Gator GatorOne v2.19 Release Note

Official Release: May 2026

Introduction

This release note provides an overview of the new features and enhancements in GatorOne v2.19, designed to simplify assay setup and provide deeper analytical insights for Gator® instrument users.

- **Product Number:** 600001
- **Supported Instruments:** Gator® Pilot, Gator® Prime, Gator® Plus and Gator® Plus+ (all serial numbers)
- **OS Compatibility**: Fully validated for use on Windows 11
- **Data Compatibility:** Supports downward compatibility (Version 2.19 can open all older files, but older versions cannot open 2.19 files)

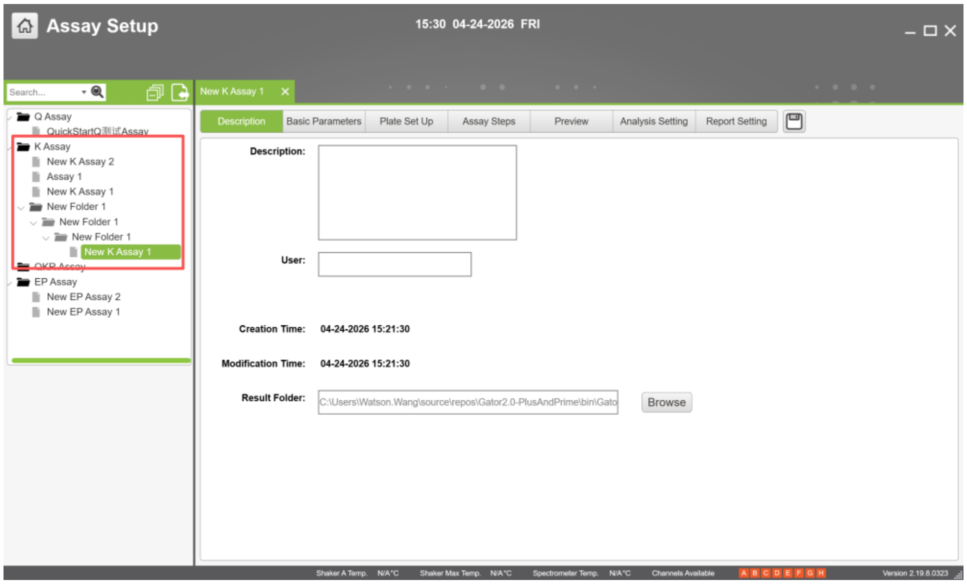
Release Highlights

- Import and export sample info and plate maps directly through Excel
- Access all 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

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.



Description:

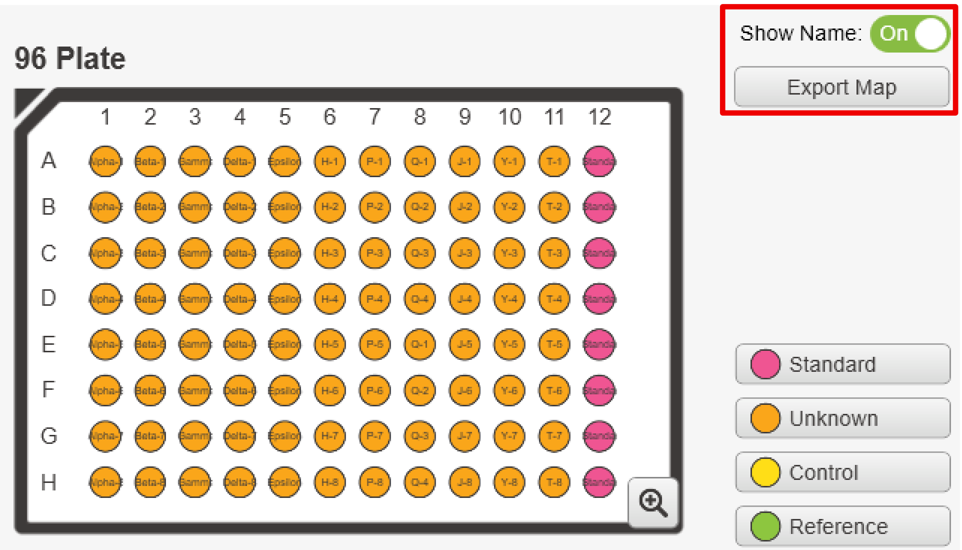
User:

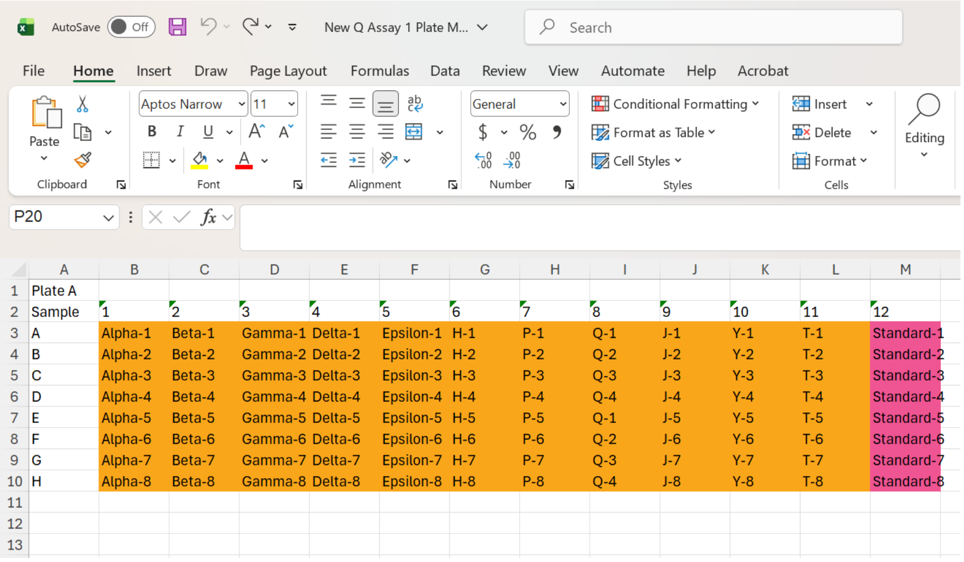
Creation Time: 04-24-2026 15:21:30

Modification Time: 04-24-2026 15:21:30

Result Folder: C:\Users\Watson.Wang\source\repos\Gator2.0-PlusAndPrime\bin\Gato

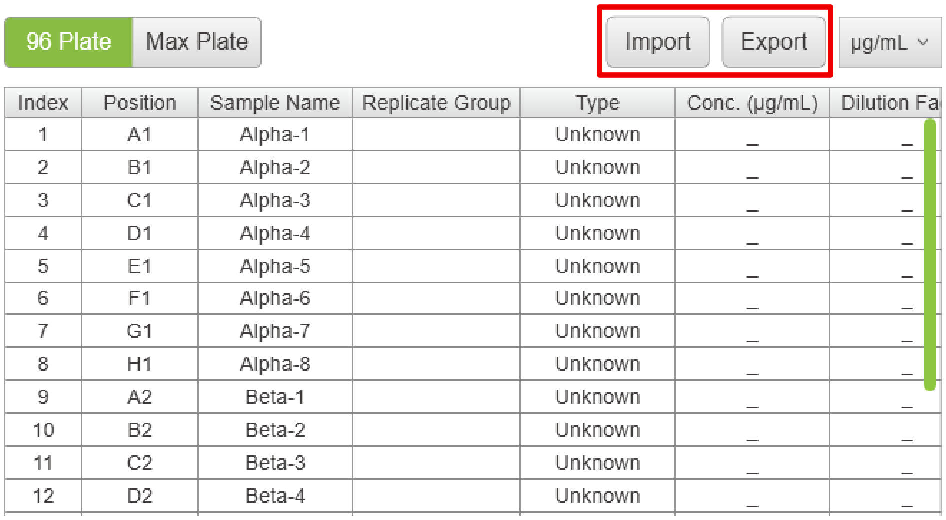
1.2. In Quantitation and Kinetics assay setup, users can now enable or disable sample names on the plate map. When enabled, the exported plate map includes sample names and color-coded step types, providing a clear reference to make pipetting easier for the user.





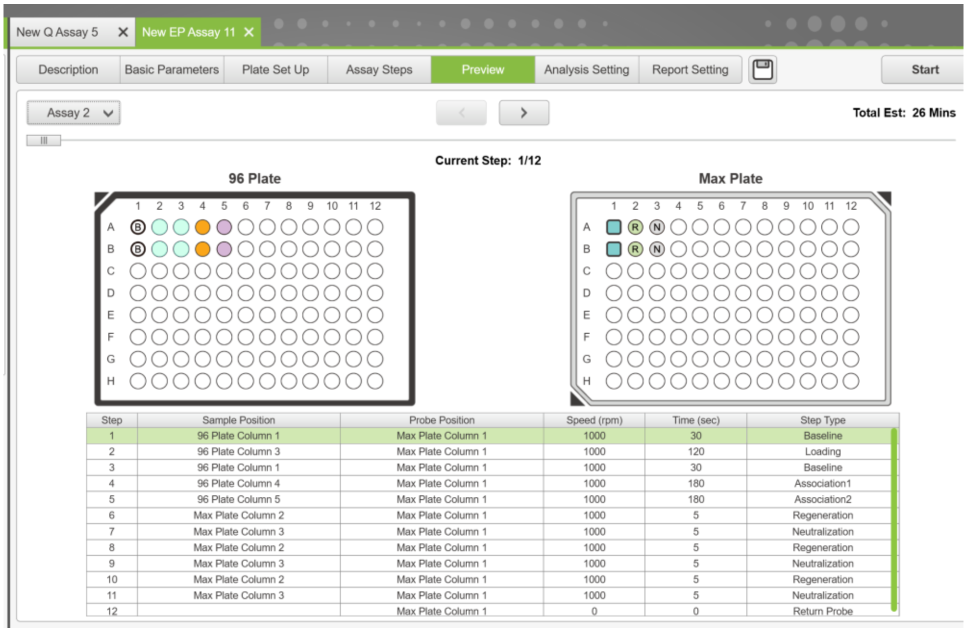
	A	B	C	D	E	F	G	H	I	J	K	L	M
1	Plate A												
2	Sample	1	2	3	4	5	6	7	8	9	10	11	12
3	A	Alpha-1	Beta-1	Gamma-1	Delta-1	Epsilon-1	H-1	P-1	Q-1	J-1	Y-1	T-1	Standard-1
4	B	Alpha-2	Beta-2	Gamma-2	Delta-2	Epsilon-2	H-2	P-2	Q-2	J-2	Y-2	T-2	Standard-2
5	C	Alpha-3	Beta-3	Gamma-3	Delta-3	Epsilon-3	H-3	P-3	Q-3	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													
12													
13													

1.3. 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	_	_

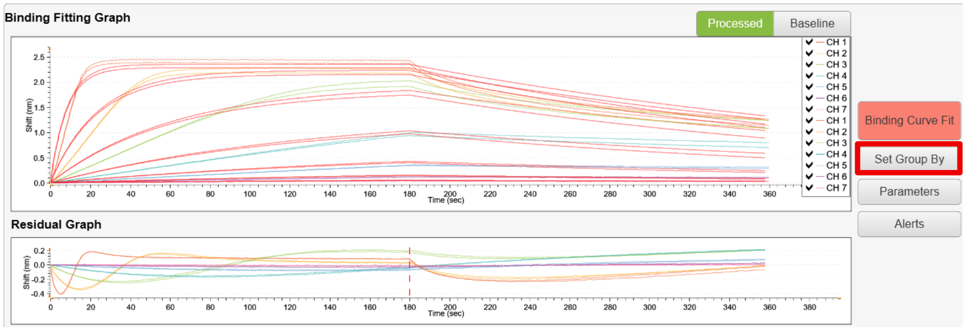
1.4. In Epitope Binning assay setup, if "Regeneration Before Assay" is active, redundant regeneration steps are now skipped when the same sensor is reused.

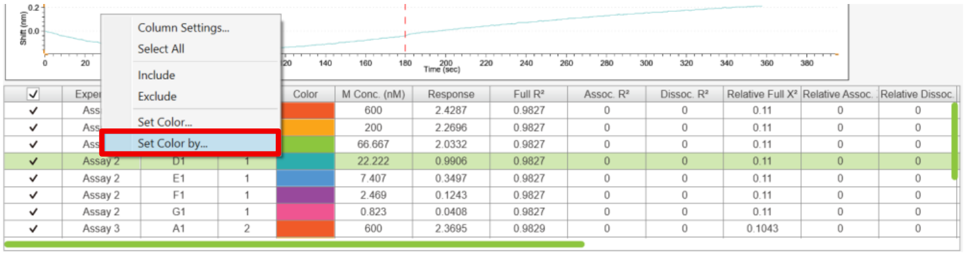


Step	Sample Position	Probe Position	Speed (rpm)	Time (sec)	Step Type
1	96 Plate Column 1	Max Plate Column 1	1000	30	Baseline
2	96 Plate Column 3	Max Plate Column 1	1000	120	Loading
3	96 Plate Column 1	Max Plate Column 1	1000	30	Baseline
4	96 Plate Column 4	Max Plate Column 1	1000	180	Association1
5	96 Plate Column 5	Max Plate Column 1	1000	180	Association2
6	Max Plate Column 2	Max Plate Column 1	1000	5	Regeneration
7	Max Plate Column 3	Max Plate Column 1	1000	5	Neutralization
8	Max Plate Column 2	Max Plate Column 1	1000	5	Regeneration
9	Max Plate Column 3	Max Plate Column 1	1000	5	Neutralization
10	Max Plate Column 2	Max Plate Column 1	1000	5	Regeneration
11	Max Plate Column 3	Max Plate Column 1	1000	5	Neutralization
12		Max Plate Column 1	0	0	Return Probe

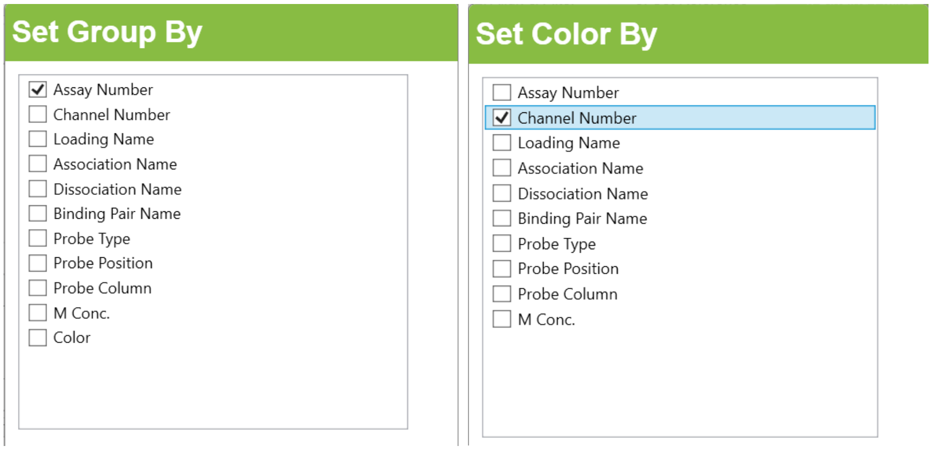
2. Result & Analysis New Features

2.1. In Kinetics analysis, users can now select multiple options to apply grouping and color-coding. This makes it more efficient to categorize results, especially when organizing large datasets during analysis.





☑	Exper			Color	M Conc. (nM)	Response	Full R²	Assoc. R²	Dissoc. R²	Relative Full X²	Relative Assoc.	Relative Dissoc.
✓	Ass			🟥	600	2.4287	0.9827	0	0	0.11	0	0
✓	Ass			🟧	200	2.2696	0.9827	0	0	0.11	0	0
✓	Ass			🟩	66.667	2.0332	0.9827	0	0	0.11	0	0
✓	Assay 2	D1	1	🟦	22.222	0.9906	0.9827	0	0	0.11	0	0
✓	Assay 2	E1	1	🟦	7.407	0.3497	0.9827	0	0	0.11	0	0
✓	Assay 2	F1	1	🟪	2.469	0.1243	0.9827	0	0	0.11	0	0
✓	Assay 2	G1	1	🟥	0.823	0.0408	0.9827	0	0	0.11	0	0
✓	Assay 3	A1	2	🟥	600	2.3695	0.9829	0	0	0.1043	0	0



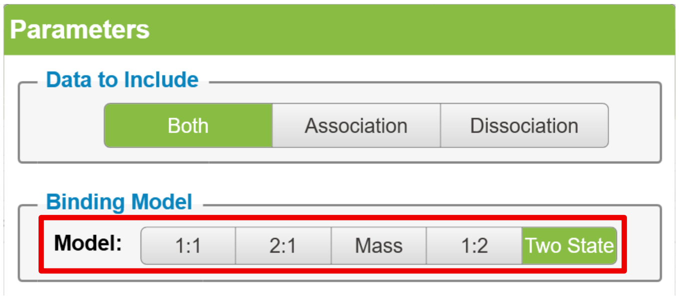
Set Group By

☑ Assay Number
☐ Channel Number
☐ Loading Name
☐ Association Name
☐ Dissociation Name
☐ Binding Pair Name
☐ Probe Type
☐ Probe Position
☐ Probe Column
☐ M Conc.
☐ Color

Set Color By

☐ Assay Number
☑ Channel Number
☐ Loading Name
☐ Association Name
☐ Dissociation Name
☐ Binding Pair Name
☐ Probe Type
☐ Probe Position
☐ Probe Column
☐ M Conc.

2.2. In Kinetics analysis, users can now apply a full suite of kinetic models, including 1:1 (Analyte:Ligand), 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.



Parameters

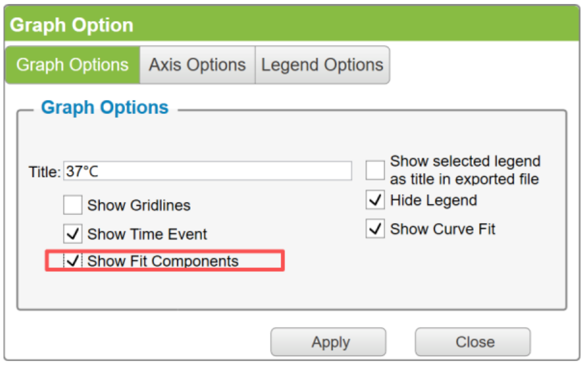
Data to Include

[✓ Both] Association Dissociation

Binding Model

Model: 1:1 2:1 Mass 1:2 [✓ Two State]

2.3. In Kinetics analysis, the Two-State binding model now allows users to enable or disable individual fit components. Since the Two-State model is calculated in two distinct phases, users can now view each component independently or combined. This allows for a more focused analysis of specific binding phases.



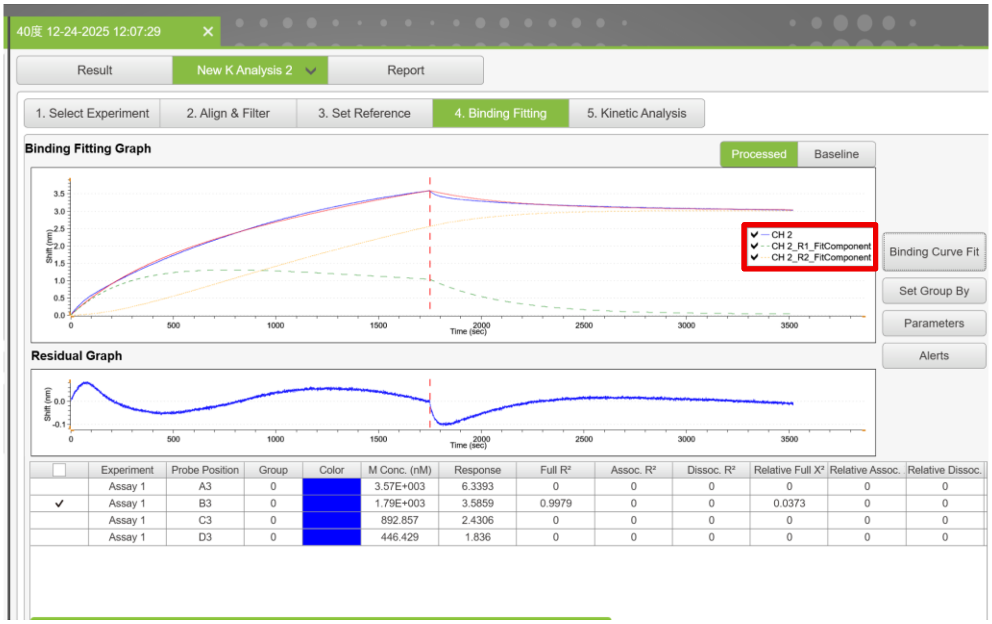
Graph Option

[✓ Graph Options] Axis Options Legend Options

Graph Options

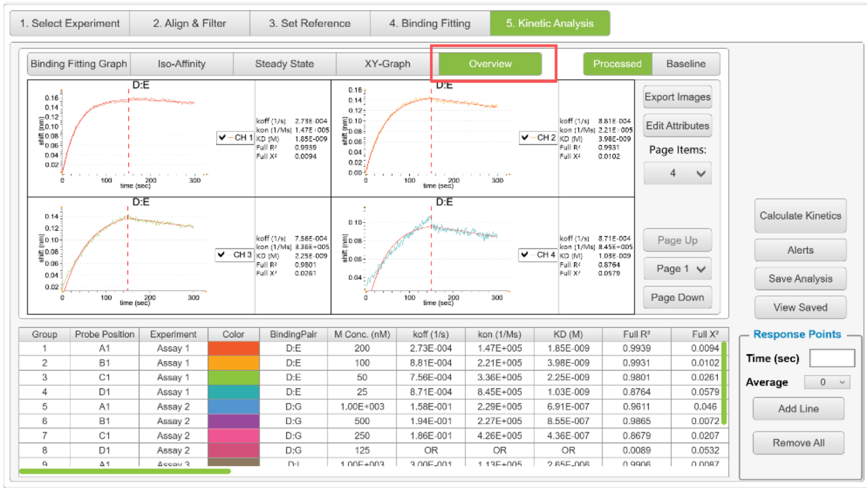
Title: 37°C

☐ Show Gridlines
☑ Show Time Event
☑ Show Fit Components
☐ Show selected legend as title in exported file
☑ Hide Legend
☑ Show Curve Fit



☐	Experiment	Probe Position	Group	Color	M Conc. (nM)	Response	Full R²	Assoc. R²	Dissoc. R²	Relative Full X²	Relative Assoc.	Relative Dissoc.
	Assay 1	A3	0	🟦	3.57E+003	6.3393	0	0	0	0	0	0
✓	Assay 1	B3	0	🟦	1.79E+003	3.5859	0.9979	0	0	0.0373	0	0
	Assay 1	C3	0	🟦	892.857	2.4306	0	0	0	0	0	0
	Assay 1	D3	0	🟦	446.429	1.836	0	0	0	0	0	0

2.4. In Kinetics analysis, results are displayed by user-defined groups, making it easier to compare different sample sets simultaneously. This provides a structured view in Overview mode for evaluating multiple interactions.



CH 1: koff (1/s) 2.73E-004; kon (1/Ms) 1.47E+005; KD (M) 1.85E-009; Full R² 0.9939; Full X² 0.0094

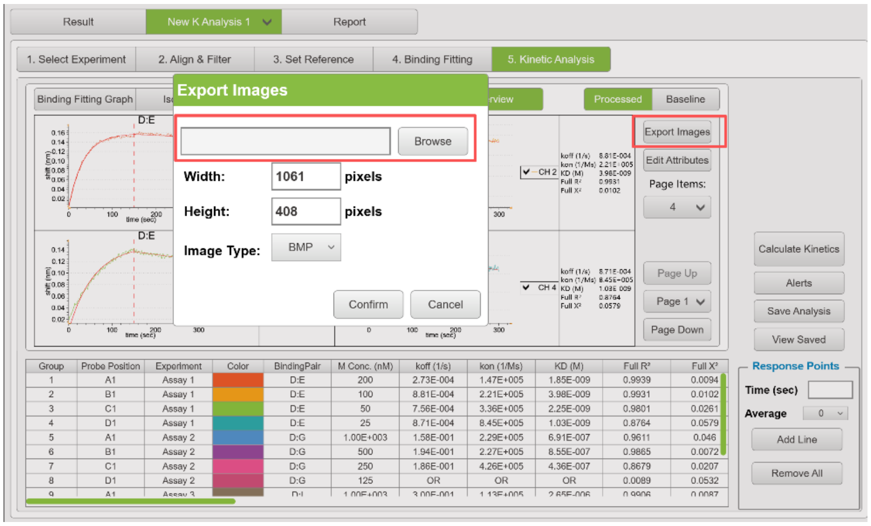
CH 2: koff (1/s) 8.81E-004; kon (1/Ms) 2.21E+005; KD (M) 3.98E-009; Full R² 0.9931; Full X² 0.0102

CH 3: koff (1/s) 7.56E-004; kon (1/Ms) 3.36E+005; KD (M) 2.25E-009; Full R² 0.9801; Full X² 0.0261

CH 4: koff (1/s) 8.71E-004; kon (1/Ms) 8.45E+005; KD (M) 1.03E-009; Full R² 0.8764; Full X² 0.0579

Group	Probe Position	Experiment	Color	BindingPair	M Conc. (nM)	koff (1/s)	kon (1/Ms)	KD (M)	Full R²	Full X²
1	A1	Assay 1	🟥	D:E	200	2.73E-004	1.47E+005	1.85E-009	0.9939	0.0094
2	B1	Assay 1	🟧	D:E	100	8.81E-004	2.21E+005	3.98E-009	0.9931	0.0102
3	C1	Assay 1	🟩	D:E	50	7.56E-004	3.36E+005	2.25E-009	0.9801	0.0261
4	D1	Assay 1	🟩	D:E	25	8.71E-004	8.45E+005	1.03E-009	0.8764	0.0579
5	A1	Assay 2	🟦	D:G	1.00E+003	1.58E-001	2.29E+005	6.91E-007	0.9611	0.046
6	B1	Assay 2	🟪	D:G	500	1.94E-001	2.27E+005	8.55E-007	0.9865	0.0072
7	C1	Assay 2	🟥	D:G	250	1.86E-001	4.26E+005	4.36E-007	0.8679	0.0207
8	D1	Assay 2	🟥	D:G	125	OR	OR	OR	0.0089	0.0532
9	A1	Assay 3	🟫	D:I	1.00E+003	3.00E-001	1.13E+005	2.65E-006	0.9906	0.0087

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



Export Images

Width: 1061 pixels

Height: 408 pixels

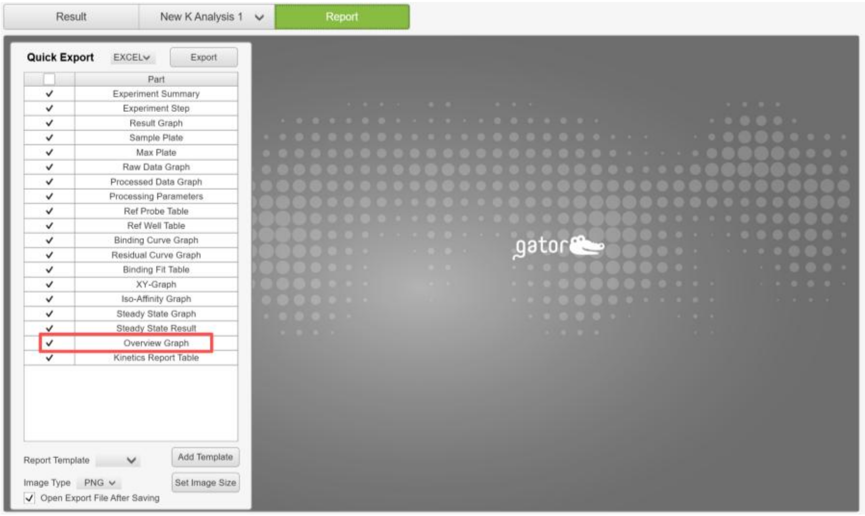
Image Type: BMP

Page Items: 4

Time (sec)

Average: 0

Group	Probe Position	Experiment	Color	BindingPair	M Conc. (nM)	koff (1/s)	kon (1/Ms)	KD (M)	Full R²	Full X²
1	A1	Assay 1	🟥	D:E	200	2.73E-004	1.47E+005	1.85E-009	0.9939	0.0094
2	B1	Assay 1	🟧	D:E	100	8.81E-004	2.21E+005	3.98E-009	0.9931	0.0102
3	C1	Assay 1	🟩	D:E	50	7.56E-004	3.36E+005	2.25E-009	0.9801	0.0261
4	D1	Assay 1	🟦	D:E	25	8.71E-004	8.45E+005	1.03E-009	0.8764	0.0579
5	A1	Assay 2	🟦	D:G	1.00E+003	1.58E-001	2.29E+005	6.91E-007	0.9611	0.046
6	B1	Assay 2	🟪	D:G	500	1.94E-001	2.27E+005	8.55E-007	0.9865	0.0072
7	C1	Assay 2	🟥	D:G	250	1.86E-001	4.26E+005	4.36E-007	0.8679	0.0207
8	D1	Assay 2	🟥	D:G	125	OR	OR	OR	0.0089	0.0532
9	A1	Assay 3	🟫	D:I	1.00E+003	3.00E-001	1.13E+005	2.65E-006	0.9906	0.0087



Quick Export EXCEL

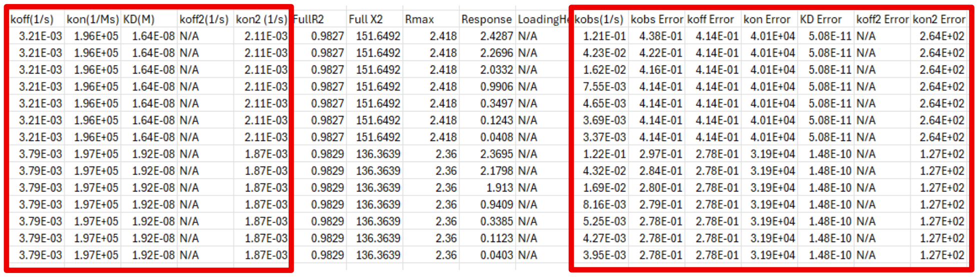
☐	Part
✓	Experiment Summary
✓	Experiment Step
✓	Result Graph
✓	Sample Plate
✓	Max Plate
✓	Raw Data Graph
✓	Processed Data Graph
✓	Processing Parameters
✓	Ref Probe Table
✓	Ref Well Table
✓	Binding Curve Graph
✓	Residual Curve Graph
✓	Binding Fit Table
✓	XY-Graph
✓	Iso-Affinity Graph
✓	Steady State Graph
✓	Steady State Result
✓	Overview Graph
✓	Kinetics Report Table

Report Template

Image Type PNG

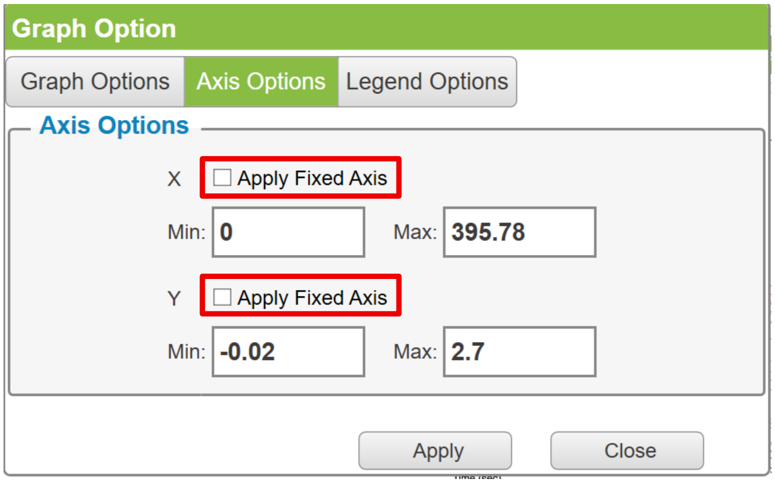
☑ Open Export File After Saving

2.6. In Kinetics analysis, kinetic data 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	LoadingHe	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

2.7. In Kinetics analysis, users can now select "Apply Fixed Axis" 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.



Axis Options

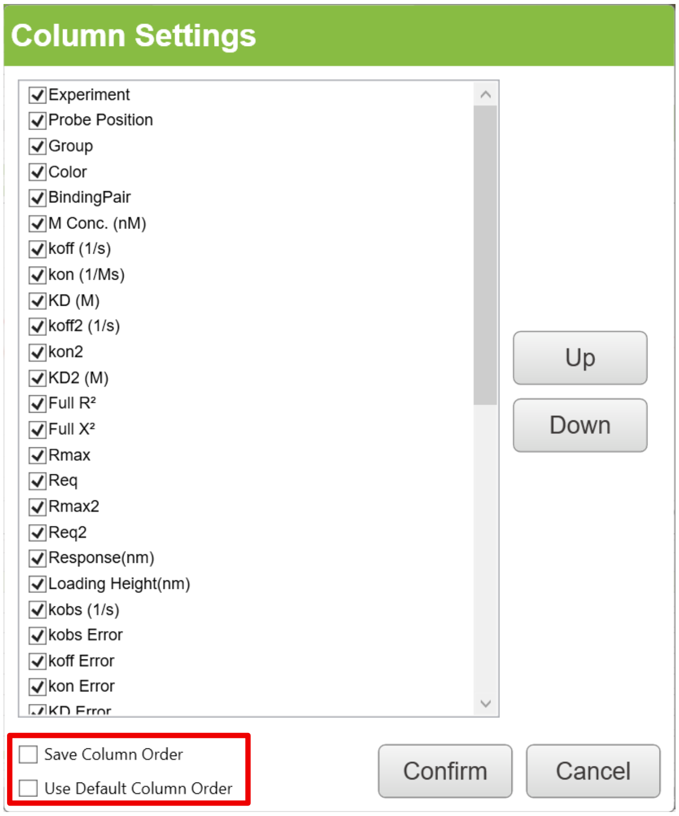
X ☐ Apply Fixed Axis

Min: 0 Max: 395.78

Y ☐ Apply Fixed Axis

Min: -0.02 Max: 2.7

2.8. In Kinetics analysis, the results table now supports column customization. When the 'Save Column Order' option is selected, these preferences are applied globally across all kinetic analyses, encompassing both current and future assay results; selecting 'Use Default Column Order' will revert the table to the original system settings.

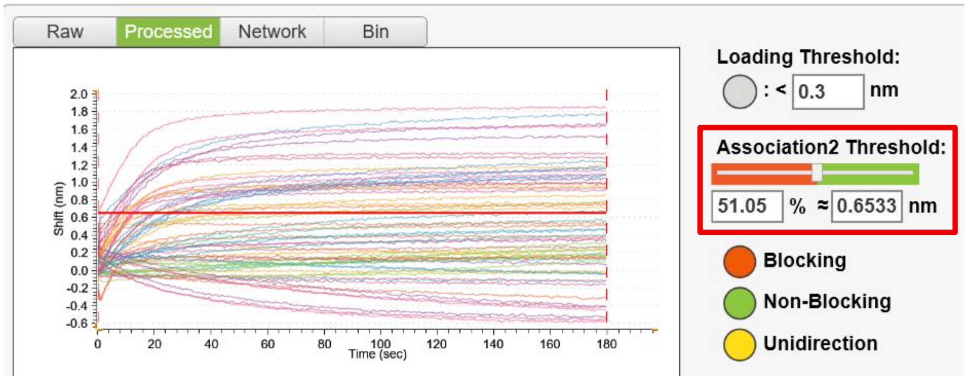


☑ Experiment
☑ Probe Position
☑ Group
☑ Color
☑ BindingPair
☑ M Conc. (nM)
☑ koff (1/s)
☑ kon (1/Ms)
☑ KD (M)
☑ koff2 (1/s)
☑ kon2
☑ KD2 (M)
☑ Full R^2
☑ Full X^2
☑ Rmax
☑ Req
☑ Rmax2
☑ Req2
☑ Response(nm)
☑ Loading Height(nm)
☑ kobs (1/s)
☑ kobs Error
☑ koff Error
☑ kon Error
☑ KD Error

☐ Save Column Order
☐ Use Default Column Order

2.9. In Epitope Binning analysis, the Association2 Threshold 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:

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

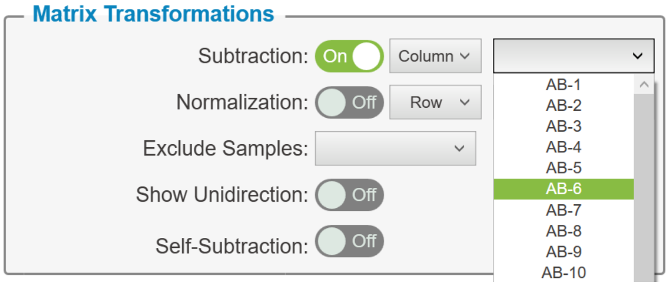


Loading Threshold: ○ : < 0.3 nm

Association2 Threshold: 51.05 % ≈ 0.6533 nm

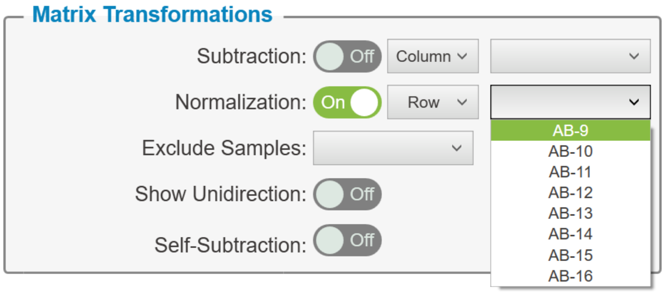
● Blocking
● Non-Blocking
● Unidirection

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



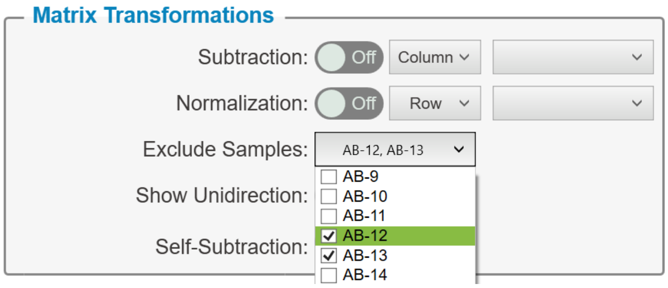
Subtraction: On Column
Normalization: Off Row
Exclude Samples:
Show Unidirection: Off
Self-Subtraction: Off

2.11. 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.



Subtraction: Off Column
Normalization: On Row
Exclude Samples:
Show Unidirection: Off
Self-Subtraction: Off

2.12. 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.



Matrix Transformations

Subtraction: Off Column

Normalization: Off Row

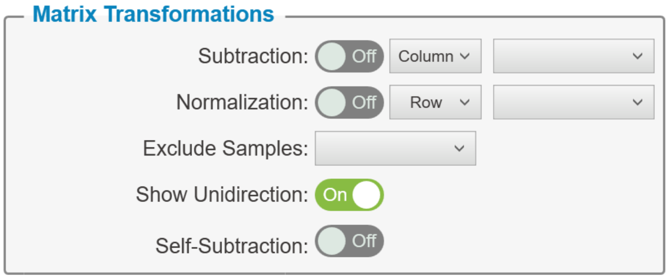
Exclude Samples: AB-12, AB-13

Show Unidirection:

Self-Subtraction:

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

2.13. 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.



Matrix Transformations

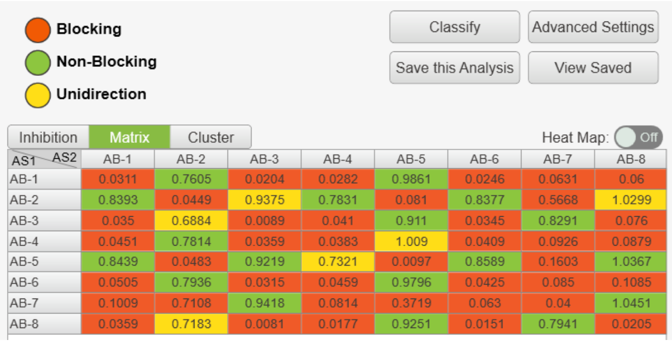
Subtraction: Off Column

Normalization: Off Row

Exclude Samples:

Show Unidirection: On

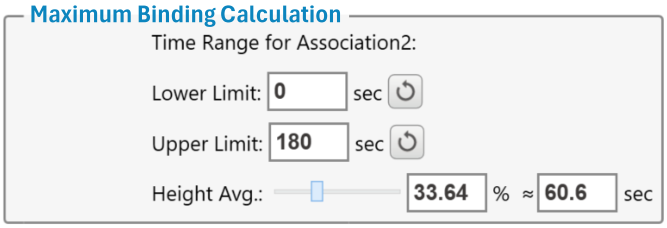
Self-Subtraction: Off



● Blocking
● Non-Blocking
● Unidirection

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

2.14. 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.



Maximum Binding Calculation

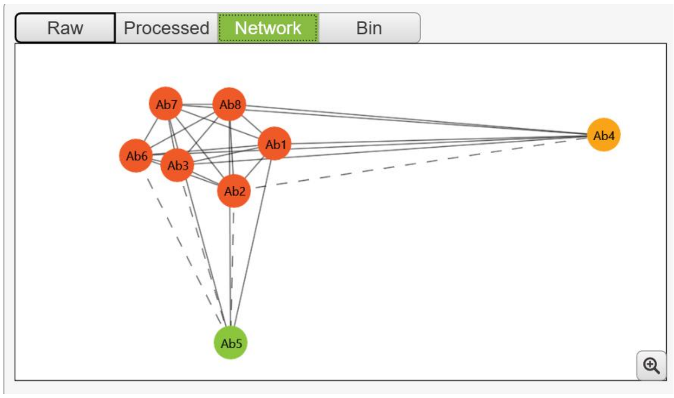
Time Range for Association2:

Lower Limit: 0 sec

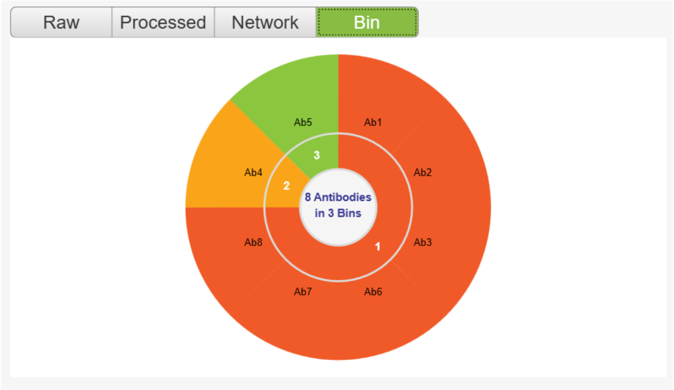
Upper Limit: 180 sec

Height Avg.: 33.64 % ≈ 60.6 sec

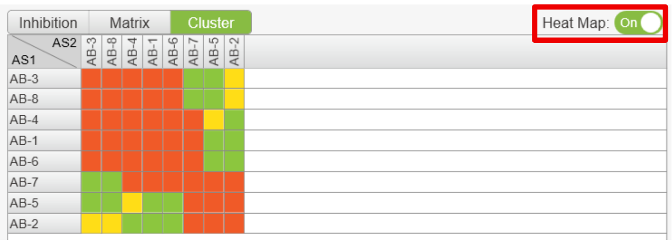
2.15. In Epitope Binning analysis, the Network Chart visualizes binding relationships by grouping samples targeting the same epitope. Connection styles represent blocking status: solid (mutual), dashed (one-way), or none (non-blocking).



2.16. 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.



2.17. 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.



Heat Map: On

AS2 / AS1	AB-3	AB-8	AB-4	AB-1	AB-6	AB-7	AB-5	AB-2
AB-3	🟥	🟥	🟥	🟥	🟥	🟩	🟩	🟨
AB-8	🟥	🟥	🟥	🟥	🟥	🟩	🟩	🟨
AB-4	🟥	🟥	🟥	🟥	🟥	🟥	🟨	🟩
AB-1	🟥	🟥	🟥	🟥	🟥	🟥	🟩	🟩
AB-6	🟥	🟥	🟥	🟥	🟥	🟥	🟩	🟩
AB-7	🟩	🟩	🟥	🟥	🟥	🟥	🟥	🟥
AB-5	🟩	🟩	🟨	🟩	🟩	🟥	🟥	🟥
AB-2	🟨	🟨	🟩	🟩	🟩	🟥	🟥	🟥

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

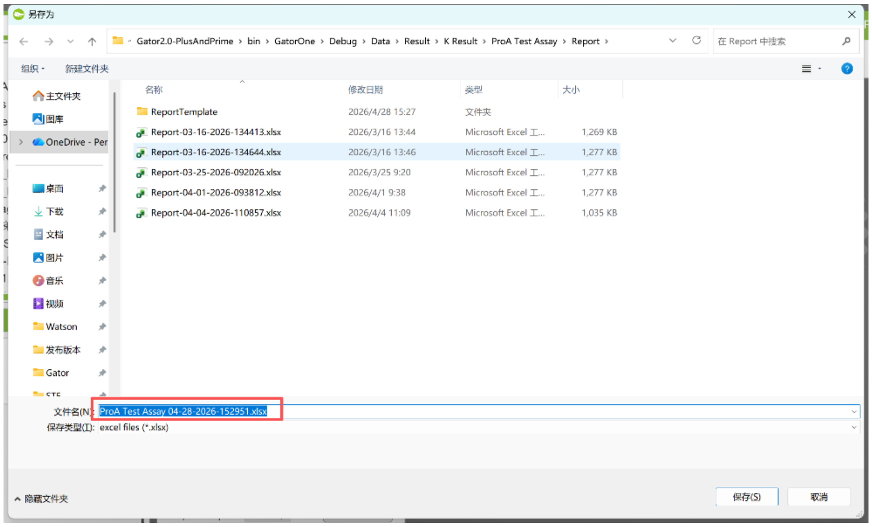
☐	Part
✓	Experiment Summary
✓	Experiment Step
✓	Result Graph
✓	Sample Plate
✓	Max Plate
✓	Raw Data Graph
✓	Processed Data Graph
✓	Processing Parameters
✓	Ref Probe Table
✓	Ref Well Table
✓	Binding Curve Graph
✓	Residual Curve Graph
✓	Binding Fit Table
✓	XY-Graph
✓	Iso-Affinity Graph
✓	Steady State Graph
✓	Steady State Result
✓	Overview Graph
✓	Kinetics Report Table

Report Template

Image Type PNG

☑ Open Export File After Saving

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



Gator2.0-PlusAndPrime › bin › GatorOne › Debug › Data › Result › K Result › ProA Test Assay › Report ›

名称	修改日期	类型	大小
ReportTemplate	2026/4/28 15:27	文件夹	
Report-03-16-2026-134413.xlsx	2026/3/16 13:44	Microsoft Excel 工...	1,269 KB
Report-03-16-2026-134644.xlsx	2026/3/16 13:46	Microsoft Excel 工...	1,277 KB
Report-03-25-2026-092026.xlsx	2026/3/25 9:20	Microsoft Excel 工...	1,277 KB
Report-04-01-2026-093812.xlsx	2026/4/1 9:38	Microsoft Excel 工...	1,277 KB
Report-04-04-2026-110857.xlsx	2026/4/4 11:09	Microsoft Excel 工...	1,035 KB

文件名(N): ProA Test Assay 04-28-2026-152951.xlsx

保存类型(T): excel files (*.xlsx)

System Requirements & Compatibility

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

PC Requirements

- **CPU**: Intel Core i9 recommended (Minimum: i5 1.6GHz).
- **Memory**: 32GB DDR5 recommended (Minimum: 8GB).
- **Storage**: 1TB SSD required.
- **Connectivity**: Ethernet, Wi-Fi, and Bluetooth ports required.

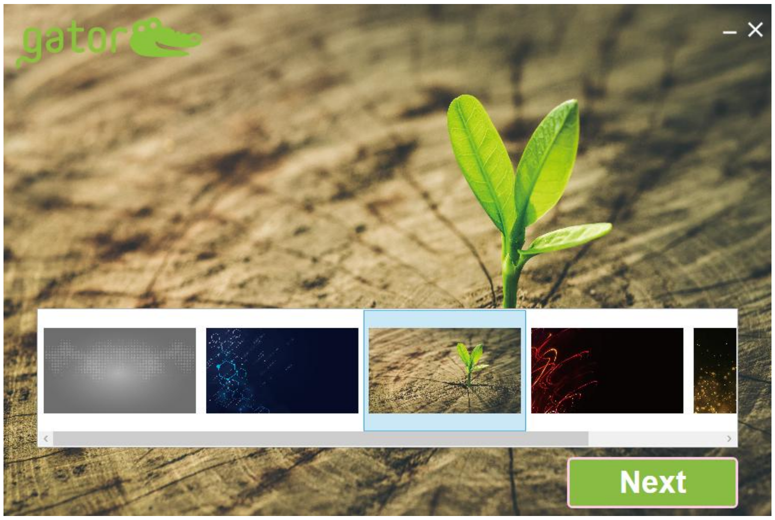
Graphics Driver Requirements

- PCs with Intel 11th and 12th Gen CPUs using Arc™ & Iris® Xe Graphics.
- Driver version 31.0.101.4091 or higher.
- Update via the Intel support website if your current version is lower.
- See the LightningChart for specific troubleshooting and workarounds.

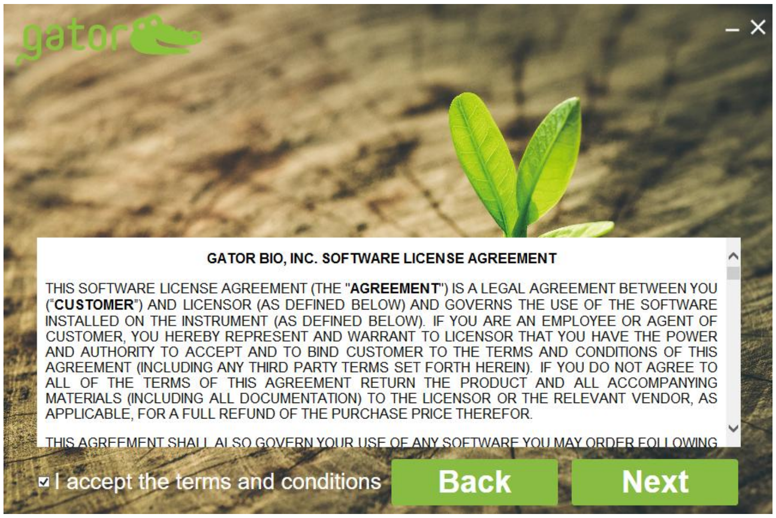
GatorOne Software Upgrade Instructions

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.



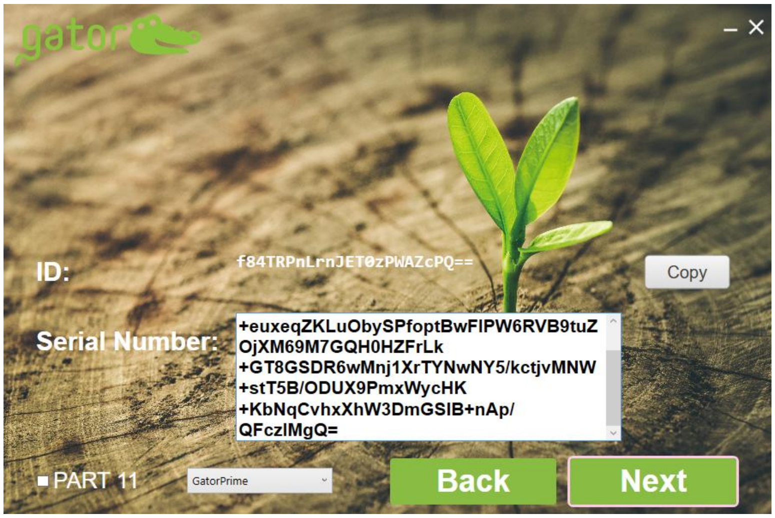
GATOR BIO, INC. SOFTWARE LICENSE AGREEMENT

THIS SOFTWARE LICENSE AGREEMENT (THE "**AGREEMENT**") IS A LEGAL AGREEMENT BETWEEN YOU ("**CUSTOMER**") AND LICENSOR (AS DEFINED BELOW) AND GOVERNS THE USE OF THE SOFTWARE INSTALLED ON THE INSTRUMENT (AS DEFINED BELOW). IF YOU ARE AN EMPLOYEE OR AGENT OF CUSTOMER, YOU HEREBY REPRESENT AND WARRANT TO LICENSOR THAT YOU HAVE THE POWER AND AUTHORITY TO ACCEPT AND TO BIND CUSTOMER TO THE TERMS AND CONDITIONS OF THIS AGREEMENT (INCLUDING ANY THIRD PARTY TERMS SET FORTH HEREIN). IF YOU DO NOT AGREE TO ALL OF THE TERMS OF THIS AGREEMENT RETURN THE PRODUCT AND ALL ACCOMPANYING MATERIALS (INCLUDING ALL DOCUMENTATION) TO THE LICENSOR OR THE RELEVANT VENDOR, AS APPLICABLE, FOR A FULL REFUND OF THE PURCHASE PRICE THEREFOR.

THIS AGREEMENT SHALL ALSO GOVERN YOUR USE OF ANY SOFTWARE YOU MAY ORDER FOLLOWING

☑ I accept the terms and conditions

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



ID: f84TRPnLrnJET0zPWAZcPQ==

Serial Number:
+euxeqZKLuObySPfoptBwFIPW6RVB9tuZ
OjXM69M7GQH0HZFrLk
+GT8GSDR6wMnj1XrTYNwNY5/kctjvMNW
+stT5B/ODUX9PmxWycHK
+KbNqCvhxXhW3DmGSIB+nAp/
QFczIMgQ=

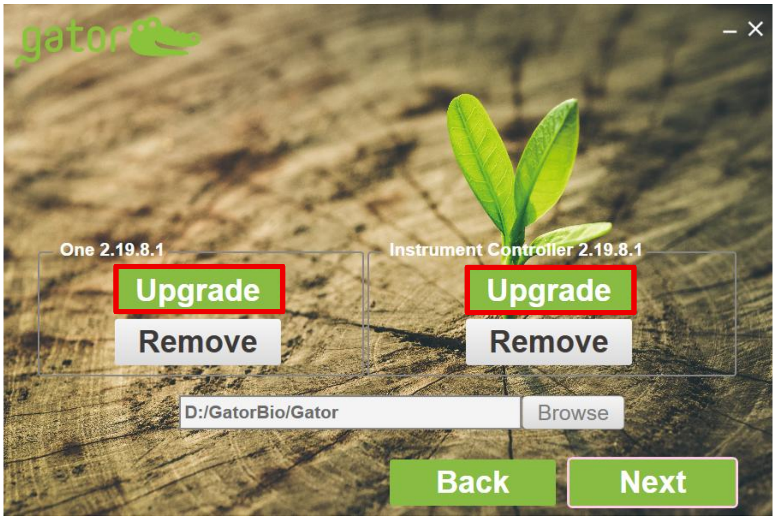
☐ PART 11 GatorPrime

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.