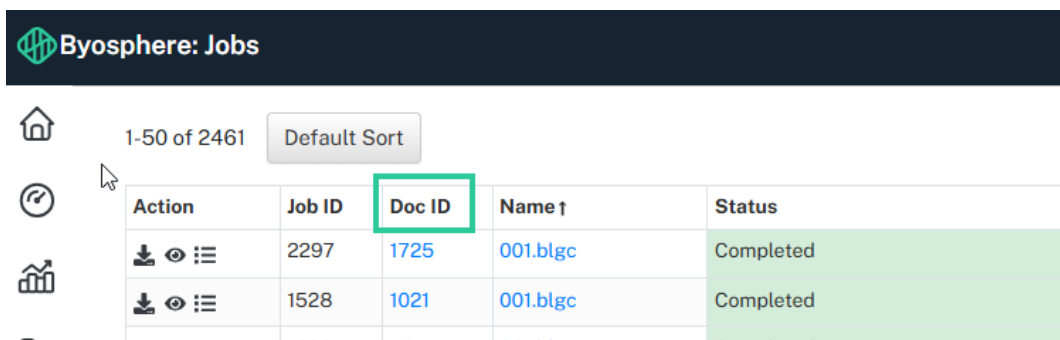
Release 2025-12 (v5.12)







Byosphere Web

- **A Doc Id column has been added to the Jobs page**

When a row in the Jobs table has a Doc ID value, the text is a hyperlink which leads to a search filtered to that specific document.

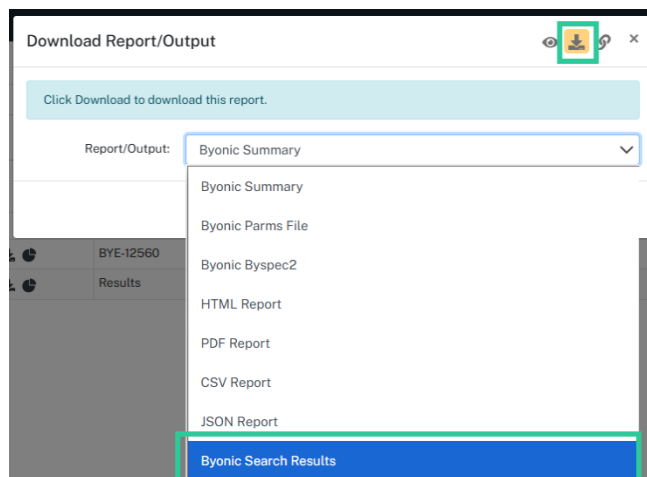
Additionally, the “ID” column has been renamed to “Job ID” to appropriately reflect the difference between the two columns.



Action	Job ID	Doc ID	Name ↑	Status
  	2297	1725	001.blgc	Completed
  	1528	1021	001.blgc	Completed

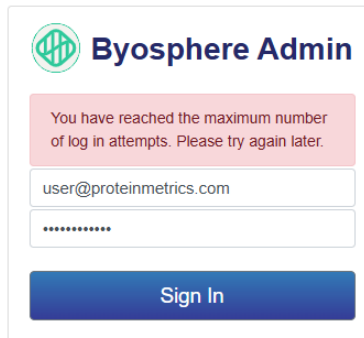
- **Byonic search result files can now be downloaded from Byosphere**

Byonic Search Results (.byrsIt) are now downloadable from Byosphere. This option can be found in the dropdown available after clicking on the download icon in the Download Report/Output dialog.



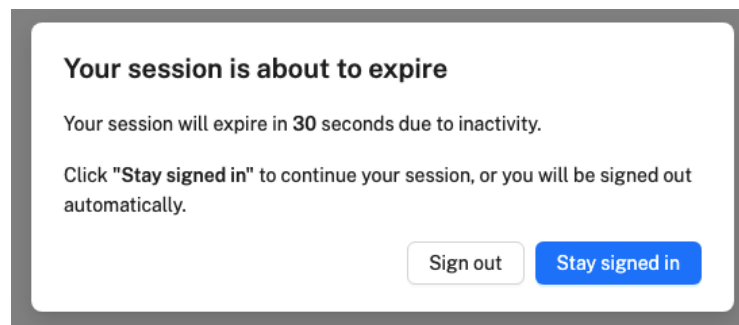
- **Rate limiting has been implemented for Admin login and password reset**

Byosphere now limits how many times an *admin* user can make login attempts within a given time.



- **Users will now be notified that their Byosphere session is about to expire**

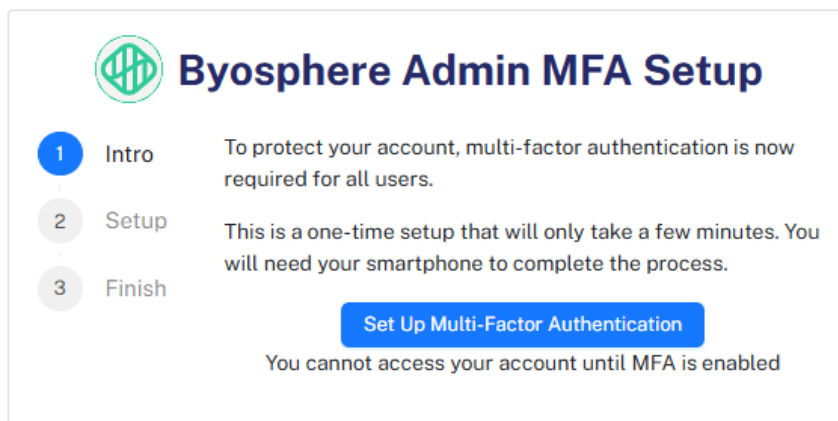
Users will now be notified 30 seconds before their session about to expire due to inactivity so that they can proactively extend it without being signed out and being interrupted mid-task. The message will provide the option to extend the session.




- **Multi-factor Authentication (MFA) will now be available for Admin users**

To enhance security for Admin user accounts, Multi-Factor Authentication will now be available as an option for Admin users.

If enabled, upon initial login, users must set up multi-factor authentication, which can be done using any standard authentication app such as Microsoft Authenticator.



Users should scan the QR code using their authentication app. Once done, the app should generate a custom six-digit code that can be entered within the Setup dialog.



Byosphere MFA Setup

✓ Intro

2 Setup

3 Finish


Setup Instructions:

1. Open your authenticator phone app
2. Tap "Add account" or "+" button
3. Choose "Scan QR code"
4. Point your camera at the QR code
5. Enter the 6-digit code below


> Cannot scan? Enter code manually.

Verify & Continue

Go Back



Once the code has been verified, the user will be informed that MFA setup is complete. Clicking **Finish** will redirect the user back to the login screen.



Byosphere Admin MFA Setup

✓ Intro

✓ Setup


3 Finish

MFA setup is complete!

Click Finish to return to the login screen.

Finish

At the login screen, the user will now be prompted to log in manually and then with the MFA code provided for use in Byosphere in their MFA app.




Byosphere Admin

Enter MFA Code

Submit Code

[Reset MFA](#)


Users can reset their multifactor authentication configuration by clicking **Reset MFA**. An email will be sent to initiate the reset process.

**Byosphere Admin**

MFA Reset request successful. Please check your Email to reset your MFA.

Sign In

Byosphere: MFA Reset Inbox xPrintShare




byos-enterprise@proteinmetrics.com
to me ▾

9:24 AM (1 minute ago) ☆ ↶ ⋮

Morgan , to reset your Byosphere MFA, click [here](#).

↶ Reply ↷ Forward

Clicking the link in the MFA reset email will redirect the user to the login page. After logging in, the user will be prompted through the entire MFA setup process again.

**Byosphere Admin**

To reset your MFA, please enter your email and password.

Reset MFA

Web Analysis

New workflow options within the Sequences room

Users can now select two new workflow options for the setup of molecule information within the Sequences room of Web Analysis: **Library** and **Chains and Compositions**. These options enhance the user experience by providing different methods of defining molecular compositions of interest to be used in mass matching and identification downstream. **Users are advised not to switch between molecule workflows once inputs have already been made as progress may be lost.**

Within the **Library** Molecule Workflow there are two tables: **Library** and **Modifications**. The **Modifications** table has not changed since the previous release (Byosphere 5.11). In the **Library** table users can provide a FASTA database reference. All the content of the selected FASTA files (sequences) will be imported.

Each uploaded FASTA reference will have its own row within the Library table where Sample associations can be provided.

Library

50Delete Selected...Add Libraryx

Molecule Class	Name	Doc ID	Sample associations	Preview Contents
<input type="text" value="Search"/>	<input type="text" value="Search"/>	<input type="text" value="Search"/>	<input type="text" value="Search"/>	<input type="text" value="Search"/>
Protein	DN29-32.fasta	2357	All samples	

Within the Library table is the **Preview Contents** column. Clicking on the eyeglass within this column will open the **Preview Contents** dialog which displays all sequences included within the FASTA file. This dialog is read-only and can be used to inspect the sequences present in the FASTA file as shown below.

Preview Contents

Name	Sequence
DN29 HC	EVQLVESGGGLVQPKGSLKLSCAASGFTFTNTYAMNWVRQAPQKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSQSLLYLQMNNLKTEDTAMYYCVR HGNFGNSYVSWFAYWQGGLTVLSAAKTTTPSVYPLAPGSAQAQNSMVTGLCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTPVPSST WPSETVTCNVAHPASSTKVDDKIIPRDCGCKPCICTVPEVSSVFIFPPKPKDVLITLTPKVTCTVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFR SVSELPIMHQDWLNGKEFKCRVNSAFAFPAIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITNFFPEDITVEWQWNGQPAENYKNTQPMIDTGS YFVYSKLVNQKSNWEAGNTFTCSVLHEQLHNHTEKLSHSPGK
DN29 LC	QAVVTQESALTTSPGETVTLCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTNKRAGVPARFSGSLIGDKAALITITGAQTEDEAIYFCALWYSNLWVFGGG TKLTVLGGQPKSSPSTLTFPPSSELETNKAATLCTITDFYPGVTVTDWKVDGTPVTQGMETTTQPSKQSNKNYMASSYLTLTARAWERHSSYSCQVTHEGHT VEKLSLRADCS
DN32 HC	QVQLQQSGAELARPGASVKMSCKASGYTFTRYTMHWVKQRPGQGLEWIGYINPSRGYTNYNQKFKDKATLTLDKSSSTAYMQLSSLTSEDSAVYYCARY DDHYCLDYWQGQTTTLTVSSAKTTAPSVYPLAPVCGDITGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQITCN VAHPASSTKVDDKIEPRGPTIKPCPPCKCAPNLLGGPSVFIFPPKIKDVLMSLSPIVTCVVDVSEDDPDVQISWFWNNVEVHTAQTQTHREDYNSTLRVVS ALPIQHQQDWMMSGKEFKCKVNNKDLPAPIERTISKPKGSRAPQVYVLPPEEEMTKKQVTLTCMVTDMPEDIYVEWTNNGKTELNYKNTPEVLDSDGSYF MYSKLRVEKKNWVERNSYSCSVVHEQLHNHHTTKFSRTPGK
DN32 LC	QIVLTQSPAISASPOEKVMTCSASSSVSYMNVYQQKSGTSPKRWYDTSKLASGVPAHFRGSGSGTSYSLTISQMEADAATYYCQQWSSNPFQSGGT KLEINRADTAPTYSIFPPSSEQLTSGGASVVCFLNNFYKPDINVKWIDGSRQNGVLNSWTDQSDKSTYSMSSTLTLDKEYERHNSYTCEATHKSTSPI VKSFRNREC

Ok

Within the **Chains and Compositions** Molecule Workflow are two tables: **Chains** and **Compositions** and **Modifications**. The **Modifications** table has not changed since the previous release (Byosphere 5.11).

Chains and compositions											
50 ▾ Delete Selected...					Import FASTA...		Add Sequence...		Add Composition...		
Molecule Class	Code	Name	Alias	Sequence	Composition	X-Links	Average Mass	Monoisotopic Mass	Expected Type	Sample associations	Actions
Search	Search	Search	Search	Search	Search	Search	Search	Search	Search	Search	Search
Protein ▾	A	DN29 HC	DN29 HC	EVQLVESGGGLVQPGSL...	Edit	A(l)	All possible	49663.8	49632.36	Desired ▾	All ... Edit
Protein ▾	B	DN29 LC	DN29 LC	QAVVTQESALTTSPGETVT...	Edit	B(l)	All possible	23078.57	23064.28	Desired ▾	All ... Edit
Protein ▾	C	DN32 HC	DN32 HC	QVQLQQSGAELARPGASV...	Edit	C(l)	All possible	49704.85	49673.34	Desired ▾	All ... Edit
Protein ▾	D	DN32 LC	DN32 LC	QIVLTQSPAIMSASPGEKV...	Edit	D(l)	All possible	23336.57	23321.95	Desired ▾	All ... Edit

Reference Mass Modifications

☒ Change N-terminal Q to pyroGlu ☒ Clip off C-terminal K

This table captures the sequences for individual protein chains and compositions of interest that are used for mass matching downstream. The Add Sequence and Import FASTA function the same as before and allows the import of sequences which can be used to create compositions within the same table. To add a composition to the table, click **Add Composition**. This will launch the corresponding dialog:

Add Composition

Name:

Alias:

Composition type:

IgG antibody
Multispecifics
Custom

Light Chain 1: ▾

Light Chain 2: Same as Light Chain 1 ▾

Heavy Chain 1: ▾

Heavy Chain 2: Same as Heavy Chain 1 ▾

X-Links:

Basic
Advanced

Disulfides: All possible ▾

Expected type: Desired ▾

Add Cancel

There are three composition types the user can choose to build: **IgG antibody**, **Multispecifics**, and **Custom**.

The **IgG antibody** composition tab allows the user to select the corresponding chain entry for each light chain and heavy chain of the IgG construct. It will build a standard IgG1 molecule.

Composition type:

IgG antibody	Multispecifics	Custom
Light Chain 1:	<input type="text"/>	
Light Chain 2:	Same as Light Chain 1	
Heavy Chain 1:	<input type="text"/>	
Heavy Chain 2:	Same as Heavy Chain 1	

The **Multispecifics** tab allows the user to select the permutation count for all included sequences, as well as set a max number of chains per composition.

Composition type:

IgG antibody	Multispecifics	Custom
--------------	-----------------------	--------

Set chains permutation count:

Molecule Class	Code	Name	Count
Protein	A	DN29 HC	0
Protein	B	DN29 LC	0
Protein	C	DN32 HC	0

Max chains per composition:

After the user sets the rules in the table and clicks **Add**, all possible chain permutations based upon the counts selected will be added to the Chains and Compositions table, starting from one chained permutations to the number defined in the Count column chained permutations, up to the Max chains per composition number of chains in a single composition. All entries created via permutation will have the same Expected Type as specified in the dialog, and the user will need to edit if they wish to change a combination to be undesired.

The **Custom** tab allows the user to provide a simple count of each sequence as well as its type.

Composition type:

IgG antibody	Multispecifics	Custom
--------------	----------------	---------------

<input type="checkbox"/>	Code	Name	Count	Type
<input checked="" type="checkbox"/>	A	DN29 HC	1	-
<input type="checkbox"/>	B	DN29 LC	1	-
<input type="checkbox"/>	C	DN32 HC	1	-

light_chain
heavy_chain

The **X-links** section is available for all composition types, with the options of Non-Reduced, Reduced, and Disulfide Count (numerical user input).

X-Links:

Basic

Advanced

Disulfides:

All possible

Figure 1: Crosslinks

The **Advanced** X-links tab allows users to define a fine grain setting of x-links between any two chains. It contains the columns for specifying the 'from' chain selection and corresponding Chain ID and 'from' residue number, and similar columns for 'to' chain. The user also specifies the Bond type to distinguish between peptide and disulfide bonds.

Composition type:

IgG antibody

Multispecifics

Custom

Light Chain 1:

B - DN29 LC

Light Chain 2:

B - DN29 LC

Heavy Chain 1:

C - DN32 HC

Heavy Chain 2:

C - DN32 HC

Basic

Advanced

Delete selected

From Chain	From Chain Id	From residue	To Chain	To Chain Id	To residue	Bond Type
B	2	1	C	3	1	Peptide
						Disulfide
						Peptide

Note that the **Chain Id** equates to each row in the Composition type table in sequential order. In the example above, the crosslink is defined as going from residue 1 of Chain B of Chain Id 2, which is Light Chain 2 in the table above, to residue 1 of Chain C of Chain Id 3, which is Heavy Chain 1 in the table above.

The **Expected Type** dropdown is also available for all composition types with the options of Desired and Undesired.

Expected type:

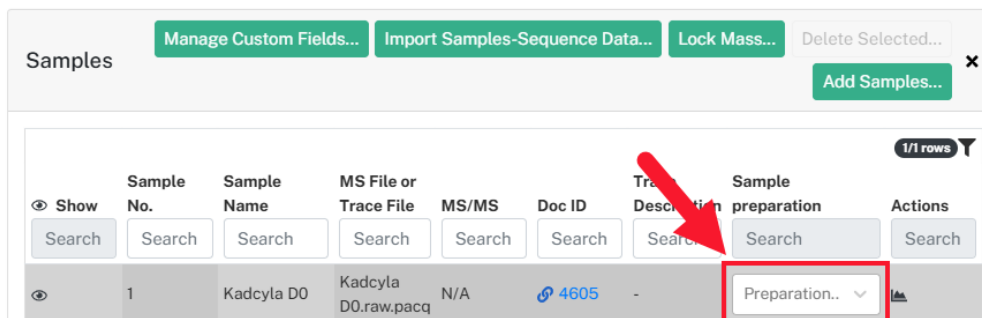
Desired

Desired

Undesired

- **New Sample Preparation column now available in the Samples table in the Samples room**

The **Sample Preparation** columns captures the inclusion of enzymes, reduction, and alkylating agents in the preparation of each sample. The Sample Preparation dialog can be launched for each sample by clicking on the dropdown within the column per sample:



The **Enzymes** section allows the user to specify the inclusion of several different enzymes, the cleavage rule, and the number of missed cleavages. Users can select multiple enzymes.

Sample Preparation

Enzymes:

<input type="checkbox"/>	Enzyme	Cleavage rule	Missed cleavages
<input type="checkbox"/>	IdeS	-	0
<input type="checkbox"/>	SpeB	-	0
<input type="checkbox"/>	IgdE	-	0
<input type="checkbox"/>	GlySERIAS	-	0
<input type="checkbox"/>	Trypsin	R, K C-termini	2

The **Reduction** section allows the user to specify whether the sample has been reduced to remove inter-chain disulfide bonds.

Reduction:
☐ Reduced ?

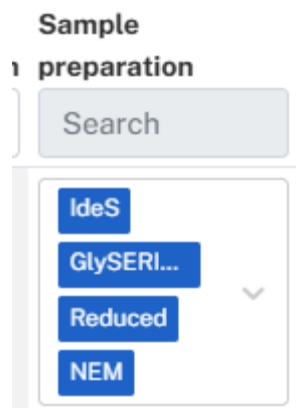
The **Alkylating agent** allows the user to select an alkylating agent used from the dropdown. Options include None, NEM, Iodo Acetic Acid, and Iodacetamide.

Alkylating agent:

None

Ok Cancel

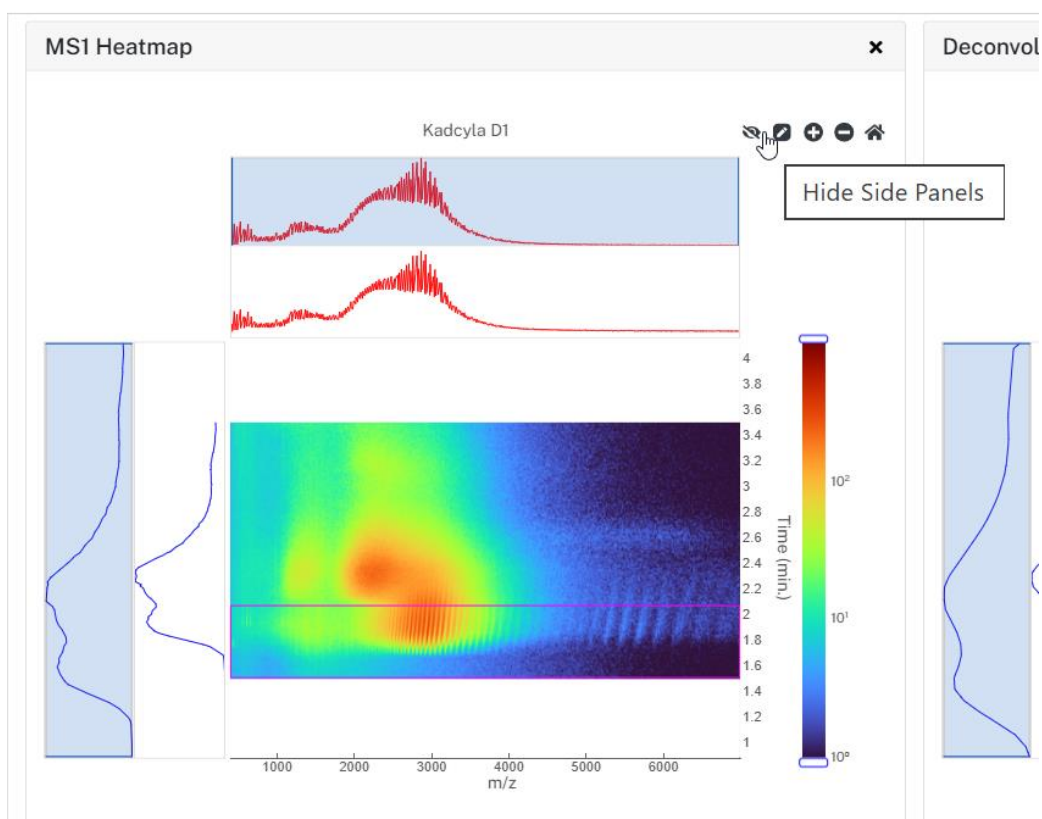
Once items are added in the Sample Preparation dialog, they are available as pills within the dropdown for the sample.



- **Heatmap improvements**

- **Users can now choose to show or hide their heatmap side panels**

Clicking on the eye icon for each sample will hide all corresponding margin plots and gradient controls. Clicking the eye icon when crossed out will hide the side panels and clicking the eye icon when fully visible will reveal the side panels.



- **Streamlined UI for adding polygons**

Polygon creation controls have been removed from the header of the MS1 heatmap widget and are now located with the zoom controls. The controls available for each heatmap are as follows:



controls side panel (gradient control, margin plot) visibility

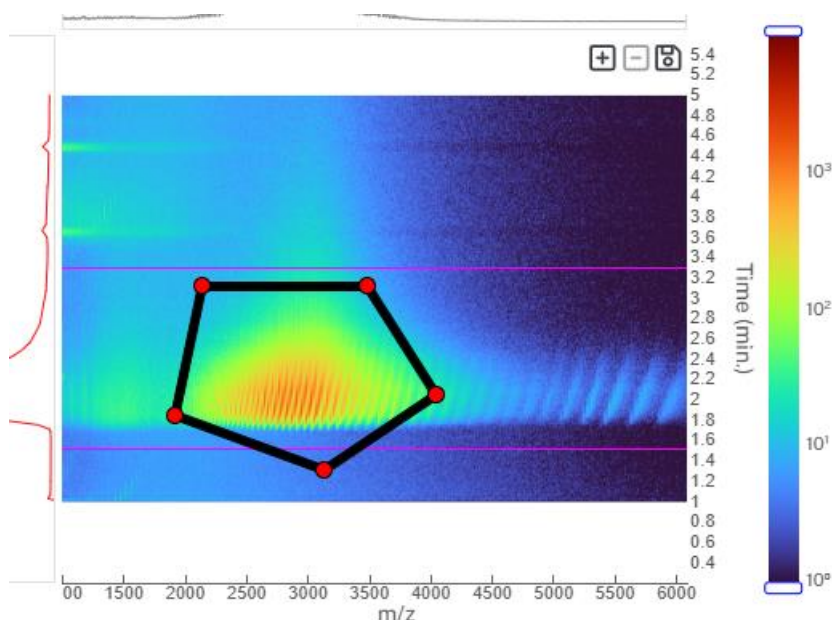
(new) enables polygon creation controls on the heatmap

zooms heatmap in

zooms heatmap out

returns heatmap to home view

When polygon controls are enabled, the edit icon turns blue . Clicking on the heatmap when polygon controls are enabled and the icon is selected adds a single red node (which will eventually be part of a polygon) to the heatmap. Clicking again will add another node which connects to the previous node.



Hovering over an existing node will illuminate it in magenta. Clicking on the node and dragging will allow the user to move it within the heatmap.

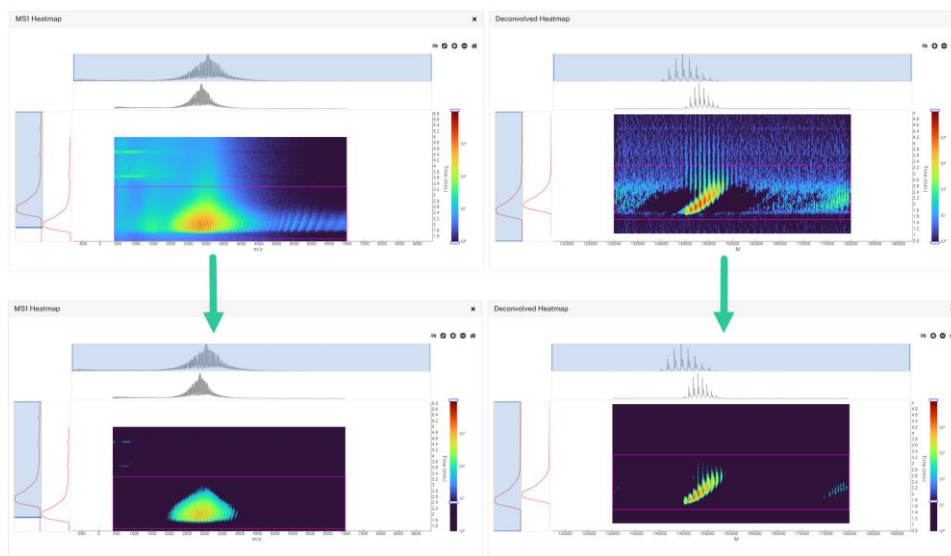


Clicking the icon turns on deletion mode. When this icon is selected, clicking on a node will delete it from the heatmap and the polygon shape will adjust accordingly. Deleting all nodes will remove the polygon all together.

Clicking the icon will save the parameters of the heatmap and add/update the Trace Peaks Table with a trace peak derived from the polygon.

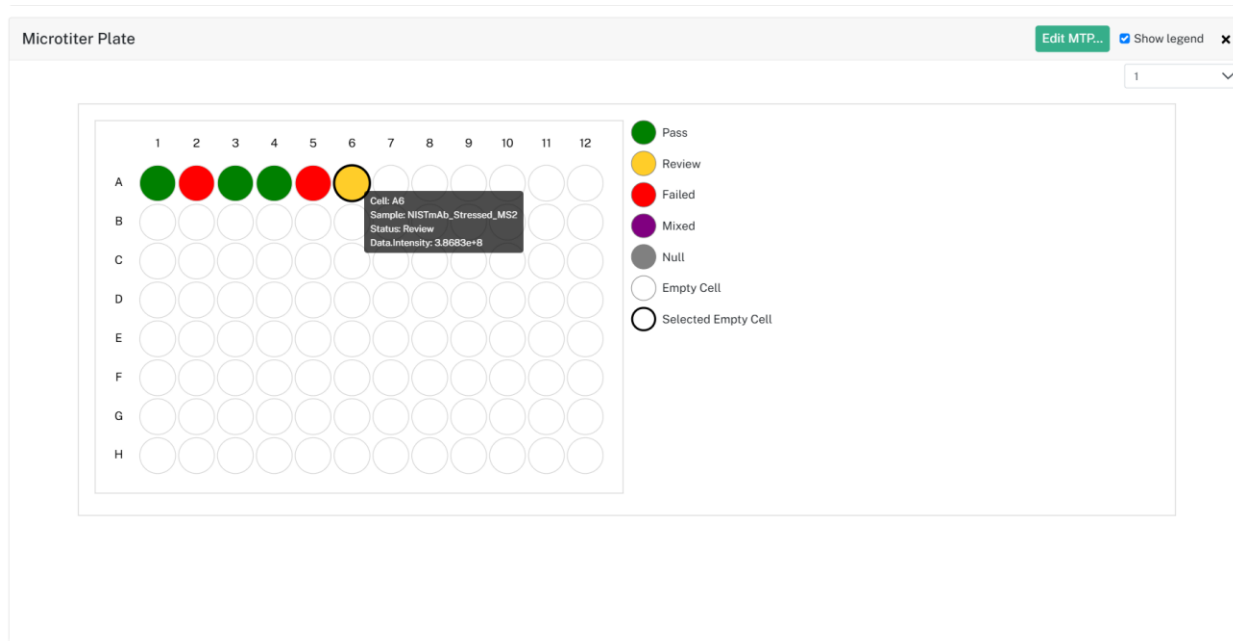
- **Heatmap gradient controls**

New interactive sliders on the heatmap color scale allow users to control the dynamic range, remove background signal, and focus on areas of interest. The gradient will be applied between the user-set positions of the sliders.



- **New Microtiter Plate widget now available in Web Analysis**

A **Microtiter Plate** widget is now available in Web Analysis in the Inspection room. This widget enables users to visualize their data in customizable plate layouts, with options for selecting additional data associated with each plate as well as connection to the Sample Status Review table.



If a user specifies a different value in the Validate column of the Sample Status Review table, this color and updated status will be reflected in the MTP widget for the corresponding sample.

Cell states are represented by the following colors, which correspond with those in the Sample Status Review Table:

- Green for Pass.

- Yellow for Review.
- Red for Failed.
- Purple for Mixed (if a well contains multiple injections with conflicting status values)
- Gray for Null. Null refers to a cell that contains a sample, but the values of interest is neither measurable nor detectable.
- White for Empty. Empty refers to a cell that contains no sample.

Information surrounding each cell can be found in a tooltip available when hovering over the cell. Information includes well identifier (e.g., A1), sample name, and metadata fields defined by the Preset.

Clicking **Edit MTP** opens a dialog which allows the user to select or define a **preset** to use which dictates the information available in the tooltip.

Edit MTP

Preset:

Default preset

▼

Dimensions:

8x12 (96-well plate)

▼

Well ID:

plate_position, plate_row, plate_column

Advanced

Fields:

Metadata.Assay

x

Metadata.Sample

x

×

Select ...

☒ Show Sample Status

Save as preset

Reset

Save

Cancel

Two system presets, **Intact** and **Default**, are available for selection in the dropdown. The Default preset is selected by default.

Parameters in the Edit MTP dialog include **Dimensions**, with available options in a dropdown:

Edit MTP

Preset: Default preset

Dimensions: 8x12 (96-well plate)

Well ID: 4x6 (24-well plate)

6x8 (48-well plate)

8x12 (96-well plate)

16x24 (384-well plate)

32x48 (1536-well plate)

Save as preset

Reset

Save

Cancel

The **Well ID** refers to the metadata fields used to form the association between a sample and its corresponding well in the microtiter plate.

Edit MTP

Preset: Default preset

Dimensions: 8x12 (96-well plate)

Well ID: plate_position, plate_row, plate_column

Advanced

Fields: Metadata.Assay Metadata.Sample Select ...

☒ Show Sample Status

Save as preset

Reset

Save

Cancel

The **Fields** specify which fields (Data or Metadata) will be included in the tooltip for each cell associated with a sample.

Edit MTP

Preset: | v

Dimensions: | v

Well ID: Advanced

Fields:

Metadata.Assay

Metadata.Sample

Select ...

x

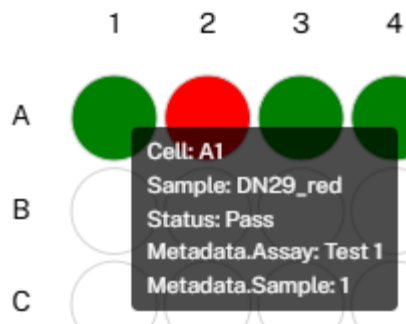
x

x

☒ Show Sample Status

Save as preset Reset Save Cancel

For example, if the **Default** preset is selected, the `Metadata.Assay` and `Metadata.Sample` information associated with a sample will be viewable in the tooltip when hovering over that sample's cell:



Users can create their own custom preset by specifying the parameters they wish to save in the Edit MTP box then clicking **Save as Preset** and providing a unique name.

Checking **Show Sample Status** enables the view of the **Sample Status Review** table widget, which provides corresponding information surrounding a sample's status.

The **Advanced Plate Configuration** is intended to shield end-users from the complexity of parsing plate, row, and column information such as A2, G:A2, G:A,2 (representing optional plate G, row A, column 2).

Advanced Plate Configuration

Sample: Add new +

Mapping:

Factor	Group	Value	Metadata Field
1	plate_position		Metadata.Plate Position ▼
2	plate_row	A	Metadata.Plate Row ▼
3	plate_col	1	Metadata.Plate Column ▼

Apply Cancel

The **Sample dropdown** provides predefined options and can also support user-defined custom samples.

Advanced Plate Configuration

Sample: ▼

Mapping:

- A1
- 1:A2
- 1:A,3
- D1F-A4
- P1-A5

3	plate_col	3	Metadata.Plate Column ▼
---	-----------	---	--------------------------------------

Apply Cancel

If the user clicks **Add new**, the **RegEx** box will be shown and populated with a preset value which supports multiple instrument sample vial configurations, but users can define custom RegEx as well.

Advanced Plate Configuration

Sample:

Inj00022-L0000006935-IM-A6

Add new

Name:

Inj00022-L0000006935-IM-A6

RegEx:

^(?(<plate_position>[A-Za-z0-9]+)[-])?(?(<plate_row>[A-Za-z]+)[,])?(?(<plate_col>[0-9]+))\$

Save

Delete

Cancel

Mapping:

Factor	Group	Value	Metadata Field
1	plate_position		Metadata.Plate Position
2	plate_row	A	Metadata.Plate Row
3	plate_col	6	Metadata.Plate Column

Apply

Cancel

The **Mapping** table outlines the parsed values based upon the selected Sample or custom RegEx which the user can then provide field associations for under the **Metadata Field**. The screenshot below shows the resultant mapping table if the user selects 1:A,3:

Advanced Plate Configuration

Sample:

1:A,3

Add new

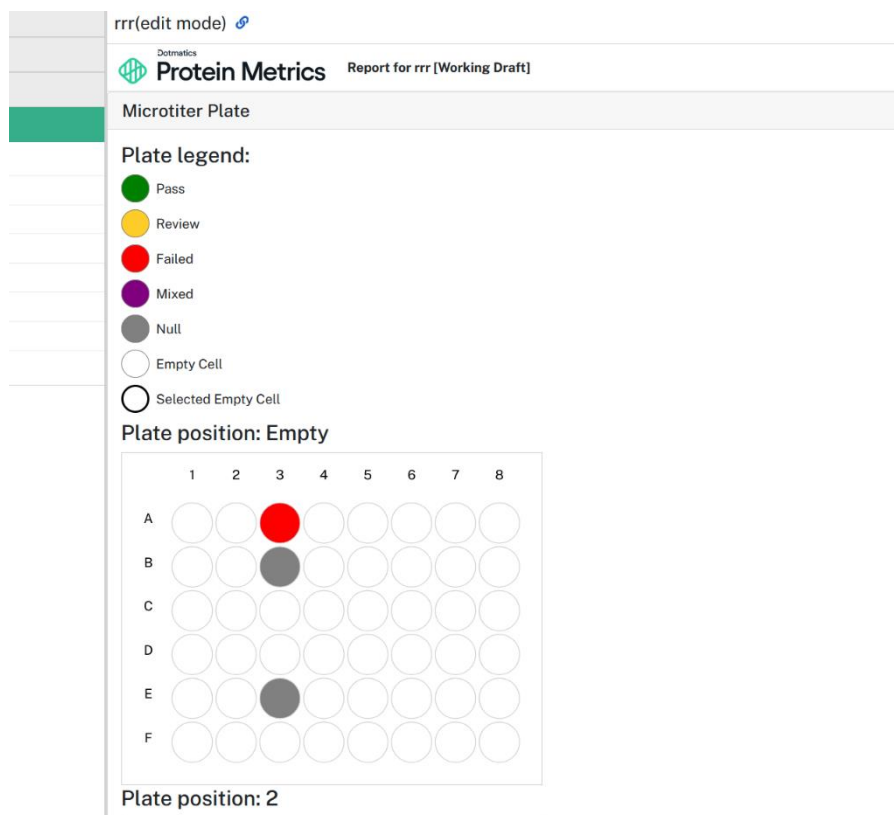
Mapping:

Factor	Group	Value	Metadata Field
1	plate_position	1	Metadata.Plate Position
2	plate_row	A	Metadata.Plate Row
3	plate_col	3	Metadata.Plate Column

Apply

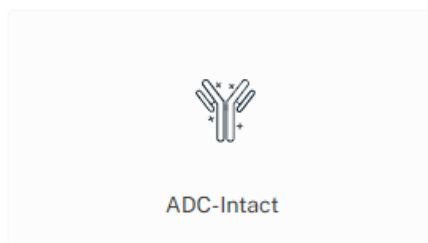
Cancel

All Micro Titer plates can be displayed within the **Report** room.



- **New ADC template available in Web Analysis**

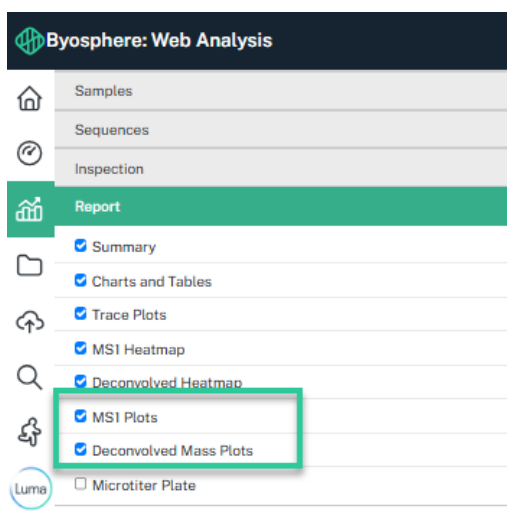
A new template, **ADC-Intact**, is now available in Web Analysis. This template uses deconvolution analysis for the purpose of analyzing Protein+Linker+toxic payload.



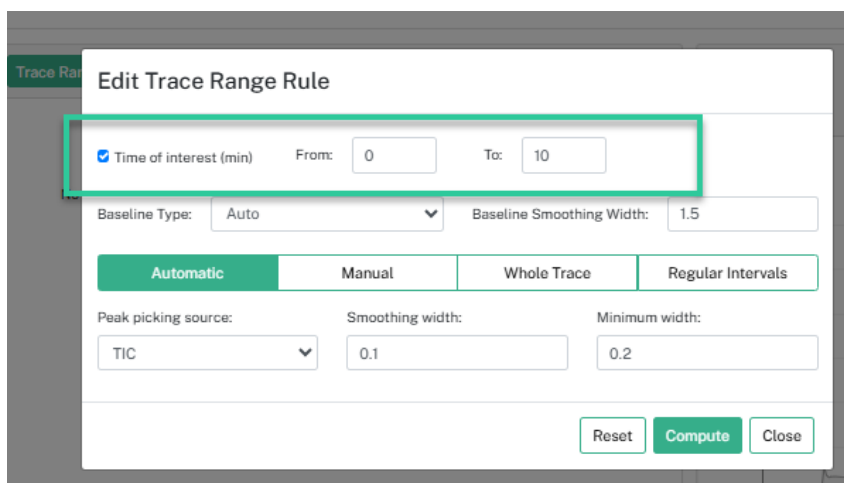
- **Updates to Progressive Deconvolution template**

The following updates have been made to the Progressive Deconvolution template in Web Analysis

- The MS1 and Deconvolved Mass plots are checked by default in the Reports room.



- A default trace range rule time of interest from 0 to 10 is now defined in the workflow



- **Optimization of Intact Deconvolution for Progressive Deconvolution**

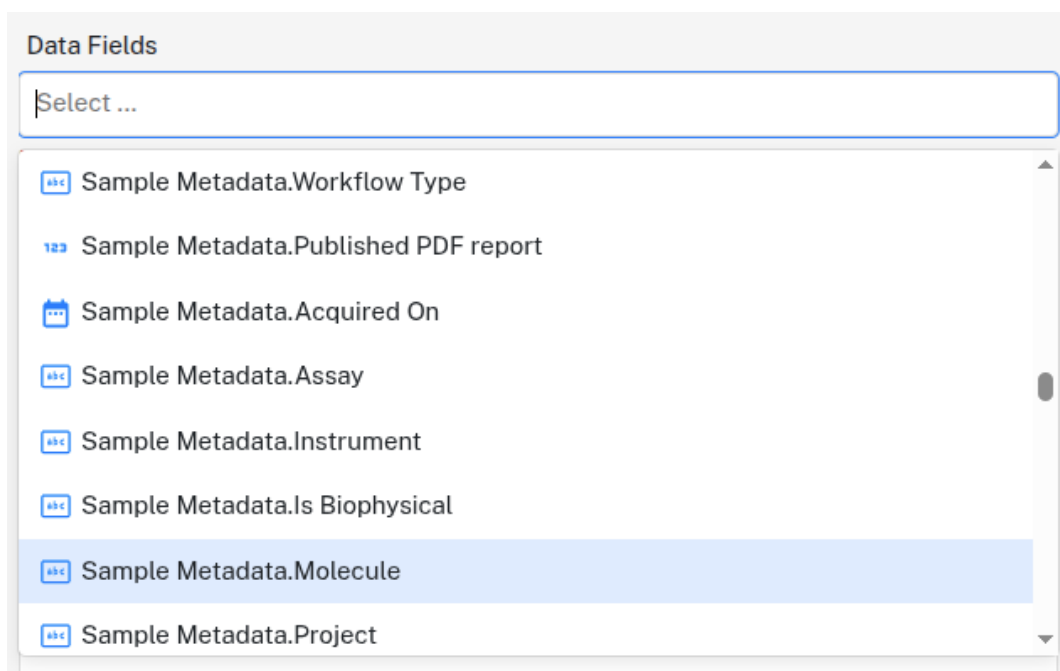
Intact Deconvolution in Web Analysis has been optimized for better progressive deconvolution results. The behavior compared to the Desktop application is therefore different. Users can expect that absolute intensities of deconvolved masses will be ~10-fold less in Web Analysis when compared to the same analysis performed using Desktop. The default behavior in Web Analysis is to avoid forcing normalization. The same behavior can be achieved when using the Desktop application with the advanced command `Intact/MatchMzIntensity=false`.

Deep Query

- **Users can now make queries using Sample-Level Metadata in Dashboards**

Sample Metadata fields have been added to Deep Query. Sample Metadata exists as a set of fields identical to the Metadata fields but are joined on the sample level (`sample_doc_id`). Users can use these fields like any other field, including filters, derived fields, etc. The prefix will show "Sample Metadata" e.g. `Sample Metadata.Molecule`.

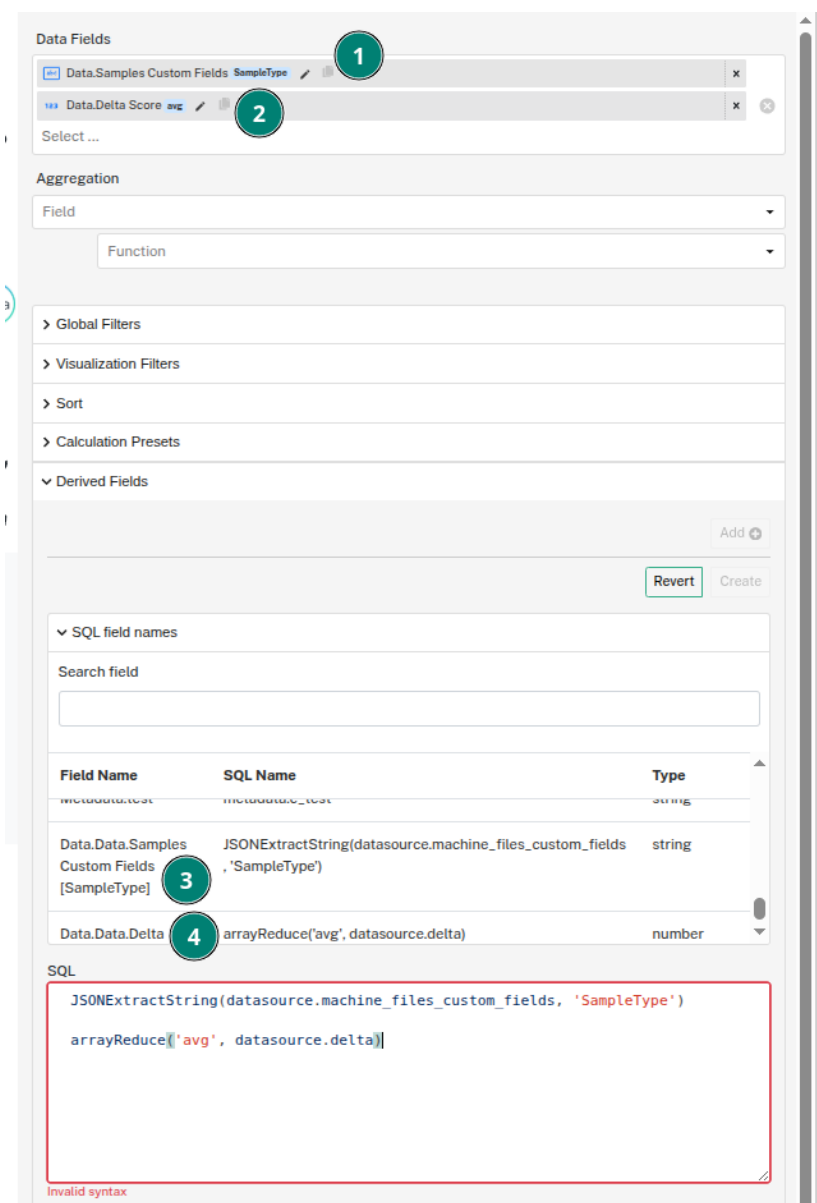
These values will be updated in real-time if the user updates the Sample Metadata within Byosphere. Data is refreshed together with any other metadata field, so it will take about 1-2 minutes to propagate.



- **More user-friendly way to add user-selected custom fields to derived fields**

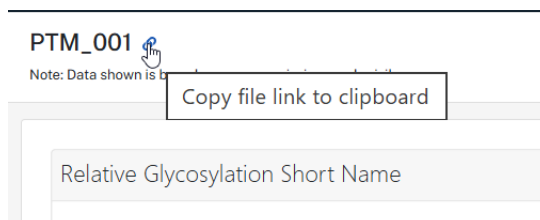
Fields parsed out from Sample Custom Fields are now easily available for selection in derived fields.

The fields created using the field-expansion property, whether for JSON or Array-based, will now appear under the list of available fields in the derived fields tab.



- **Users can now copy their Dashboard ID for sharing in both View and Edit mode**

Added a document sharing icon that allows users to copy the dashboard ID either in edit mode or not.



- **The Data.Peaks # data field in the Chromatogram data source has been updated to match the peak number values in Byos**

The Data.Peaks # field has been updated to a String value and will now reflect Peak# values found in corresponding Byos projects.

Search: 492 records...			Obs. m/z		132.391	
Data.Peaks #	Data.Sequence	Data.Apex Time	[Ref. Sequence]		132.871	133.300
46		136.3771	Pop_Label		133.879	134.009
46		136.5381	_prot_id		134.52	134.413
46a	VVSVLTVLHQDWLNGK	136.4110	Apex time original		134.424	134.487
46a	VVSVLTVLHQDWLNGK	136.4328	Area		134.577	134.628
46a	VVSVLTVLHQDWLNGK	136.5558	End AA		134.413	134.453
46a	VVSVLTVLHQDWLNGK	136.6585	End time		134.488	134.608
46a	VVSVLTVLHQDWLNGK	137.3787	End time Original		137.279	137.792
46a	VVSVLTVLHQDWLNGK	137.7521	Glycans		137.792	137.792
47	THTCPPCPAPELGGPSVFLFPPK	139.4312	Imported comment		139.451	139.451
47	THTCPPCPAPELGGPSVFLFPPK	139.5180	MS2 Score		139.451	139.451
47	THTCPPCPAPELGGPSVFLFPPK	139.5563			139.451	139.451

- The derived field for DAR in the ADC template has been updated to account for the presence of linkers

The derived field which is used to calculate DAR, present in multiple Visualizations within the ADC Dashboard template, has been updated to appropriately capture the presence of linkers within the delta mass.

- New “Number of Peptides” derived field added to HCP Dashboard template

New dashboards created using the HCP template include a derived field called **Number of Peptides** which accounts for both modified, as well as unmodified peptides in the "Concentration Calculation per Protein relative to Recombinant using Top 3 Peptides per Protein" table.

Search: 4 records...			
Data.Protein Accession Name	Data.Sequence	Data.Modifications Name List	Number of Peptides
tr A0A061HZZ5 A0A061HZZ5_CRIGR Ig kappa chain V-l region (Fragment) OS=Cricetulus griseus GN=H671_8g19444 PE=4 SV=1	FSGSGSGTQFSLKISSLEAEDAGIYFCQ QGYNPPSTVIHAMS	Deamidated/0.9840	3
tr A0A061HZZ5 A0A061HZZ5_CRIGR Ig kappa chain V-l region (Fragment) OS=Cricetulus griseus GN=H671_8g19444 PE=4 SV=1	FSGSGSGTQFSLKISSLEAEDAGIYFCQ QGYNPPSTVIHAMS	Oxidation/15.9949	3
tr A0A061HZZ5 A0A061HZZ5_CRIGR Ig kappa chain V-l region (Fragment) OS=Cricetulus griseus GN=H671_8g19444 PE=4 SV=1	FSGSGSGTQFSLKISSLEAEDAGIYFCQ QGYNPPSTVIHAMS		3
tr A0A061HZZ5 A0A061HZZ5_CRIGR Ig kappa chain V-l region (Fragment) OS=Cricetulus griseus GN=H671_8g19444 PE=4 SV=1	VSIACKASEGISDELSWYQKPGK		3

This change will not be reflected in templates created in previous releases. If you wish to reuse a previous template, please copy the derived field code from the latest (Byosphere version 5.12) system template and update your old dashboards.

- New rolling data filter options for Dashboard and Visualization filters

Added two new options for date fields in DQ:

- in the last (duration of time *including* the present)
- in the previous (duration of time *previous to* the present)

Examples:

The screenshot displays the Byosphere Web interface. On the left, a sidebar lists various metadata fields with checkboxes: Metadata.File Name, Metadata.Created On, Metadata.Changed On, Metadata.Acquired On, Metadata.Request On, Metadata.File Size, Data.Apex Time, Data.Charge, and Metadata.Sample ID. Below this is a section titled "Apply Global Filters" which contains a filter configuration panel. This panel shows a filter for "Metadata.Acquired On" set to "is in last 5 Months". The main area of the interface is a table with 1339 records. The table has columns for Metadata.Created On, Metadata.Changed On, Metadata.Acquired On, Metadata.Request On, Metadata.File Size, Data.Charge, and Metadata.Sample ID. The "Metadata.Acquired On" column is highlighted with a green box. Below the table, there is a summary row with labels: Metadata.Crea, Metadata.Chan, Metadata.Acqu, Metadata.Requ, Metadata.Fil, Data.Apex, Data.Charg, and Metadata.Sam.

Virtual Client

- **The Virtual Client expiration time is now set independently from user session expiration**

The expiration time for the Virtual Client is now set independently from user session expiration. Thus, a user's session may expire and they may be logged out of Byosphere, but Virtual Client may continue running.

An admin configuration option exists to set the Virtual Client expiration time. The default the Virtual Client expiration time is 15 minutes

The Virtual Client will not be shut down when the user explicitly signs out and will only be shut down once the Virtual Client's own timer expires.

- **Virtual Client idle time behavior**

A user's session of Virtual Client will remain active and accessible while Byos for Byosphere is actively being used (i.e. interacting with the UI) or while Byos for Byosphere is performing a long-running background process.

A user's sessions of Virtual Client will be idled (stopped, suspended) after 15 minutes of inactivity (e.g., the user is neither interacting with Byos for Byosphere nor performing a long-running background process).

After a Virtual Client session has been idled, the user can restart the session by clicking on the Virtual Client tab in the Web Client and pick up where they left off. Local changes will still be preserved if the Virtual Client goes idle.

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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.



Byosphere

Enter your Email and click Submit to request a password reset.

[Back to Sign In](#)

Submit


- **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**

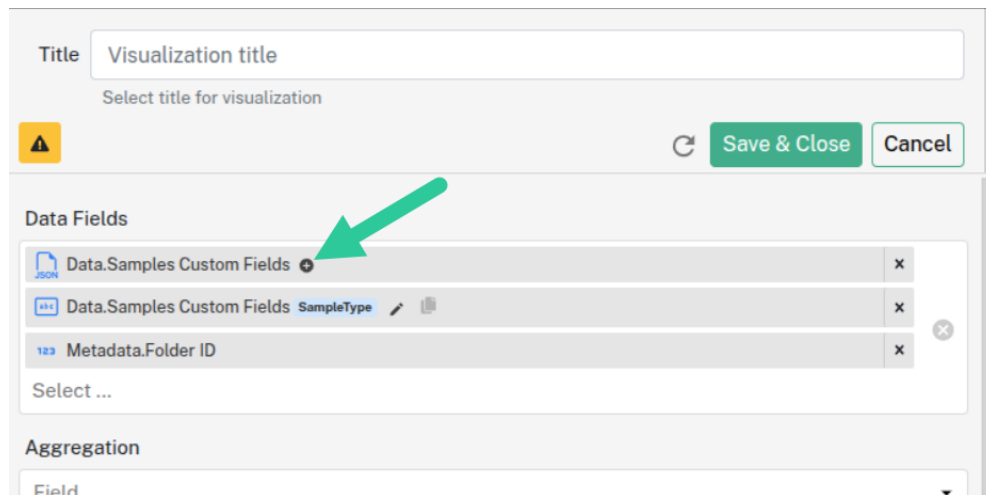
Publishing a Web Analysis will now generate a Deep Query Import job associated with the analysis that can be seen within the Jobs page.

 	3779	doc_7770_1_test.wa	Completed	DQ Import
	3774	doc_7770_1_test.wa	Failed	DQ Import

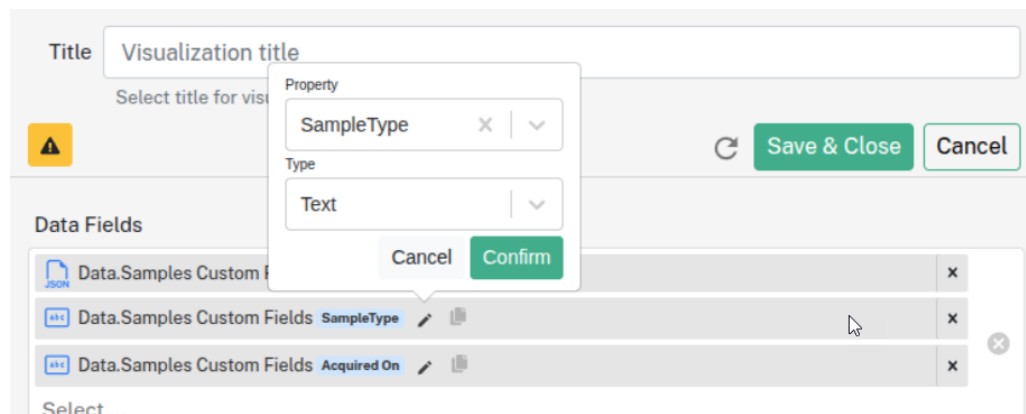
Deep Query

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

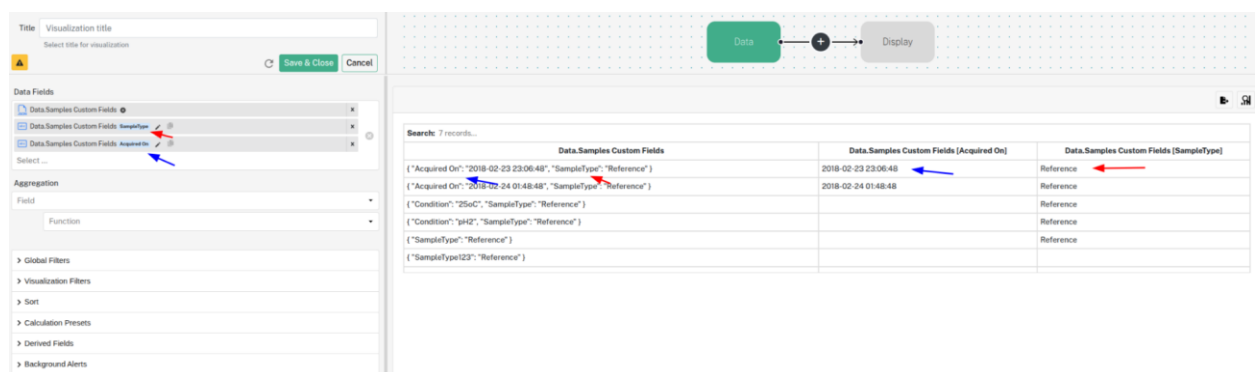
Users can parse individual fields from "Data.Samples Custom Fields" to use in querying, filtering, visualization, and calculations. A plus sign icon displayed next to this field indicates the ability to parse.



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.

Sample 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**

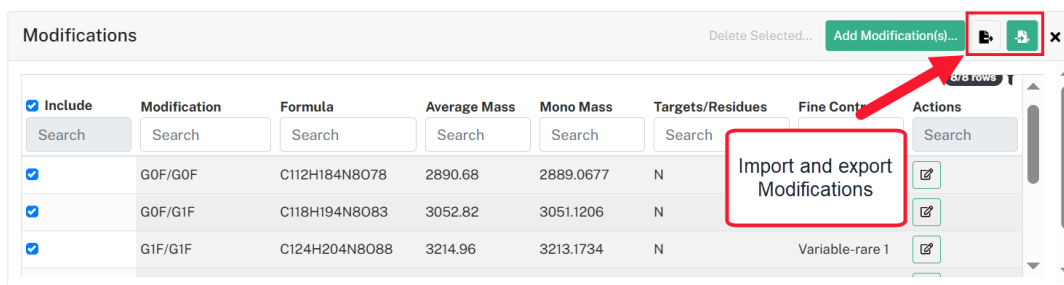
- **Glycan Adduct**

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.



Modifications

Delete Selected... Add Modification(s)...


<input checked="" type="checkbox"/> Include	Modification	Formula	Average Mass	Mono Mass	Targets/Residues	Fine Cont	Actions
Search	Search	Search	Search	Search	Search	Search	Search
<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

- > Deep Query Dashboards
- > Deep Query Golden Projects
- Fasta
- ▼ Files
 - Analysis Results
 - Large files
 - > Report Templates
 - Small files
- Metadata
- PMI - Automation
- > QA - Automation

File name:

Likewise, CSV files containing the values required to populate the Modifications table can also be imported by clicking the  icon which will launch a dialog where the user can select which modification file they wish to import into the table.

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.

Trace Peaks Table

Progressive deconvolution

Trace peak deconvolution

Edit Deconv. preset

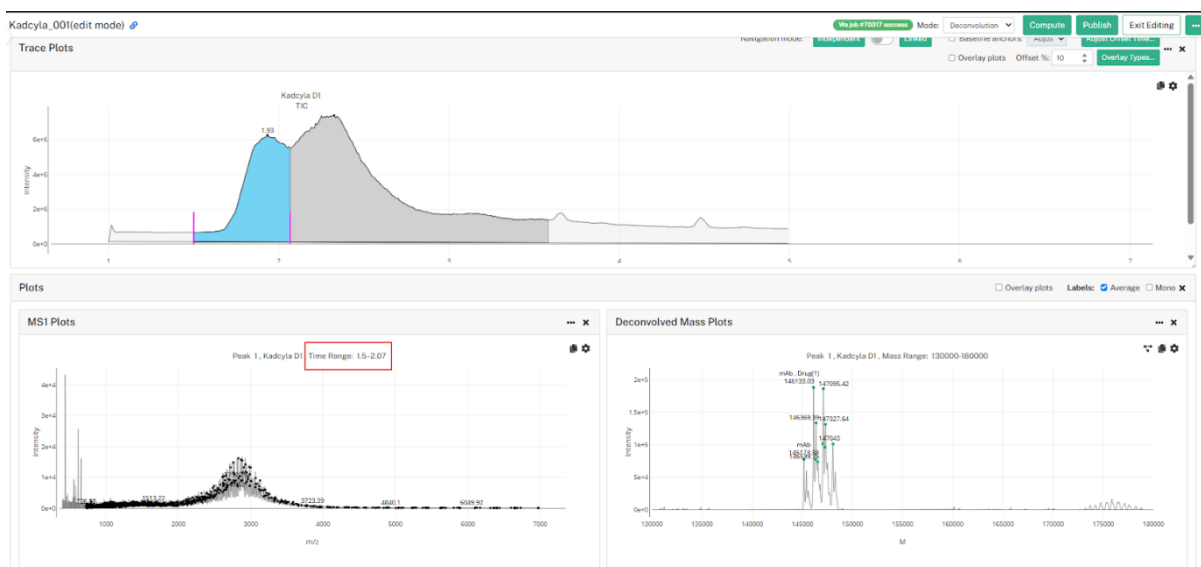
Delete Selected...

Update

17/17 rows

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

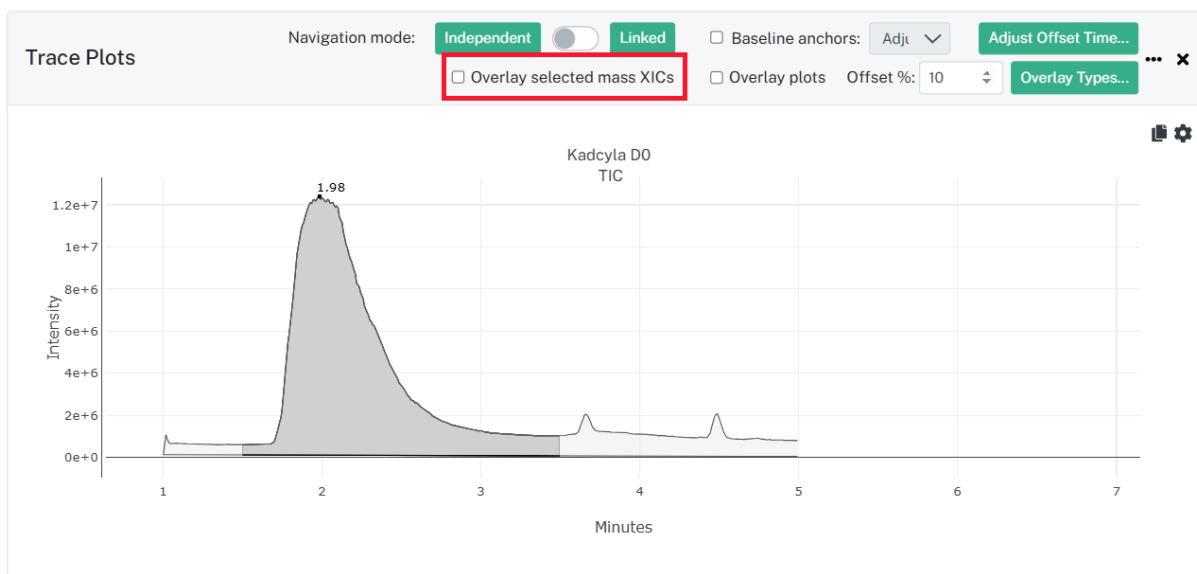
For example, when a user selects **Trace Peak Deconvolution**, the range used for deconvolution is directly associated with the range from trace peak integration. The figure below shows the range for the MS1 plot corresponds with the highlighted peak, where the time range is 1.5-2.07 minutes.



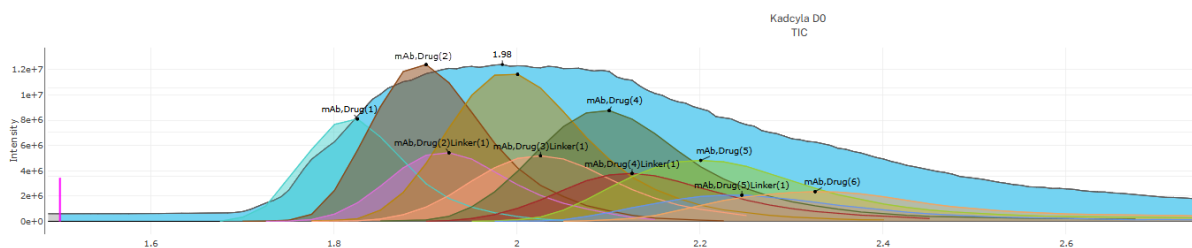
When a user selects **Progressive Deconvolution**, deconvolution is no longer restricted to the integrated trace peaks. Instead, a user may specify windows to produce multiple slices for deconvolution. They may also specify an overlap between these windows. In this way, Deconvolution is no longer restricted 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)
--------	---------------------	--------------------	----------------------------------	------------------

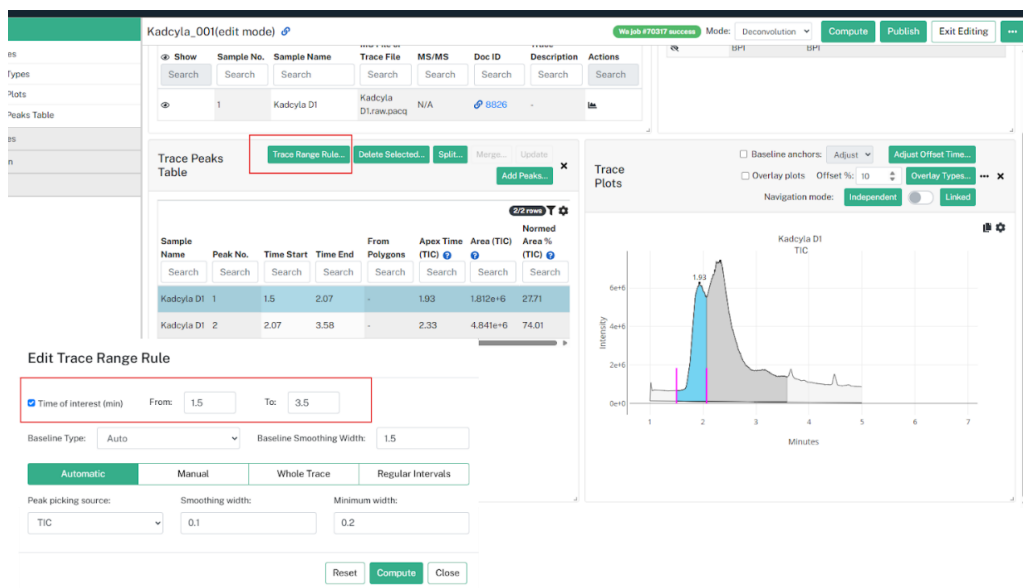
Sliding window width (min)

Sliding window overlap (min)

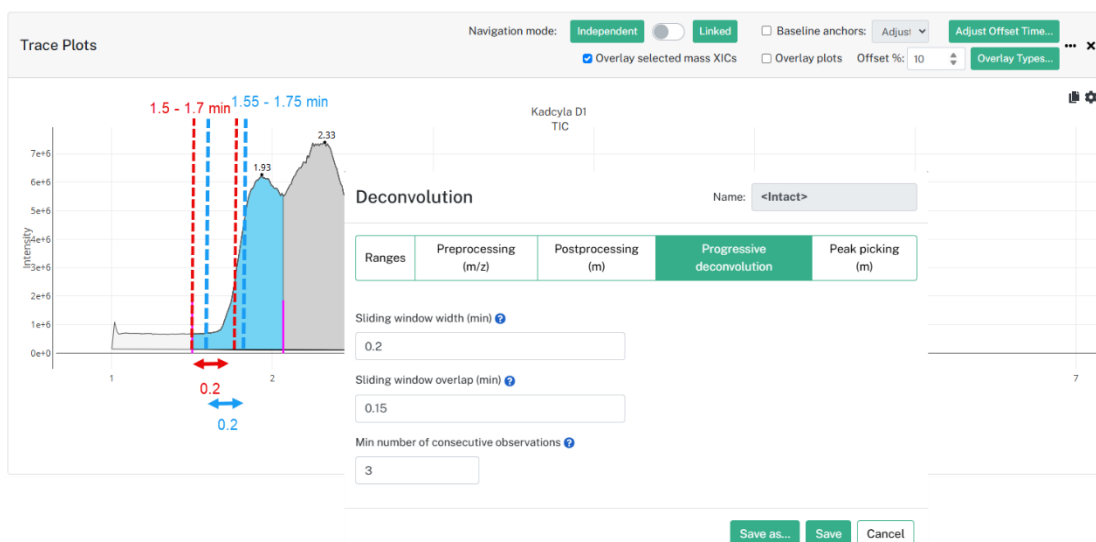
Min number of consecutive observations

- **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).

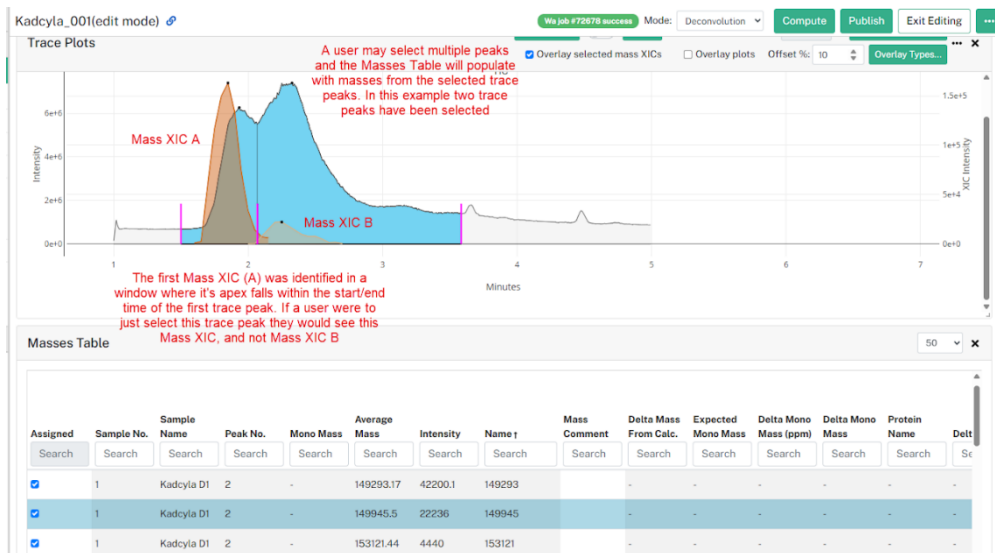
Again, as the window is set to 0.2, the second slice will end at **1.75**, making the time range of the second slice **1.55 - 1.75 minutes** ($1.55 + 0.2 = 1.75$). Deconvolution will be performed on *each* slice using the deconvolution parameters specified in the preset tab. The table below shows all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

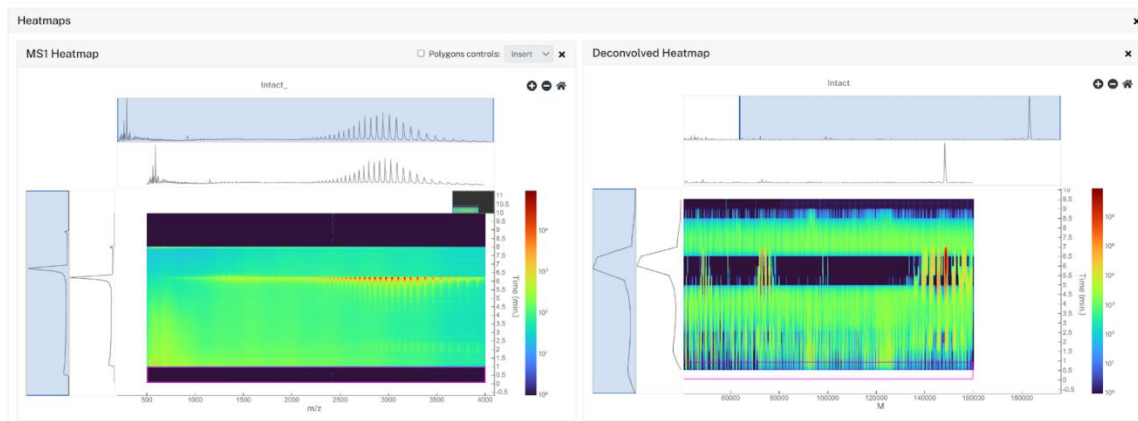


When a user selects a mass from the Masses Table, the MS1 and Deconvolution plots displayed are taken from this slice:

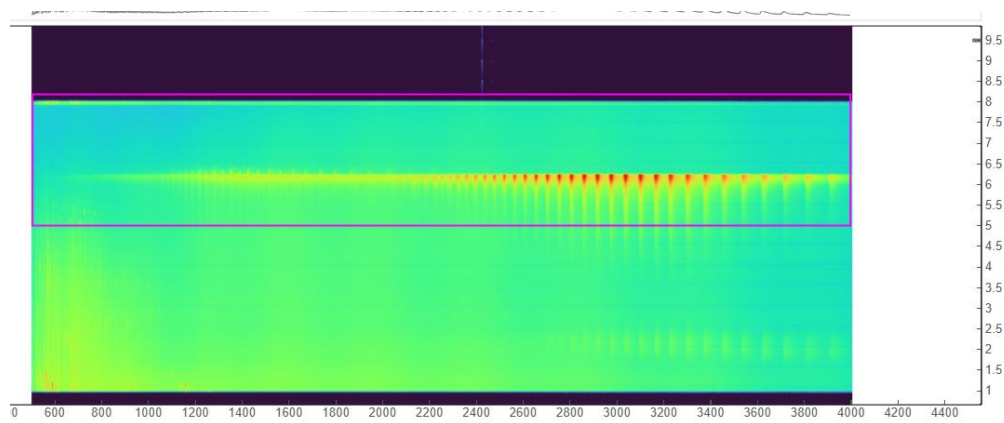


- **New Heatmap Widget now available within Deconvolution Web Analysis**

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.

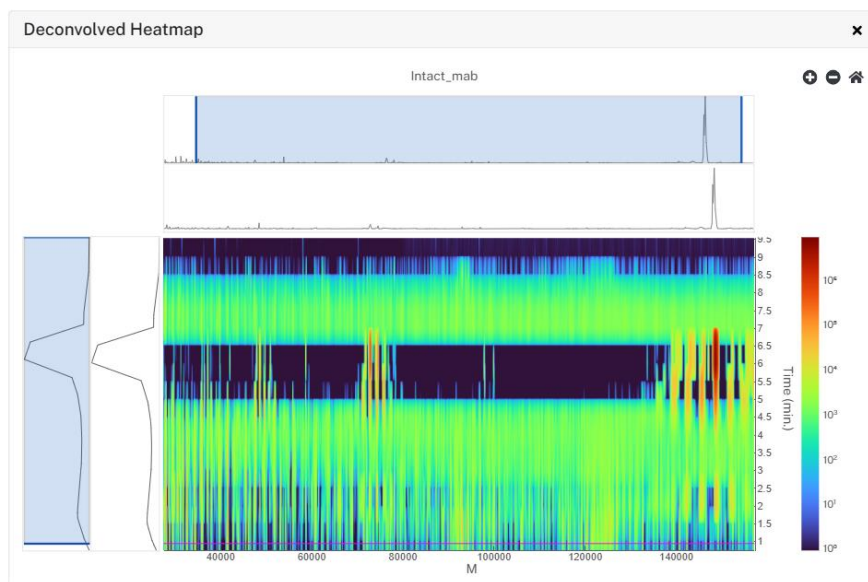


If multiple rows are selected in the trace peaks table, multiple regions will be highlighted on the heatmap. Heatmaps are generated for each input sample. For a sample's heatmap to be displayed, a trace peak from that sample must be selected.

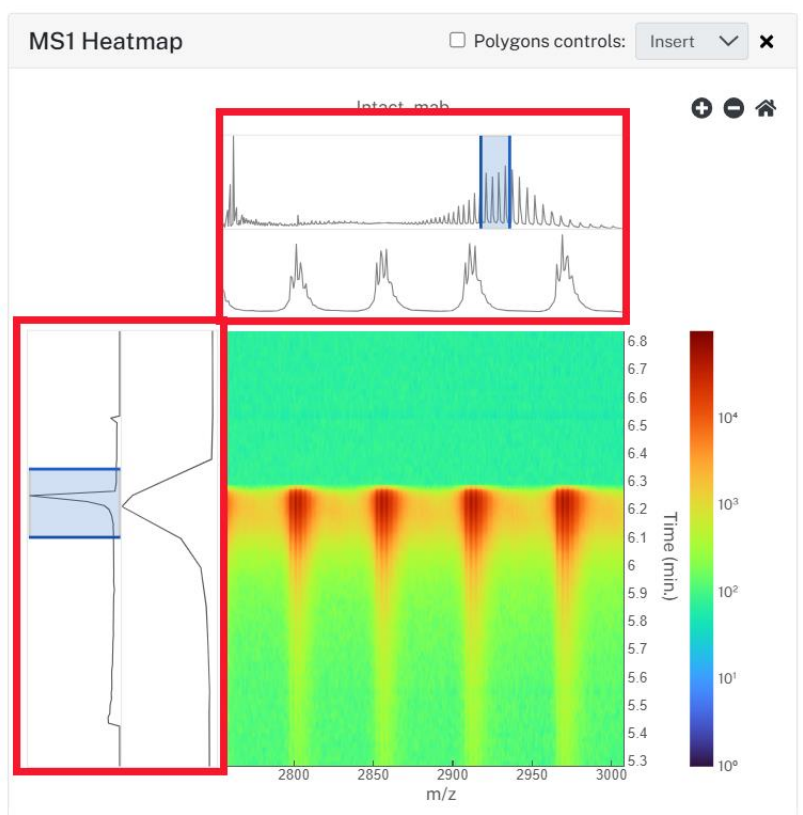
The heatmaps have the following dynamic zoom controls:

- 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

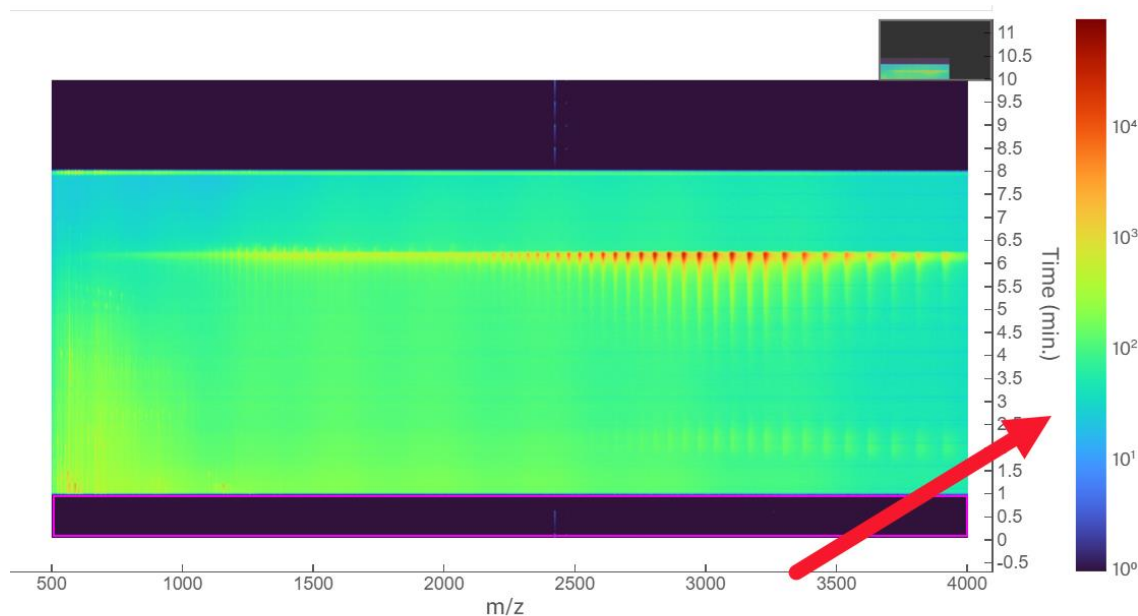
When a user selects **Progressive Deconvolution** mode, deconvolution is no longer restricted to the integrated trace peaks. Instead, a user may specify windows to produce multiple slices for deconvolution. As a part of selecting Progressive Deconvolution, an additional Deconvolved heatmap is created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



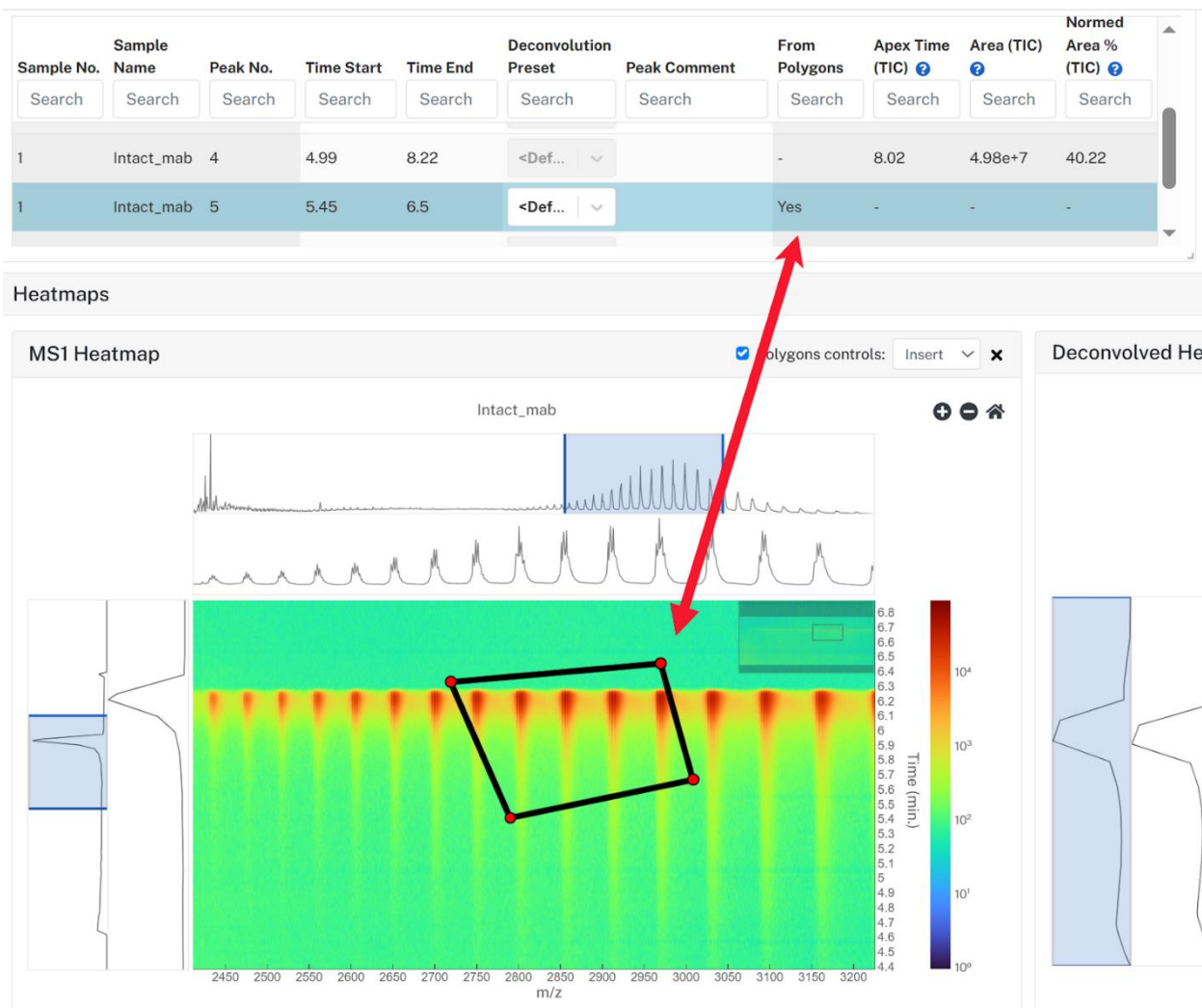
Alongside each heatmap are **margin plots** which display the corresponding trace plot and the m/z or M spectra, respectively. Each margin plot contains two stacked instances of the same data – the bottom trace will change boundaries as the user zooms into areas of the heatmap. The top trace will remain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



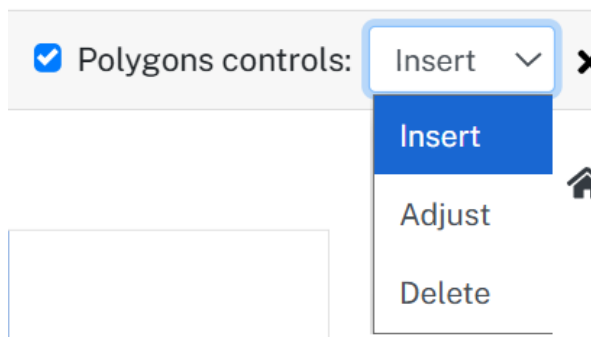
A color scale on the right side of the Heatmap denotes the relationship between pixel colors and signal intensity.



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.

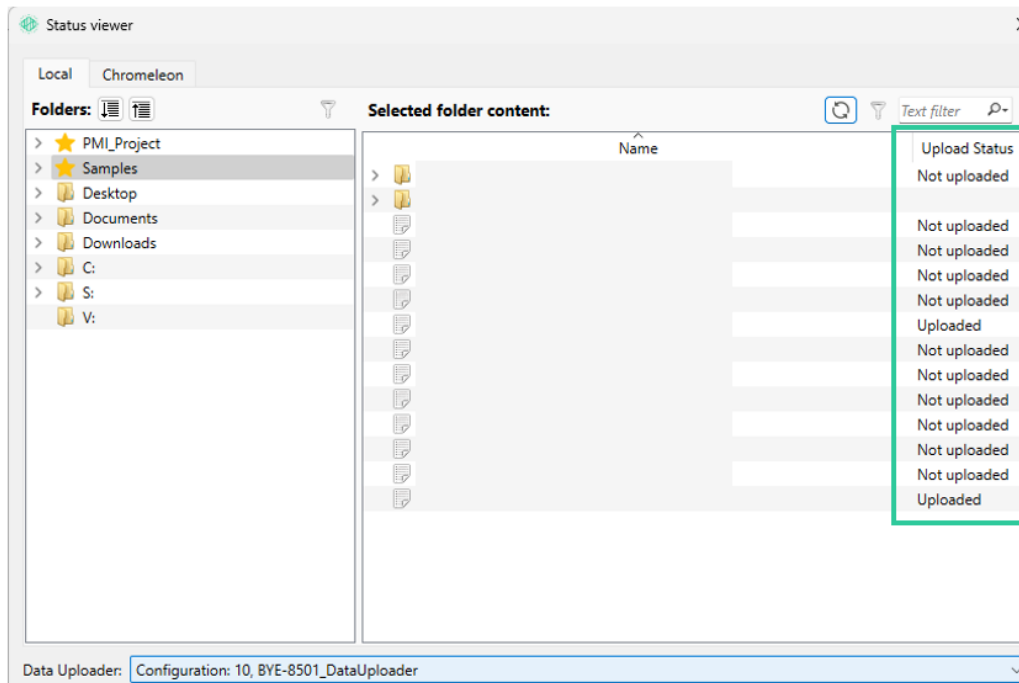


Release 2025-07 (v5.10)

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.MS Alias Name	Glycan Short Name	SUM(Relative Glycan Quant)
09315_E_SN_NIST_Guanidine_CTryptsin	G2F NA	0.507553603609197
09315_E_SN_NIST_Guanidine_CTryptsin	GlcNAc	0.09663941557671231
09315_E_SN_NIST_Guanidine_CTryptsin	Man3	0.12819015909568296
09315_E_SN_NIST_Guanidine_CTryptsin	Man3 + GlcNAc	0.17689039263642065
09315_E_SN_NIST_Guanidine_CTryptsin	Man3F	0.40373345402184335
09315_E_SN_NIST_Guanidine_CTryptsin	Man4	0.038639133949044516
09315_E_SN_NIST_Guanidine_CTryptsin	Man5	0.3014283145592117
09315_E_SN_NIST_Guanidine_CTryptsin	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	
Oligonucleotide Analysis	
Intact Analysis	
Combined Analysis	
Chromatogram Analysis	
Biophysical Analysis	

Description
A data source containing data from multiple Oligonucleotide Projects involving Charge State Deconvolution.

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

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.

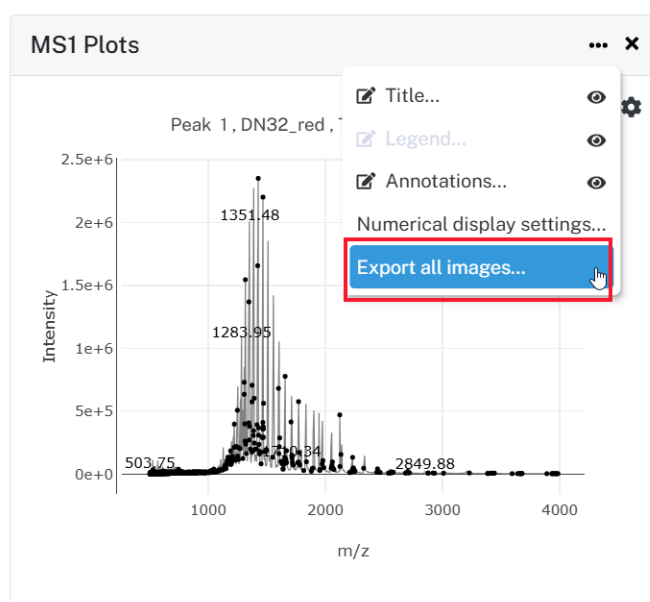
- **New column in the Sequences table, "Molecule Type"**

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**

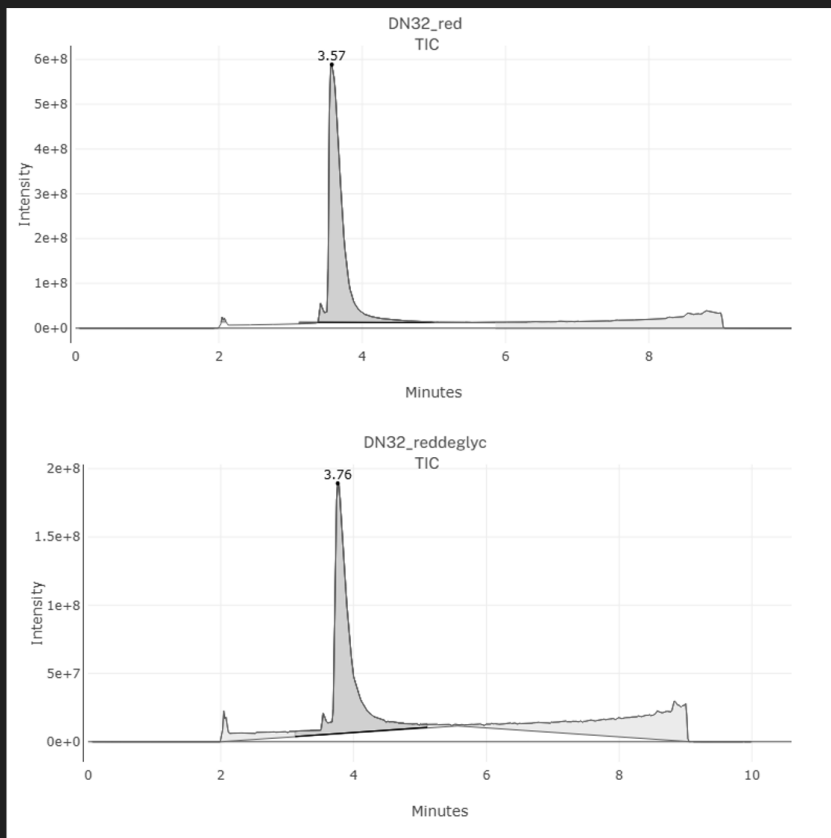
Users can now export an image including all stacked plots within a widget in WA. This feature is available from the three-dot icon in the header of each plot widget.



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”**

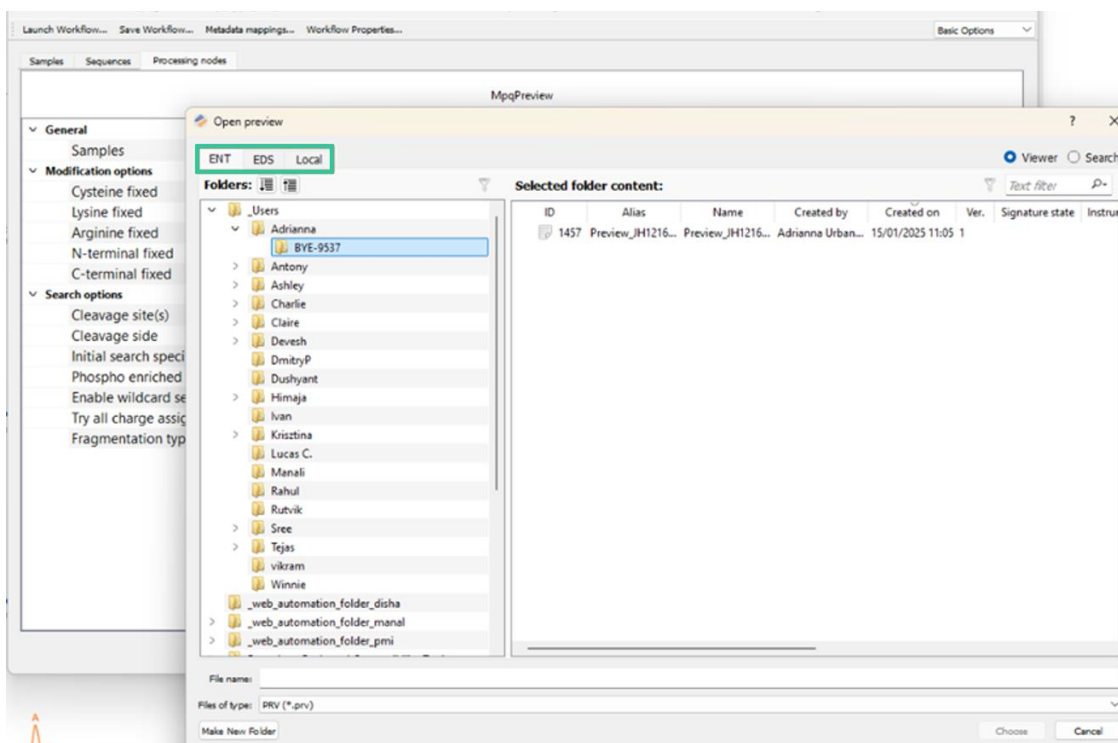
A new reserved metadata field exists in Byosphere called “Acquired on”, which includes the date and time of acquisition of a raw data file if available. This field has the format YYYY-MM-DD HH:mm:ss.SS.

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

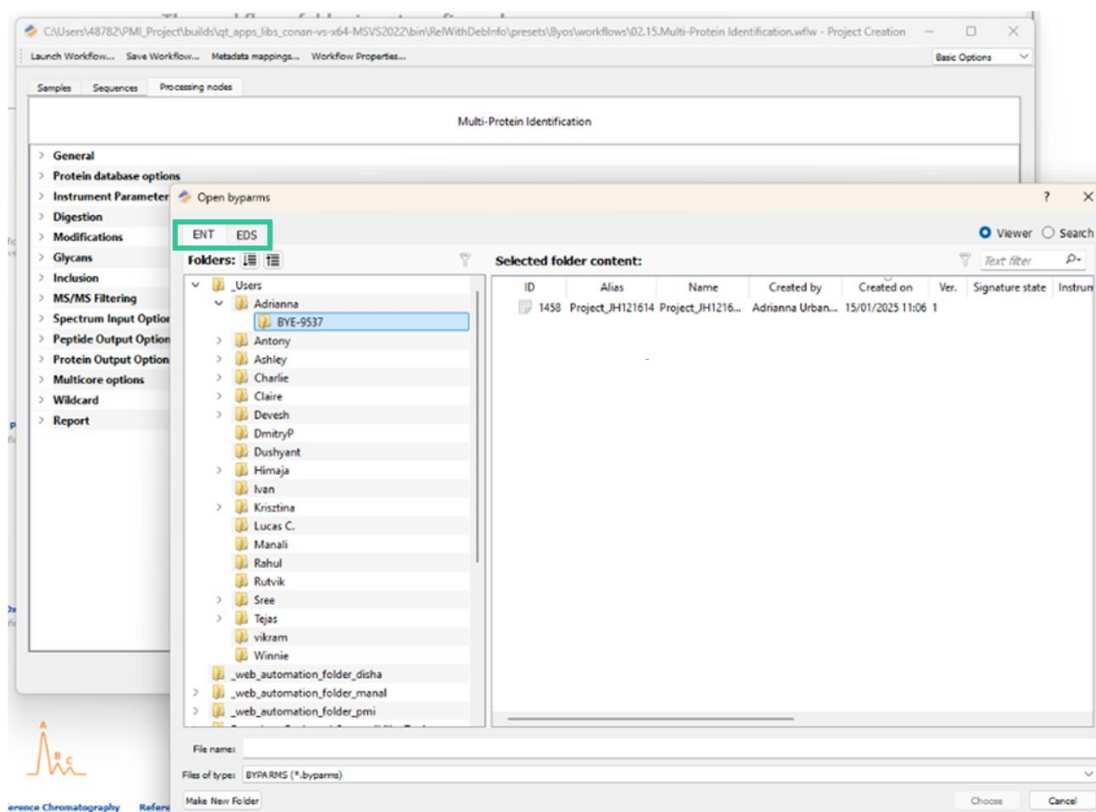
Virtual Client, Byosphere

- 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**

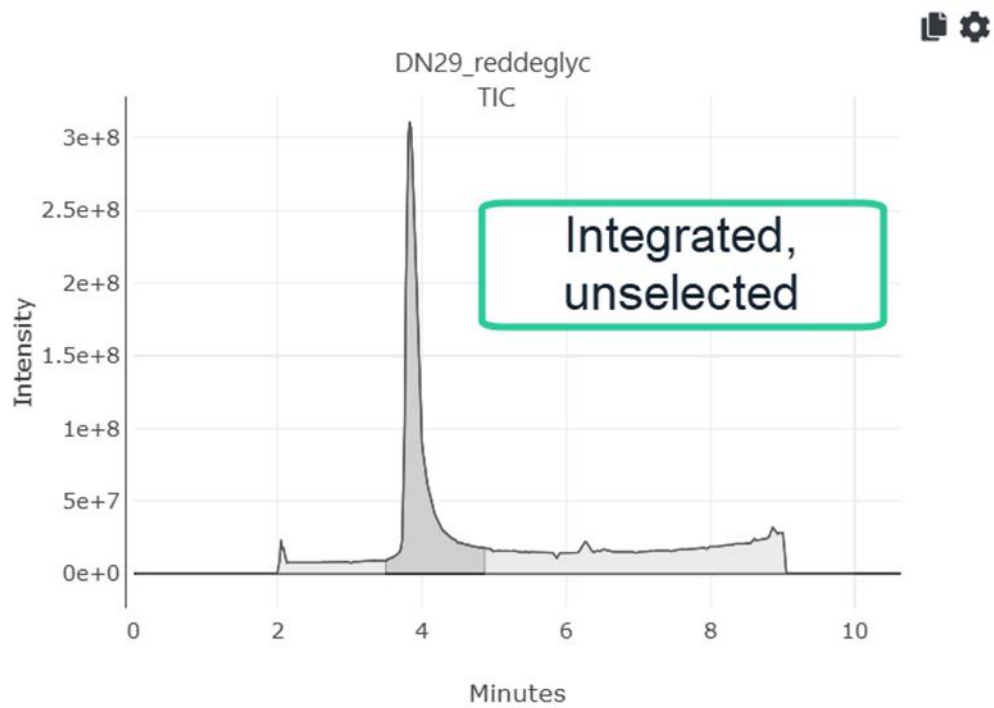
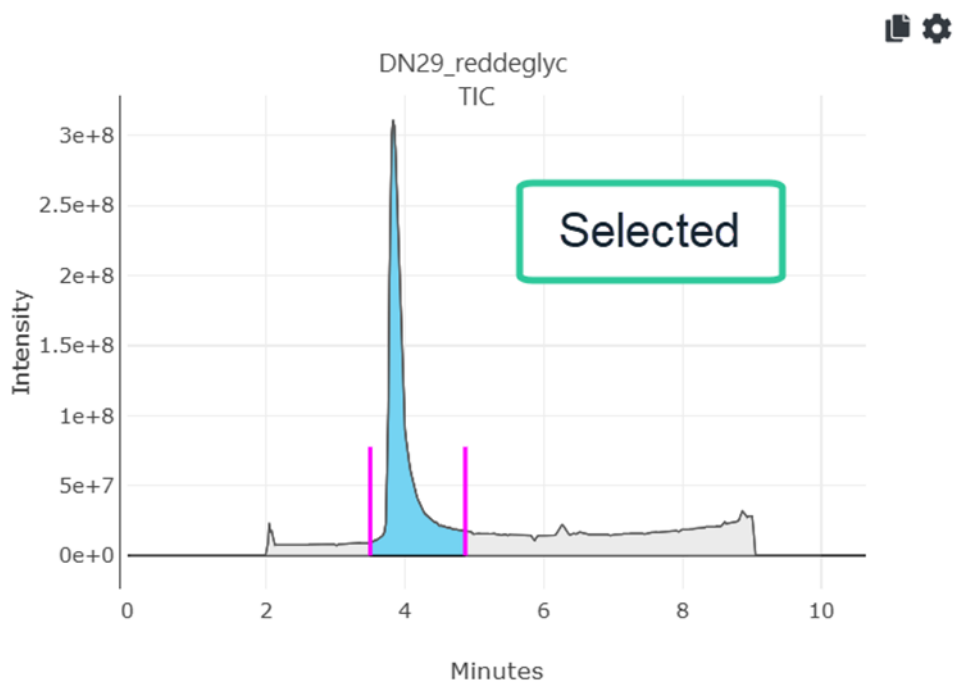
When users use Web Analysis templates to create a new analysis, they are now immediately greeted with their Analysis in Edit Mode for ease of use.

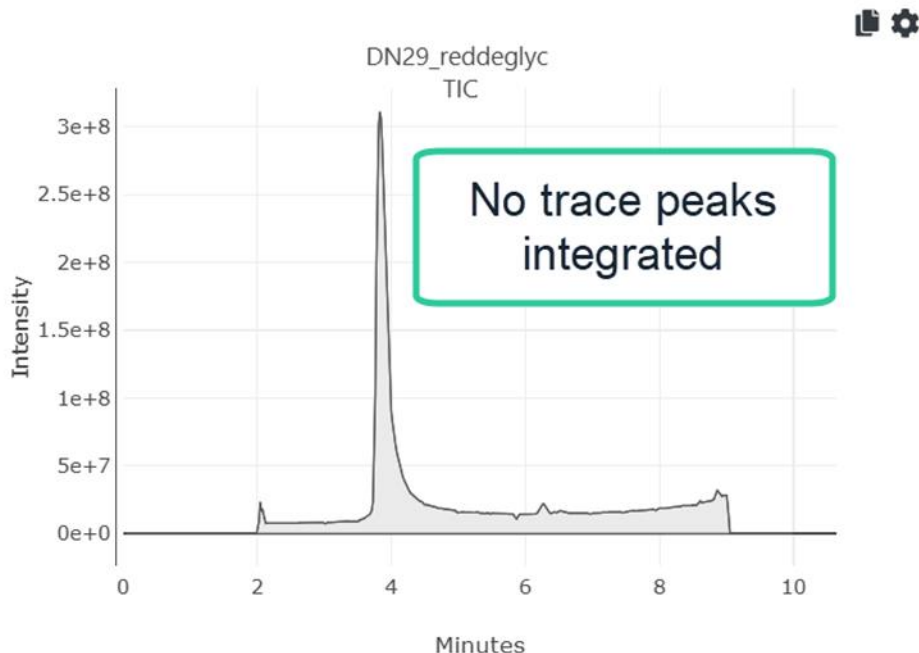
- **Improved behavior for annotations in Trace Plots**

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:

Deep Query, Byosphere

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

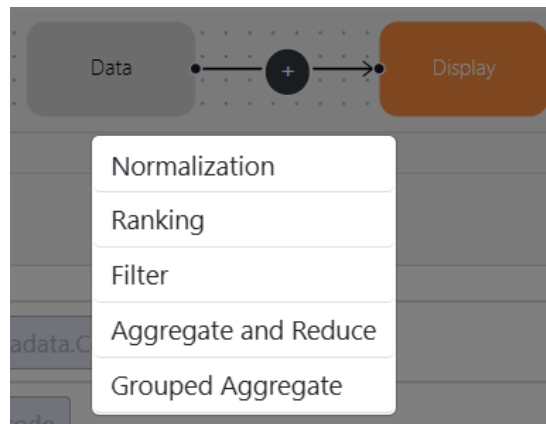
Deep Query Dashboards has been updated with the new Deep Query **Visualization Builder**. This flowchart tool enables users to visualize the flow of all changes that occur on their dataset, from project data ingestion to Visualization generation and display.

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.

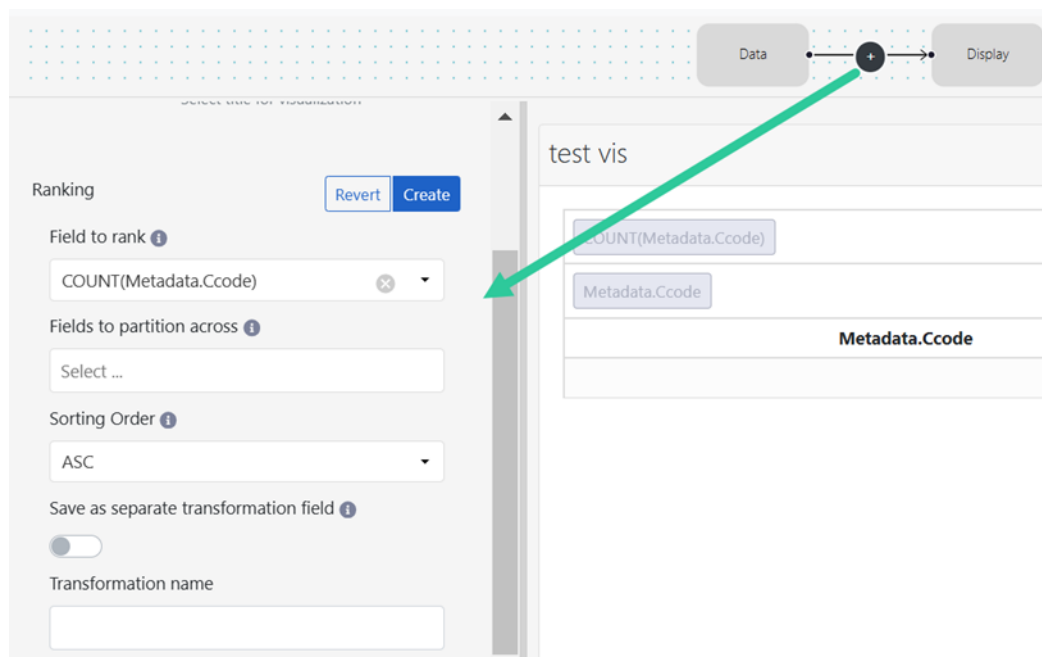
The screenshot displays the Deep Query Visualization Builder interface. At the top, a flowchart shows a sequence: Data (orange box) → + (black circle with a plus sign) → Display (grey box). Below this, the interface is divided into several panels. On the left, the 'Data Settings' panel is active, showing options for 'Select Visualization Type' (Pivot Table), 'Chart type' (Pivot Table), 'Rows' (Select ...), 'Columns' (Select ...), 'Data' (Field), and 'Aggregation' (Aggregation). The 'Display Settings' panel is also visible. In the center, a 'test vis' panel shows a title 'test vis' and a 'Select title for visualization' dropdown. On the right, a data table is displayed with columns: Data.Average PPM, Data.Apex Pout Time, and Data.Document ID. The table contains 10 rows of data. A green box labeled 'v5.8' is overlaid on the 'Rows' field in the Data Settings panel. Another green box labeled 'v5.9' is overlaid on the 'Select Visualization Type' dropdown in the center panel. A green arrow points from the 'v5.9' box to the 'Data' box in the flowchart. Another green arrow points from the 'v5.8' box to the 'Rows' field in the Data Settings panel.

Data.Average PPM	Data.Apex Pout 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

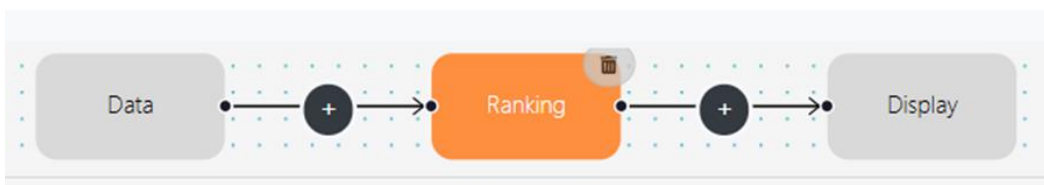
Transformations can be added by clicking on the **+** icon within the flow. Users will be prompted with all available Transformation options for their selected Visualization. Once selected, the lefthand sidebar will populate with options to configure the Transformation and once added, the Transformation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

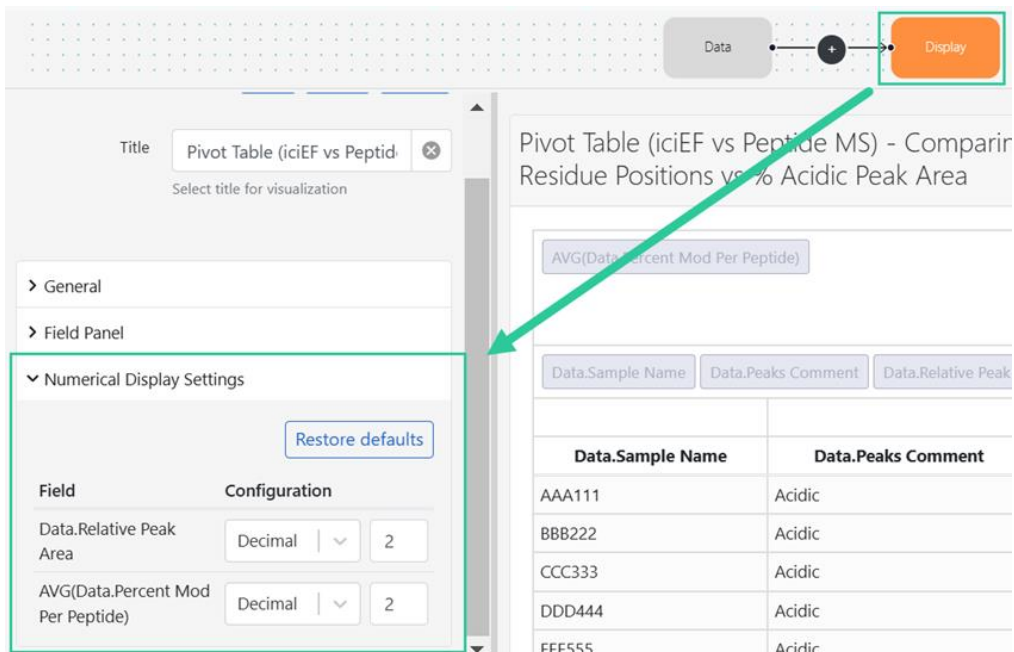


Note that Data and Display are fundamental steps and cannot be deleted.

- **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



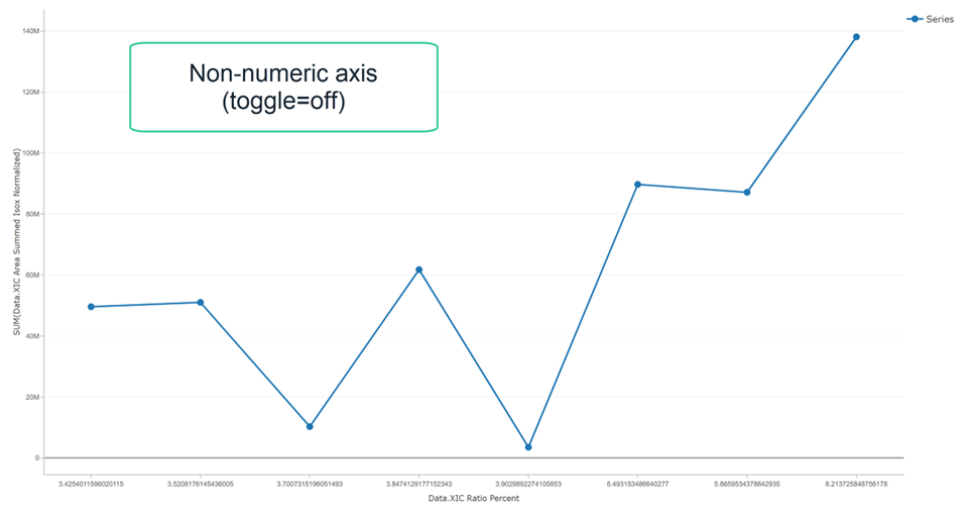
Chart position of X axis

Numeric x-axis

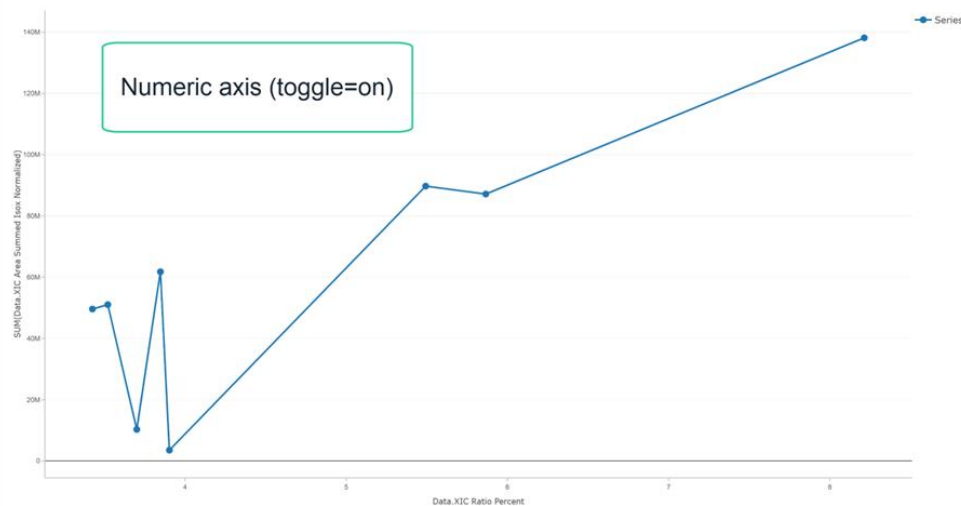


Set x-axis spacing and labels to numeric values

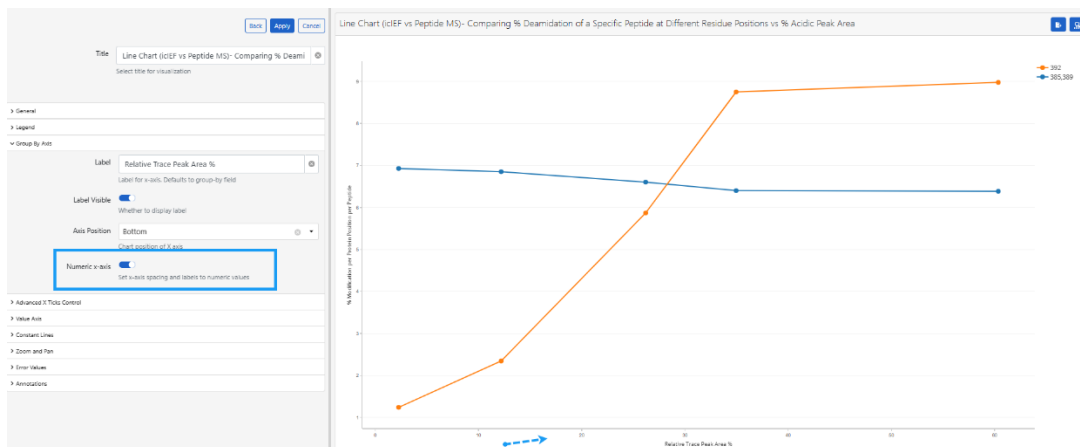
Line Chart Example for numeric X axis



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

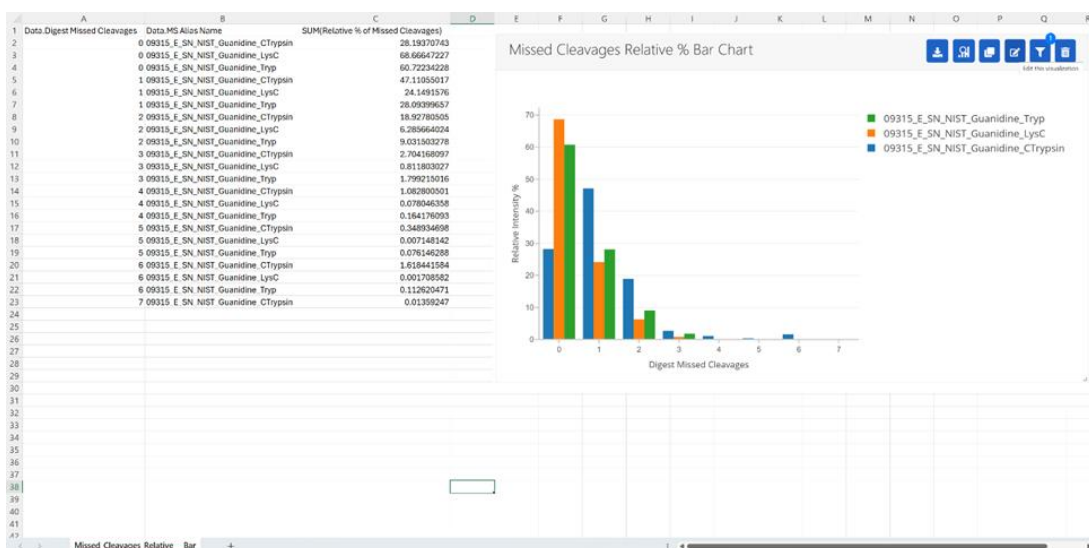


- Users can now export XY data from all Visualizations

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.



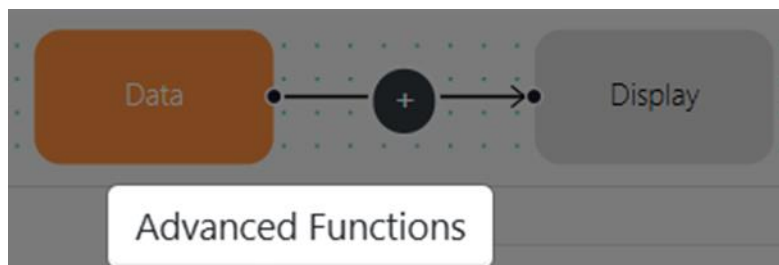
Example output with Visualization on the right for comparison:



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.



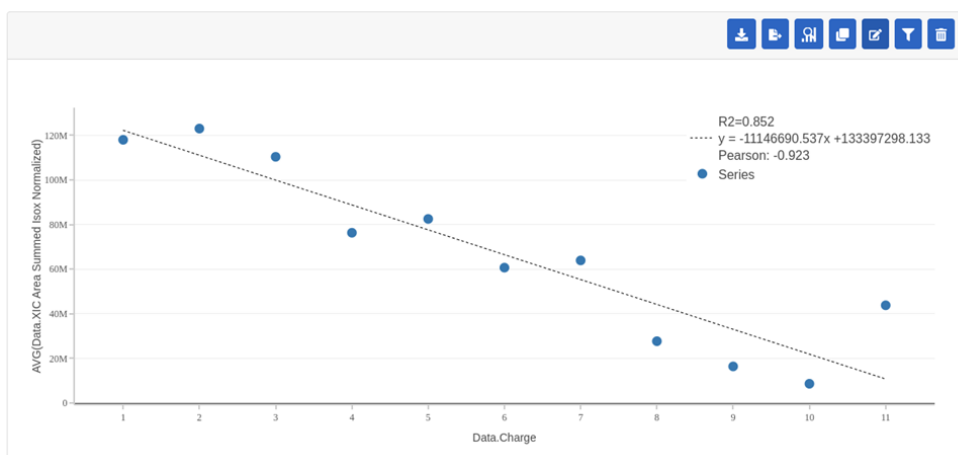
The first Advanced Function introduced in Byosphere v5.9 is **Linear Regression**. Adding Linear Regression will calculate the equation for the line of best fit, the Pearson Correlation, and the R^2 value.

The screenshot shows the 'Advanced Functions' configuration panel. It includes a 'Function' dropdown menu set to 'Linear Regression', an 'Independent Variable' field containing 'Data.Charge', and a 'Dependent Variable' field containing 'AVG(Data.XIC Area Summed Isox Normalized)'. There are 'Revert' and 'Update' buttons at the top right.

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 the 'Display' settings for the Linear Regression function. A toggle switch is turned on, indicating that the results (R², Slope, Intercept, and Pearson's Correlation) are enabled for display.

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" }