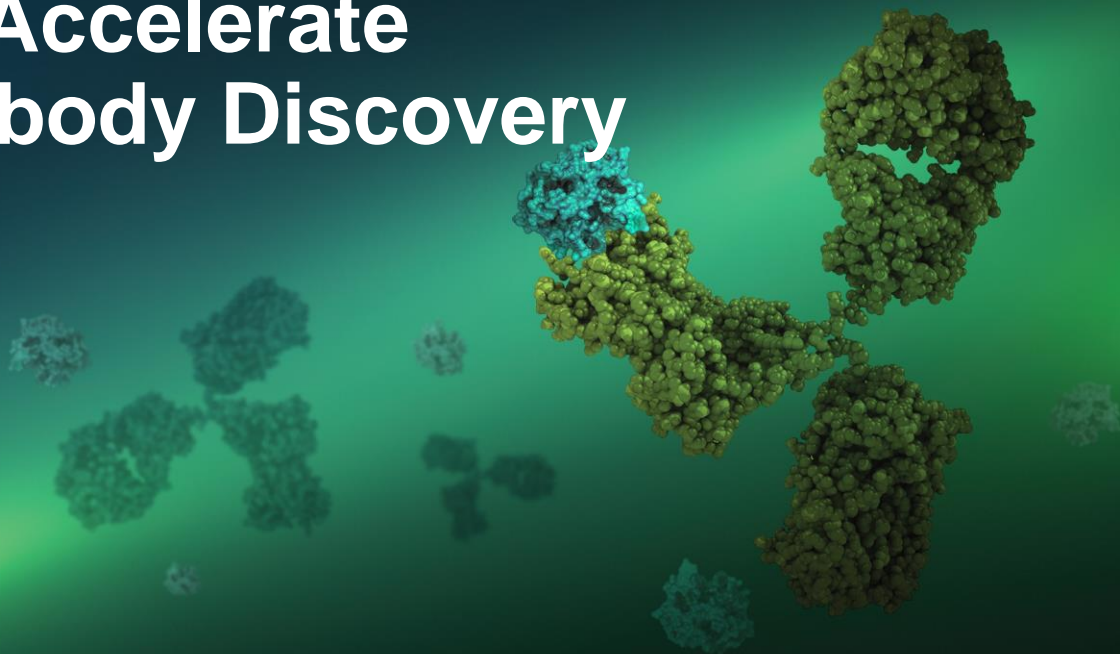




# Expanding SPR Throughput Orders of Magnitude to Accelerate Therapeutic Antibody Discovery

Yasmina Noubia Abdiche, PhD  
Chief Scientific Officer, Carterra

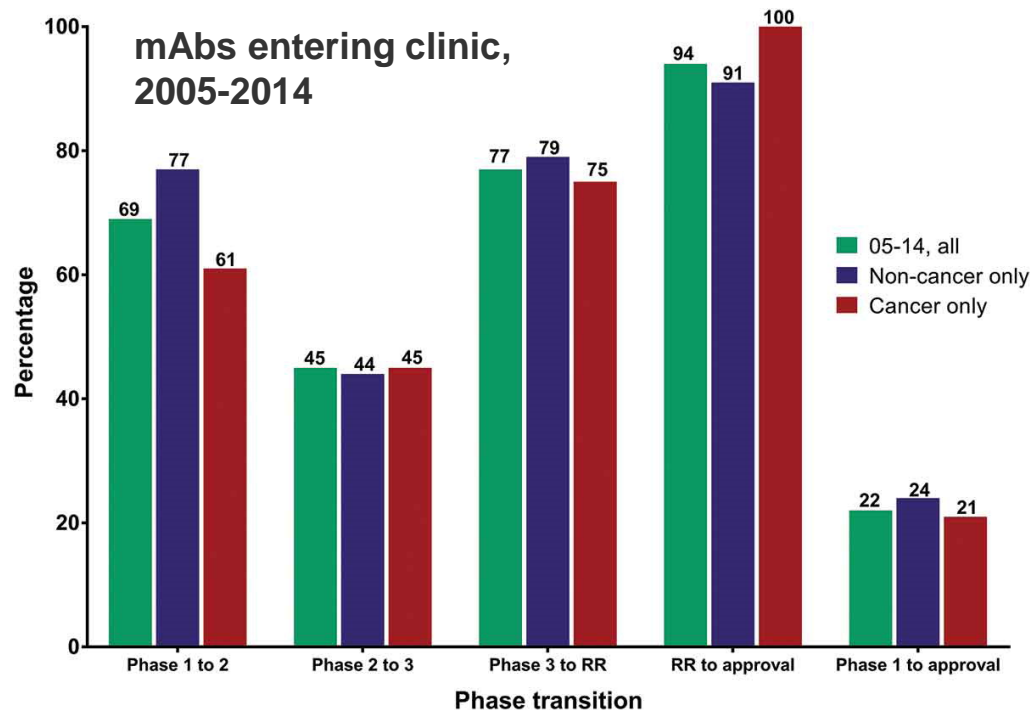


# The Therapeutic Antibody Market is Lucrative and Growing



- mAbs are bringing transformative medicines, even “cures”, to patients
- mAbs dominate the top 10 blockbuster drugs
- A diverse, innovative and robust clinical pipeline ensures market growth
- Also, mAbs provide biosimilars, companion diagnostics, and reagents

# Drug Discovery is Costly, Tedious, and Fraught with Failure

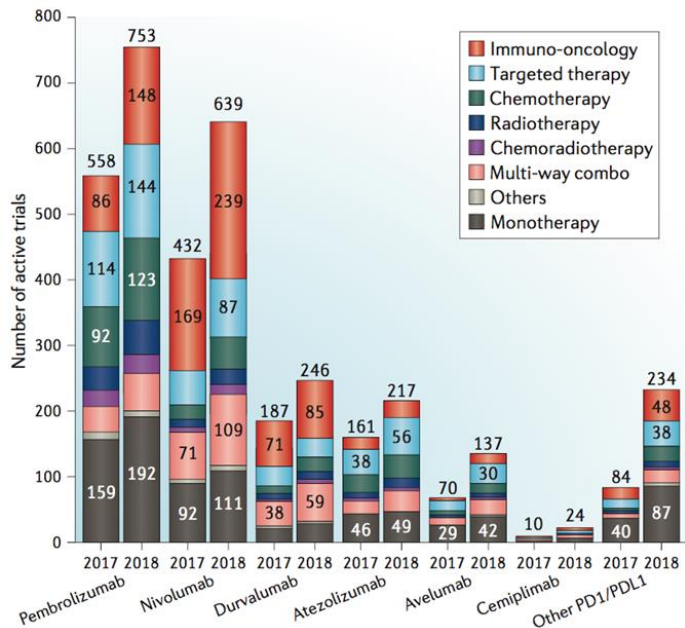


- Only 20% Phase I drugs achieve market approval
- On average, US\$ 1 billion and 12 years from bench to market
- Understanding Mechanism of Action (MOA) is key to clinical success

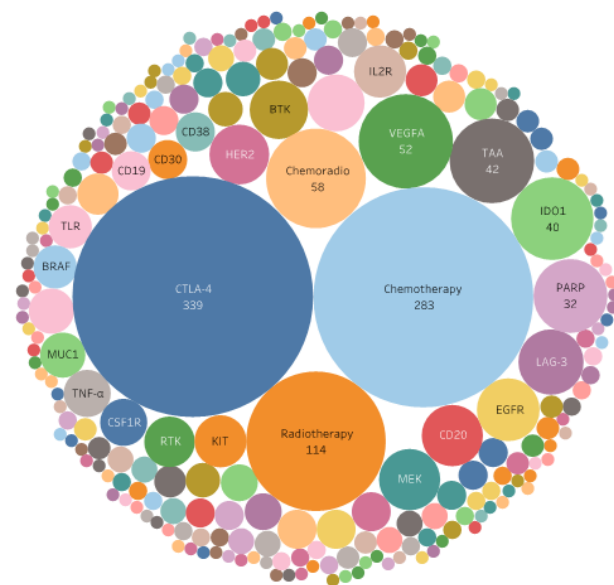
*Antibodies to watch in 2019,  
Kaplon and Reichert, MABS 2018*

# Prominence of Immuno-Oncology: PD-1/PD-L1 Clinical Landscape

Breakdown of trials (total 2,250 in 2018) by mAb and their combination with other targets/therapies

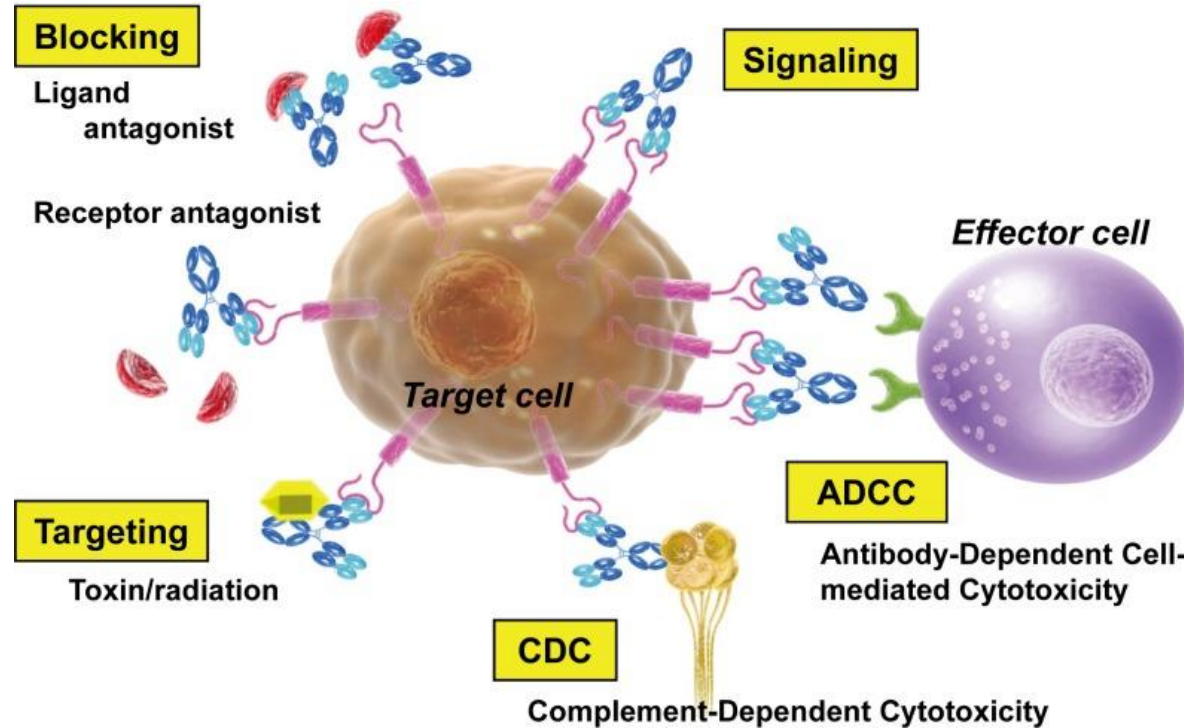


Distribution of trials (total 1,716) in combo with other (250) targets/therapies



*The clinical trial landscape for PD1/PDL1 immune checkpoint inhibitors  
Tang et al, Nature Reviews Drug Discovery 2018*

# Therapeutic mAbs Work via Different MOAs



*Therapeutic antibodies: their mechanisms of action and the pathological findings they induce in toxicity studies (review), Suzuki et al, J Toxicol Pathol 2015*

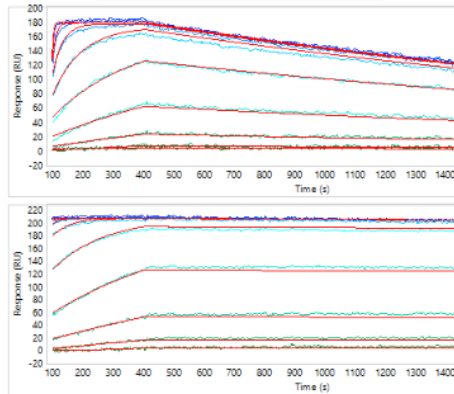
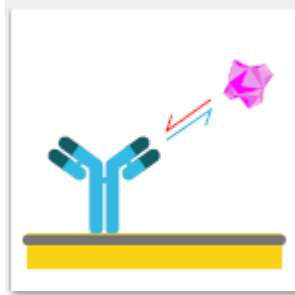
# High Throughput SPR: A Disruption in Antibody Characterization

- MAbs can achieve high specificity and affinity - leveraged in drug discovery
- Binding kinetics, affinity, and epitope are crucial parameters in assessing a mAb's quality and fitness for a given therapeutic application, because they inform **Mechanism Of Action**
- SPR is the *de facto* technique for measuring binding kinetics and affinity
- Carterra's LSA expands the throughput of SPR orders of magnitude compared with other platforms, shifting the role of SPR upstream to screening stages where it can streamline the library-to-leads triage
- Additionally, the LSA's 384-ligand capacity enables high throughput epitope binning studies, transforming the binning paradigm and revealing exquisite epitope resolution to guide lead selection and secure IP
- Minimal sample consumption and facile assay set-up
- Fast and intuitive data analysis via dedicated Kinetic and Epitope software

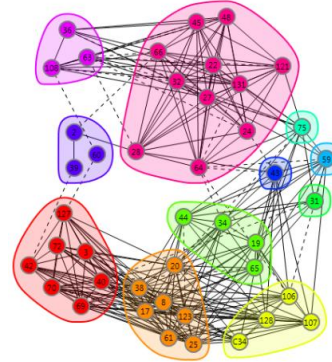
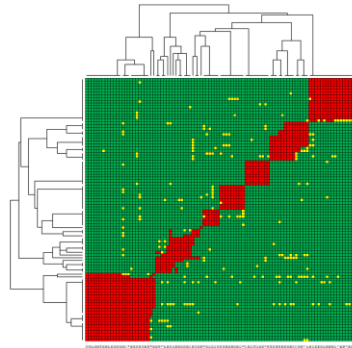
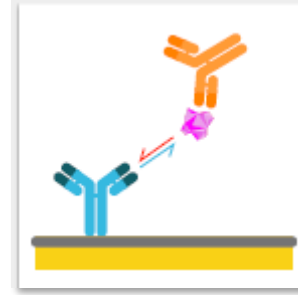
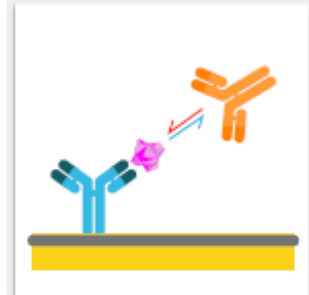


# LSA's Core Applications

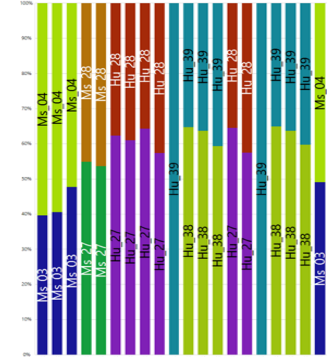
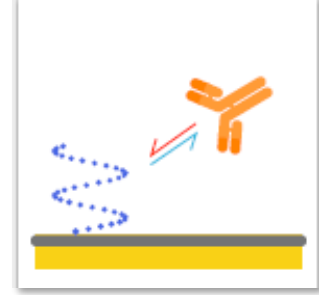
## Kinetics/Affinity



## Epitope Binning

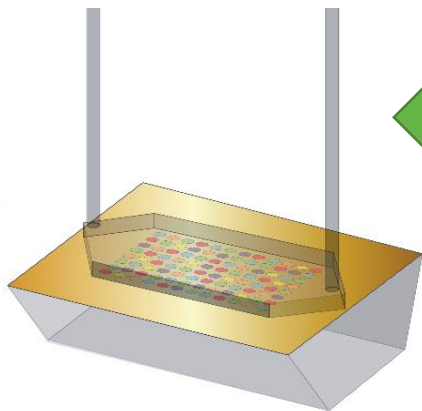


## Mapping

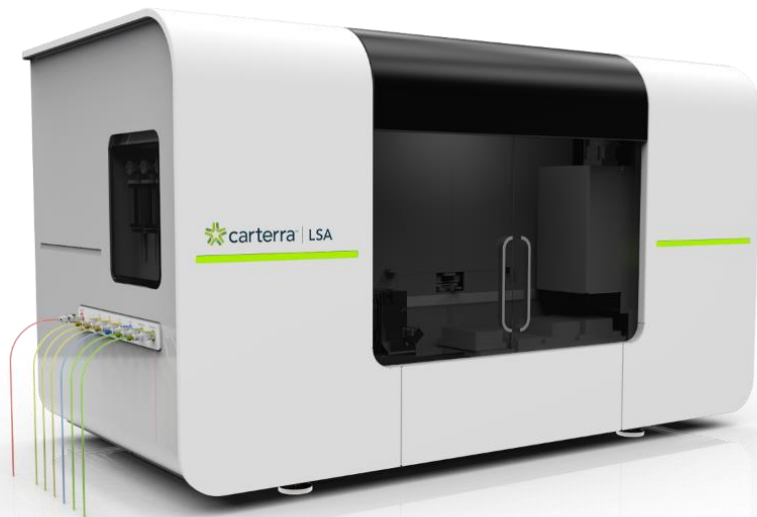
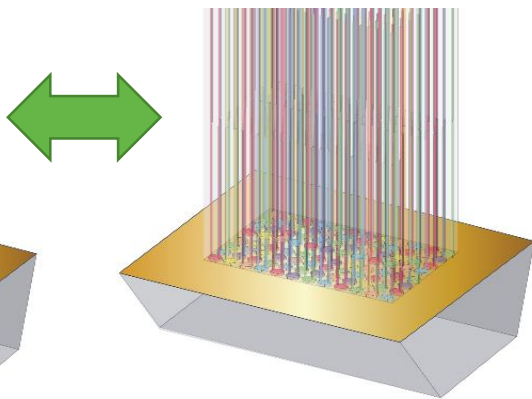


# The LSA Automates a Choreography between Two Microfluidic Modules

Single Flow Cell  
(SFC)



96-Channel Printhead  
(96PH)

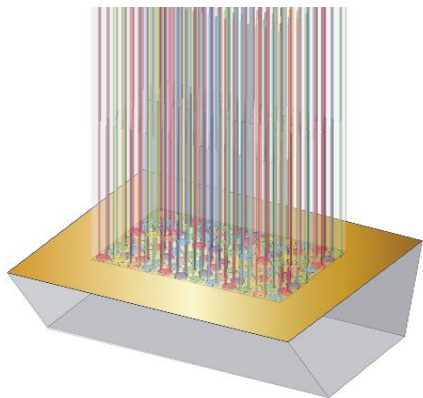


- Inject 250 $\mu$ l over entire array
- 1-on-384 (analyte-on-ligand) mode
- Coat chips as a “lawn”
- Exceptional sample efficiency
- Functionalize discrete spots using 200 $\mu$ l/spot
- Create 384-ligand array using 4 serial docks of 96PH
- Recover samples (-15 $\mu$ l/print)

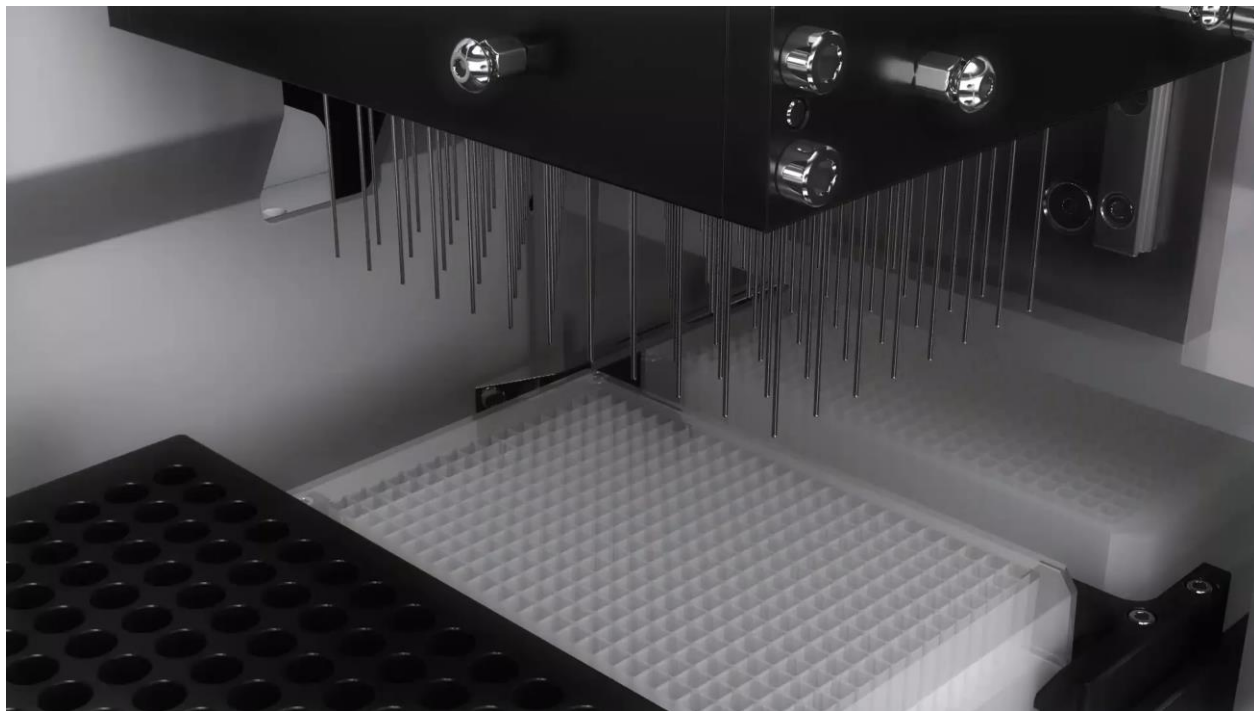


# LSA Integrates Flow Printing

96-Channel Printhead  
(96PH)



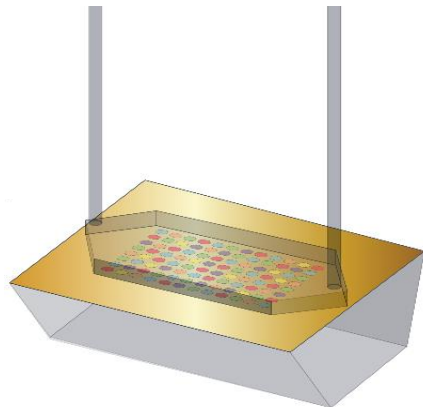
Create 384-ligand  
array via 4 serial  
docks of 96PH



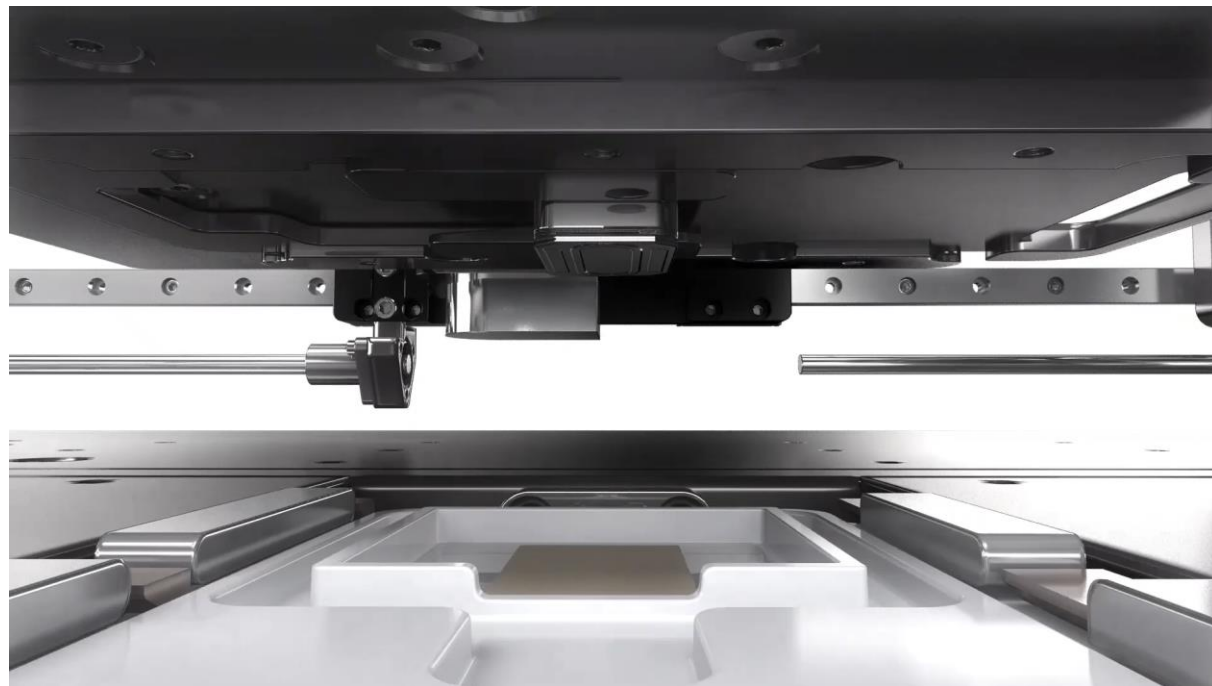
Deck accommodates 3x 96/384 plates

# LSA Integrates High Throughput SPR

Single Flow Cell  
(SFC)

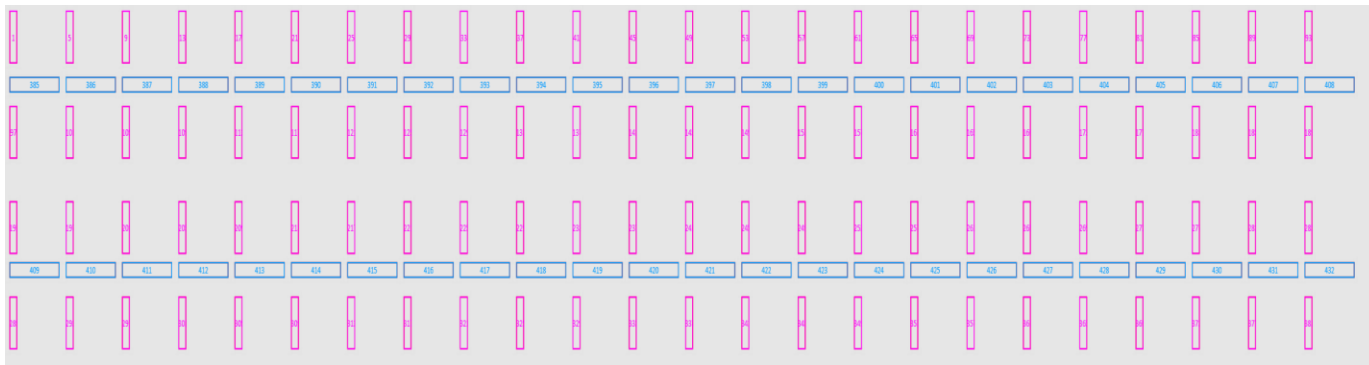


Inject 250 $\mu$ l analyte  
over entire array in a  
“1-on-384” analyte-  
on-ligand mode

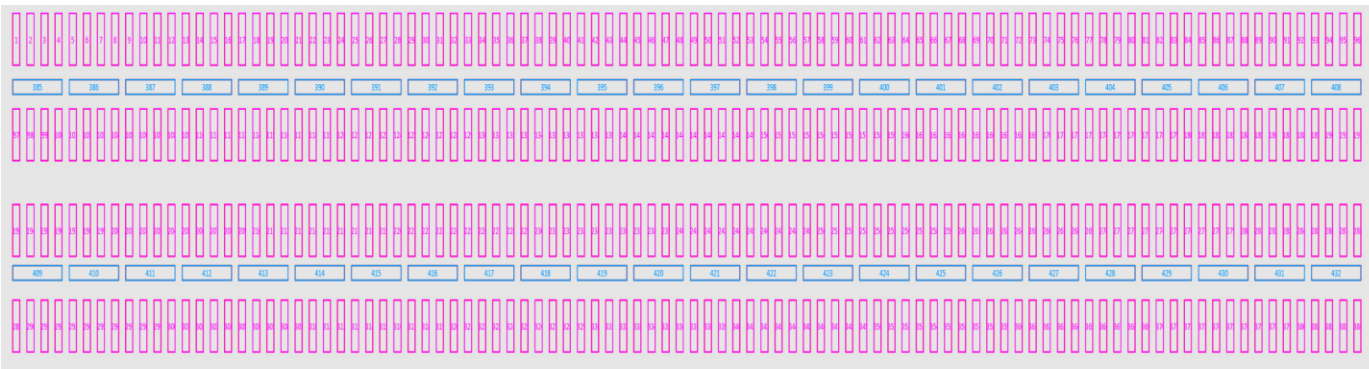


Deck accommodates 2 plate positions:  
sample block and 96/384 plate

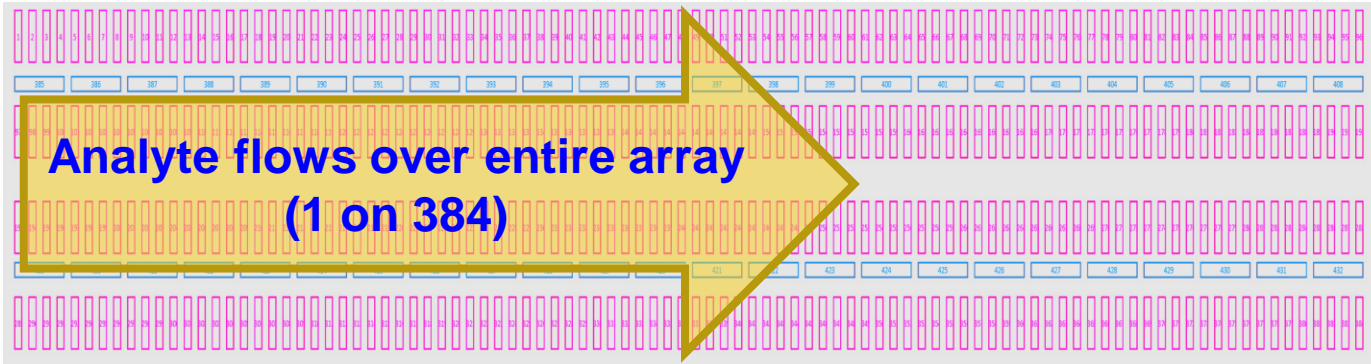
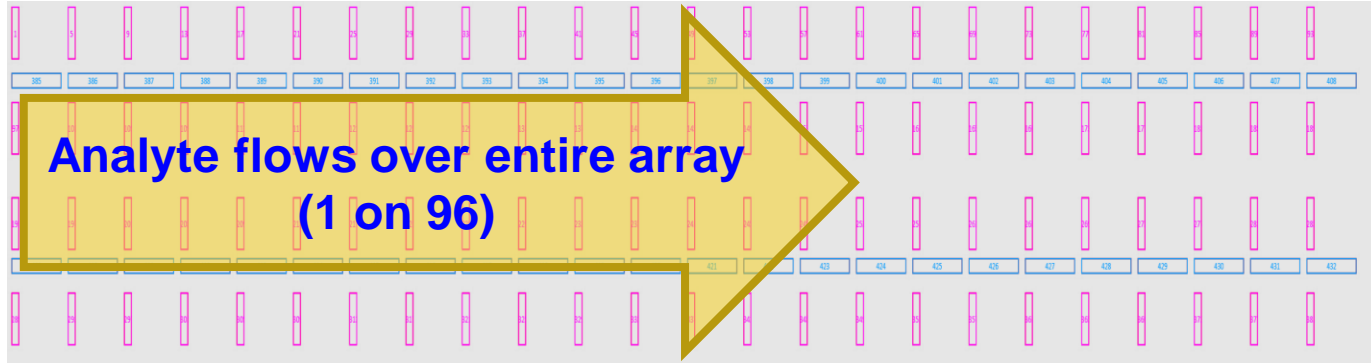
# Flow Print a 384-Ligand Array on the LSA



**Serially dock the 96PH at 4 nested locations to create a 384-ligand array**



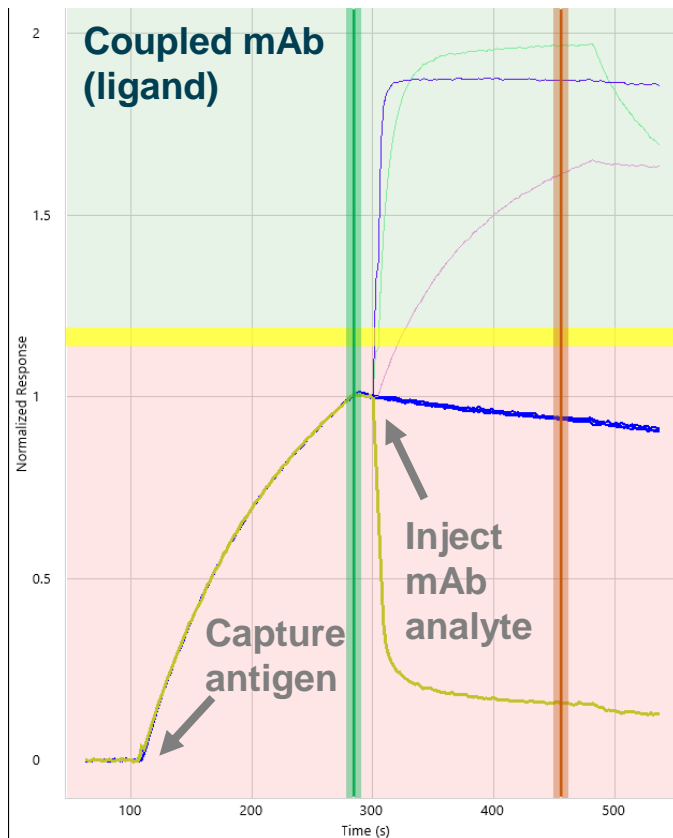
# Minimal Sample Consumption



# Why It's All About The Epitope

- Epitope influences a mAb's MOA
- Epitope is innate; it can neither be predicted by *in silico* methods, nor rationally shifted/optimized by engineering, so must be SELECTED
- Epitope can be used to secure IP
- Combining different MOA's often produces superior therapeutic outcome
- High throughput binning can reveal the epitope landscape of an antibody library, and when merged with functional data, can identify biologically-significant epitope clusters.
- **Epitope diversity is a surrogate for functional diversity**

# Epitope Binning on the LSA



Analytes that sandwich pair with ligand

Buffer (no sandwiching/blocked)

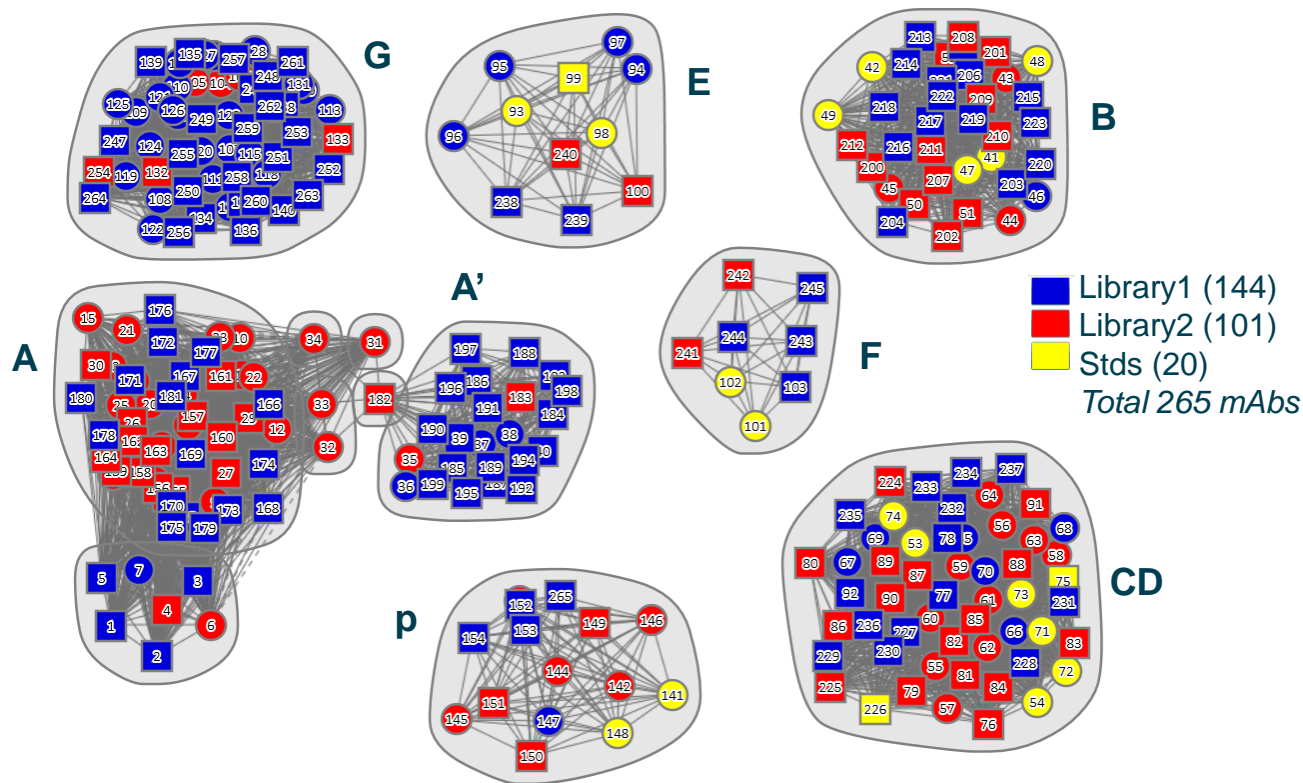
Displacement (< buffer baseline)



antigen + mAb  
analyte captures  
are cycled over the  
array

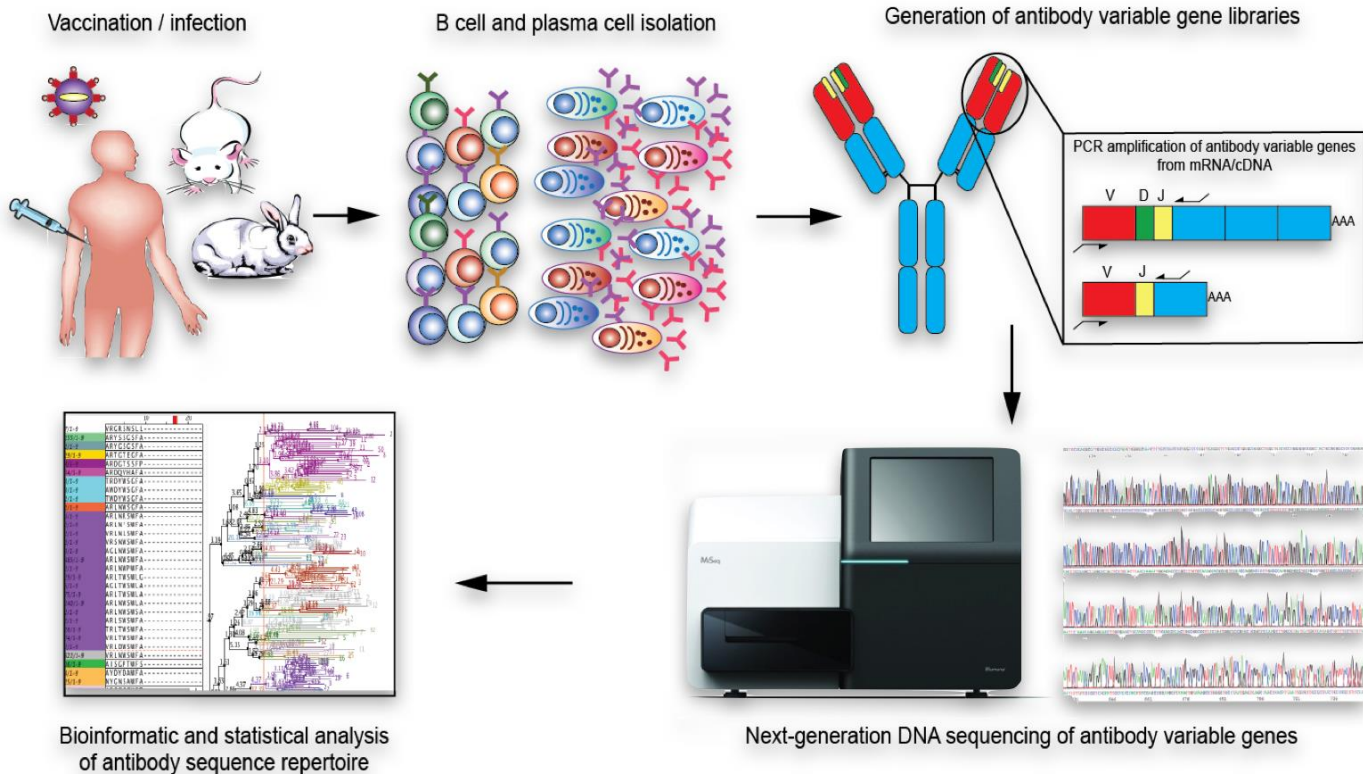
- A comprehensive epitope binning experiment scales geometrically with the size of the mAb panel
- The LSA provides a simple way to explore a full 384 x 384 competition matrix on a single chip using <10 $\mu$ g/mAb and <200 $\mu$ g antigen
- Powerful analysis software

# Using Epitope Binning to Benchmark Discovery Platforms – OmniChicken<sup>®</sup>



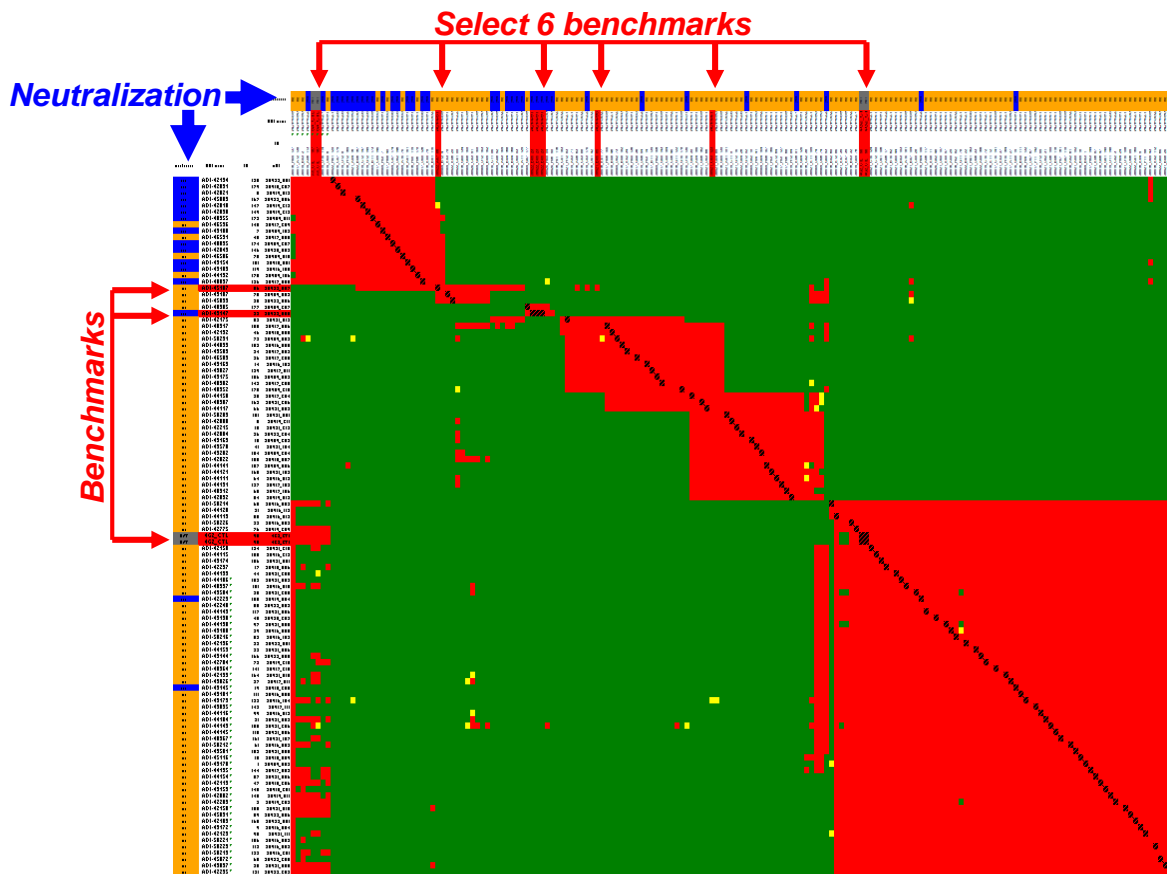


# Therapeutic mAb Cocktails for Infectious Disease



- The human immune response can be used to source therapeutic mAbs to treat infectious disease
- Isolate mAbs by B-cell cloning of vaccinated/infected individuals
- Sequence diversity is necessary **but not sufficient** to produce functional diversity
- Epitope diversity is a surrogate for functional diversity
- Epitope binning can reveal the epitope landscape

# Therapeutic mAb Cocktails for Infectious Disease



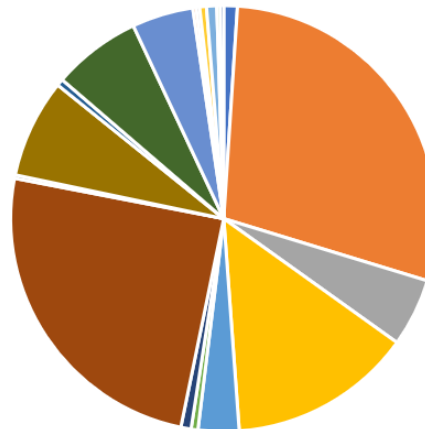
- High throughput binning revealed the epitope landscape of the human immune response
- Inform selection of a few benchmark clones to probe a bigger library
- Merge with neutralization data to understand the **functional space**

*Manuscript submitted to Nature Immunology*

# Therapeutic mAb Cocktails for Infectious Disease




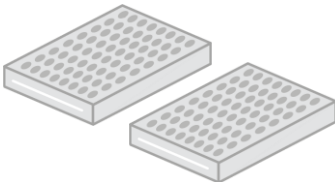
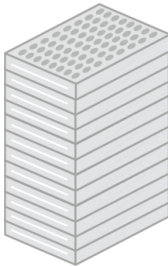
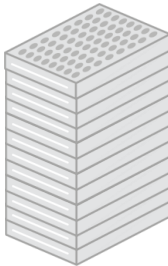
Bin name	CTL-1	CTL-2	CTL-3	CTL-4	CTL-5	CTL-6	Tally	#Neutralizers
0	0	0	0	0	0	0	4	0
1	1	0	0	0	0	0	111	5
2	0	1	0	0	0	0	20	8
3	0	0	1	0	0	0	54	2
4	0	0	0	1	0	0	12	1
5	0	0	0	0	1	0	2	0
6	0	0	0	0	0	1	3	2
12	1	1	0	0	0	0	96	9
23	0	1	1	0	0	0	1	1
24	0	1	0	1	0	0	29	16
34	0	0	1	1	0	0	2	0
35	0	0	1	0	1	0	26	1
45	0	0	0	1	1	0	18	2
135	1	0	1	0	1	0	1	0
245	0	1	0	1	1	0	1	0
345	0	0	1	1	1	0	2	1
1235	1	1	1	0	1	0	3	0
2345	0	1	1	1	1	0	1	0
12345	1	1	1	1	1	0	1	0
total							387	48

Bin Distribution  
(387 mAbs, 19 bins)



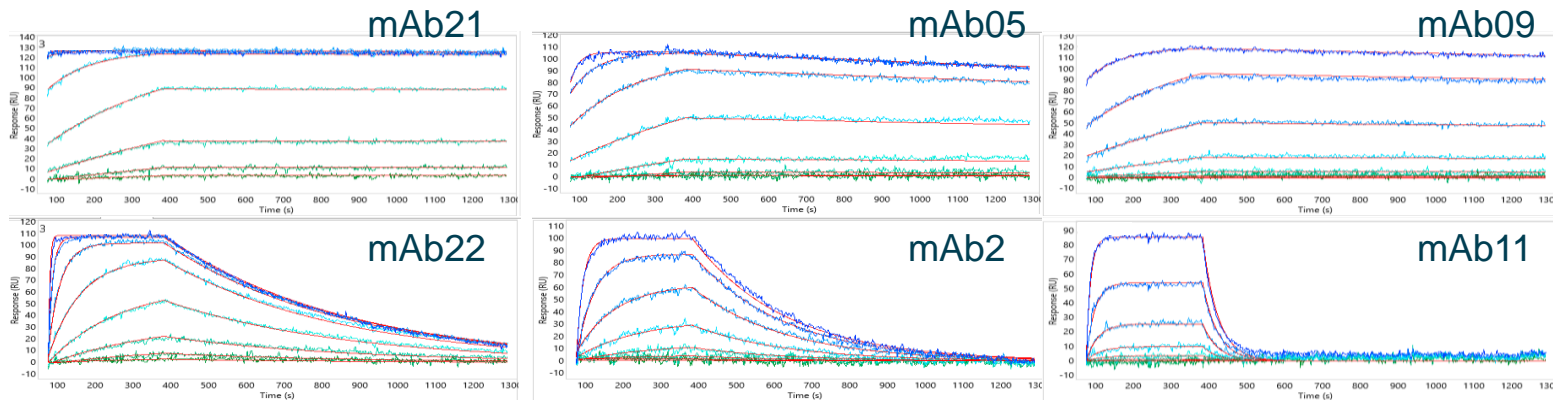
- Multiple bins were functional
- Some rare bins showed exceptionally **potent** neutralization
- Inform the design of a broadly neutralizing cocktail

# Transforming the Binning Paradigm

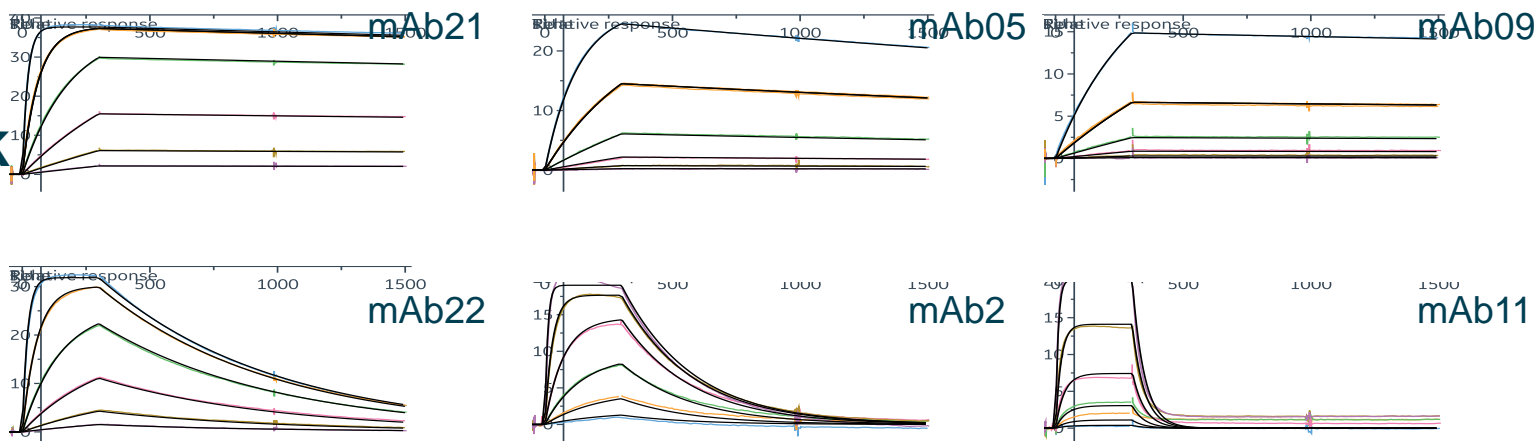
	LSA	8K	HTX
Antibody consumption per mAb	 5 µg	 >1000 µg	 >1000 µg
384-well plates required	 2 plates / 6 days	 10 to 100+ / 1 month	 10 to 100+ / 1 month

# LSA Kinetics Benchmarked against Biacore 8K

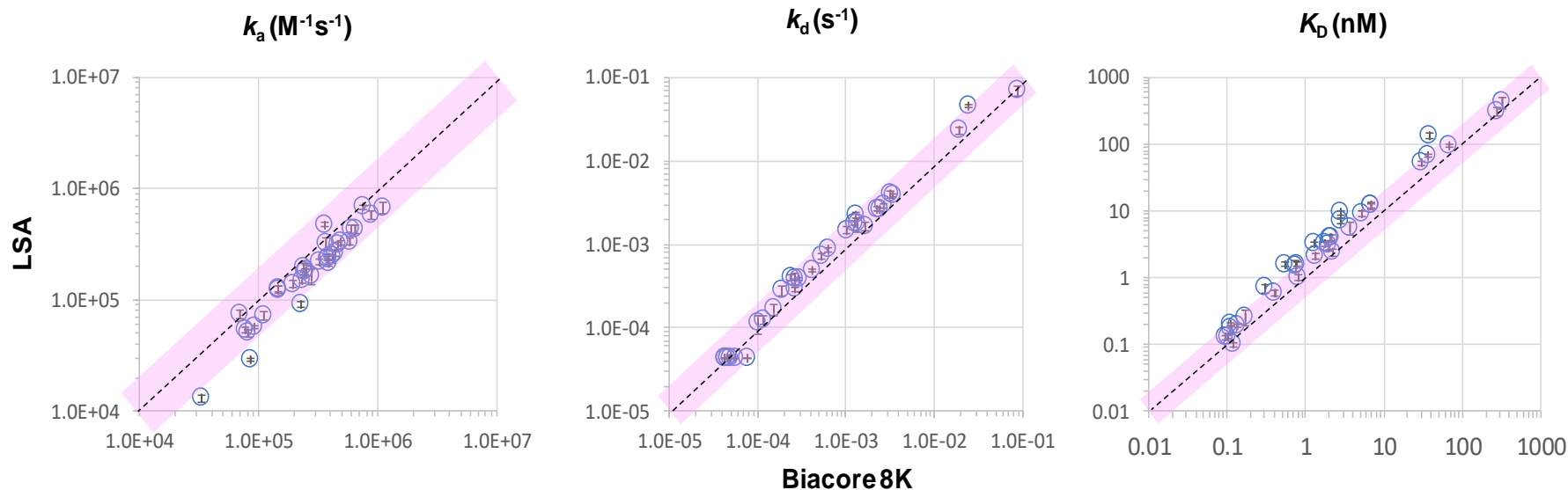
LSA



Bia8K



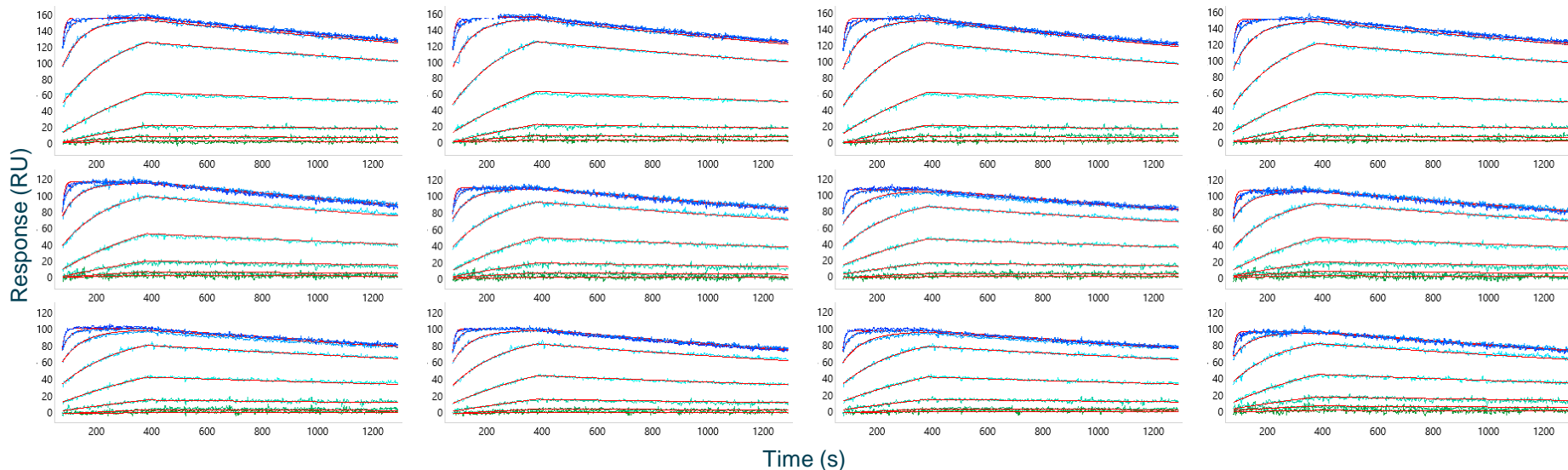
# LSA Kinetics Benchmarked against Biacore 8K



- Near-identical kinetic rate and affinity constants (within 2fold) across platforms
- Tested a panel of 32 kinetically-diverse mAbs
- LSA measurements are Mean  $\pm$  StDev for 8-12 reps (spots) per mAb
- Biacore are single measurements

# LSA Kinetics: Intra-Assay (Spot-To-Spot) Reproducibility

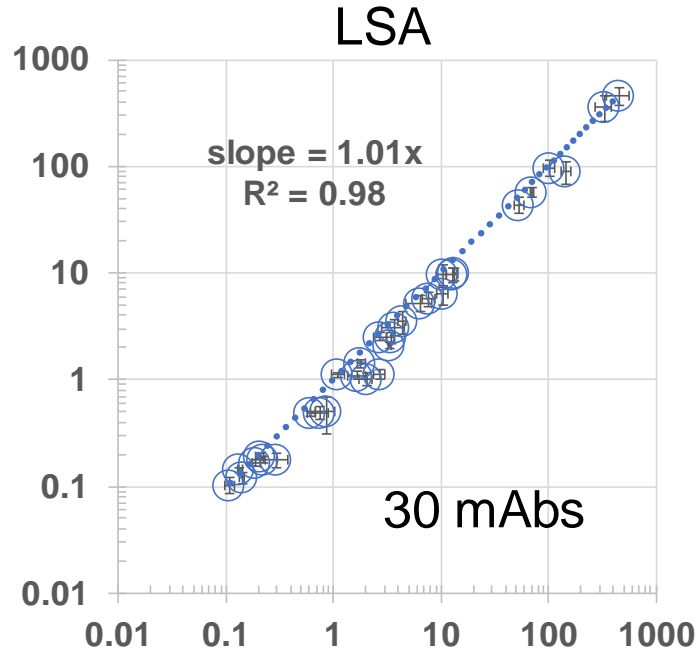
mAb 23,  $K_D = 1.5 \pm 0.3$  nM for  $N = 12$



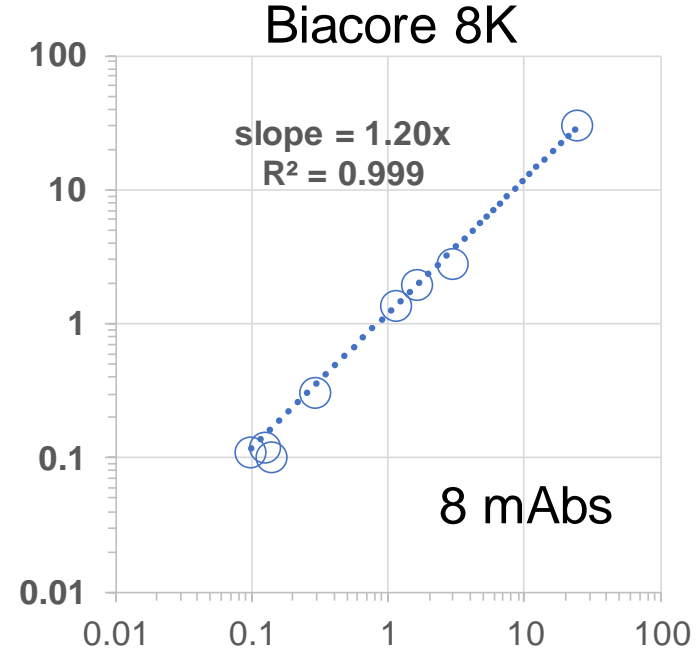
- For small panels of mAbs, use the full capacity of the 384-ligand array to explore surface capacity
- Combine measurements from optimum capacity spots and report parameters with statistical confidence (Mean  $\pm$  StDev)



# Inter-Assay Reproducibility: $K_D$ values



Each measurement is Mean  $\pm$  StDev  
(error bars) for 8-12 reps per interaction

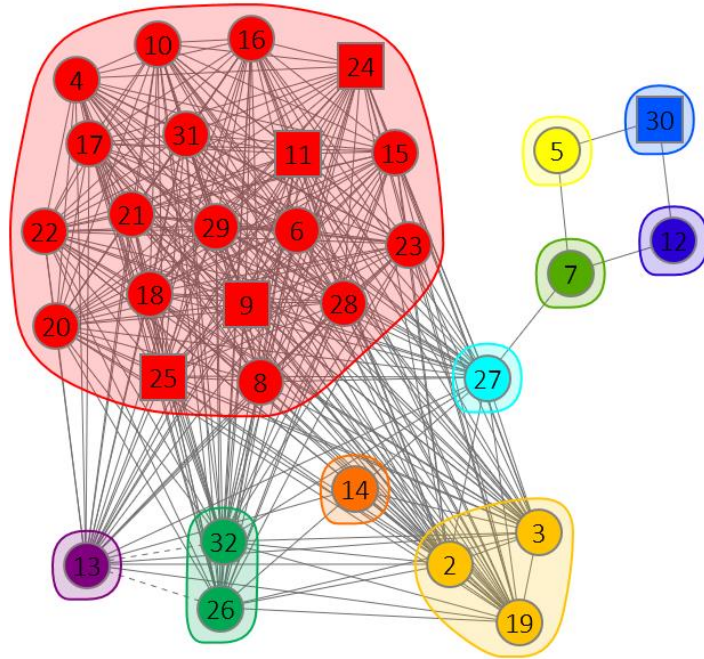


Single measurements

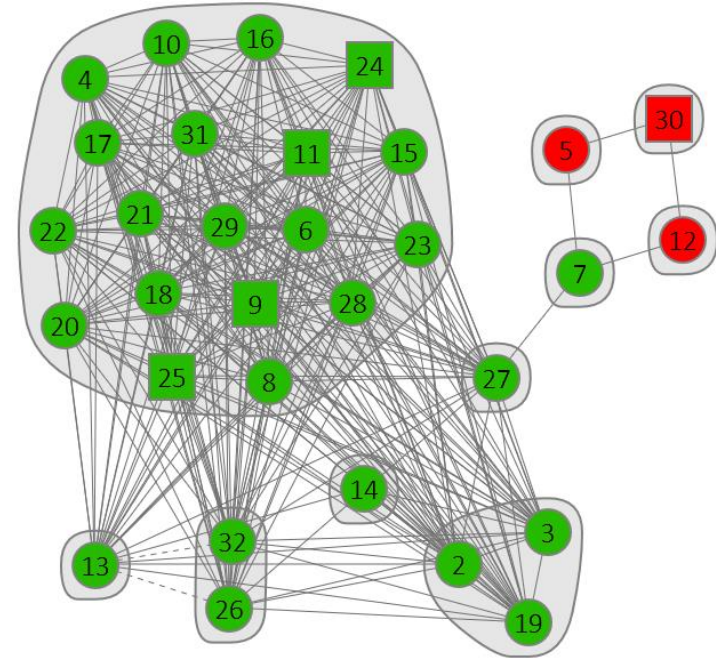
Manuscript submitted to PlosOne, Aug 2019

# High Throughput Binning Provides Exquisite Epitope Resolution

Color by bin



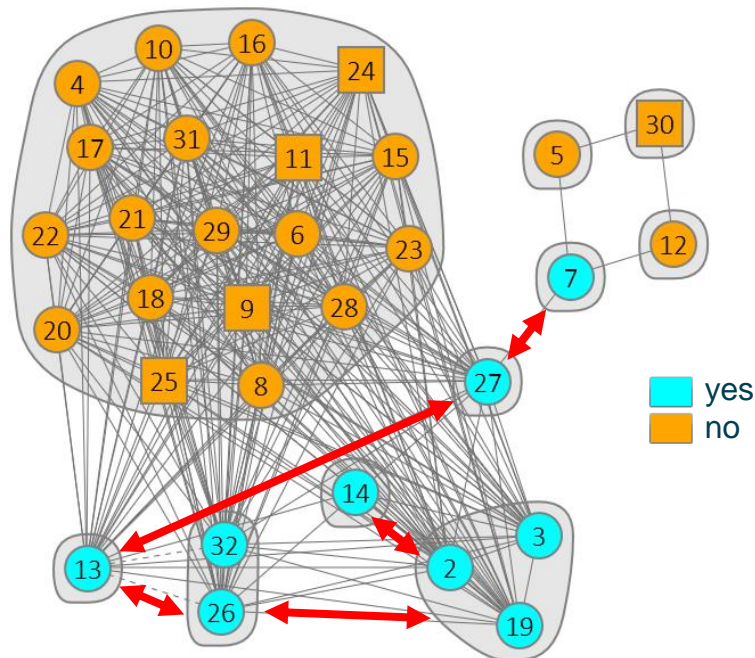
Color by ligand blockade



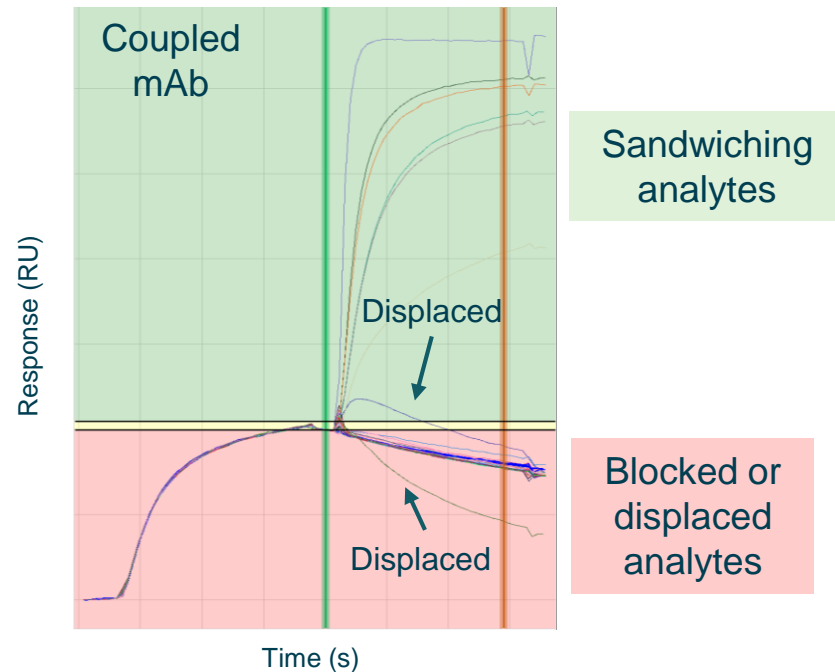
Manuscript submitted to PlosOne, Aug 2019

# High Throughput Binning Provides Exquisite Epitope Resolution

Color by displacement



Sensorgram Overlay Plot



Manuscript submitted to PlosOne, Aug 2019

# The LSA is Disrupting Antibody Analytics

- **Our value proposition:**
  - unprecedented throughput (50x Bia8K)
  - minimal sample consumption and facile assay set-up
  - high quality, reliable kinetics (within 2fold of Bia8K)
  - industry-leading analysis software to expedite getting to the results
- **The LSA's high throughput shifts the role of SPR upstream in drug discovery, where it can impact the library-to-leads triage**
- **High throughput binning reveals the epitope landscape quickly, enabling exquisite epitope resolution and the identification of mAbs with unique and mechanistically-differentiated MOA's**