Gator GatorOne v2.8 Release Note

Official Release: May 2026

Introduction

This release note provides an overview of the new features and enhancements in GatorOne v2.8, designed to simplify assay setup and provide deeper analytical insights for Gator® instrument users.

- **Product Number:** 600006
- **Supported Instruments:** Gator® Pivot and Gator® Pro (all serial numbers)
- **OS Compatibility**: Fully validated for use on Windows 11
- **Data Compatibility:** Supports downward compatibility (Version 2.8 can open all older files, but older versions cannot open 2.8 files)

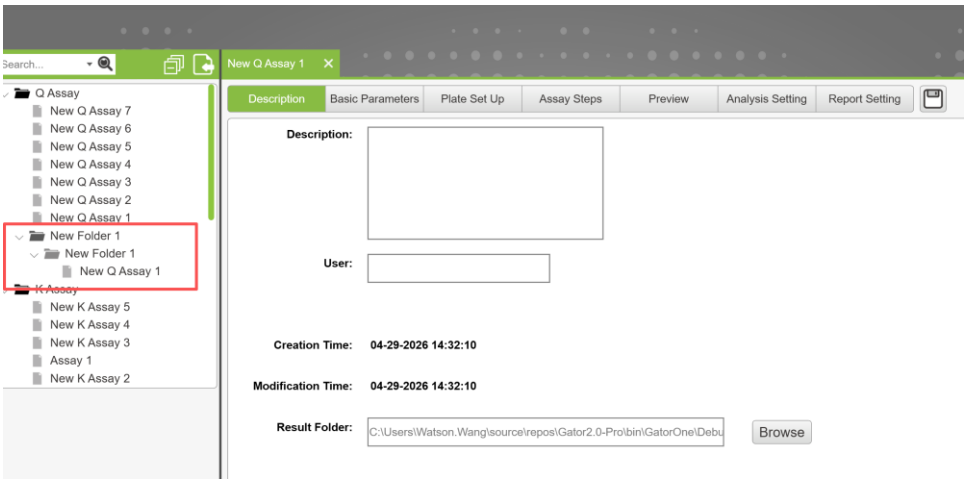
Release Highlights

- Import and export sample info and plate maps directly through Excel
- Apply a full suite of kinetic models (1:1, 2:1, 1:2, Mass Transport, and Two-state)
- Group and color-code results faster using enhanced multi-selection tools
- Visualize EP data more effectively with interactive synchronization and charts
- Support offline simulation via the automation interface

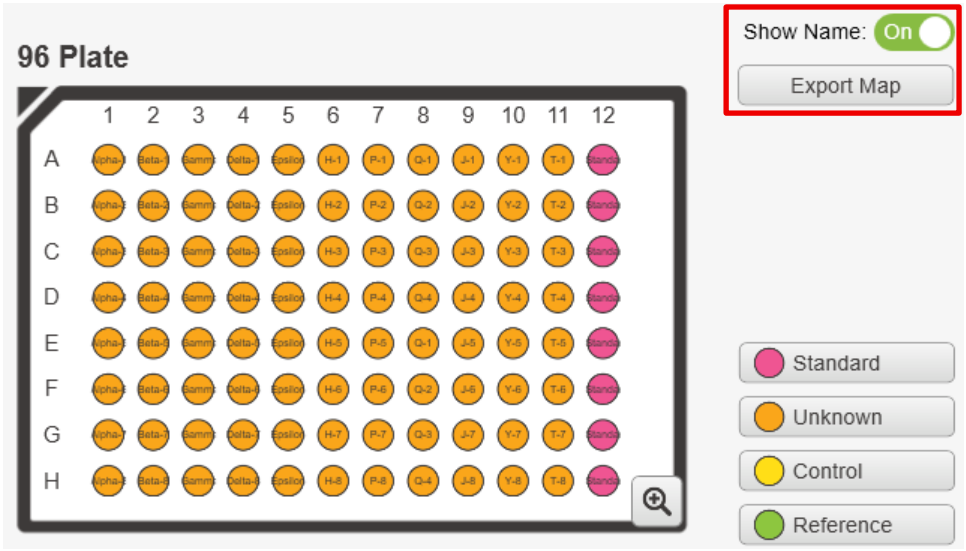
New Features & Improvements

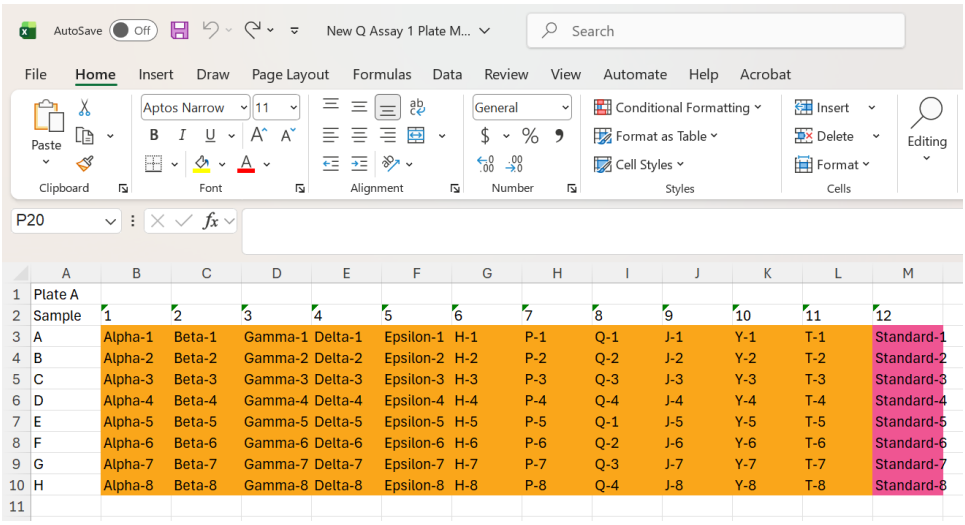
1. Assay Setup New Features

1.1. In Quantitation, Kinetics, and Epitope Binning assay setup, users can now create nested folders that automatically sync to the Results and Analysis section, ensuring data stays organized throughout the workflow.



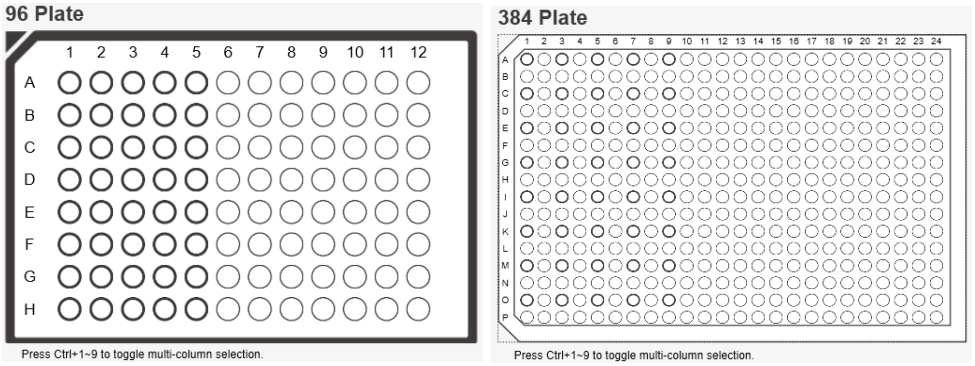
1.2. In Quantitation and Kinetics assay setup, users can now enable or disable sample names on the plate map. When enabled, the exported plate map includes sample names and color-coded step types, providing a clear reference to make pipetting easier for the user.



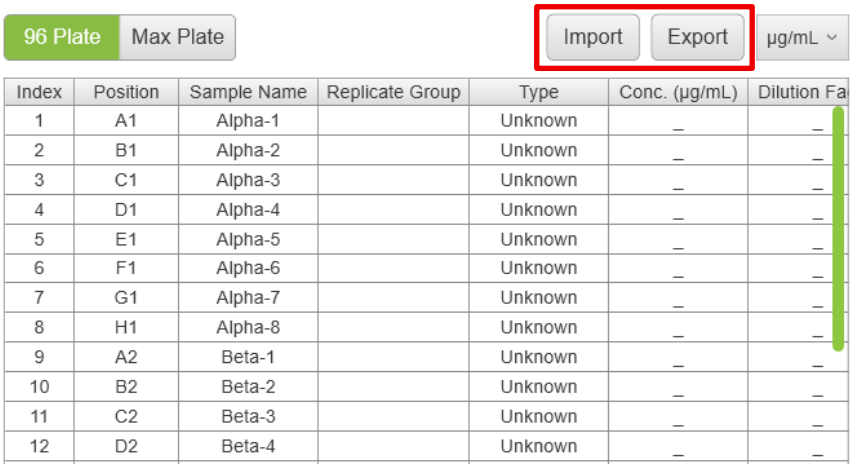


	A	B	C	D	E	F	G	H	I	J	K	L	M
1	Plate A												
2	Sample	1	2	3	4	5	6	7	8	9	10	11	12
3	A	Alpha-1	Beta-1	Gamma-1	Delta-1	Epsilon-1	H-1	P-1	Q-1	J-1	Y-1	T-1	Standard-1
4	B	Alpha-2	Beta-2	Gamma-2	Delta-2	Epsilon-2	H-2	P-2	Q-2	J-2	Y-2	T-2	Standard-2
5	C	Alpha-3	Beta-3	Gamma-3	Delta-3	Epsilon-3	H-3	P-3	Q-3	J-3	Y-3	T-3	Standard-3
6	D	Alpha-4	Beta-4	Gamma-4	Delta-4	Epsilon-4	H-4	P-4	Q-4	J-4	Y-4	T-4	Standard-4
7	E	Alpha-5	Beta-5	Gamma-5	Delta-5	Epsilon-5	H-5	P-5	Q-1	J-5	Y-5	T-5	Standard-5
8	F	Alpha-6	Beta-6	Gamma-6	Delta-6	Epsilon-6	H-6	P-6	Q-2	J-6	Y-6	T-6	Standard-6
9	G	Alpha-7	Beta-7	Gamma-7	Delta-7	Epsilon-7	H-7	P-7	Q-3	J-7	Y-7	T-7	Standard-7
10	H	Alpha-8	Beta-8	Gamma-8	Delta-8	Epsilon-8	H-8	P-8	Q-4	J-8	Y-8	T-8	Standard-8
11													

1.3. In Quantitation, Kinetics, and Epitope Binning assay setups, users can now use CTRL + [Number 1–9] to quickly select multiple columns at once or press the shortcut again to clear the selection. Pressing the keys selects the corresponding number of columns (e.g., CTRL + 5 selects 5 columns). The number of wells selected per column is plate-dependent: for 96-well plates, the shortcut selects eight consecutive wells, while for 384-well plates, it selects every other well in the column.



1.4. In Quantitation, Kinetics, and Epitope Binning assay setup, users can now import and export sample information. This minimizes manual data entry and saves time when setting up complex experiments.



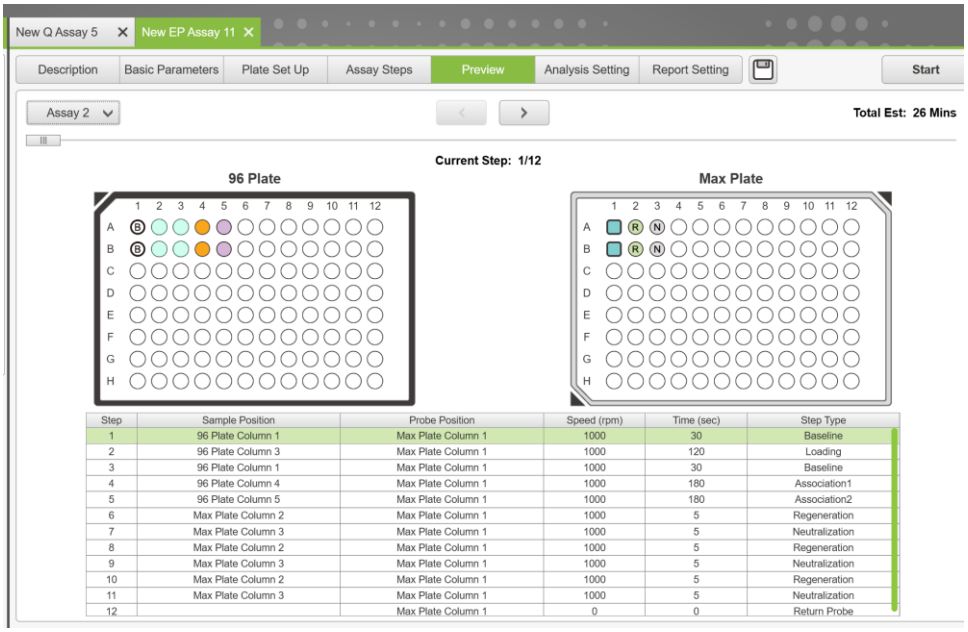
Index	Position	Sample Name	Replicate Group	Type	Conc. (µg/mL)	Dilution Fa
1	A1	Alpha-1		Unknown	_	_
2	B1	Alpha-2		Unknown	_	_
3	C1	Alpha-3		Unknown	_	_
4	D1	Alpha-4		Unknown	_	_
5	E1	Alpha-5		Unknown	_	_
6	F1	Alpha-6		Unknown	_	_
7	G1	Alpha-7		Unknown	_	_
8	H1	Alpha-8		Unknown	_	_
9	A2	Beta-1		Unknown	_	_
10	B2	Beta-2		Unknown	_	_
11	C2	Beta-3		Unknown	_	_
12	D2	Beta-4		Unknown	_	_

1.5. In the Quantitation, Kinetics, and Epitope Binning assay setups, users can now click Position in the table header to toggle the sort of plate positions between row and column order.

Index	Position	Sample Name	Type	Conc. (µg/mL)	MW (kD)	M Conc. (m
1	A1	FcRn in pH5.5	Buffer	-	-	500
2	B1	FcRn in pH5.5	Buffer	-	-	250
3	C1	FcRn in pH5.5	Buffer	-	-	125
4	D1	FcRn in pH5.5	Buffer	-	-	62.5
5	E1	FcRn in pH5.5	Buffer	-	-	31.25
6	F1	FcRn in pH5.5	Buffer	-	-	15.625
7	G1	FcRn in pH5.5	Buffer	-	-	7.813
8	H1	FcRn in pH5.5	Buffer	-	-	3.906

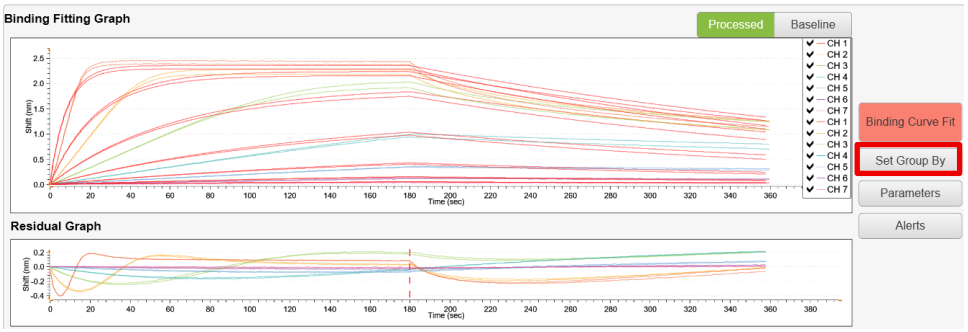
Index	Position	Sample Name	Type	Conc. (µg/mL)	MW (kD)	M Conc. (m
1	A1	FcRn in pH5.5	Buffer	-	-	500
9	A2	FcRn in pH5.5	Buffer	-	-	500
17	A3	FcRn in pH5.5	Buffer	-	-	500
25	A4	FcRn in pH5.5	Buffer	-	-	500
33	A5	FcRn	Sample	-	-	600
41	A6	FcRn	Sample	-	-	600
49	A7	FcRn	Sample	-	-	600
57	A8	FcRn	Sample	-	-	600
65	A9		Buffer	-	-	-
73	A10		Buffer	-	-	-
81	A11		Buffer	-	-	-
89	A12		Buffer	-	-	-

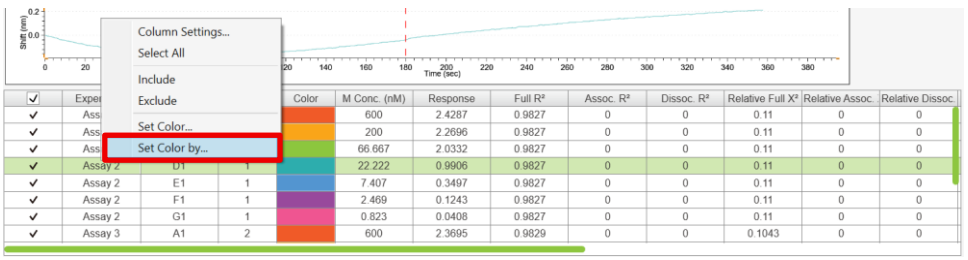
1.6. In Epitope Binning assay setup, if "Regeneration Before Assay" is active, redundant regeneration steps are now skipped when the same sensor is reused.

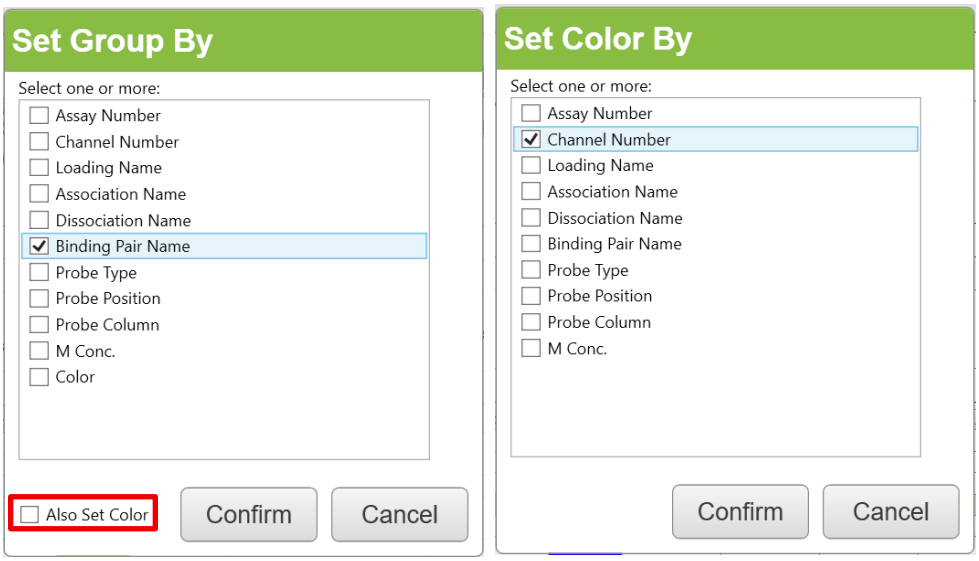


2. Result & Analysis New Features

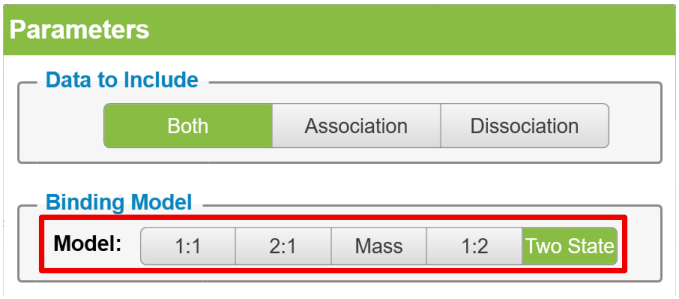
2.1. In Kinetics analysis, users can now select multiple options to apply grouping and color-coding, making it much more efficient to categorize large datasets. Additionally, only when the 'Set Color' option is enabled within the 'Set Group By' settings, the data groups will automatically be color-coded based on their assigned group.



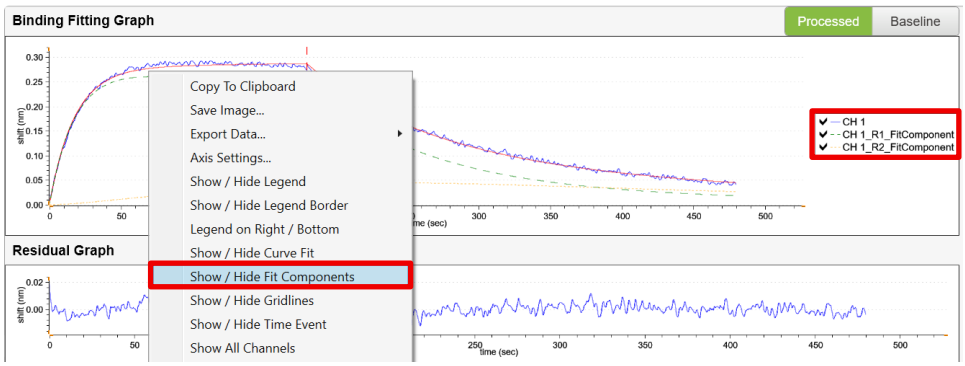




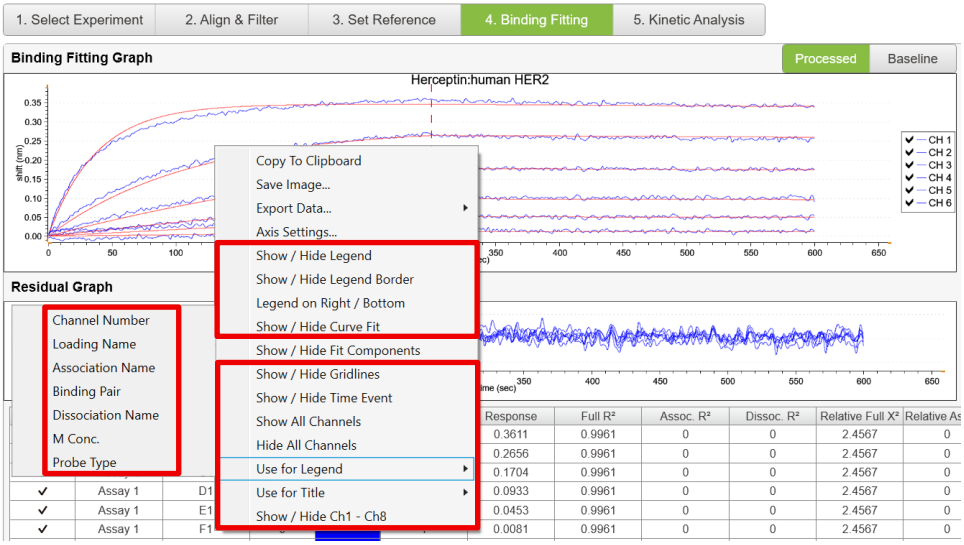
2.2. In Kinetics analysis, users can now apply a full suite of kinetic models, including 1:1, 2:1, 1:2, Mass Transport, and Two-state. This allows for the accurate characterization of complex binding behaviors across a wider range of biomolecular interactions.



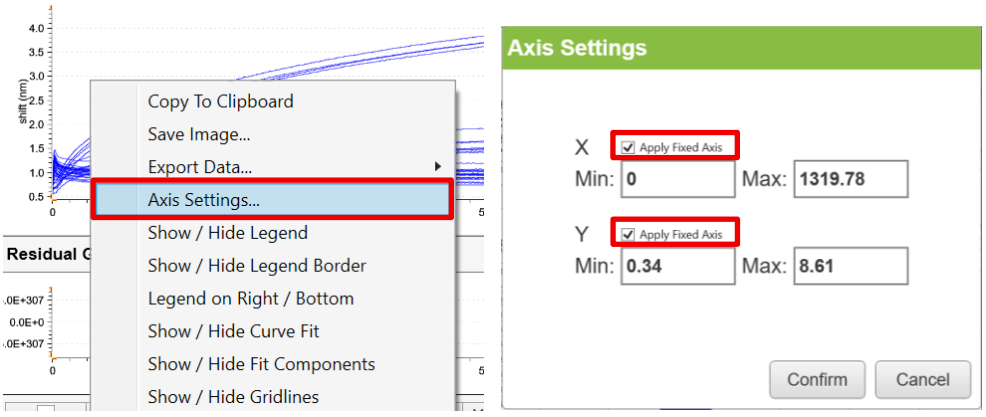
2.3. In Kinetics analysis, the binding fitting graph for the Two-state binding model now allows users to right-click the graph to enable or disable individual fit components. This works for both association and dissociation, providing a more focused view of specific binding phases.



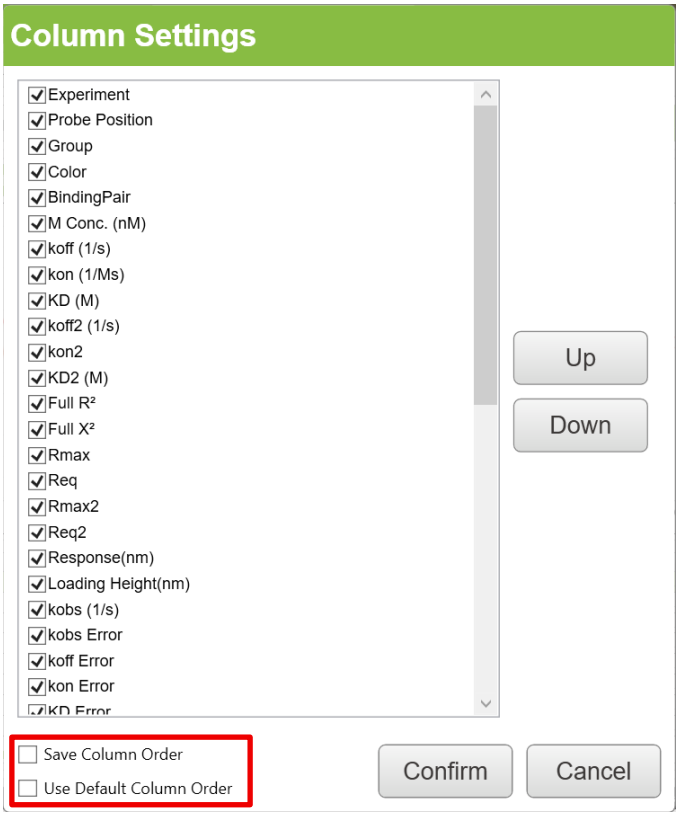
2.4. In Kinetics analysis, users can now right-click the binding fitting graph to quickly toggle options such as curve fitting, channel displays, the legend, and the title settings.



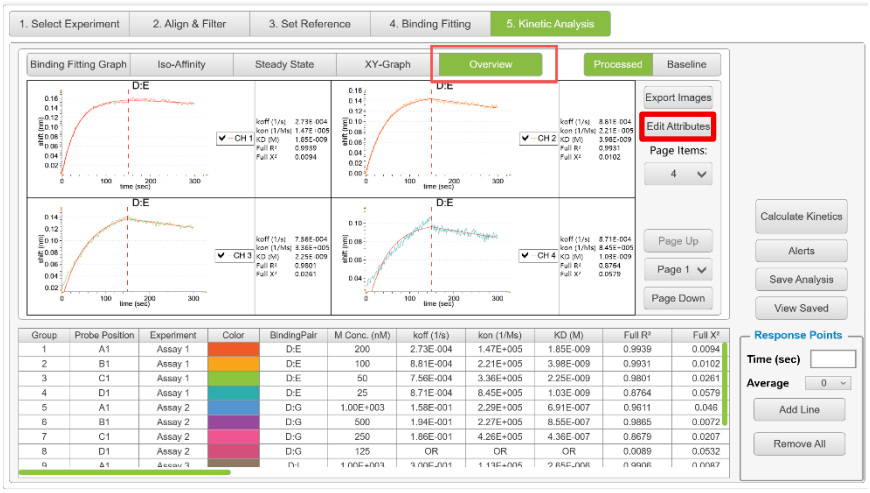
2.5. In Kinetics analysis, users can now select "Apply Fixed Axis" in Axis Settings to maintain customized graph dimensions and scales during report export. This ensures that the visual presentation remains consistent from the software interface to the final report.

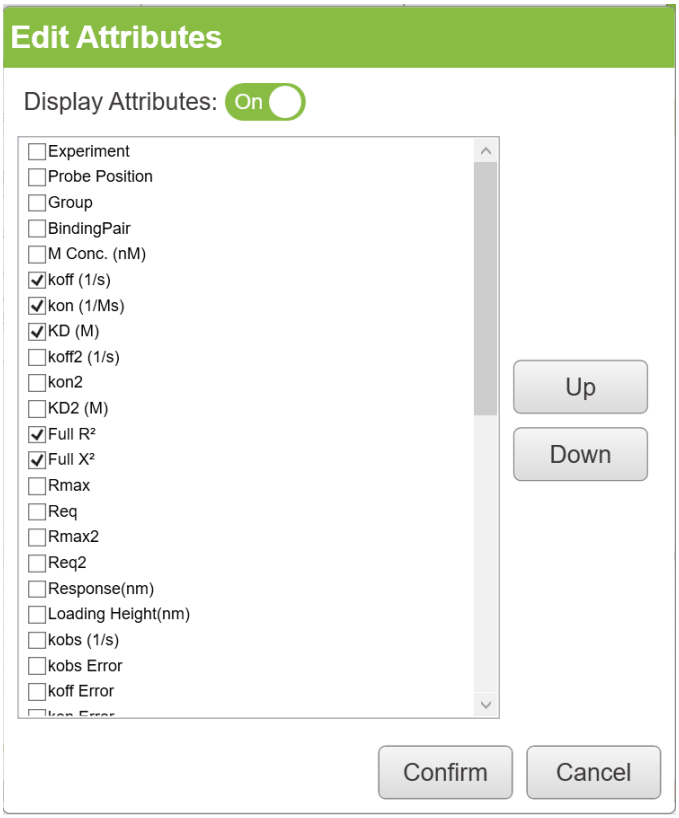


2.6. In Kinetics analysis, the results table now supports column customization. Right-click the table to open Column Settings, where selecting 'Save Column Order' applies the layout globally to all current and future results. Selecting 'Use Default Column Order' will revert the table to the original system layout.

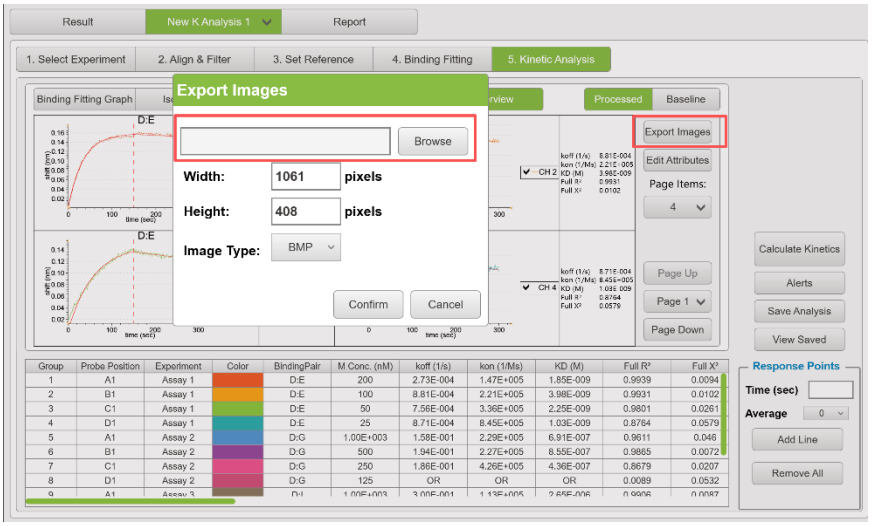


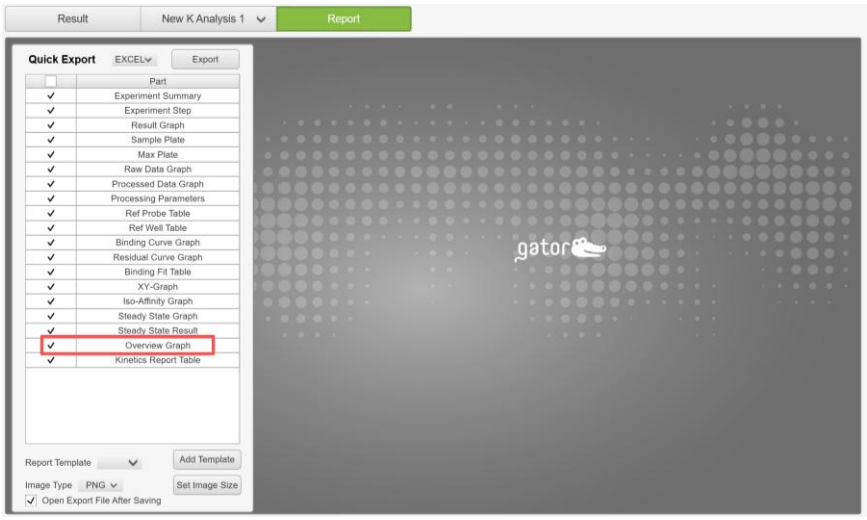
2.7. In Kinetics analysis, results can now be displayed by user-defined groups, providing a structured layout in Overview mode for comparing multiple interactions simultaneously. To customize which kinetic results appear next to the binding curves, click Edit Attributes.





2.8. In Kinetics analysis, Overview mode results can be exported directly to a selected folder or included in the "Overview" tab within the final report.



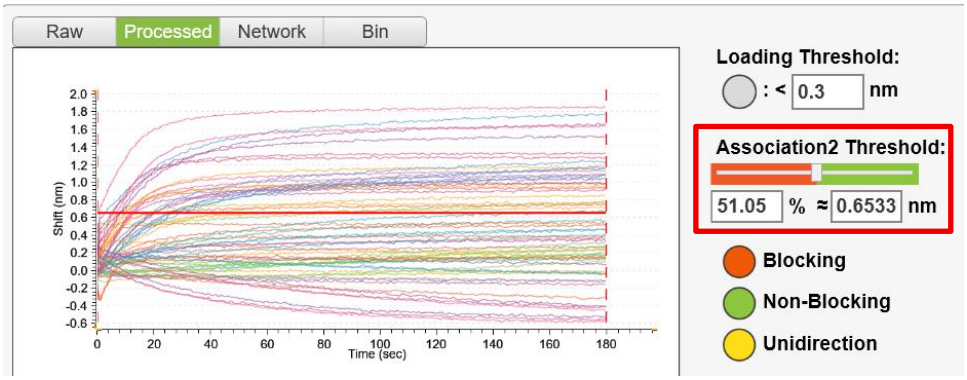


2.9. In Kinetics analysis, kinetic constants are now exported in scientific notation to improve readability.

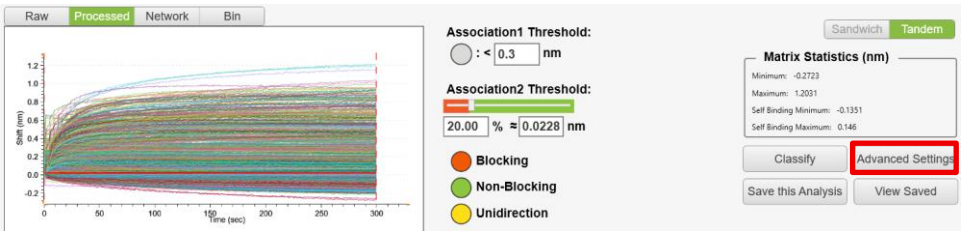
koff(1/s)	kon(1/Ms)	KD(M)	koff2(1/s)	kon2 (1/s)	FullR2	Full X2	Rmax	Response	LoadingH	kobs(1/s)	kobs Error	koff Error	kon Error	KD Error	koff2 Error	kon2 Error
3.21E-03	1.96E+05	1.64E-08	N/A	2.11E-03	0.9827	151.6492	2.418	2.4287	N/A	1.21E-01	4.38E-01	4.14E-01	4.01E+04	5.08E-11	N/A	2.64E+02
3.21E-03	1.96E+05	1.64E-08	N/A	2.11E-03	0.9827	151.6492	2.418	2.2696	N/A	4.23E-02	4.22E-01	4.14E-01	4.01E+04	5.08E-11	N/A	2.64E+02
3.21E-03	1.96E+05	1.64E-08	N/A	2.11E-03	0.9827	151.6492	2.418	2.0332	N/A	1.62E-02	4.16E-01	4.14E-01	4.01E+04	5.08E-11	N/A	2.64E+02
3.21E-03	1.96E+05	1.64E-08	N/A	2.11E-03	0.9827	151.6492	2.418	0.9906	N/A	7.55E-03	4.14E-01	4.14E-01	4.01E+04	5.08E-11	N/A	2.64E+02
3.21E-03	1.96E+05	1.64E-08	N/A	2.11E-03	0.9827	151.6492	2.418	0.3497	N/A	4.65E-03	4.14E-01	4.14E-01	4.01E+04	5.08E-11	N/A	2.64E+02
3.21E-03	1.96E+05	1.64E-08	N/A	2.11E-03	0.9827	151.6492	2.418	0.1243	N/A	3.69E-03	4.14E-01	4.14E-01	4.01E+04	5.08E-11	N/A	2.64E+02
3.21E-03	1.96E+05	1.64E-08	N/A	2.11E-03	0.9827	151.6492	2.418	0.0408	N/A	3.37E-03	4.14E-01	4.14E-01	4.01E+04	5.08E-11	N/A	2.64E+02
3.79E-03	1.97E+05	1.92E-08	N/A	1.87E-03	0.9829	136.3639	2.36	2.3695	N/A	1.22E-01	2.97E-01	2.78E-01	3.19E+04	1.48E-10	N/A	1.27E+02
3.79E-03	1.97E+05	1.92E-08	N/A	1.87E-03	0.9829	136.3639	2.36	2.1798	N/A	4.32E-02	2.84E-01	2.78E-01	3.19E+04	1.48E-10	N/A	1.27E+02
3.79E-03	1.97E+05	1.92E-08	N/A	1.87E-03	0.9829	136.3639	2.36	1.913	N/A	1.69E-02	2.80E-01	2.78E-01	3.19E+04	1.48E-10	N/A	1.27E+02
3.79E-03	1.97E+05	1.92E-08	N/A	1.87E-03	0.9829	136.3639	2.36	0.9409	N/A	8.16E-03	2.79E-01	2.78E-01	3.19E+04	1.48E-10	N/A	1.27E+02
3.79E-03	1.97E+05	1.92E-08	N/A	1.87E-03	0.9829	136.3639	2.36	0.3385	N/A	5.25E-03	2.78E-01	2.78E-01	3.19E+04	1.48E-10	N/A	1.27E+02
3.79E-03	1.97E+05	1.92E-08	N/A	1.87E-03	0.9829	136.3639	2.36	0.1123	N/A	4.27E-03	2.78E-01	2.78E-01	3.19E+04	1.48E-10	N/A	1.27E+02
3.79E-03	1.97E+05	1.92E-08	N/A	1.87E-03	0.9829	136.3639	2.36	0.0403	N/A	3.95E-03	2.78E-01	2.78E-01	3.19E+04	1.48E-10	N/A	1.27E+02

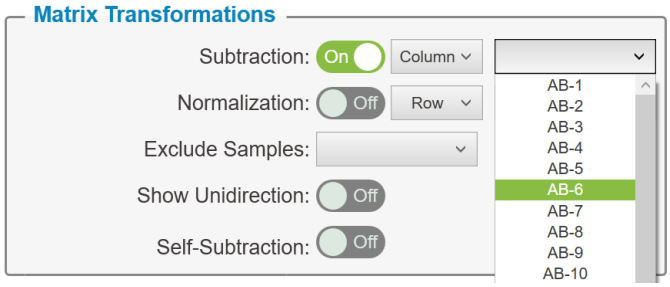
2.10. In Epitope Binning analysis, the Association2 Threshold setting now features an interactive slider for easier adjustment. This setting controls the threshold for Association2, which is the binding of secondary or competing antibodies. The value is calculated as:

$$\boldsymbol{Threshold\ Value = Min + (Max - Min) \times \left(\frac{Slider\%}{100}\right)}$$

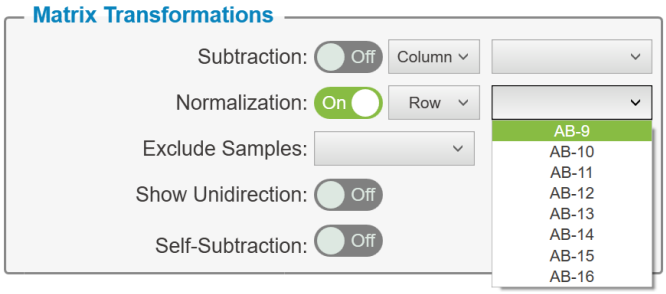


2.11. In Epitope Binning analysis, users can now select a specific row or column as a reference to subtract from the dataset.

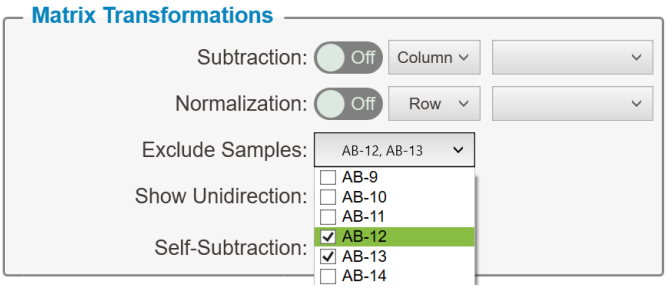




2.12. In Epitope Binning analysis, users can now select a row or column as a normalization factor, where all other data points are divided by the reference.

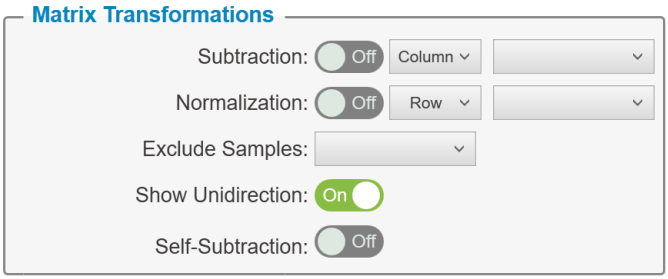


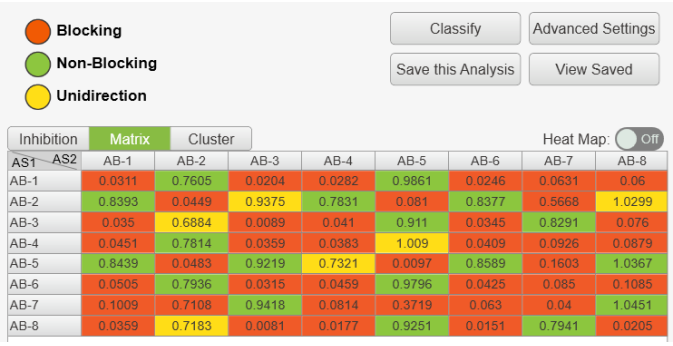
2.13. In Epitope Binning analysis, users can now manually exclude specific samples from the dataset. This provides flexibility to remove outliers, resulting in a more focused view of the matrix.



AS1 \ AS2	AB-1	AB-2	AB-3	AB-4	AB-5	AB-6	AB-7	AB-8
AB-9	0.0577	0.0632	0.9219	0.0559	0.0984	0.8388	0.0744	1.1026
AB-10	0.9761	0.146	1.0316	0.6466	0.1739	0.9521	0.159	1.1359
AB-11	0.0784	0.7179	0.0608	0.0812	0.9088	0.0791	0.8348	0.138
AB-12	0.118	0.3636	0.7022	0.0726	0.068	0.7022	0.3612	0.9402
AB-13	0.4826	0.1127	0.5299	0.4797	0.1978	0.5281	0.5349	0.7101
AB-14	0.3691	0.6731	0.3613	0.3649	0.8074	0.3575	0.7534	0.526
AB-15	0.101	0.76	0.0434	0.08	0.9115	0.0488	0.8687	0.0851
AB-16	0.8936	0.0498	0.9648	0.9082	0.0456	0.9186	0.0397	1.0823

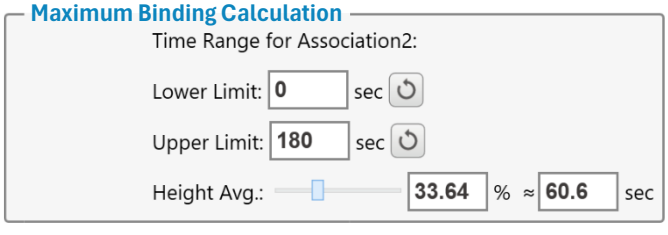
2.14. In Epitope Binning analysis, users can now choose to show or hide unidirectional binding events. This provides a cleaner view of the matrix by focusing only on confirmed bidirectional interactions when necessary.





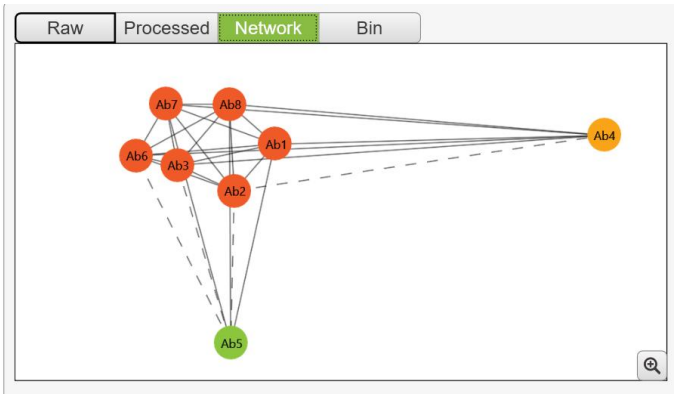
AS1 \ AS2	AB-1	AB-2	AB-3	AB-4	AB-5	AB-6	AB-7	AB-8
AB-1	0.0311	0.7605	0.0204	0.0282	0.9861	0.0246	0.0631	0.06
AB-2	0.8393	0.0449	0.9375	0.7831	0.081	0.8377	0.5668	1.0299
AB-3	0.035	0.6884	0.0089	0.041	0.911	0.0345	0.8291	0.076
AB-4	0.0451	0.7814	0.0359	0.0383	1.009	0.0409	0.0926	0.0879
AB-5	0.8439	0.0483	0.9219	0.7321	0.0097	0.8589	0.1603	1.0367
AB-6	0.0505	0.7936	0.0315	0.0459	0.9796	0.0425	0.085	0.1085
AB-7	0.1009	0.7108	0.9418	0.0814	0.3719	0.063	0.04	1.0451
AB-8	0.0359	0.7183	0.0081	0.0177	0.9251	0.0151	0.7941	0.0205

2.15. In Epitope Binning analysis, the maximum binding can now be calculated using a user-specified percentage of the final data points from the Association 2 loading height.

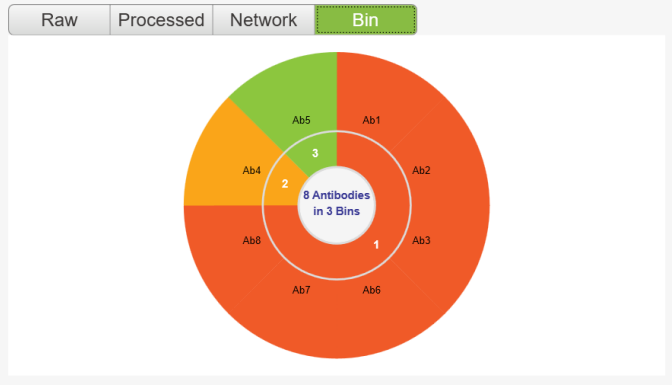


2.16. In Epitope Binning analysis, the Network Chart visualizes binding relationships by grouping samples targeting the same epitope.

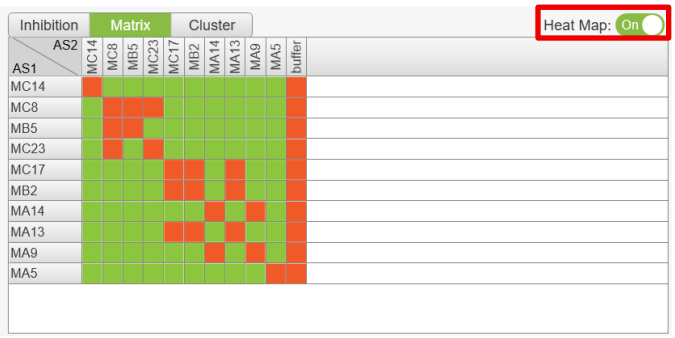
Connection styles represent blocking status: solid (mutual), dashed (one-way), or none (non-blocking).



2.17. In Epitope Binning analysis, the Bin Chart provides a categorized view of results based on sample epitope targets, offering a clear summary of how a library is distributed across different binding sites.

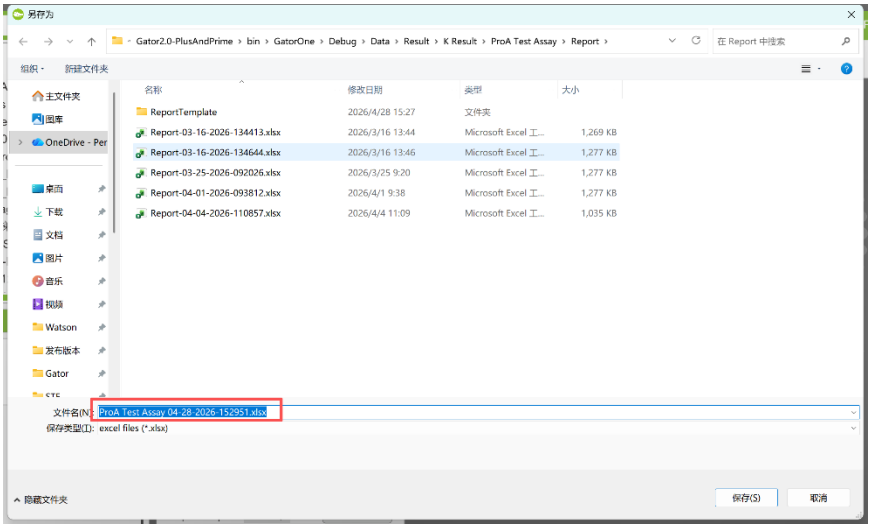


2.18. In Epitope Binning analysis, the updated Heat Map provides a simple, color-coded view of all sample interactions, making it easy to identify binding patterns across the entire dataset.



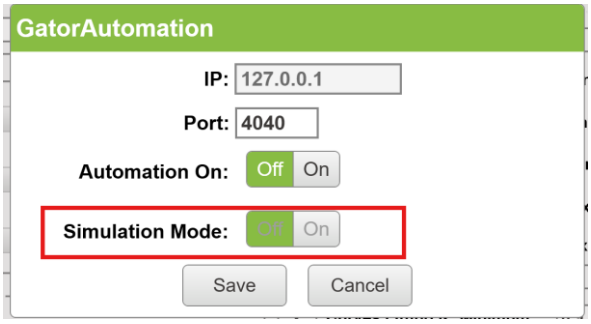
2.19. In Report, users can now select a preferred image format for exported figures, while the Overview section remains in PNG format.

2.20. In Report, default report names now combine the Assay Name and Timestamp for improved traceability.



3. Automation New Features

3.1. The automation interface now includes an offline simulation mode, allowing users to validate and test integration workflows without requiring a physical connection to the instrument.



3.2. Automation connection settings are now saved locally, eliminating the requirement to manually re-enable automation each time the software is restarted.

3.3. For a comprehensive list of automation-related updates, please refer to the Automation API Documentation. To request access, contact support@gatorbio.com.

System Requirements & Compatibility

To ensure full compatibility with new software features and maintain optimal system stability, please confirm that your hardware and drivers adhere to the following specifications.

PC Hardware Requirements

- **CPU**: Intel Core i9 recommended (Minimum: i5 1.6 GHz).
- **Memory**: 32 GB DDR5 RAM recommended (Minimum: 16 GB).
- **Storage**: 1TB Solid-State Drive (SSD) required.
- **Connectivity**: Ethernet, Wi-Fi, and Bluetooth ports required.
- **Expansion:** PCI-E USB 3.0 host controller card installed.

Graphics Driver Requirements

- PCs with Intel 11th and 12th Gen CPUs using Arc or Iris Xe Graphics.
- Driver version 31.0.101.4091 or higher required.
- Update via the Intel support website if your current version is lower.
- For specific troubleshooting steps and rendering workarounds, please refer to LightningChart documentation.

Other Driver Requirements

- .NET SDK version 8.0.408
- Microsoft .NET Framework 4.8
- Spectrometer communication driver version 2.56
- Light source driver version V01
- Vision system SDK version 6.4.1
- Vision system software version 5.7.2 CR1

GatorOne Software Upgrade Instructions

1. **Coordinate with Gator Support Team**

   Contact the Gator Support Team at support@gatorbio.com to obtain the software installer.

2. **Preparation and Extraction**

   2.1. Right-click the software ZIP file and select "Extract" to unzip the contents using the Windows extraction tool.

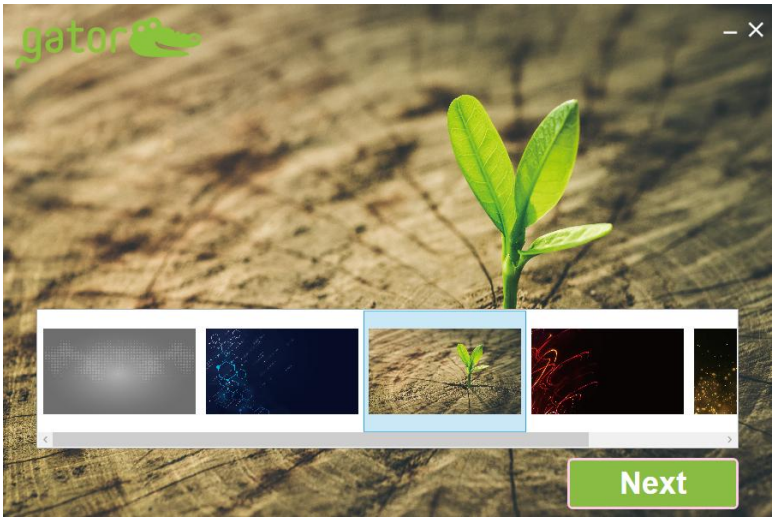
   2.2. Move the extracted .exe file to the C:\ Drive of the computer workstation connected to the Gator instrument.

   2.3. Ensure the GatorOne application is closed before initiating the upgrade.

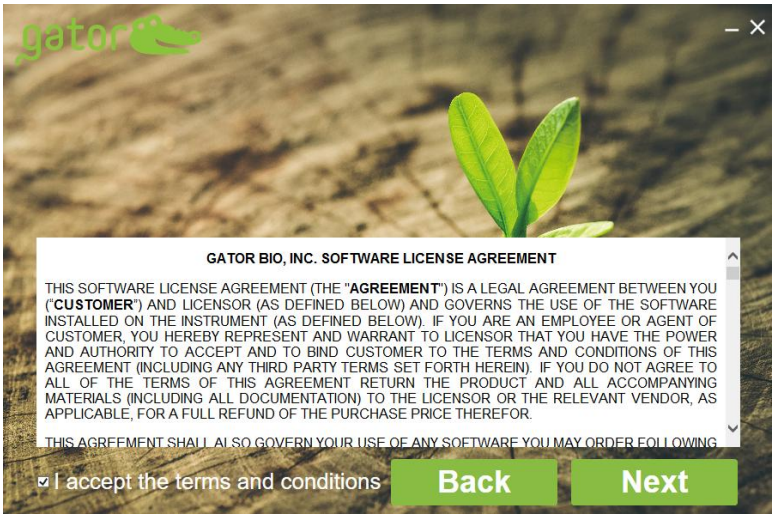
   2.4. Right click and run as administrator to begin the upgrade process.

3. **Configuration and Validation**

   3.1. Choose one of the five available color themes and click Next.



   3.2. Review the Software License Agreement, check the box to accept the terms, and click Next.



3.3. Select the appropriate Gator model from the drop-down menu located at the bottom left of the interface.

3.4. **Copy the unique ID and email it to the Gator Support Team** at support@gatorbio.com to request your Serial Number.

3.5. **Enter the valid Serial Number provided by Support** and click Next.

3.6. DO NOT select the "PART 11" checkbox unless you are installing the CFR Part 11 compliant package for regulated environments.

3.7. For software upgrades, ensure both GatorOne and Instrument Controller remain selected (system default) and click Next.

3.8. Once the installation finishes, click Finish to exit the installer and finalize the upgrade.