Gator[®] Plus Next Generation Biolayer Interferometry for Label-Free Analysis



Next Generation BLI Design

- Patented V-grooze coupling provides consistent biosensorfiberoptic alignment for enhanced signal
- Insulated low-volume sample compartment enhances stability and minimizes evaporation
- Adjustable orbital flow minimizes mass transfer effects and decreases rebinding
- User-configurable Max Plate houses biosensors, reagents, wash, or samples
- 96-well or 384-well sample plates
- · Automated sample plate tilt provides reproducible positioning

Variety of Biosensors

- HFC (Anti-HIgG Fc) Protein A
- MFC (Anti-MIgG Fc) Protein G
- Anti-His

• Protein L

- Amine-Reactive
- Streptavidin
- SMAP (Small Molecule, Antibodies, and Proteins)
- APS (Aminopropylsilane)
- Custom-Made Biosensors (eg SARS-CoV-2 RBD Biosensors). Contact us for more information!

Gator® Plus is the next generation in biolayer interferometry (BLI) instrumentation for label-free, real-time measurements of biomolecular interactions from inventor of BLI. This premier system incorporates patented advances in optics, coupling mechanics, and surface chemistry to provide state-of-the-art sensitivity, reproducibility, and robust operation to meet the demands of research, development, manufacturing, and quality control.

Gator[®] Plus enables a broad range of applications:

- Antibody titer determination
- Yes/no binding to target antigen
- Isotyping
- Epitope binning
- Cross-reactivity testing
- Affinity determination
- Small molecule measurements
- Off-rate ranking
- Binding rates determination
- Protein expression optimization

Integrated Data Acquisition and Analysis

- Intuitive software with integrated data analysis and report generation tools
- Quantitation, kinetics, and regeneration in a single run
- Built-in algorithms and models accelerate design-of experiment
- Dynamic data acquisition with real-time quantitation, results, and heat map







Small molecule kinetics



	Gator Bio BLI	SPR	
k _{off} (1/s)	4.86 E-02	4.96 E-02	
k _{on} (1/Ms)	1.00 E+05	9.66 E+04	
K _D (M)	4.85 E-07	5.13 E-07	

Association and dissociation of furosemide (330 Da) to carbonic anhydrase II bound using SMAP biosensors. Global-fit analysis results shown in the table. Values match those obtained with SPR.

Efficient setup and analysis of epitope binning experiments

Gator Bio software includes pre-built templates for tandem and sandwich epitope binning methods. Large data sets can be created in one run to evaluate entire antibody libraries. Data analysis takes only minutes.



Sandwich experiment with loading of mAb's, blocking, antigen, and then a large number of different mouse antibodies.

Robust regeneration for consistent quantitation



Standard curve of mIgG (1 mg/mL to 0.0003 mg/mL) using Protein A biosensors. Twenty-four consecutive measurements with regeneration in graph above. Calculated binding rates, SD, and CV are shown in the table.

n = 24	Binding Rate		
Standard (µg/mL)	avg	SD	CV
1000	1.581	0.016	1.0%
300	0.733	0.010	1.4%
100	0.273	0.006	2.2%
30	0.082	0.002	2.1%
10	0.026	0.0005	1.7%
3	0.0081	0.00015	1.9%
1	0.0035	0.00012	3.4%
0.3	0.0013	0.00002	1.7%
		Overall	1.9%

Kinetics analysis from start to finish

Gator® Plus provides stable baselines for the measurement of pM to mM affinities. From small molecules to large biomolecules, Gator Bio BLI enables the detection, measurement, and analysis of interactions across a wide molecular weight range.



KD (M) $k_{off} (1/s)$ k_{on}(1/Ms) 4.30E-09 0.00284 6.61E+05

PERFORMANCE

Dissociation rate koff

Affinity constant K_D

Dilution series of PD-1 binding to anti PD1. Global-fit analysis yielded the kinetics parameters shown in the table.

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GENERAL	
Detection method	Biolayer interferometry (BLI)
Number of spectrometers/channels	8
Data acquisition rate	2, 5, 10 Hz
Instrument size	630 mm x 730 mm x 440 mm (H x W x D); 45 kg
Electrical	110V – 220V 5A
Power consumption	200 W
Temperature control	Ambient – 40°C

Proteins, antibodies, peptides, Sample types nucleic acids, liposomes, viruses, small molecules Plate capacity 96-well or 384-well Maximum Sample Capacity 456 Yes/no binding, quantitation, Type of analysis kinetics, affinity, off-rate ranking, epitope binning **Orbital flow** 100 - 2000 RPM Minimum sample volume 40 µL Baseline noise (RMS) $\leq 4 \text{ pm} (\text{RMS})$ **Baseline drift** ≤ 0.1 nm/hour Association rate kon 101 to 107 M-1S-1

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10-6 to 10-1 S-1

10 pM - 1 mM

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