

GatorOne v2.7 Release Note

Release Oct 2025

Introduction

Version 2.7 of GatorOne is intended to operate the Gator® instrument.

This document is intended for current Gator Bio customers who have a Gator instrument and use the GatorOne software for assay setup and data analysis.

Product Number: 600006

Supported Instruments: Gator® Pivot and Gator® Pro (all serial numbers)

Supported operating systems: Windows 10

Important note:

This software supports downward compatibility only. Data collected using Version 2.7 cannot be imported into earlier versions. However, all data from previous versions can be seamlessly imported and analyzed in Version 2.7.

Highlighted Features:

- AI-Powered Smart Monitoring
- EP Template Auto Generator
- Kinetics or EP Data Combination

Release Note Contents:

- Changes Since Last Release
- Upgrade Instruction

1.0 SELECTED CHANGES SINCE LAST RELEASE

1.1 AI-Powered Smart Monitoring

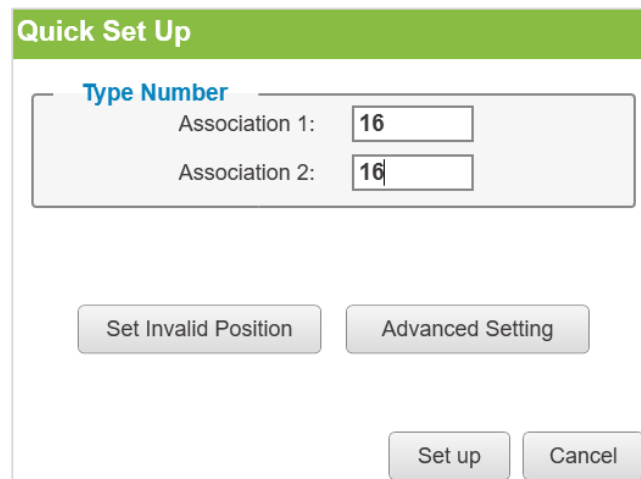
- 1.1.1 GatorOne now includes **AI-powered smart monitoring**, utilizing a built-in camera and advanced machine learning to automatically detect operational issues - such as incorrect plate placement or workflow deviations - before they affect your experiment.

This proactive system improves reliability, reduces user error, and enhances lab efficiency by catching mistakes in real time.

Note: To ensure activation of this feature, please contact Gator Bio Support at support@gatorbio.com to schedule on-site service for compatibility verification and activation, especially if your Pivot or Pro system was shipped or installed prior to this software release.

1.2 Assay Setup New Features

- 1.2.1 In the Epitope Binning assay setup, “Quick Set Up” enables auto-generation of the assay design based on user preferences, optimized for common settings, minimum assay time, or minimum sample usage. Users can select different settings for each step type to match their assay design. Additionally, if there are microplate wells that should not be used, users can choose to configure them as blocking wells.



Quick Set Up

Type Number

Association 1: 16

Association 2: 16

Set Invalid Position Advanced Setting

Set up Cancel

Advanced Setting

Optionals

Baseline: 1

Activation: 0

Quench: 0

Wash: 0

RN: 1

Probe Reuse: 10

Strategy: Classic

Save

Cancel

Invalid Position

Max Plate

1 2 3 4 5 6 7 8 9 10 11 12

A

B

C

D

E

F

G

H

Plate A

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24

A

B

C

D

E

F

G

H

I

J

K

L

M

N

O

P

Block

Unassigned

Plate B

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24

A

B

C

D

E

F

G

H

I

J

K

L

M

N

O

P

Plate C

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24

A

B

C

D

E

F

G

H

I

J

K

L

M

N

O

P

Confirm

Cancel

1.2.2 In the Epitope Binning assay setup, add a toggle option to show sample names in the plate layout. When enabled, export the plate layout as an Excel file that includes sample names and color-coded step types for easy printing and pipetting.

GATOR BIO | 2455 FABER PLACE, PALO ALTO, CA 94303 USA | INFO@GATORBIO.COM | 1-855-208-0743

SW-09 Rev-0 PAGE 2

Plate A

Plate B

Plate C

384 Plate

Sandwich Tandem

Show Name: ☒ On

Export

B Buffer

Loading

Association1

Association2

A Activation

Q Quench

Press Ctrl+S to Activate/Deactivate Quick Select

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y
1	Plate B																								
2	Sample	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24
3	A	Ab1	Ab1	Ab9	Ab9	Ab1	Ab1	Ab9	Ab9	Ab17	Ab17	Ab25	Ab25	Ab17	Ab17	Ab25	Ab25	Ag	Ag	Ag	Ag	Ag	Ag	Ag	Ag
4	B	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer
5	C	Ab2	Ab2	Ab10	Ab10	Ab2	Ab2	Ab10	Ab10	Ab18	Ab18	Ab26	Ab26	Ab18	Ab18	Ab26	Ab26	Ag	Ag	Ag	Ag	Ag	Ag	Ag	Ag
6	D	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer
7	E	Ab3	Ab3	Ab11	Ab11	Ab3	Ab3	Ab11	Ab11	Ab19	Ab19	Ab27	Ab27	Ab19	Ab19	Ab27	Ab27	Ag	Ag	Ag	Ag	Ag	Ag	Ag	Ag
8	F	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer
9	G	Ab4	Ab4	Ab12	Ab12	Ab4	Ab4	Ab12	Ab12	Ab20	Ab20	Ab28	Ab28	Ab20	Ab20	Ab28	Ab28	Ag	Ag	Ag	Ag	Ag	Ag	Ag	Ag
10	H	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer
11	I	Ab5	Ab5	Ab13	Ab13	Ab5	Ab5	Ab13	Ab13	Ab21	Ab21	Ab29	Ab29	Ab21	Ab21	Ab29	Ab29	Ag	Ag	Ag	Ag	Ag	Ag	Ag	Ag
12	J	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer
13	K	Ab6	Ab6	Ab14	Ab14	Ab6	Ab6	Ab14	Ab14	Ab22	Ab22	Ab30	Ab30	Ab22	Ab22	Ab30	Ab30	Ag	Ag	Ag	Ag	Ag	Ag	Ag	Ag
14	L	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer
15	M	Ab7	Ab7	Ab15	Ab15	Ab7	Ab7	Ab15	Ab15	Ab23	Ab23	Ab31	Ab31	Ab23	Ab23	Ab31	Ab31	Ag	Ag	Ag	Ag	Ag	Ag	Ag	Ag
16	N	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer
17	O	Ab8	Ab8	Ab16	Ab16	Ab8	Ab8	Ab16	Ab16	Ab24	Ab24	Ab32	Ab32	Ab24	Ab24	Ab32	Ab32	Ag	Ag	Ag	Ag	Ag	Ag	Ag	Ag
18	P	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer	Buffer
19																									
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34																									
35																									

1.2.3 The EP and K experiment setup now supports cycle reordering, giving users greater flexibility and control in experiment design.

Cycle 1

Position

Step Type

Time (sec)

Speed (rpm)

Step 1

96 1 2 3 4 5 6 7 8 9 10 11 12 M 1 2 3 4 5 6 7 8 9 10 11 12

Baseline

120

1000

Step 2

96 1 2 3 4 5 6 7 8 9 10 11 12 M 1 2 3 4 5 6 7 8 9 10 11 12

Loading

120

1000

Step 3

96 1 2 3 4 5 6 7 8 9 10 11 12 M 1 2 3 4 5 6 7 8 9 10 11 12

Baseline

120

1000

Add Step

Cycle 2

Position

Step Type

Time (sec)

Speed (rpm)

Step 1

96 1 2 3 4 5 6 7 8 9 10 11 12 M 1 2 3 4 5 6 7 8 9 10 11 12

Baseline

120

1000

Step 2

96 1 2 3 4 5 6 7 8 9 10 11 12 M 1 2 3 4 5 6 7 8 9 10 11 12

Loading

120

1000

Step 3

96 1 2 3 4 5 6 7 8 9 10 11 12 M 1 2 3 4 5 6 7 8 9 10 11 12

Baseline

120

1000

Add Step

Cycle 3

Position

Step Type

Time (sec)

Speed (rpm)

Step 1

96 1 2 3 4 5 6 7 8 9 10 11 12 M 1 2 3 4 5 6 7 8 9 10 11 12

Baseline

120

1000

Step 2

96 1 2 3 4 5 6 7 8 9 10 11 12 M 1 2 3 4 5 6 7 8 9 10 11 12

Loading

120

1000

Step 3

96 1 2 3 4 5 6 7 8 9 10 11 12 M 1 2 3 4 5 6 7 8 9 10 11 12

Baseline

120

1000

Add Step

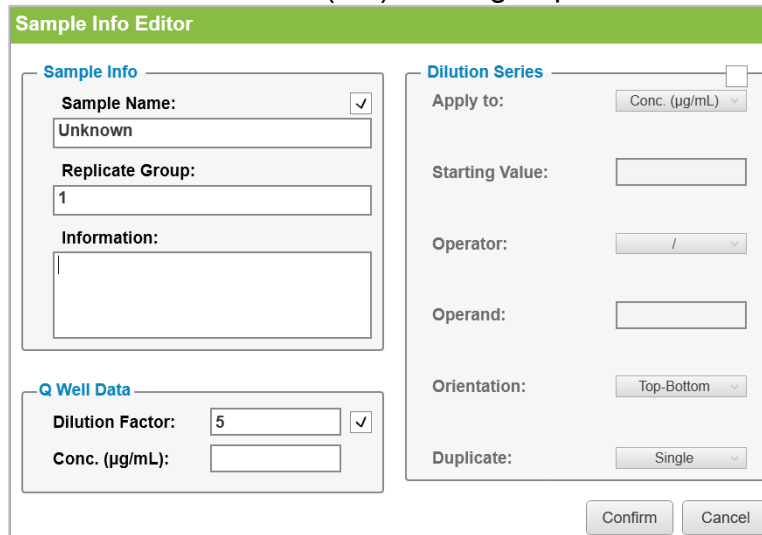
Add Cycle

Regeneration Settings: Off

Regeneration Before Assay: Off

Threshold Settings: Off

- 1.2.4 Enhanced Quantitation Assay Setup, enabling users to assign groups for calculating average concentrations and coefficient of variation (CV) within groups.



- 1.2.5 Introduced a disk space warning message to alert users when storage is running low (default threshold: 1 GB), helping to prevent data loss or storage issues.
- 1.2.6 Implemented a temperature detection process during experiments, triggering an alert for any temperature difference exceeding 2°C to ensure accurate and reliable results.

1.3 Assay Setup Amendment

- 1.3.1 Improved assay panel management: Imported assay protocols will now remain accessible and will not be automatically removed by the software, ensuring greater flexibility and data retention.
- 1.3.2 Enhanced real-time experiment flexibility by allowing users to reliably skip or extend steps, improving overall performance and reliability.

1.4 Result & Analysis New Features

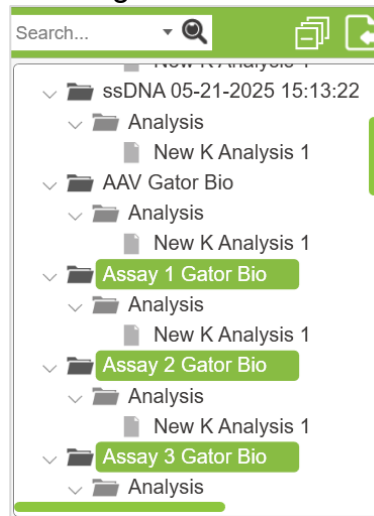
- 1.4.1 Combine multiple Kinetics or Epitope Binning assay files for batch analysis in a single report, helping to streamline your workflow and reduce analysis time.
To combine files:
- In the navigation panel, hold Ctrl and click to select multiple files.
 - Right-click the selection and choose "Combine".

- GatorOne will generate a new assay file named: CombinedResult_mm-dd-yyyy_hh-mm-ss
The assays will be concatenated in the order in which they are selected.

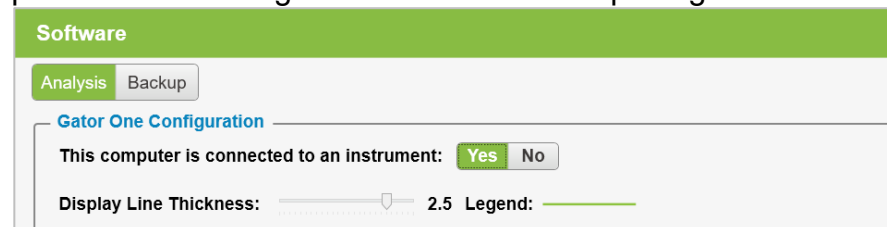
Note:

- For Kinetics, we recommend keeping assay steps and step durations consistent across all selected files to ensure better visualization and comparison.
- For Epitope Binning, aligning pairwise settings and assay step durations is also recommended for clearer interpretation.
- The sequence of plate types, either 96- or 384-well, loaded on the shakers must remain consistent across all experiment files to ensure accurate data combination. If mismatched formats are selected, the software will display a warning message and prevent combining.
- GatorOne supports combining 10 or more experiment files, offering unmatched flexibility for large-scale analysis.

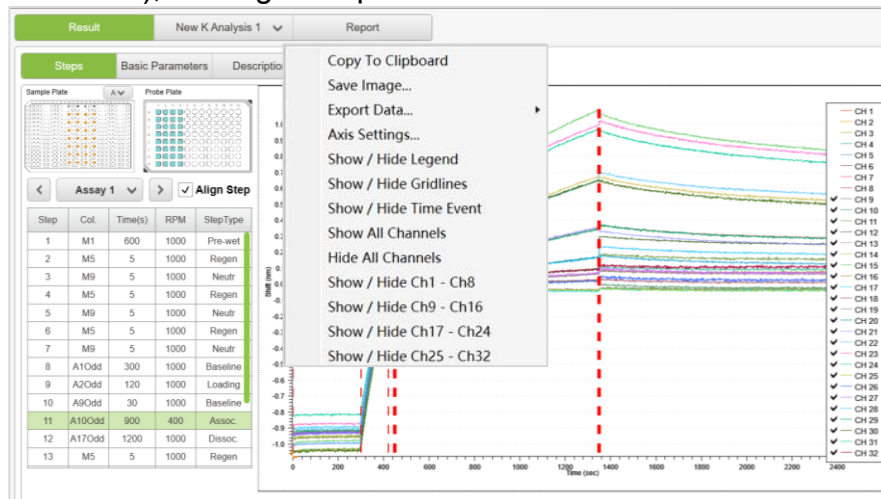
For the best performance and responsiveness, we recommend keeping combined assays under 128, ensuring a balance between power and usability.



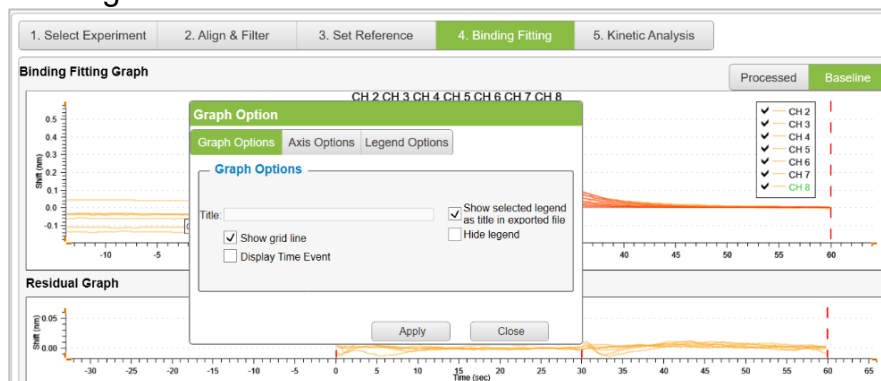
- 1.4.2 Added customization for sensorgram line thickness in the Settings page, allowing users to adjust the display to their preferences. Changes take effect after reopening the data file.



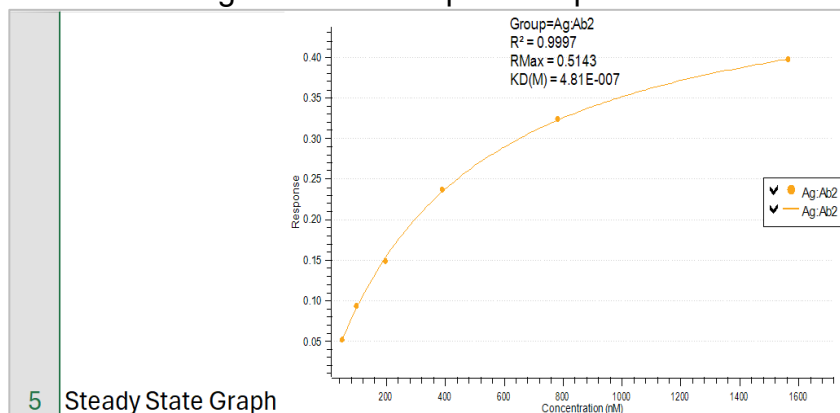
- 1.4.3 Users can now show or hide legends by group (based on the readhead), making it simpler to focus on the most relevant data



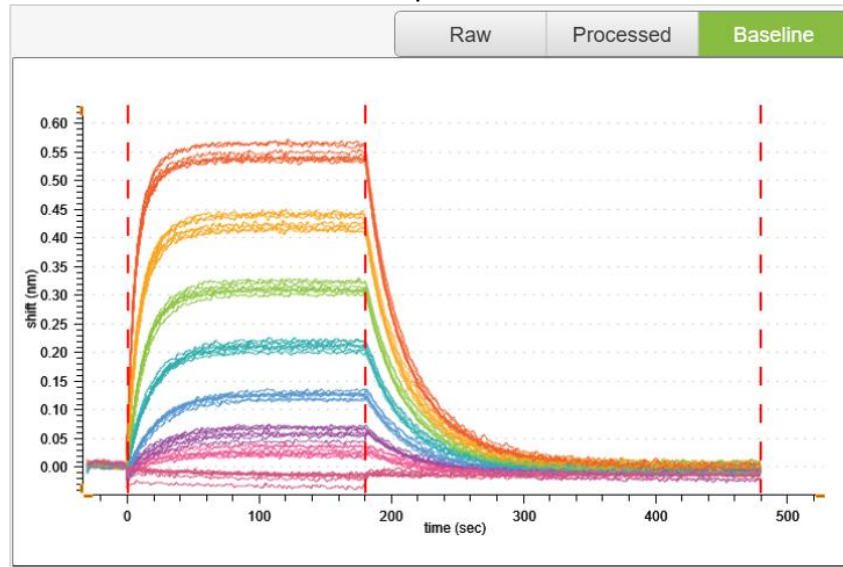
- 1.4.4 Introduced an option to show or hide time events on sensorgrams.



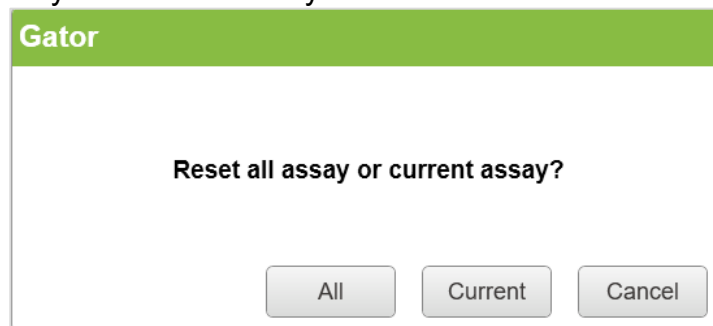
- 1.4.5 Sample information is now displayed in Steady State results, both on sensorgrams and in exported reports.



- 1.4.6 Added an option to display previous baseline sensorgrams for association and dissociation phases.



- 1.4.7 Update K analysis default alignment settings: align Y to the end of baseline, and align the interaction phase to the end of dissociation.
- 1.4.8 Added K_D error calculation.
- 1.4.9 Add units to the column headers in the Kinetic Analysis results table.
- 1.4.10 Introduced an optional reset feature for assay reference settings/formulas, allowing users to reset either all assays or only the current assay.



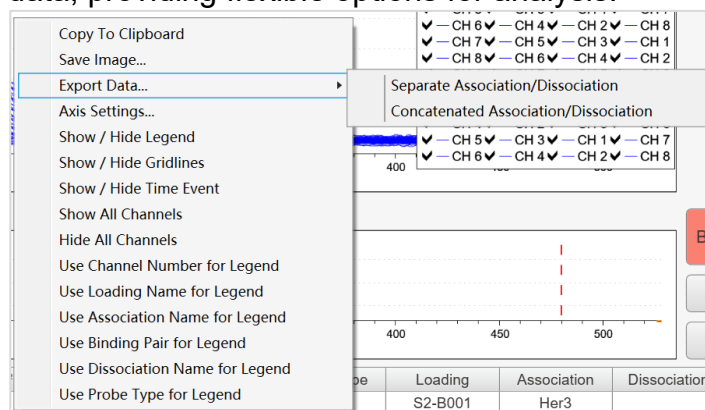
- 1.4.11 Added loading threshold information and file location to the exported Excel.

A	B
Experiment Summary	
Experiment Summary	Value
Assay Description	
Assay User	
Acquisition Time	MM-DD-YYYY HH-MM-SS
Refinement Time	MM-DD-YYYY HH-MM-SS
Result Path	C:\GatorOne\Release\Data\Result\K Result\Gator Bio MM-DD-YYYY hh-mm
Result Name	GB MM-DD-YYYY HH-MM-SS
Analysis Name	AssociationBeginLocalFull
History Analysis record Name	
Current Login User	
Product Version :	2.7.4.0905
Loading Threshold :	On
Initial Value :	1.2 nm
Apply To :	All Channel

- 1.4.12 Introduced Concentration as an optional legend for kinetics analysis.

- 1.4.13 Added loading concentration details under the tab “5. Kinetic Analysis” result table and exported Excel report.

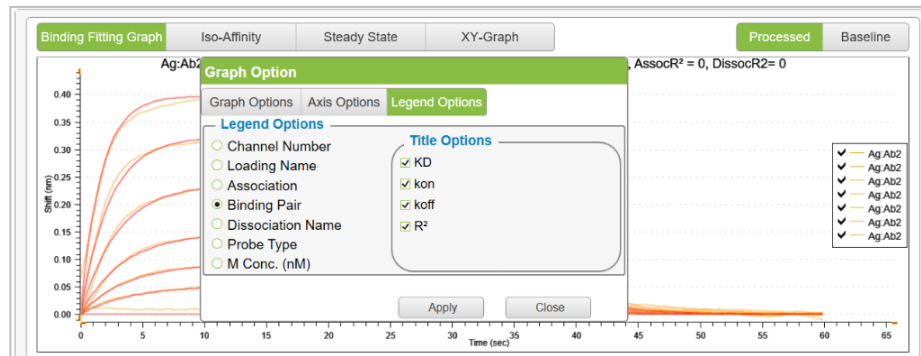
- 1.4.14 Under Kinetics Step 4: Binding Fitting, Export CSV Data now allows binding curve sensorgrams to be exported with association and dissociation signals either separated or concatenated per column, for both fitted and raw processed data, providing flexible options for analysis.



- 1.4.15 The export data file format in the K Binding Fitting and Kinetic Analysis tabs has been updated with additional headers - including Assay, Channel, Probe Position, Group Index, and Binding Pair - and each trace now contains only one time column, making it easier to identify and organize sample data.

	A	B	C	D	E	F	G	H	I
1	Assay		1	Assay		1	Assay		1
2	Channel		1	Channel		2	Channel		3
3	Probe Position	A1		Probe Position	B1		Probe Position	C1	
4	Group Number		1	Group Number		1	Group Number		1
5	Binding Pair	S2-B001:Her3		Binding Pair	S2-B001:Her3		Binding Pair	S2-B001:Her3	
6	Time CH1	Data CH1	Fit CH1	Time CH2	Data CH2	Fit CH2	Time CH3	Data CH3	Fit CH3
7	0	0.046401223	0	0	0.044510146	0	0	0.013242618	0
8	0.2	0.055206637	0.01812	0.2	0.04678913	0.008496	0.2	0.016492235	0.004199
9	0.4	0.064340777	0.035657	0.4	0.049521184	0.01683	0.4	0.019885424	0.008345
10	0.6	0.073803644	0.052629	0.6	0.05270631	0.025006	0.6	0.023422185	0.01244
11	0.8	0.083595238	0.069055	0.8	0.056344505	0.033026	0.8	0.027102519	0.016485
12	1	0.093715558	0.084952	1	0.060435772	0.040893	1	0.030926425	0.020479
13	1.2	0.104164605	0.100338	1.2	0.064980109	0.048611	1.2	0.034893904	0.024424
14	1.4	0.114942378	0.115228	1.4	0.069977517	0.056181	1.4	0.039004956	0.02832
15	1.6	0.126048877	0.129638	1.6	0.075427995	0.063607	1.6	0.043259579	0.032167
16	1.8	0.137484104	0.143585	1.8	0.081331544	0.070893	1.8	0.047657775	0.035967

1.4.16 Expanded graph customization options to include title information.



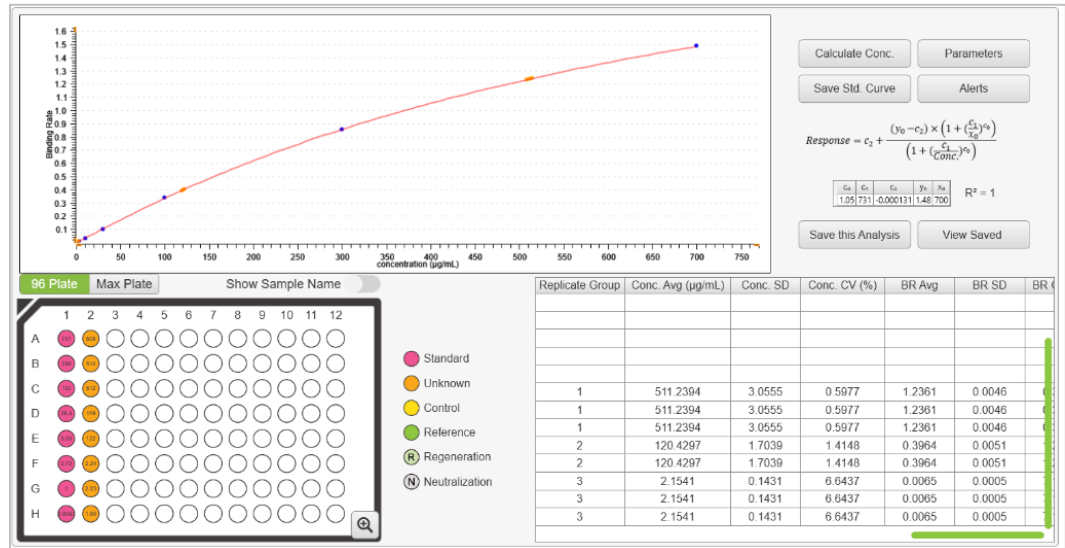
1.4.17 The result table for K assays now includes loading concentration, making it easier to review and interpret experiment data.



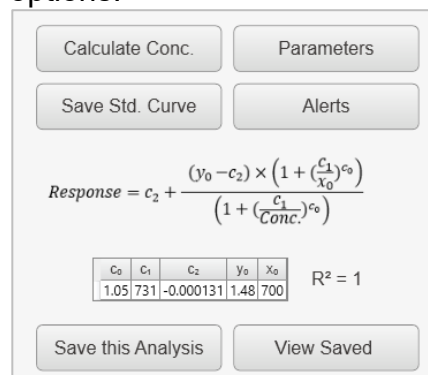
1.4.18 Added Sample Name and Concentration as legend options in quantitation results.

1.4.19 Quantitation results now support replicate grouping assignments to calculate:

- Average calculated concentration
- Standard deviation of concentration
- CV of calculated concentration
- Average binding rate (BR)
- Standard deviation of BR
- CV of BR



1.4.20 Added Quantitation Standard Curve fitting formula details, including Linear Regression, 4PL, and 5PL with weighting options.



For more details, please contact support@gatorbio.com or your local support team for further information.

1.4.21 Update the column header from 'Residual' to '% Recovery' in the Q Assay

1.4.22 Improved readability by displaying scientific notation for extremely low concentrations.

- 1.4.23 Under Q Result, legends can now display sample names and concentrations, making it easier to identify and interpret assay data at a glance.
- 1.4.24 EP results now support self-subtraction, simplifying background correction and improving data clarity.
- 1.4.25 Removed the Canvas feature.
- 1.4.26 Curve Fitting Improvements in BLI Analysis. For more details, see **Appendix**

1.5 Result & Analysis Amendment

- 1.5.1 Resolved the issue where the table of contents did not refresh properly in the graph legend
- 1.5.2 Restored the latest analysis session parameters for Advanced Quantitation under kinetics analysis.
- 1.5.3 Corrected an issue causing abnormal double reference subtraction.
- 1.5.4 The % recovery calculation is now omitted when no known concentration is provided for quantitation.
- 1.5.5 Updated the EP Tandem Inhibition calculation to correctly handle cases where the inhibition value approaches infinity.

2.0 UPGRADE INSTRUCTIONS

- 2.1** (For US customers only) Visit www.gatorbio.com. In the upper-right corner, click “Shop” and log in using a valid email and password, then proceed to Step 2.3.
- 2.2** If you do not have access through “Shop”, navigate to the “Products” tab, click “Software”, select “Request Software Download.” Complete the form and click “Submit”, then proceed to Step 2.5.



Download GatorOne Software

GatorOne is required to operate your Gator Bio instrument and analyze BLI data. Download the latest version below to ensure compatibility, access updates, and maintain reliable performance.

We ask for your contact information before download so we can notify you about important software updates, compatibility notes, and new features that may affect your experiments.

All fields required.



First Name*	Last Name*
Gator	Bio
Company*	Email*
Gator Bio	info@gatorbio.com
Country*	
United States	
State*	Postal Code*
California	94303
Instrument*	Software Requested
☐ Gator Pilot ☐ Gator Plus ☐ Gator Prime ☐ Gator Pivot ☒ Gator Pro	Gator Pivot / Pro
protected by reCAPTCHA Privacy - Terms	
Gator Bio needs the contact information you provide to us to contact you about our products and services. You may unsubscribe from these communications at any time. For information on how to unsubscribe, as well as our privacy practices and commitment to protecting your privacy, please review our Privacy Policy.	
Submit	

- 2.3** Click “Add to Cart” or “Add to Quote”, then go to your cart (upper-right corner) to proceed with checkout.
- 2.4** Complete the order form and submit. You will see an “Order Received” confirmation, and a Gator Bio representative will follow up.
- 2.5** For questions about eligibility for a complimentary software upgrade, contact Gator Bio Support at support@gatorbio.com, your regional Gator Bio representative, or your authorized

distributor, or use the request form from Step 2.2.

2.5.1 After submitting the request form or receiving order approval, please follow up with your Gator Bio representative and provide the Installation ID displayed during software installation or upgrade. The representative will verify your eligibility and provide a valid Serial Number, which you can use during the installation or upgrade at Step 2.12.

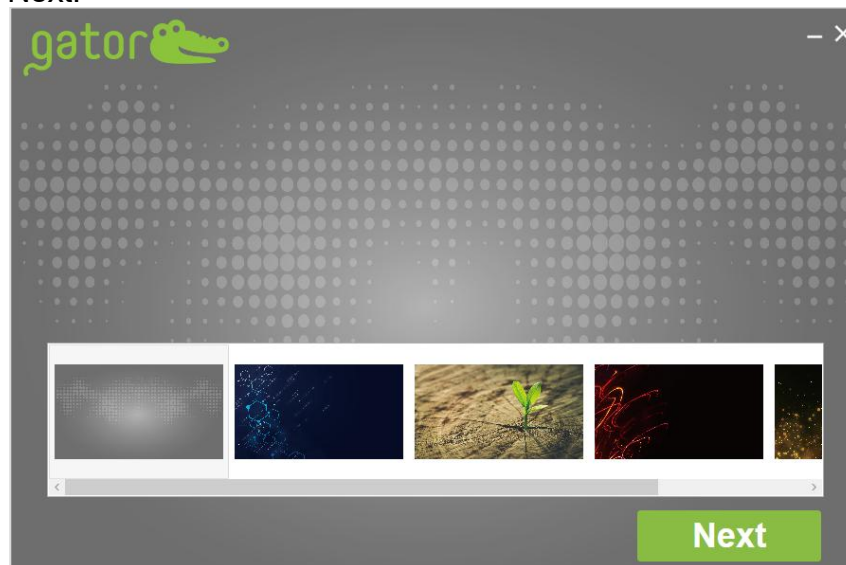
2.6 After submission, you will receive a download link from Gator Bio. Click the link to download the software ZIP package.

2.7 Right-click the downloaded ZIP file and select “Extract” to unzip it using the Windows extraction tool.

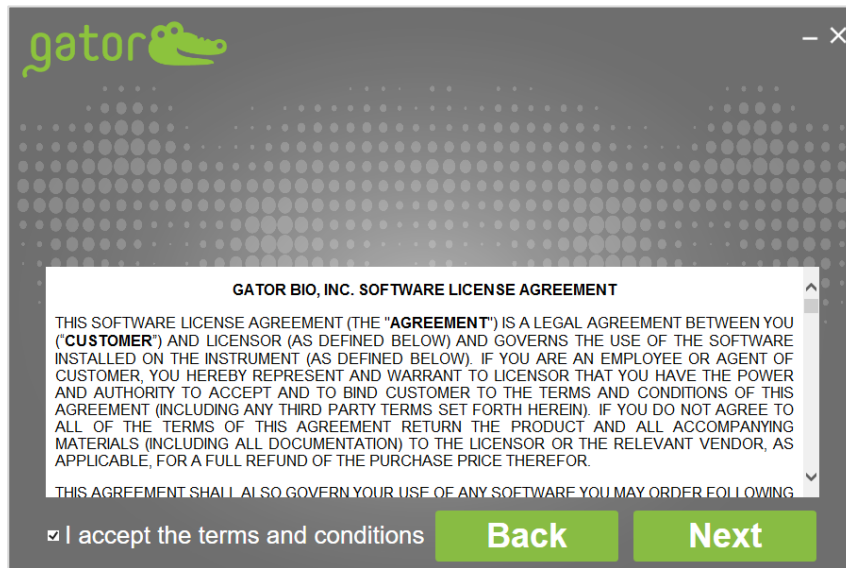
2.8 Move the extracted .exe file to the C:\ Drive on the computer connected to your Gator instrument.

2.9 Close the GatorOne software, then right-click the installer (.exe) and select “Run as administrator” to begin the upgrade.

2.10 Select one of the five color themes for the software and then click Next.



2.11 Read through the Software License Agreement and check the box to agree. Click Next.



The screenshot shows a window titled "gator" with a close button. Inside, there is a scrollable text area containing the "GATOR BIO, INC. SOFTWARE LICENSE AGREEMENT". The text describes the legal agreement between the user and Gator Bio, Inc. regarding the use of the software. Below the text area, there is a checkbox labeled "I accept the terms and conditions" which is checked. To the right of the checkbox are two green buttons: "Back" and "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

Back **Next**

2.12 Choose the correct **Gator model** from the drop-down list at the bottom left to upgrade or install the GatorOne Software.

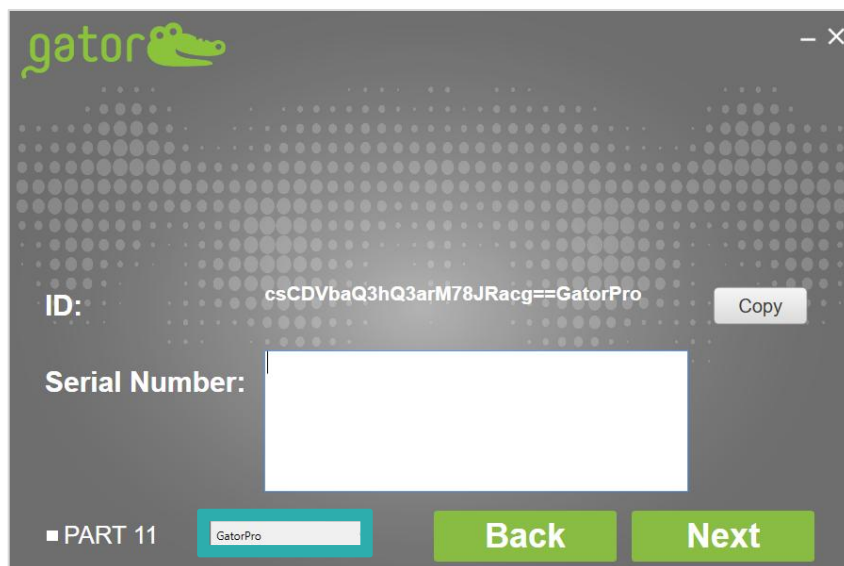
Note: A **new Serial Number is required** for both upgrades and new installations. Please obtain this from your Gator Bio representative after eligibility verification.

2.12.1 Click the "Copy" button and share the Serial Number with your Gator Bio representative if requested.

2.12.2 Enter the Serial Number in the field provided.

2.12.3 Click Next to continue.

2.12.4 Important: Do not check the "PART 11" box unless you are installing the CFR Part 11–compliant package.



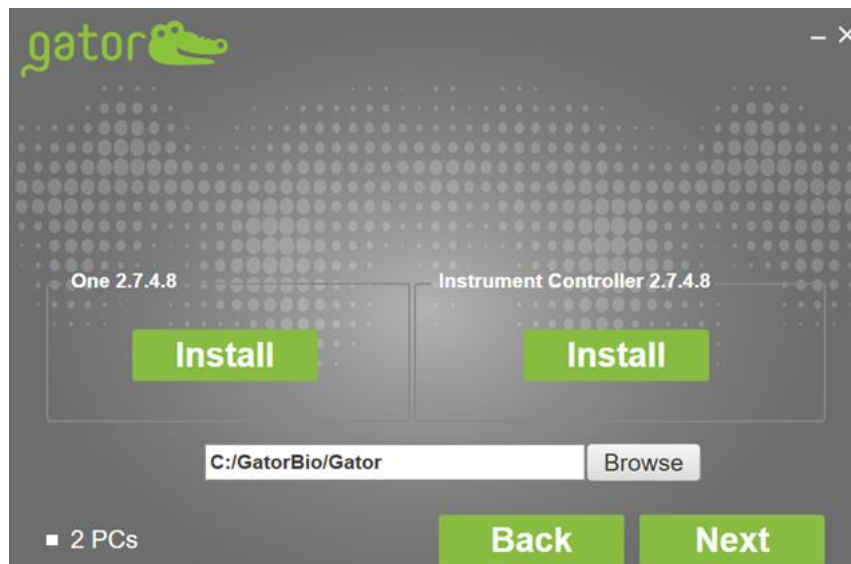
The screenshot shows a window titled "gator" with a close button. Inside, there is a text field labeled "ID:" containing the value "csCDVbaQ3hQ3arM78JRacg==GatorPro". To the right of the text field is a "Copy" button. Below the text field is a label "Serial Number:" followed by a large empty text input field. At the bottom left, there is a checkbox labeled "PART 11" which is unchecked. To the right of the checkbox is a dropdown menu currently showing "GatorPro". To the right of the dropdown menu are two green buttons: "Back" and "Next".

ID: csCDVbaQ3hQ3arM78JRacg==GatorPro **Copy**

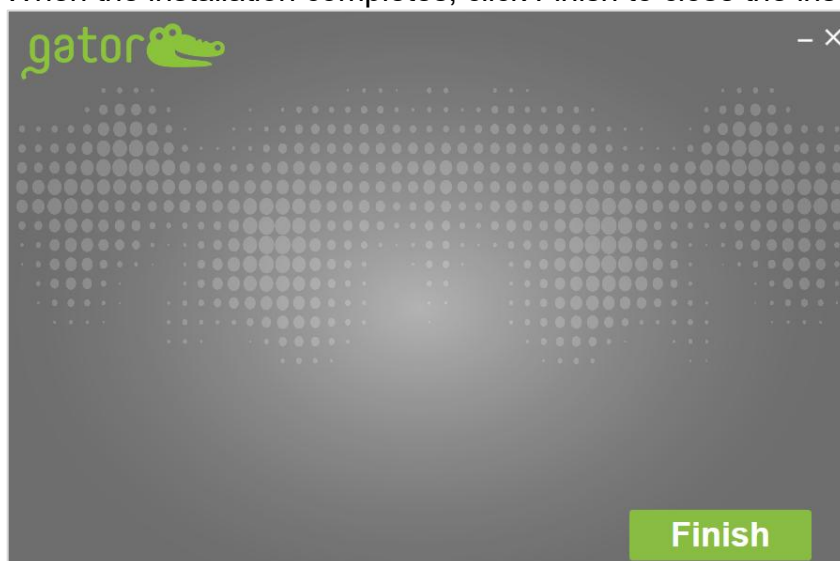
Serial Number:

☐ **PART 11** **GatorPro** **Back** **Next**

- 2.12** Leave the default setting to Upgrade both GatorOne and GatorController, then click Next. DO NOT select “2 PCs” unless advised by a Gator Bio representative.



- 2.13** When the installation completes, click Finish to close the installer.



3.0 APPENDIX

The latest updates to our curve fitting algorithms provide greater robustness and reliability across a wide range of experimental conditions. These improvements ensure that users obtain accurate kinetic results even in challenging datasets, while preserving legacy fitting modes for direct comparison and continuity with previous studies.

Key Enhancements

- Reliable Handling of Fast-Rate Curves

Calculations are now constrained within a defined confidence range, ensuring stable, consistent, and trustworthy results.

Example:

Fast-Rate, Enhanced Off



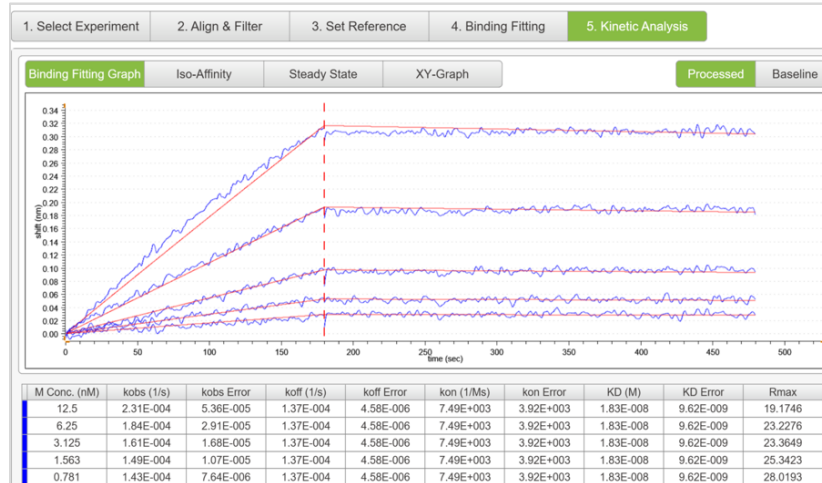
Fast-Rate, Enhanced On



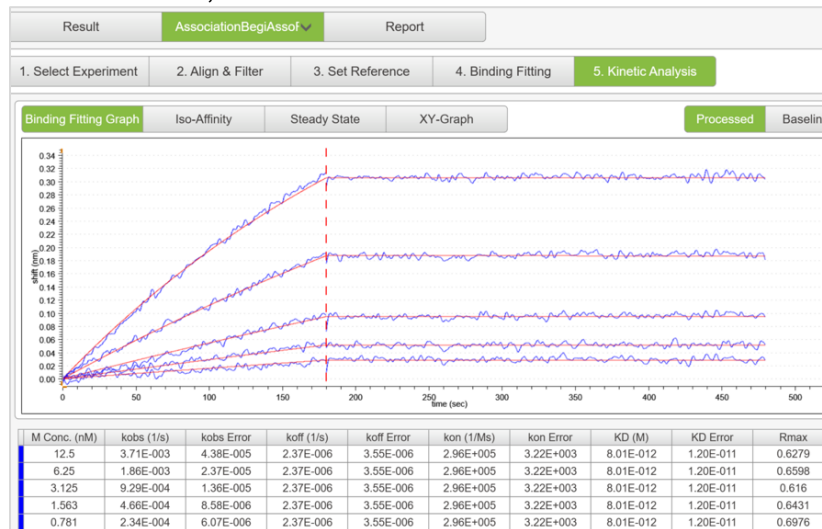
- **Stability in Underdetermined Systems**
Linear or near-linear curves are managed with controlled limits, avoiding infinite or non-physical outputs.

Example:

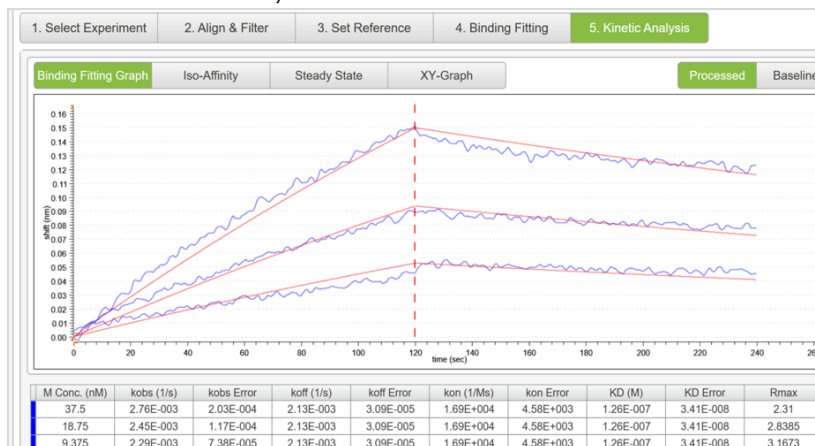
Linear Curves, Enhanced Off



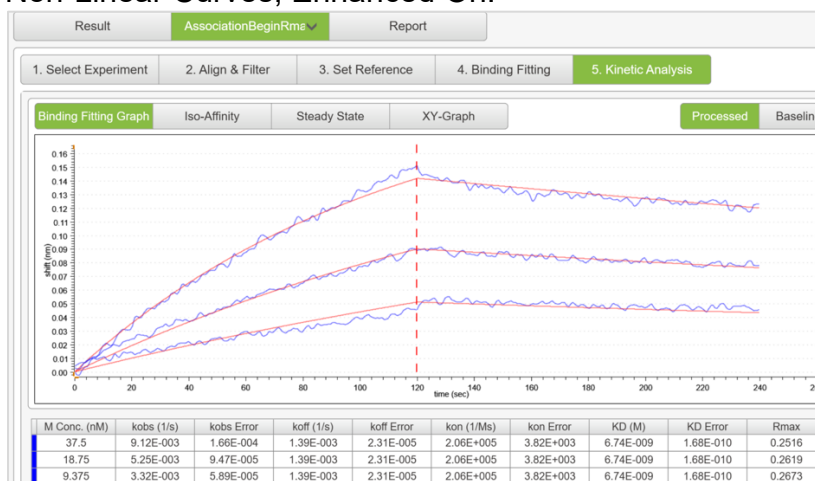
Linear Curves, Enhanced On



Example Non-Linear Curves, Enhanced Off:



Non-Linear Curves, Enhanced On:



- Improved Global Fitting with Data Screening
Poorly fitting datasets are automatically flagged and filtered, improving the accuracy and reliability of global fitting.
- Legacy Fitting Preserved for Continuity
Original fitting methods remain available, enabling direct comparison with historical data and a smooth transition to the improved workflow.

Parameters

Data to Include

Both Association Dissociation

Binding Model

Model: 1:1 2:1 Mass 1:2

Fitting

Type: Local Global

On Enhanced 1:1 fit (edge-aware) ⓘ

Explores a wider parameter space; processing may take slightly longer.

Sub Options

Full Partial

☐ Full Stitch Average 0

Window of Interest

Association: 0 to 108 secs ⓘ

Dissociation: 0 to 105 secs ⓘ

Confirm Cancel

Performance Enhancements

- More reliable kinetic constants across diverse assay conditions.
- Minimized risk of non-physical results in challenging datasets.
- Increased confidence in small molecule and weak binder analysis.
- Improved stability and reproducibility of fitting results.
- More accurate and dependable global fitting for complex datasets.
- Continuity with past results while benefiting from improved fitting accuracy.