

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)

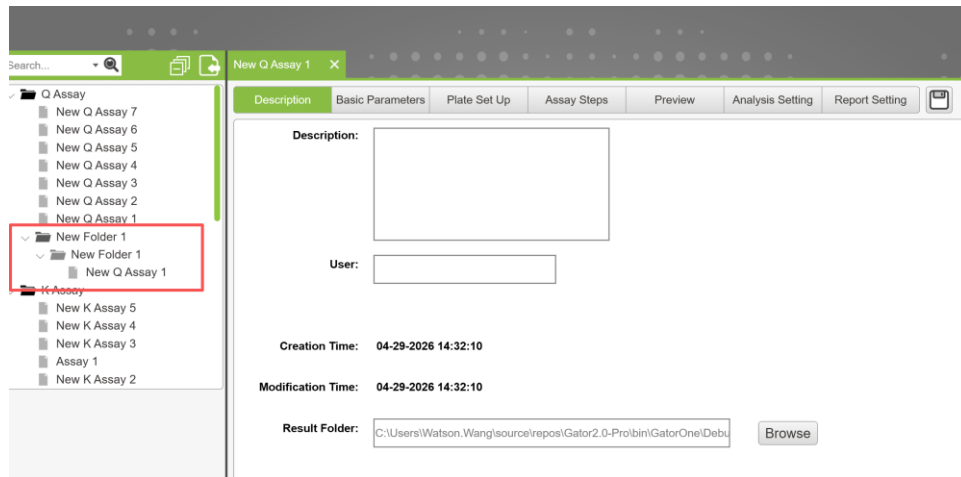
Release Highlights

- 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

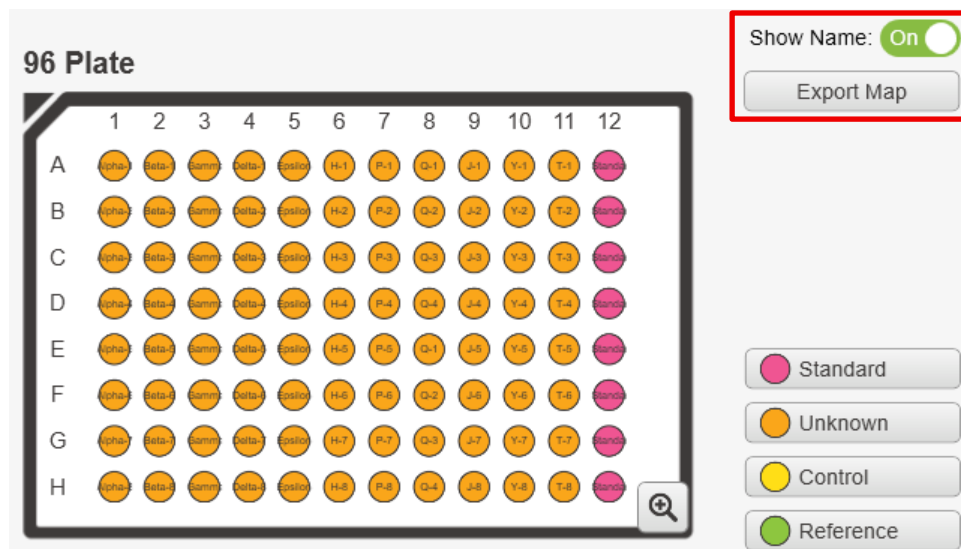
New Features & Improvements

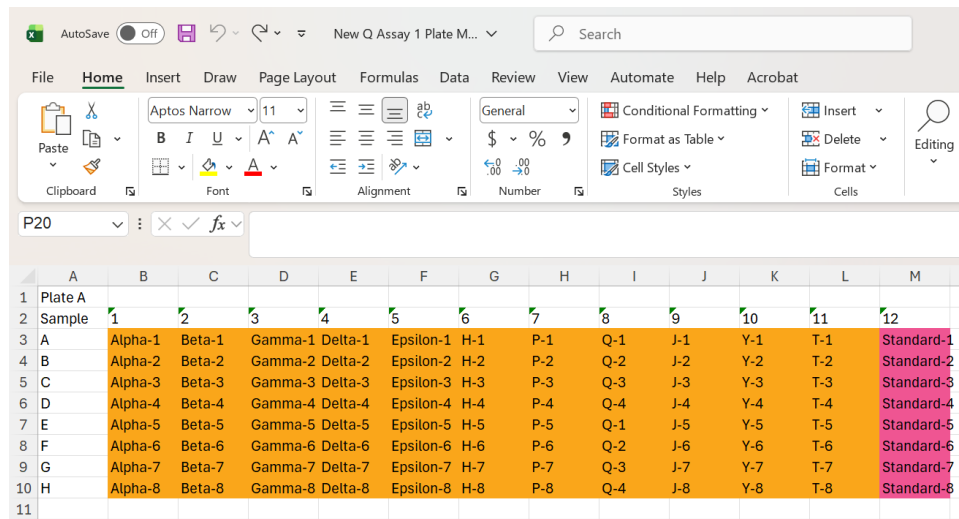
1. Assay Setup New Features

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.

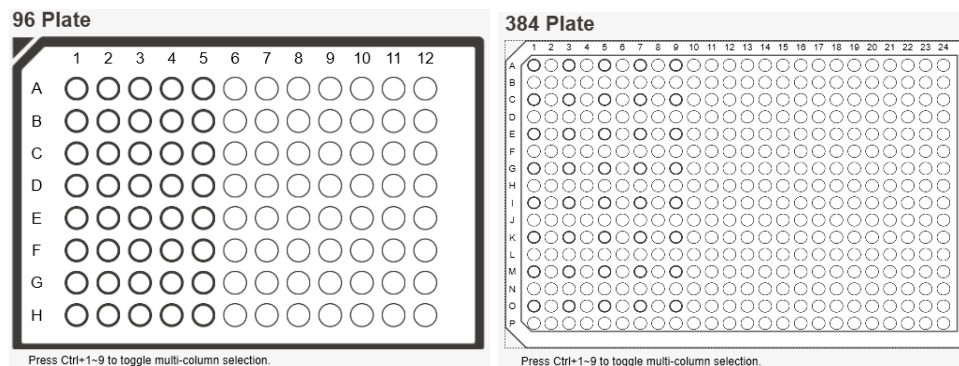


1.2. In Quantitation and Kinetics assay setup, users can now enable or disable sample names on the plate map. When enabled, the exported plate map includes sample names and color-coded step types, providing a clear reference to make pipetting easier for the user.





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.

96 Plate Max Plate Import Export µg/mL ▾

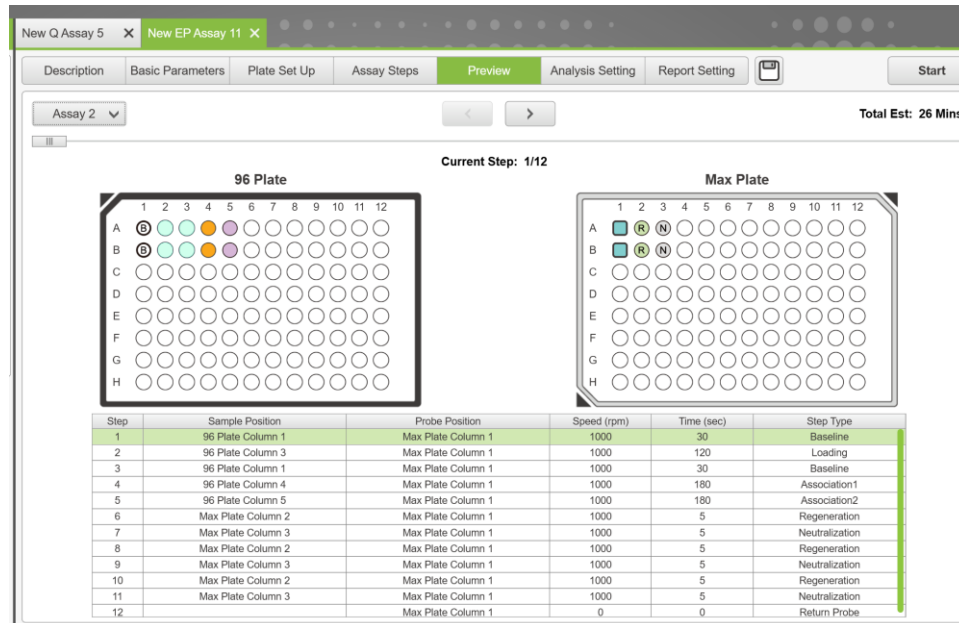
Index	Position	Sample Name	Replicate Group	Type	Conc. (µg/mL)	Dilution Fa
1	A1	Alpha-1		Unknown	—	—
2	B1	Alpha-2		Unknown	—	—
3	C1	Alpha-3		Unknown	—	—
4	D1	Alpha-4		Unknown	—	—
5	E1	Alpha-5		Unknown	—	—
6	F1	Alpha-6		Unknown	—	—
7	G1	Alpha-7		Unknown	—	—
8	H1	Alpha-8		Unknown	—	—
9	A2	Beta-1		Unknown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

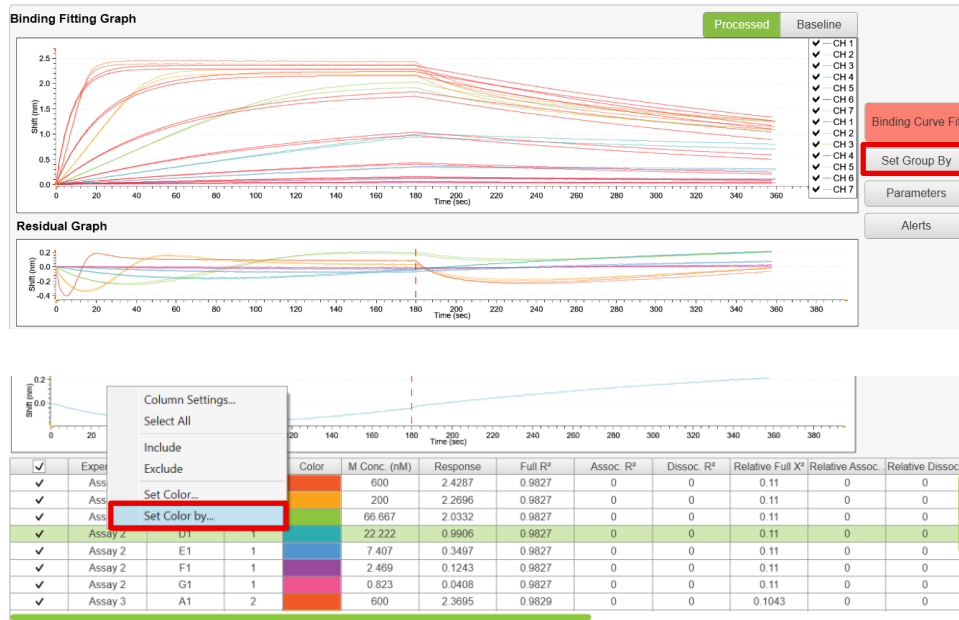
1.6. In Epitope Binning assay setup, if "Regeneration Before Assay" is active, redundant regeneration steps are now skipped when the same sensor is reused.



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, 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.



Assay	Exp	Color	M Conc. (nM)	Response	Full R ²	Assoc. R ²	Dissoc. R ²	Relative Full X ²	Relative Assoc.	Relative Dissoc.	
Ass	✓	600	2.4287	0.9827	0	0	0.11	0	0	0	
Ass	✓	200	2.2696	0.9827	0	0	0.11	0	0	0	
Ass	✓	66.667	2.0332	0.9827	0	0	0.11	0	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

Select one or more:

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

Also Set Color

Set Color By

Select one or more:

- 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, 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

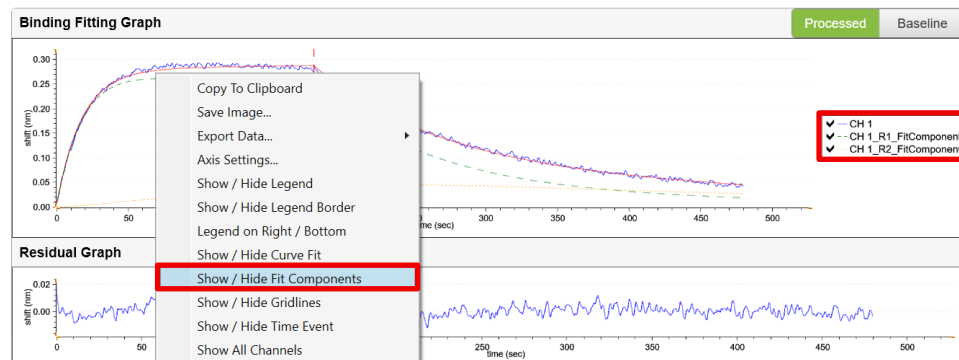
Both
Association
Dissociation

Binding Model

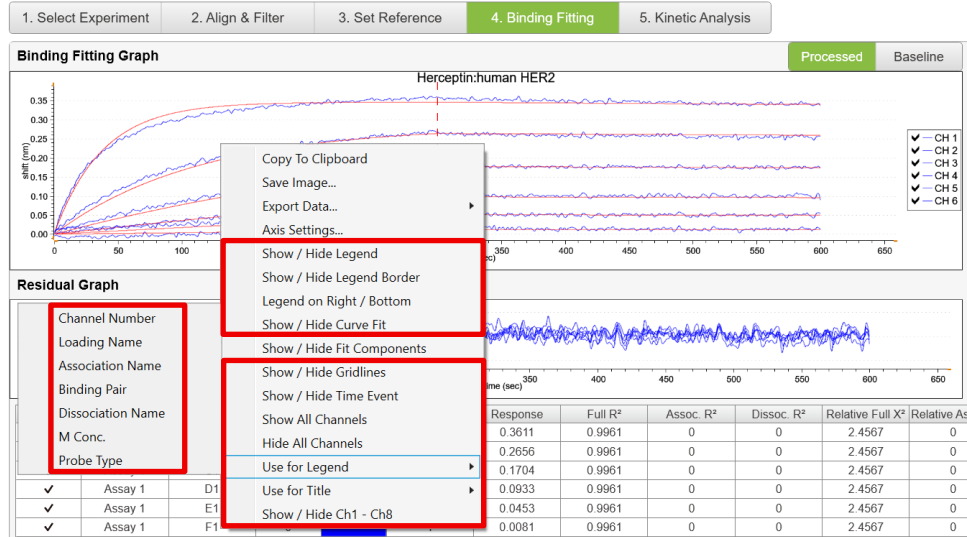
Model:

1:1
2:1
Mass
1:2
Two State

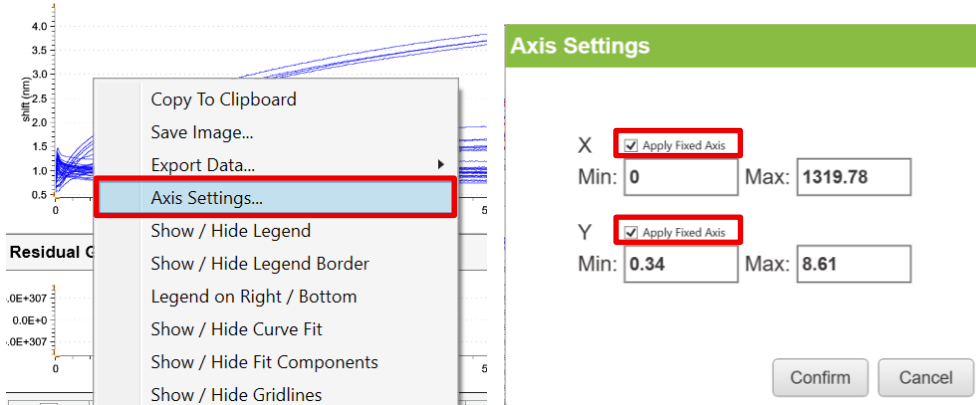
2.3. In Kinetics analysis, the binding fitting graph for the Two-state binding model now allows users to right-click the graph to enable or disable individual fit components. This works for both association and dissociation, providing a more focused view of specific binding phases.



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.

Column 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 R²
- Full X²
- Rmax
- Req
- Rmax2
- Req2
- Response(nm)
- Loading Height(nm)
- kobs (1/s)
- kobs Error
- koff Error
- kon Error
- KD Error

Up
Down

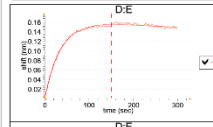
Save Column Order
 Use Default Column Order

Confirm
Cancel

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.

1. Select Experiment
2. Align & Filter
3. Set Reference
4. Binding Fitting
5. Kinetic Analysis

Binding Fitting Graph
Iso-Affinity
Steady State
Overview
Processed
Baseline



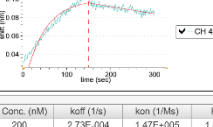
koff (1/s) 2.75E-004
kon (1/Ms) 1.47E+005
KD (M) 1.65E-009
Full R² 0.9939
Full X² 0.0094



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



koff (1/s) 3.88E-004
kon (1/Ms) 8.26E+005
KD (M) 2.29E-009
Full R² 0.9901
Full X² 0.0261



koff (1/s) 8.71E-004
kon (1/Ms) 8.45E+005
KD (M) 1.03E-009
Full R² 0.9876
Full X² 0.0579

Export Images
Edit Attributes
Page Items:
4
Page Up
Page 1
Page Down

Group	Probe Position	Experiment	Color	BindingPair	M Conc. (nM)	koff (1/s)	kon (1/Ms)	KD (M)	Full R ²	Full X ²
1	A1	Assay 1		D-E	200	2.73E-004	1.47E+005	1.65E-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	0.048
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	Δ1	Assay 1		FR	1.00E+003	1.00E+001	1.10E+006	2.00E+006	0.0000	0.0007

Calculate Kinetics
Alerts
Save Analysis
View Saved

Response Points
Time (sec)
Average 0
Add Line
Remove All

Edit Attributes

Display Attributes: On

- Experiment
- Probe Position
- Group
- BindingPair
- M Conc. (nM)
- koff (1/s)
- kon (1/Ms)
- KD (M)
- koff2 (1/s)
- kon2
- KD2 (M)
- Full R²
- Full X²
- Rmax
- Req
- Rmax2
- Req2
- Response(nm)
- Loading Height(nm)
- kobs (1/s)
- kobs Error
- koff Error
- kon Error

Up
Down

Confirm Cancel

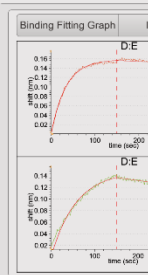
2.8. In Kinetics analysis, Overview mode results can be exported directly to a selected folder or included in the "Overview" tab within the final report.

Result | New K Analysis 1 | Report

1. Select Experiment | 2. Align & Filter | 3. Set Reference | 4. Binding Fitting | 5. Kinetic Analysis

Export Images

Binding Fitting Graph



Width: pixels

Height: pixels

Image Type:

Confirm Cancel

Export Images

Page Items:

Page Up
Page 1
Page Down

Group	Probe Position	Experiment	Color	BindingPair	M Conc. (nM)	koff (1/s)	kon (1/Ms)	KD (M)	Full R ²	Full X ²
1	A1	Assay 1	Orange	D-E	200	2.73E-004	1.47E+005	1.85E-009	0.9939	0.0094
2	B1	Assay 1	Green	D-E	100	8.81E-004	2.21E+005	3.98E-009	0.9931	0.0102
3	C1	Assay 1	Blue	D-E	50	7.56E-004	3.36E+005	2.25E-009	0.9801	0.0261
4	D1	Assay 1	Red	D-E	25	8.71E-004	8.45E+005	1.03E-009	0.8764	0.0579
5	A1	Assay 2	Yellow	D-G	1.00E+003	1.58E-001	2.29E+005	6.91E-007	0.9611	0.046
6	B1	Assay 2	Purple	D-G	500	1.94E-001	2.27E+005	8.55E-007	0.9865	0.0072
7	C1	Assay 2	Light Blue	D-G	250	1.86E-001	4.26E+005	4.36E-007	0.8679	0.0207
8	D1	Assay 2	Light Green	D-G	125	OR	OR	OR	0.0089	0.0532
9	A1	Assay 3	Light Purple	D-I	1.00E+003	3.00E-001	1.15E+004	3.65E-006	0.9006	0.0067

Calculate Kinetics

Alerts

Save Analysis

View Saved

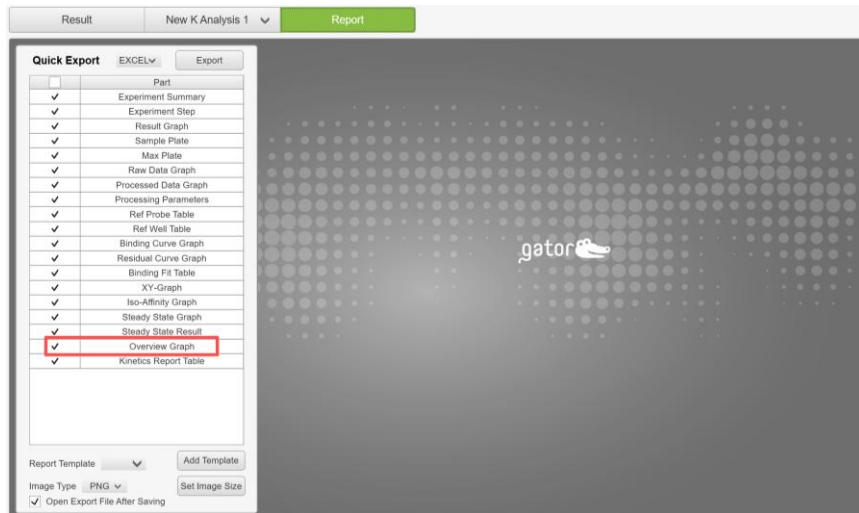
Response Points

Time (sec)

Average

Add Line

Remove All

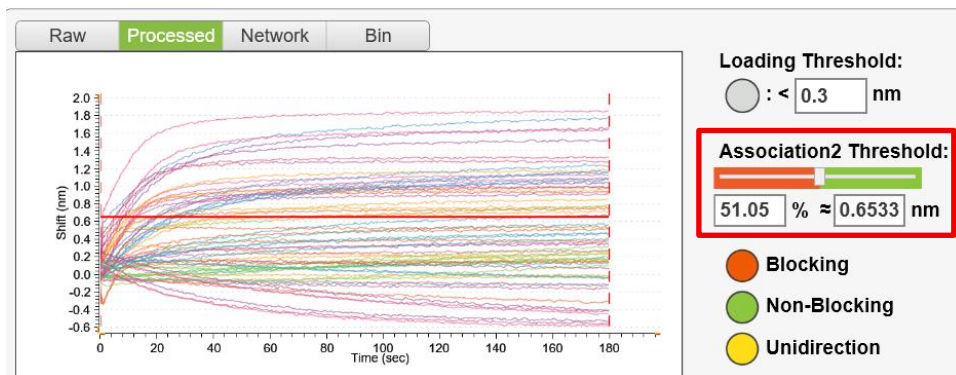


2.9. In Kinetics analysis, kinetic constants are now exported in scientific notation to improve readability.

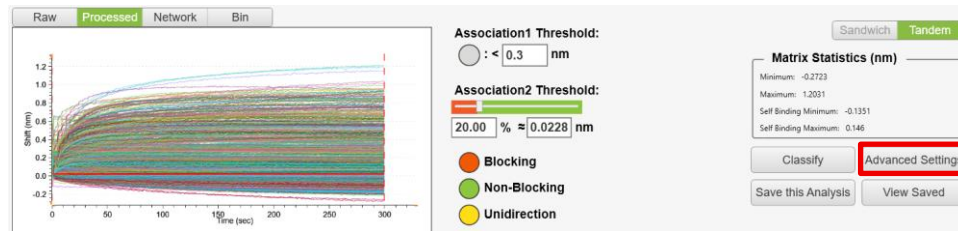
koff(1/s)	kon(1/Ms)	KD(M)	koff2(1/s)	kon2(1/s)	FullR2	FullX2	Rmax	Response	Loading	kobs(1/s)	kobs Error	koff Error	kon Error	KD Error	koff2 Error	kon2 Error
3.21E-03	1.96E+05	1.64E-08	N/A	2.11E-03	0.9827	151.6492	2.418	2.4287	N/A	1.21E-01	4.38E-01	4.14E-01	4.01E+04	5.08E-11	N/A	2.64E+02
3.21E-03	1.96E+05	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:

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



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



Matrix Transformations

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

Dropdown menu contents: AB-1, AB-2, AB-3, AB-4, AB-5, **AB-6**, AB-7, AB-8, AB-9, AB-10

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.

Matrix Transformations

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

Dropdown menu contents: **AB-9**, AB-10, AB-11, AB-12, AB-13, AB-14, AB-15, AB-16

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.

Matrix Transformations

- Subtraction: Off Column ▼
- Normalization: Off Row ▼
- Exclude Samples: AB-12, AB-13 ▼
- Show Unidirection: Off
- Self-Subtraction: AB-12, AB-13, AB-14

Inhibition	Matrix	Cluster							Heat Map: <input type="radio"/> Off
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.

Matrix Transformations

Subtraction: Off Column ▼

Normalization: Off Row ▼

Exclude Samples: ▼

Show Unidirection: On

Self-Subtraction: Off

Blocking
 Non-Blocking
 Unidirection

Inhibition	Matrix	Cluster							Heat Map: <input type="radio"/> Off
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	0.5568	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.

Maximum Binding Calculation

Time Range for Association2:

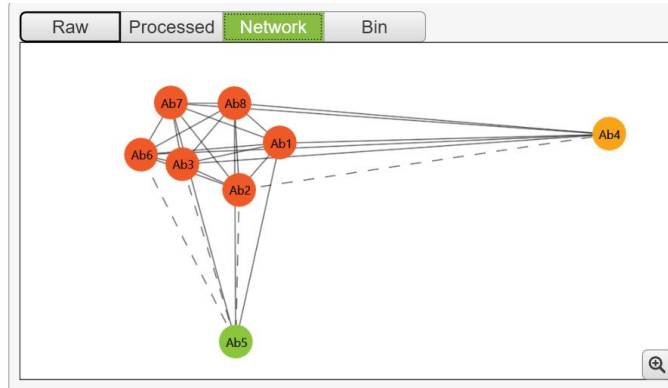
Lower Limit: sec

Upper Limit: sec

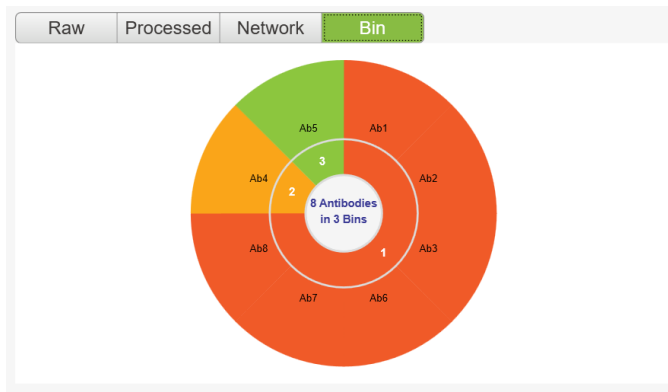
Height Avg.: % ≈ sec

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

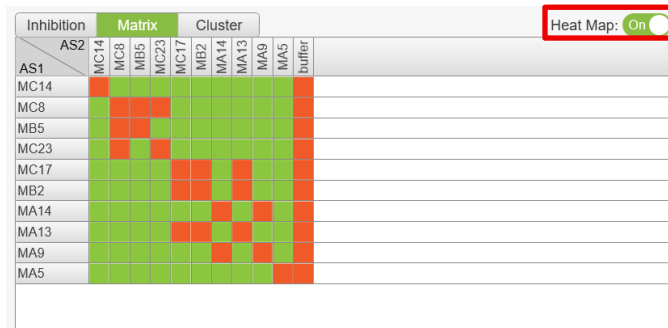
Connection styles represent blocking status: solid (mutual), dashed (one-way), or none (non-blocking).



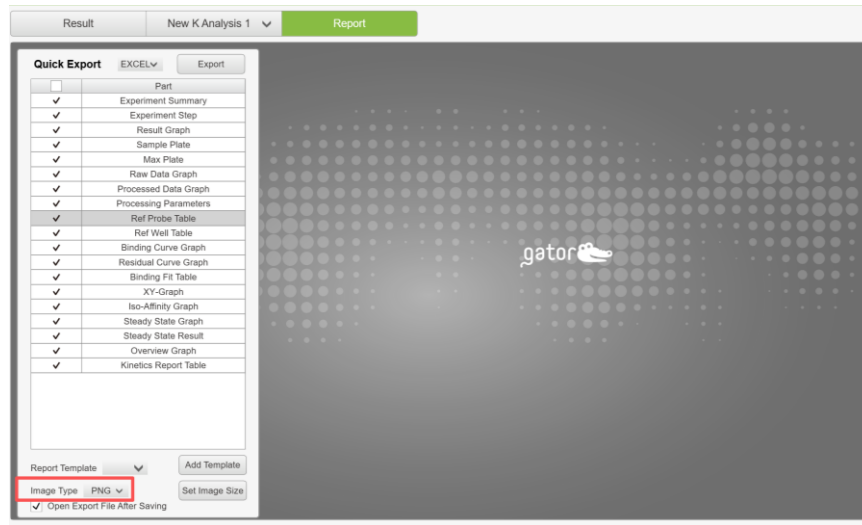
2.17. In Epitope Binning analysis, the Bin Chart provides a categorized view of results based on sample epitope targets, offering a clear summary of how a library is distributed across different binding sites.



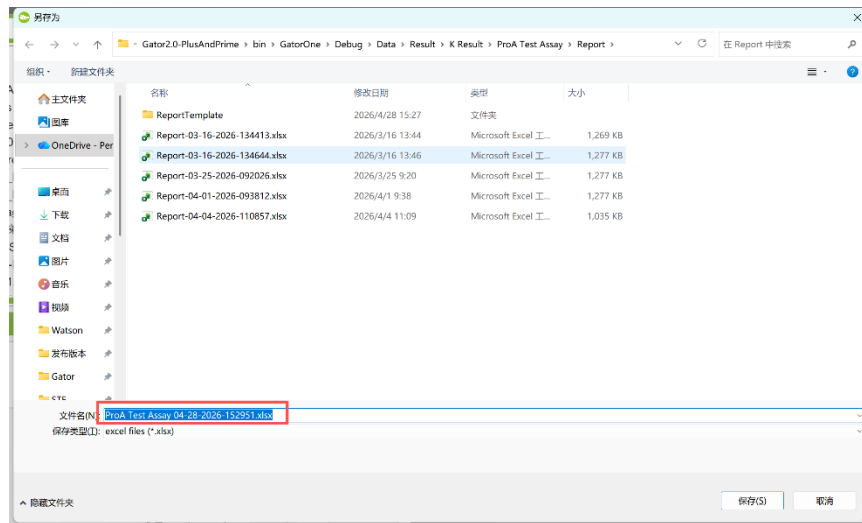
2.18. In Epitope Binning analysis, the updated Heat Map provides a simple, color-coded view of all sample interactions, making it easy to identify binding patterns across the entire dataset.



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

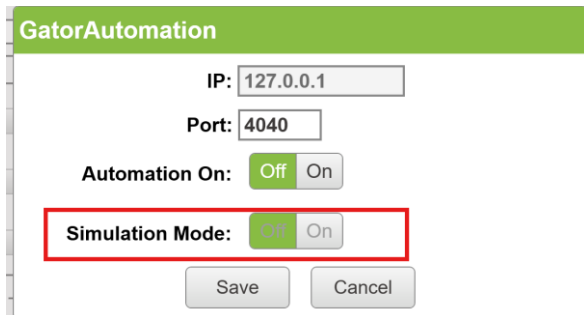


2.20. In Report, default report names now combine the Assay Name and Timestamp for improved traceability.



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.



The screenshot shows a dialog box titled "GatorAutomation". It contains the following elements:

- IP: 127.0.0.1
- Port: 4040
- Automation On: Off On
- Simulation Mode: Off On (highlighted with a red box)
- Save button
- Cancel button

- 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.

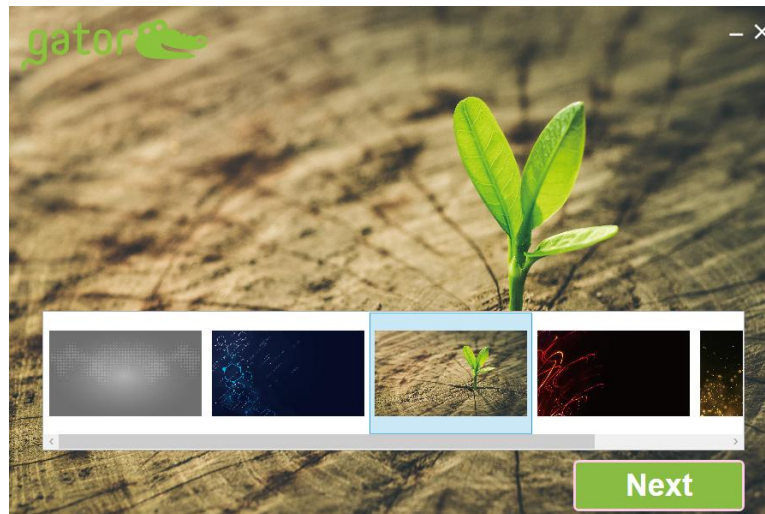
2.2. Move the extracted .exe file to the C:\ Drive of the computer workstation connected to the Gator instrument.

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

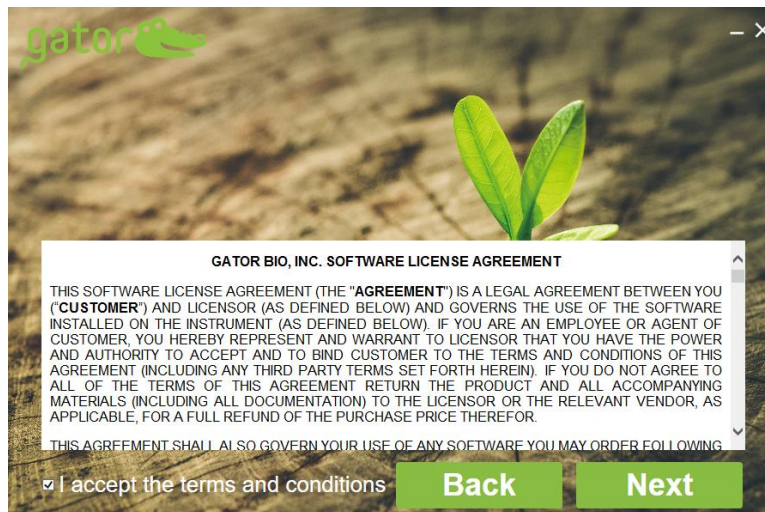
2.4. Right click and run as administrator to begin the upgrade process.

3. Configuration and Validation

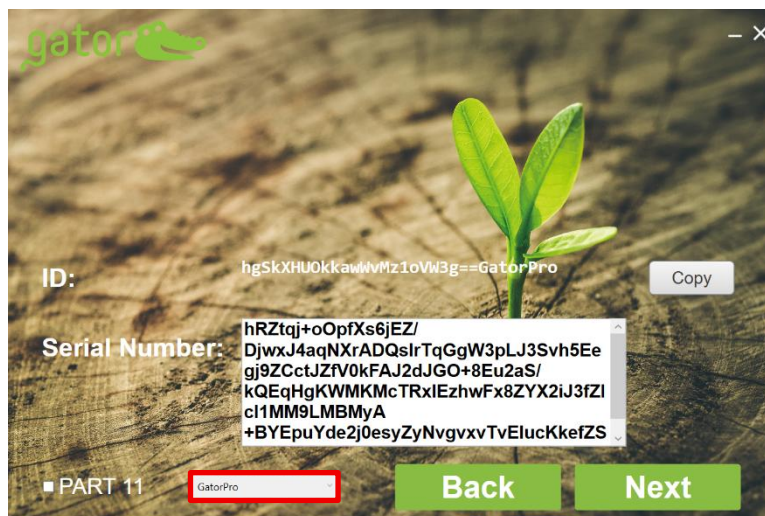
3.1. Choose one of the five available color themes and click Next.



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.

