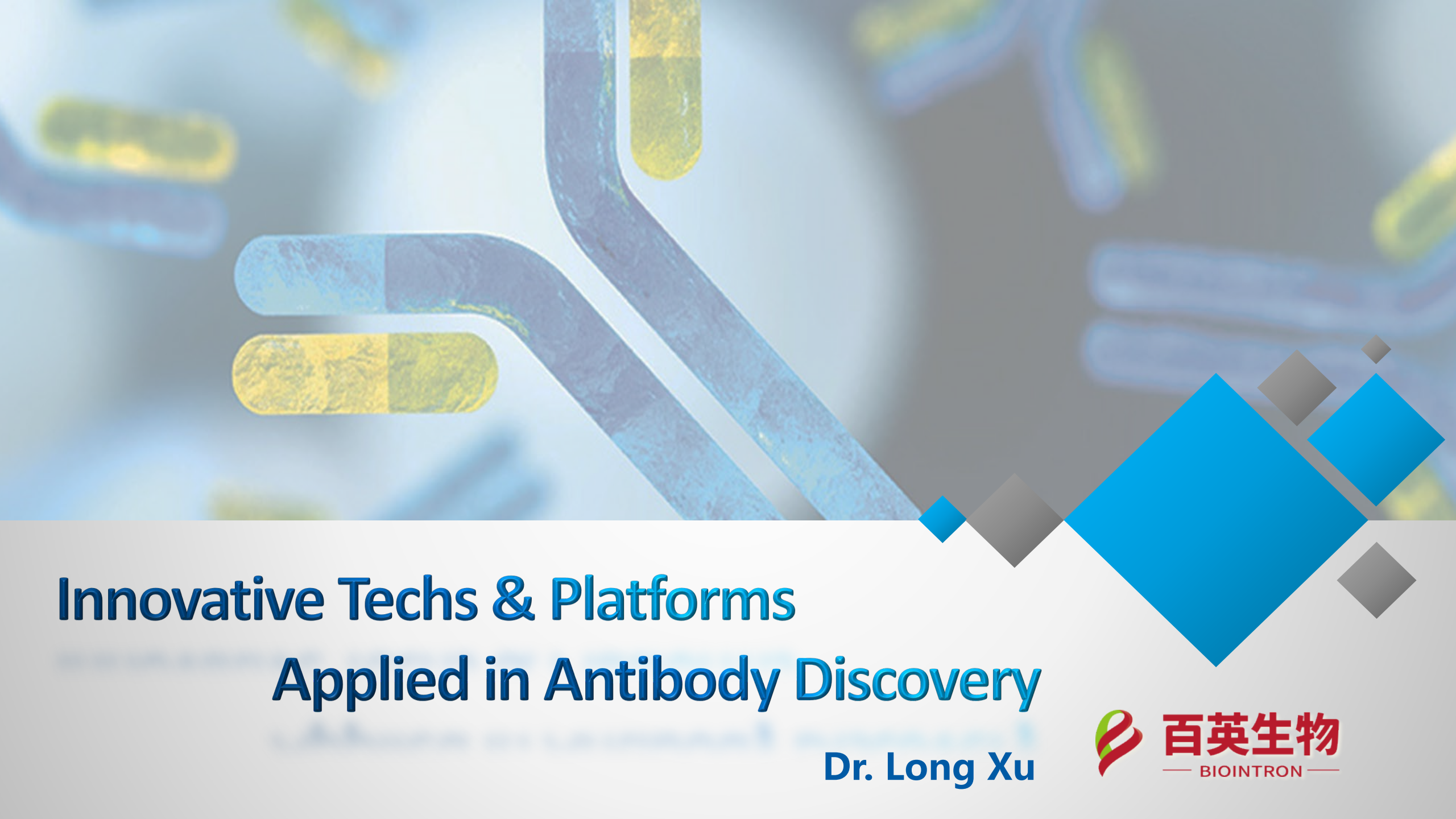


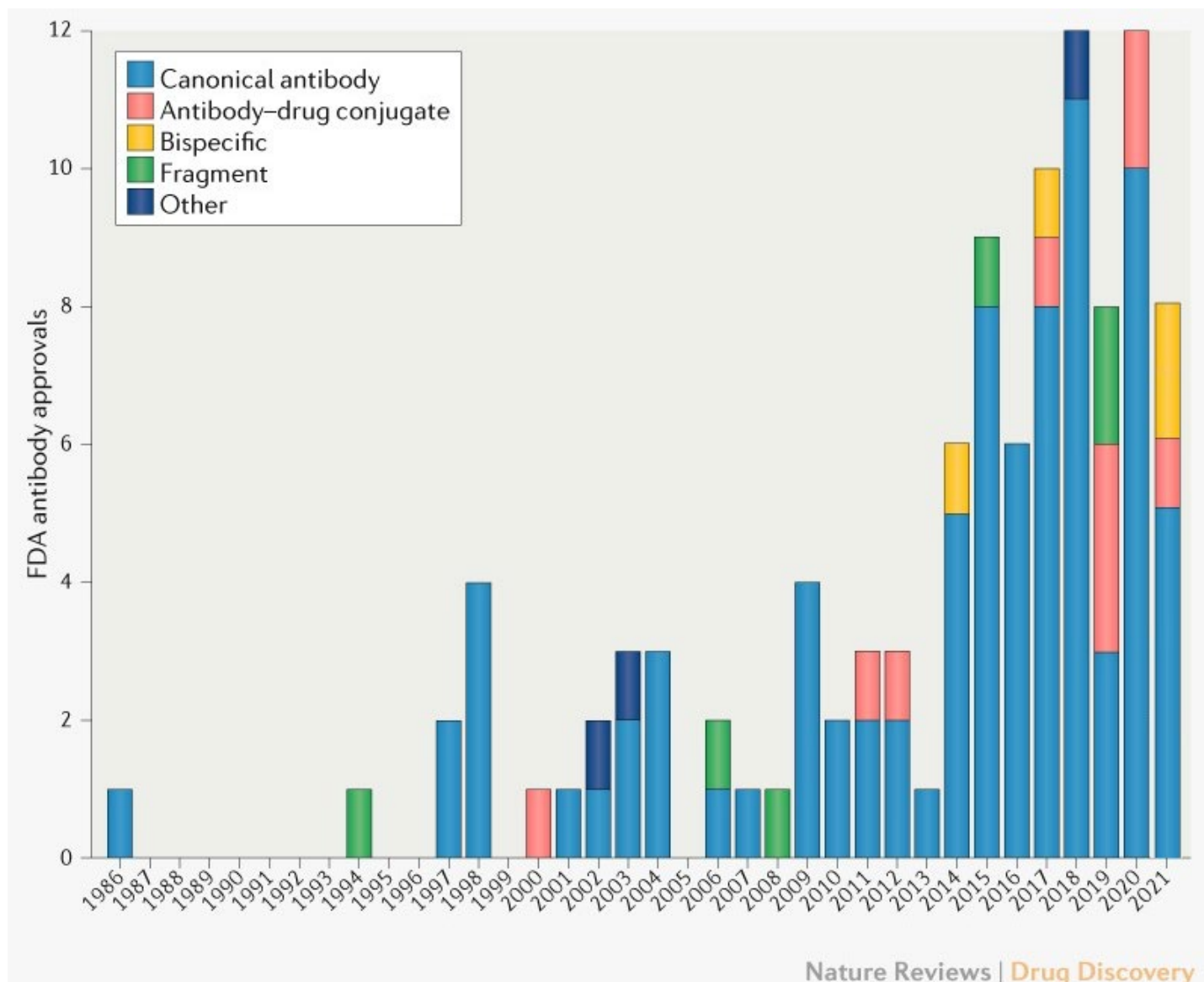


Innovative Techs & Platforms Applied in Antibody Discovery

Dr. Long Xu



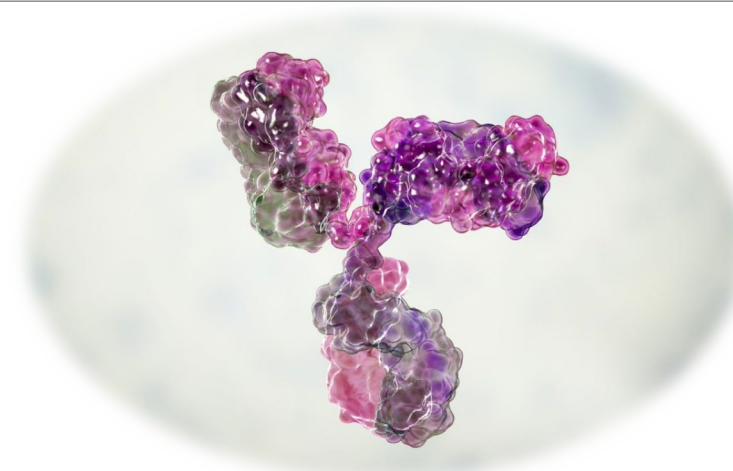
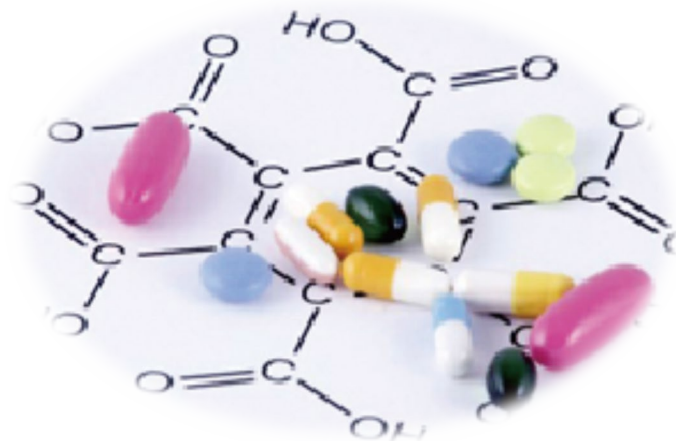
We've Entered the Era of "100+ Antibody Drugs"



7 of Top 10 Best-Selling Drugs in H1 2023 are Antibodies

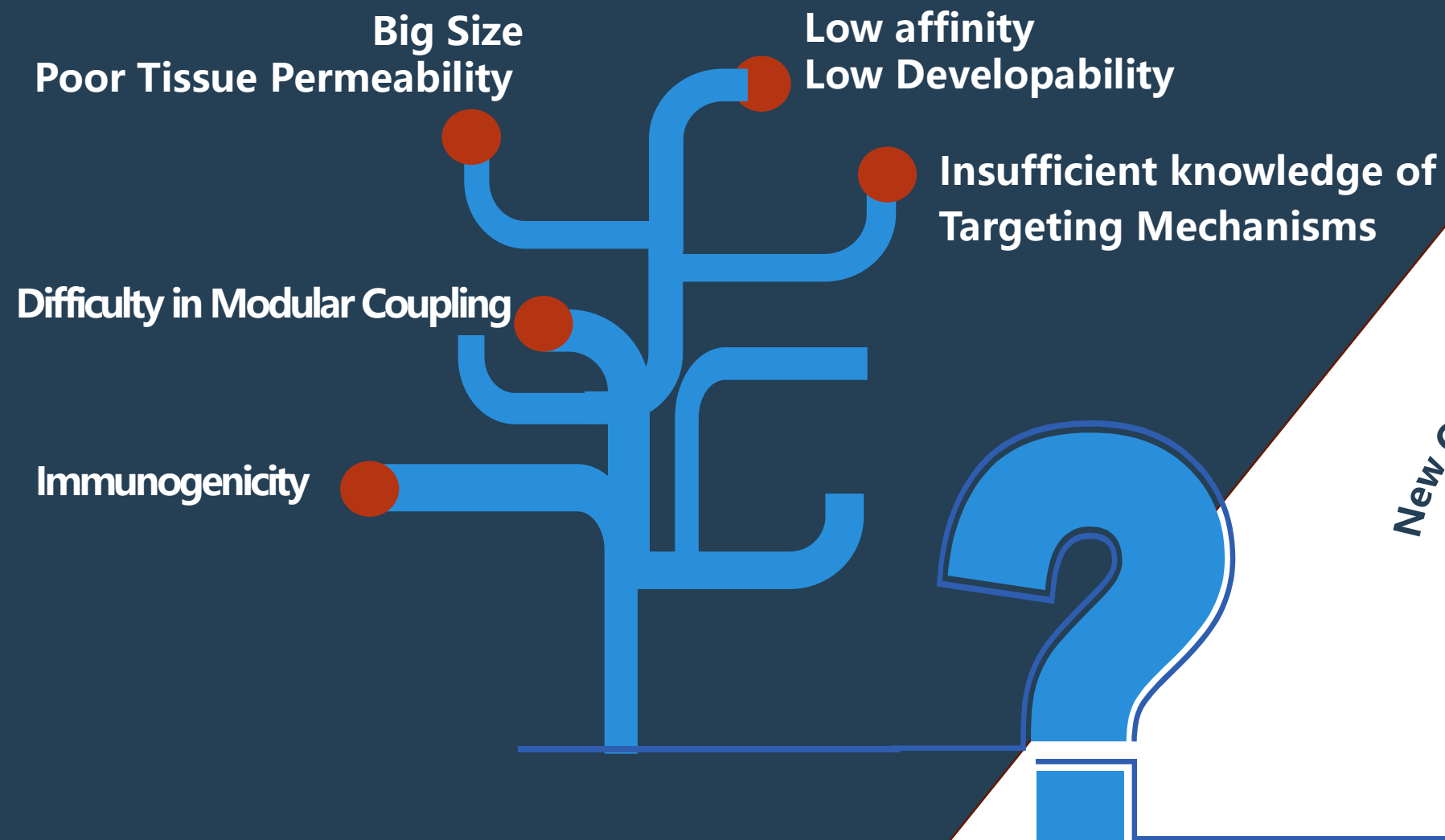
Drug		Target	Company	Sales (in billion U.S. dollars)			
				2020	2021	2022	2023
1	Keytruda	PD-1	Merck	14.38	17.19	20.94	12.07
2	Humira	TNFA	AbbVie/Eisai	19.83	20.70	21.24	7.55
3	Eliquis	FXa	BMS/Pfizer	9.17	10.76	11.79	6.63
4	Ozempic	GLP-1R	Novo Nordisk	3.51	5.86	8.47	6.18
5	Biktarvy		Gilead	7.26	8.62	10.39	5.66
6	Dupixent	IL-4R	Sanofi/Regeneron	4.05	6.20	8.68	5.35
7	Stelara	IL-12/IL-23	Janssen/Mitsubishi Tanabe	7.95	9.55	9.72	5.24
8	Opdivo	PD-1	BMS/Ono	7.92	8.48	9.36	4.88
9	Jardiance	SGLT2	ELI LILLY/BI	385.40	5.90	7.30	4.80
10	Darzalex	CD38	JANSSEN	4.19	6.02	7.98	4.70

Small Molecule Drugs vs Biologics

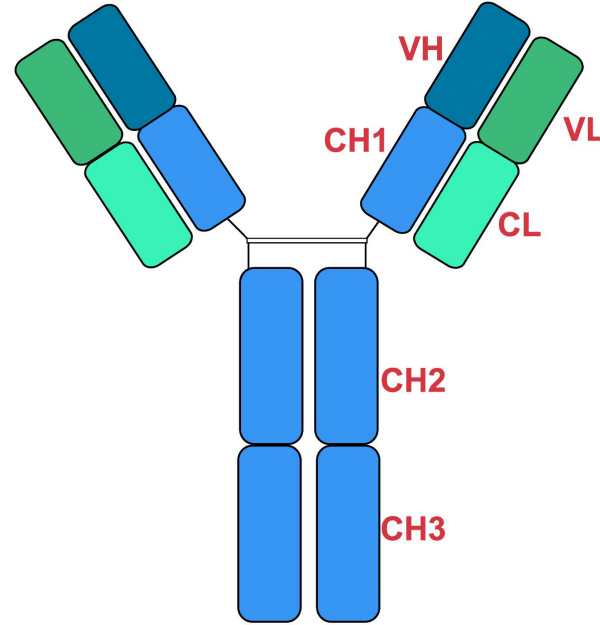


	Small Molecule Drugs	Biologics
Size	Small	Large
Structure	Defined structure & physicochemical properties	Structure & physicochemical properties less well defined
Stability	Stable; not heat-labile	Not stable; heat- and shear-labile
Affinity	Low	Better
Specificity	Low	Better specificity for target binding
Selectivity	Low tissue selectivity	Better tissue selectivity

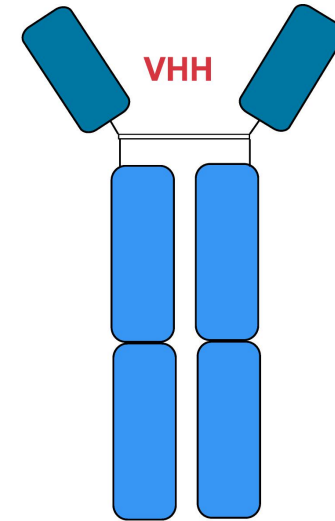
Bottlenecks in Antibody Drug Discovery



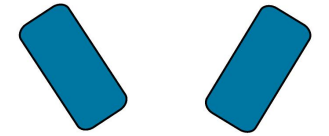
sdAbs Offer New Options for Antibody Drug Discovery



Conventional antibody
150 kDa



Heavy chain antibody
90 kDa



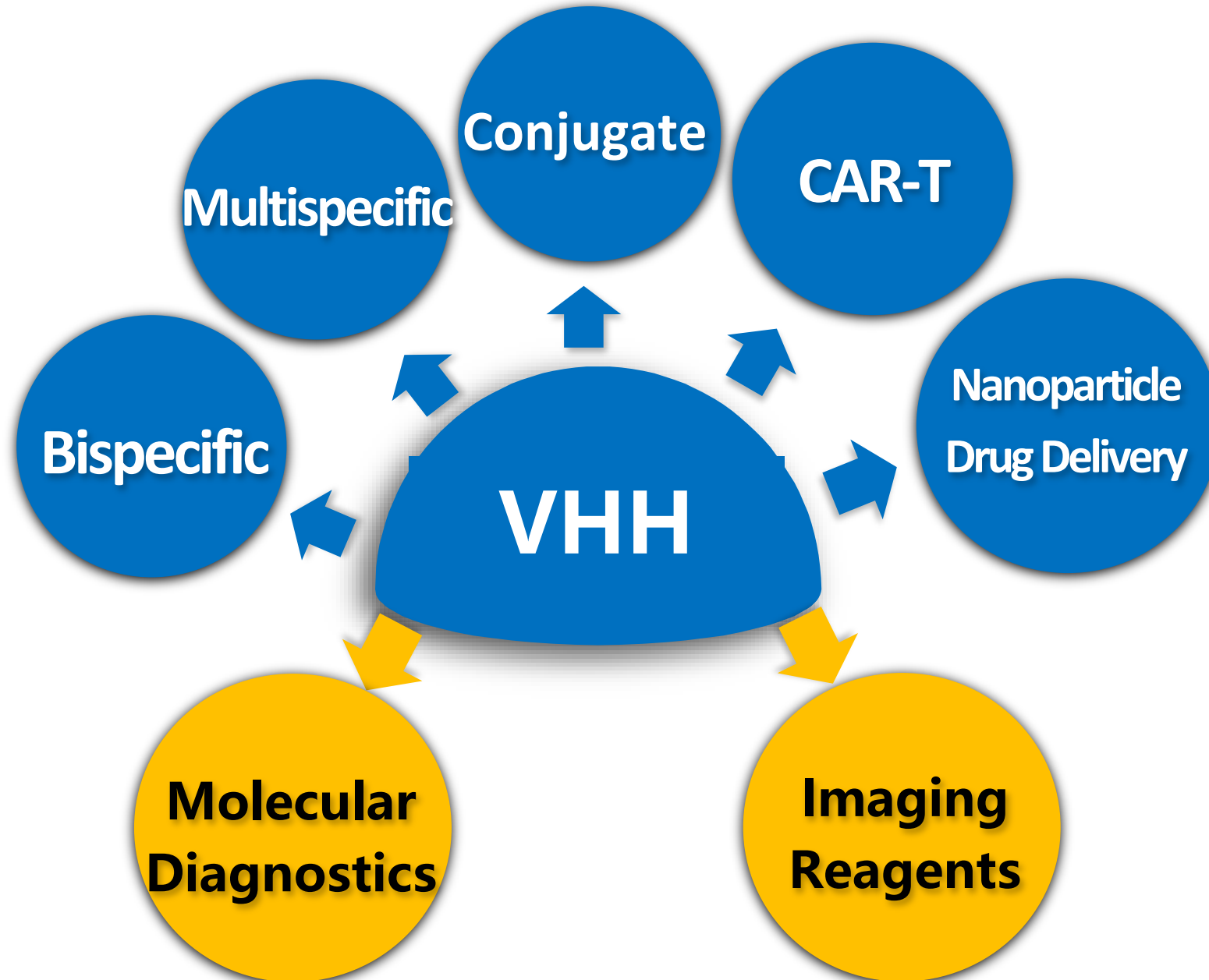
VHH/nanobody
15 kDa

VHH (variable domain of heavy chain of heavy-chain antibody)

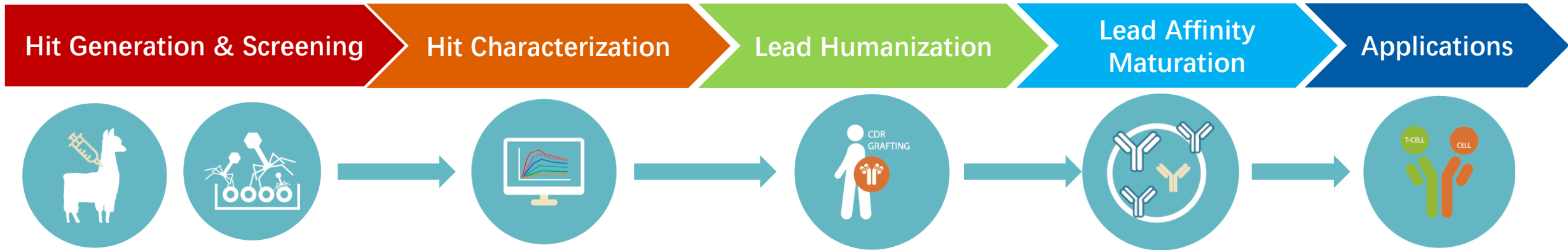
Favorable Biophysical-chemical Properties of VHH



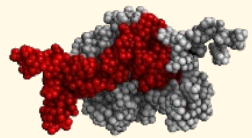
Wide Range of Applications of VHH



VHH Antibody Discovery



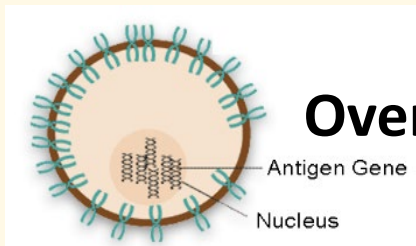
Immunization strategy



Protein



DNA



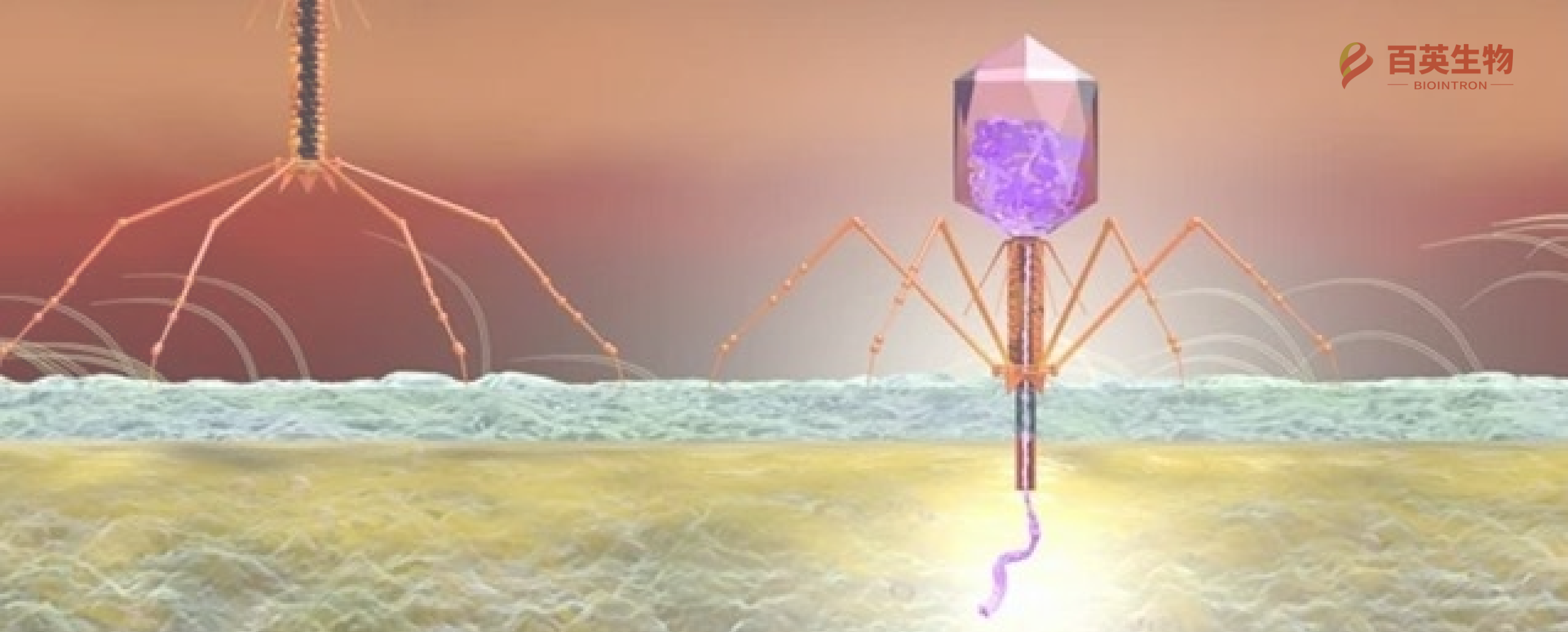
Over-expression cell

PBMC isolation



Phage Display
1.5 month/high-throughput

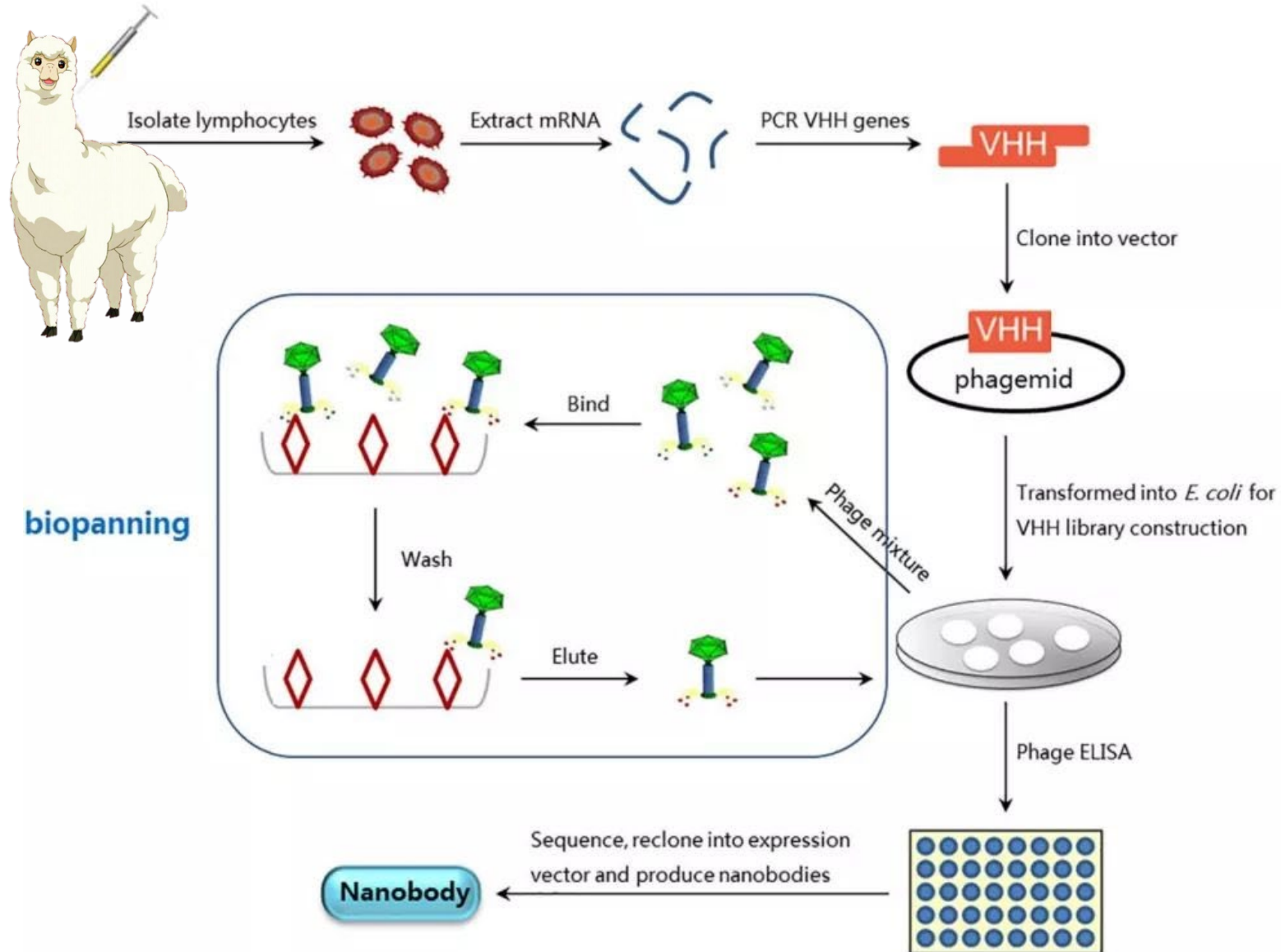
NGS Sequencing &
Data Mining



Phage Display

VHH Discovery Platform

Phage Display as a Reliable Method for VHH Discovery



Anti-X Nanobody Discovery Case

Target X, a cell surface receptor expressed on T cells, is a co-stimulator for T cell activation.

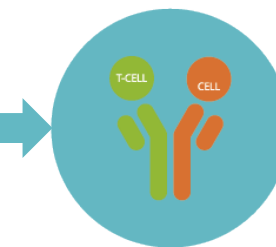
Hit Generation & Screening

Hit Characterization

Lead Humanization

Lead Affinity
Maturation

Construction of
Bispecific Antibody



From the alpaca immune antibody library, **phage display** tech was used to screen the nanobodies targeting **X**.

The selected hits were functionally characterized & validated.

SPP

ELISA

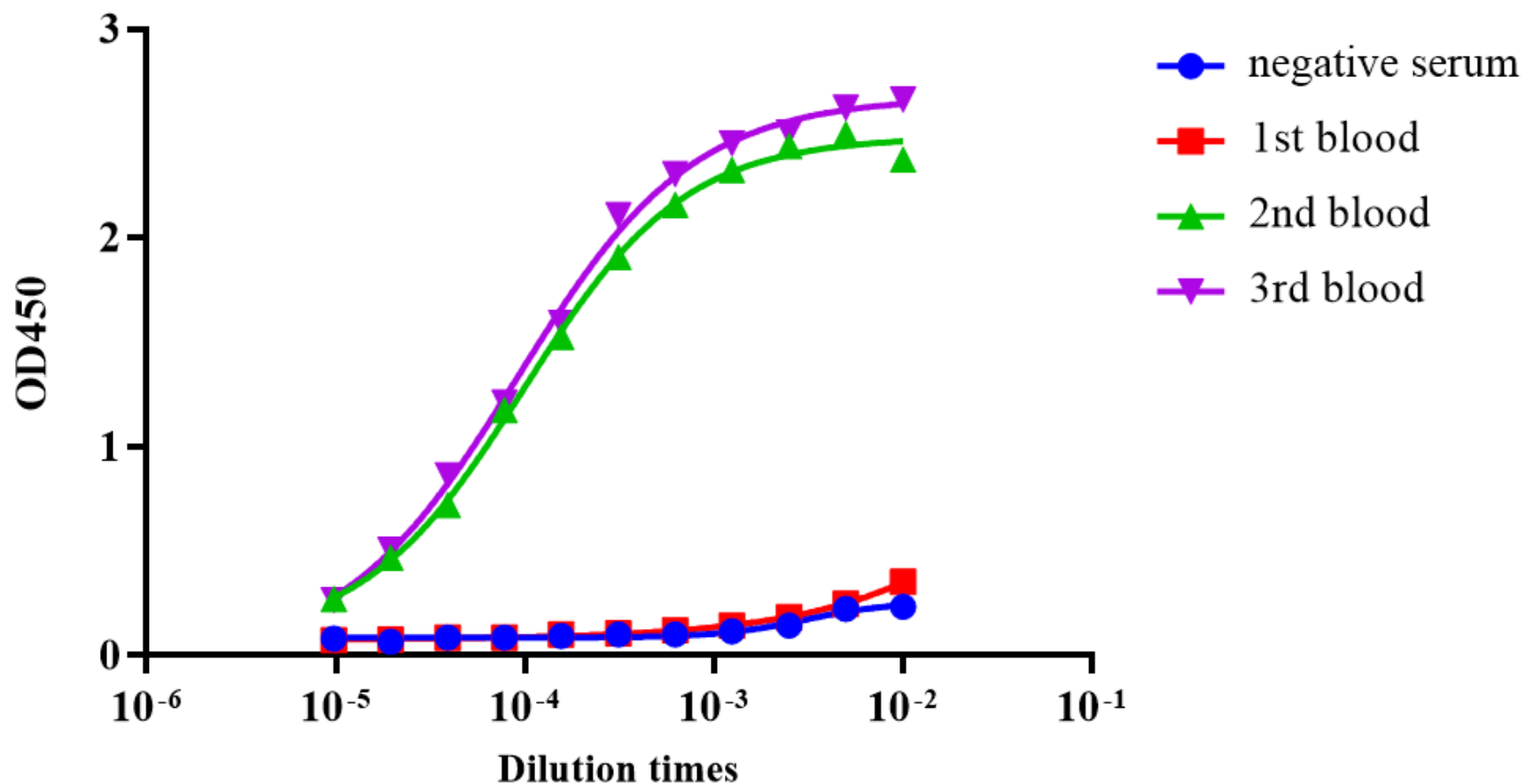
FACS

Agonist

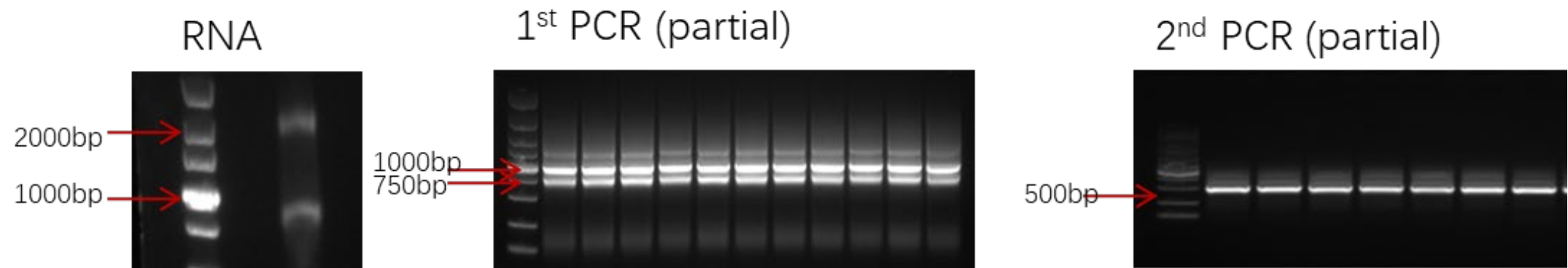
Blocking

The candidate sequences have been selected. **Humanization & affinity maturation** are being carried out in preparation for the final construction of the **bispecific antibody**.

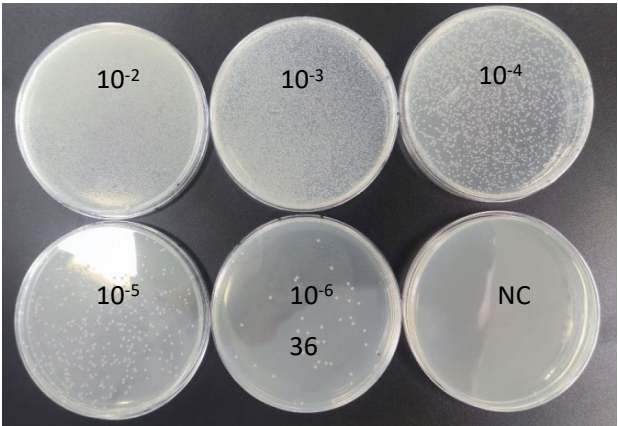
Immunization of Alpaca with Antigen X



VHH Phage Display Library Construction



Library Diversity Evaluation



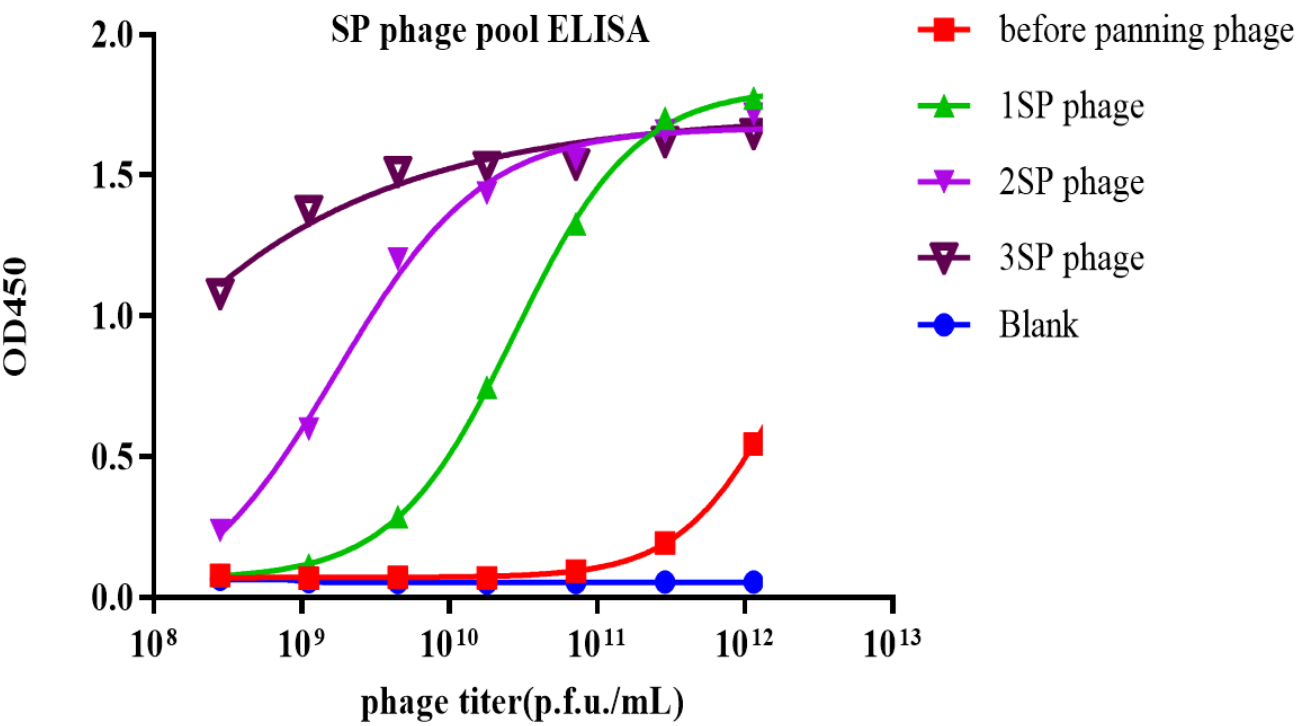
The library size = 5.18×10^9

Clone #	CDR1	CDR2	CDR3	Clone #	CDR1	CDR2	CDR3
Diversity-A-3M-1	GFNL		GFDDY	Diversity-Z045-3、4M-16	GFTF		
Diversity-A-3M-25	GFNL		GFDDY	Diversity-Z045-3、4M-17	GISV		
Diversity-A-3M-2	GSPF			Diversity-Z045-3、4M-18	GSIS		
Diversity-A-3M-3	GDTM		DDY	Diversity-Z045-3、4M-19	GFNV		GSYAY
Diversity-A-3M-4	GFTF		AYGMDY	Diversity-Z045-3、4M-20	GFIL		
Diversity-A-3M-5	GIVF			Diversity-Z045-3、4M-21	RSGF		
Diversity-A-3M-6	GSIF		DDY	Diversity-Z045-3、4M-22	GSTF		
Diversity-A-3M-7	GFAF			Diversity-Z045-3、4M-23	GFTF		
Diversity-A-3M-8	GFTF			Diversity-Z045-3、4M-24	GVPS		KY
Diversity-A-3M-9	GRSI			Diversity-Z045-3、4M-25	GTTL		FGS
Diversity-A-3M-10	GFTL		GPPEYNF	Diversity-Z045-3、4M-26	GGTF		
Diversity-A-3M-28	GFSL		SHYNDMDY	Diversity-Z045-3、4M-27	GGGF		
Diversity-A-3M-18	GFTL		RTYDY	Diversity-Z045-3、4M-28	GCMY		
Diversity-A-3M-21	ETML		RFHG VKY	Diversity-Z045-3、4M-29	GFTL		
Diversity-A-3M-24	GFTS			Diversity-Z045-3、4M-30	GDIF		

2 repetitive sequences in 48 clones sent for sequencing。

Output/Input

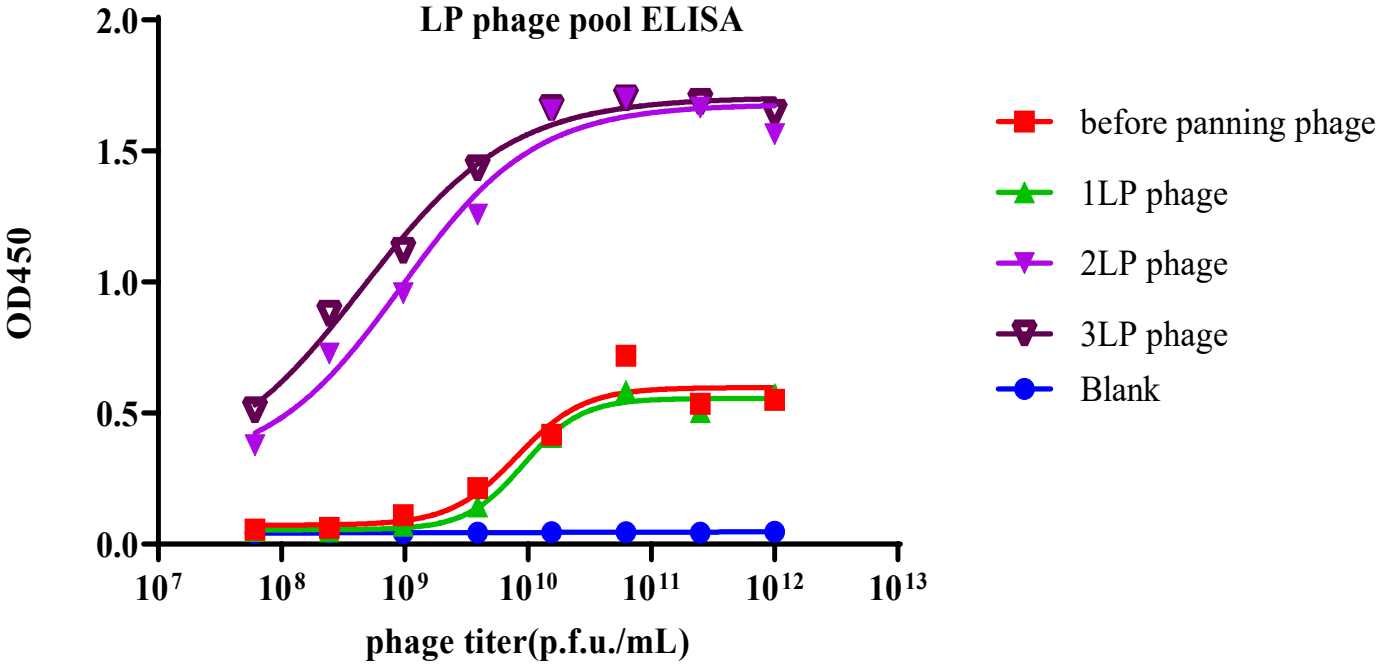
Solid phase panning (SP)	Input	Output	Output/Input
Round 1 SP	2.00E+12	1.20E+07	6.00E-06
Round 2 SP	1.53E+12	1.50E+08	9.78E-05
Round 3 SP	1.15E+13	1.17E+10	1.02E-03



360 positive clones were obtained, 11 unique sequences were obtained & expressed in HTP system (CHO).

Output/Input

Liquid phase panning (LP)	Input	Output	Output/Input
Round 1 LP	2.00E+12	2.40E+06	1.20E-06
Round 2 LP	3.33E+11	4.20E+09	1.26E-02
Round 3 LP	4.10E+12	7.50E+09	1.83E-03

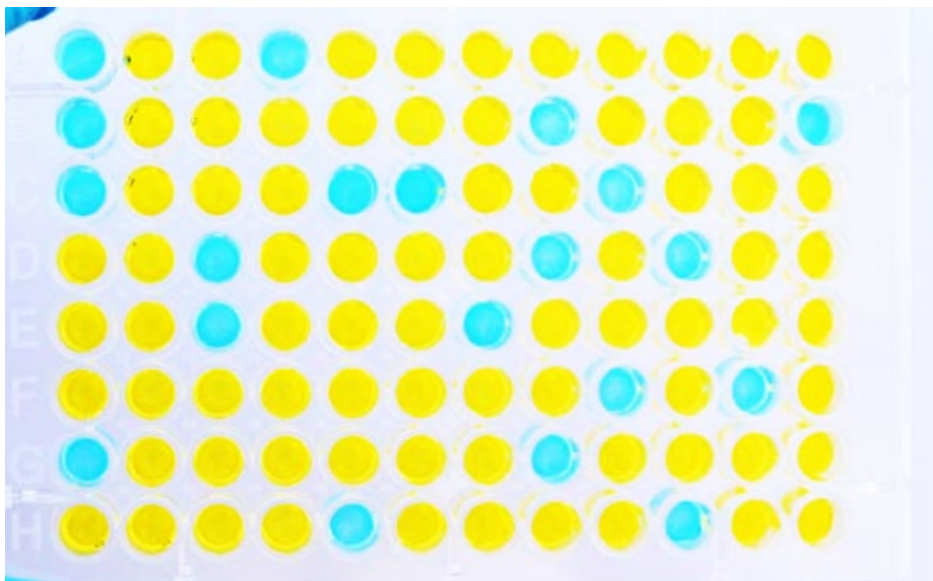


952 positive clones were obtained, **43** unique sequences were obtained & expressed in HTP system (CHO).
11 + 43 = 54 unique sequences

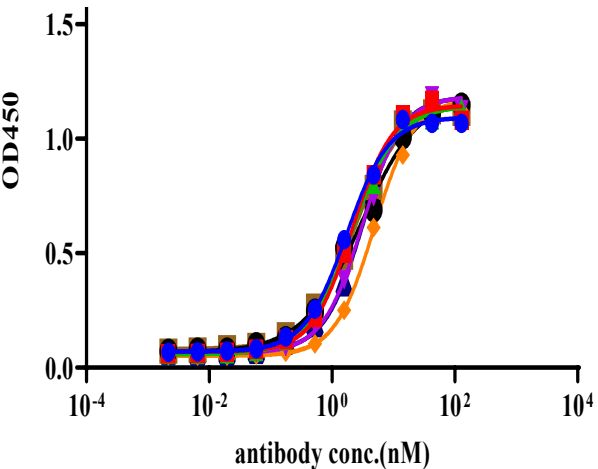
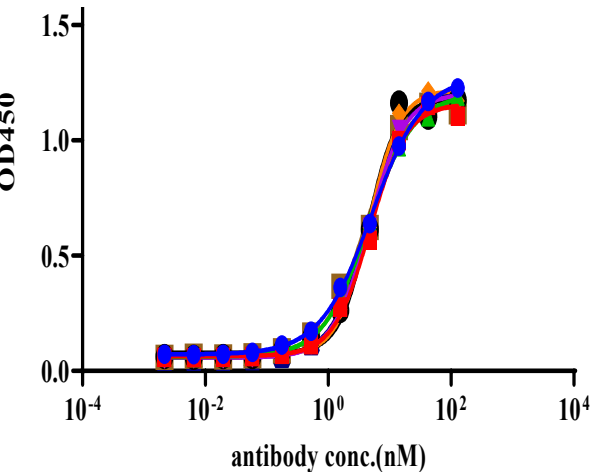
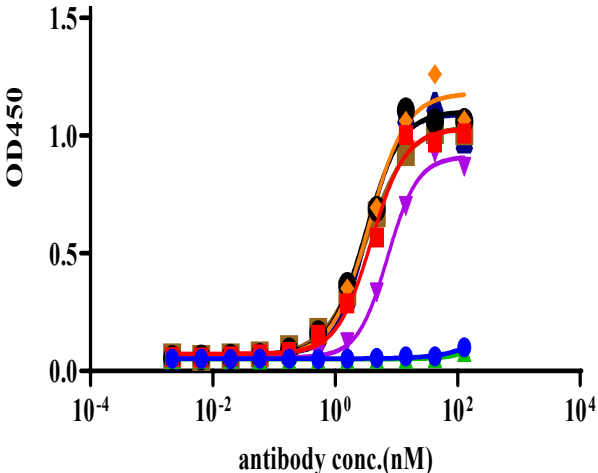
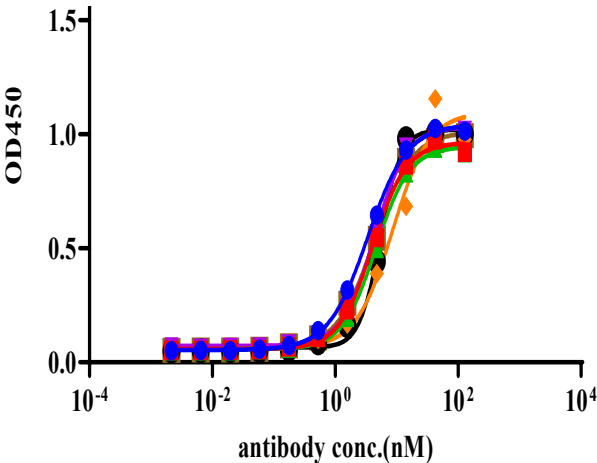
Antibody Characterization

ELISA BINDING ASSAY

54 VHH antibodies were expressed in HTP CHO expression system, purified, & validated by ELISA against Antigen X.

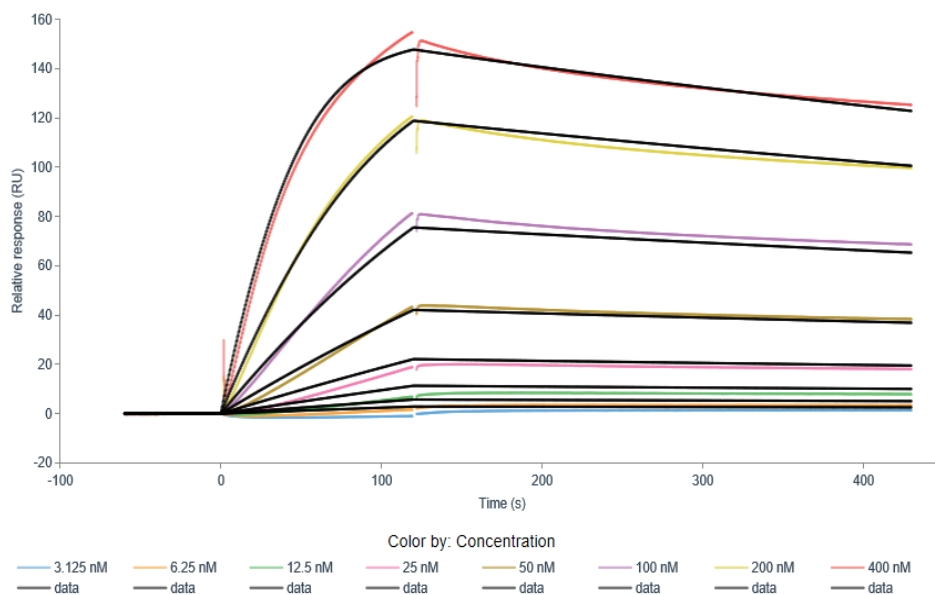


35 of 54 VHH Antibodies Bound to X in ELISA Assay



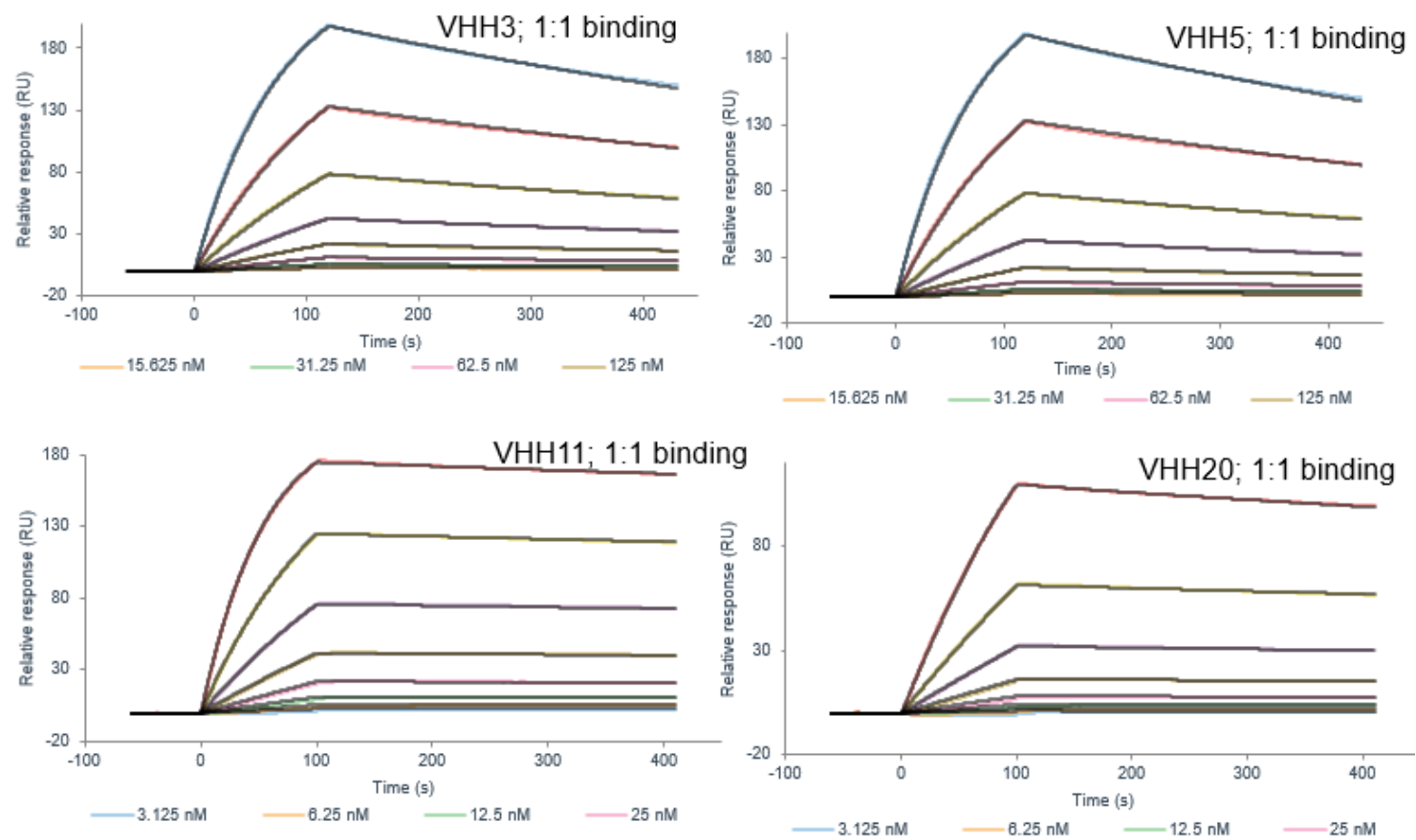
Antibody Characterization

SPR AFFINITY MEASUREMENT

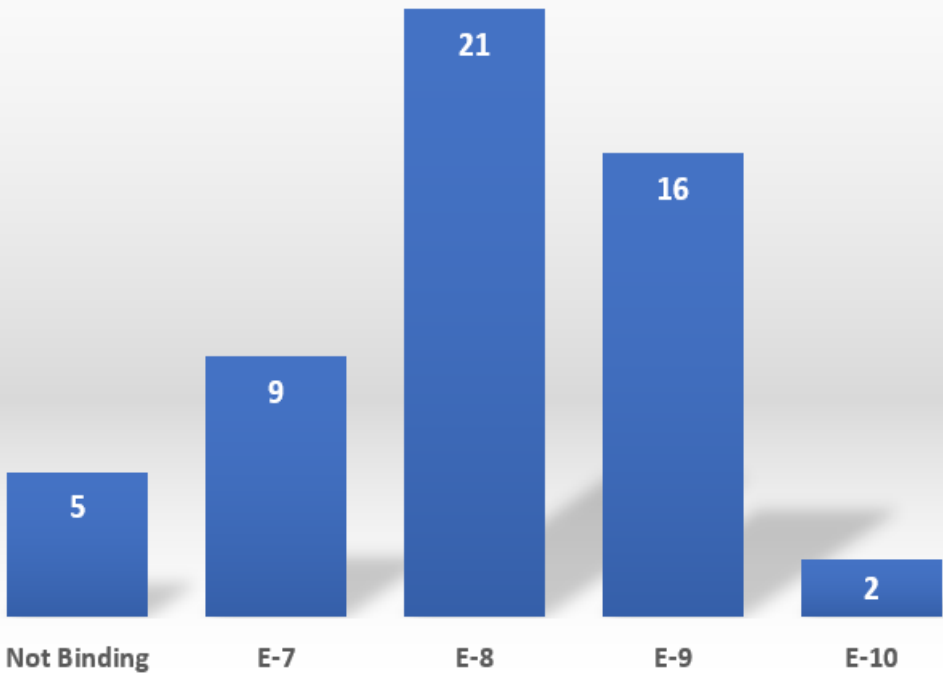


54 VHH antibodies were expressed in HTP CHO expression system, purified, & subjected to SPR test on BIAcore 8k system against Antigen X.

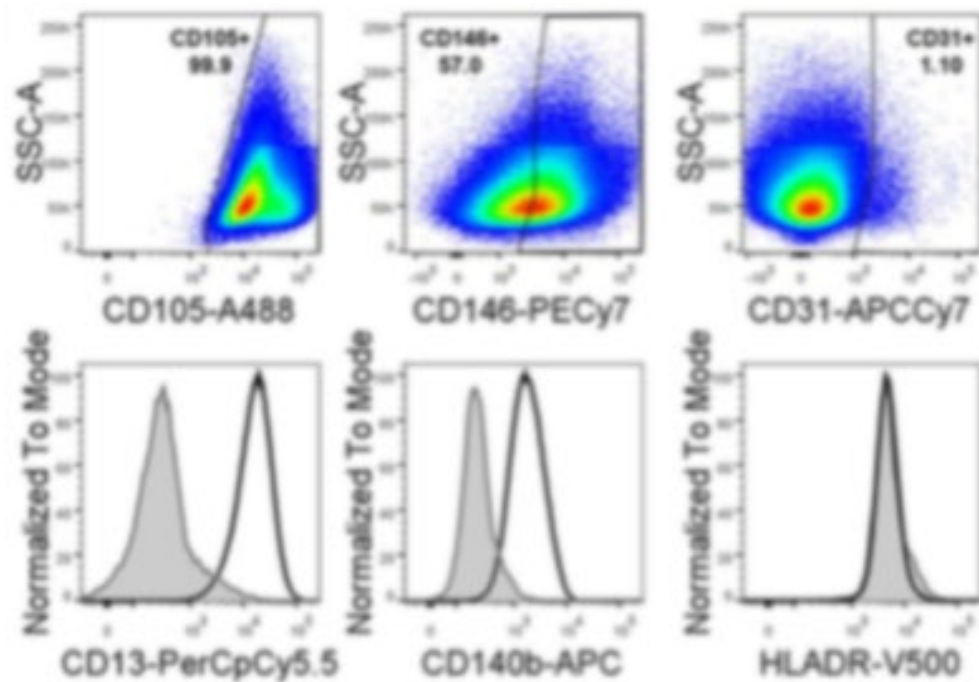
49 of 54 VHH Antibodies Bound to X in SPR Tests



Affinity Distribution



Affinity range 5.36×10^{-7} M to 7.66×10^{-10} M.

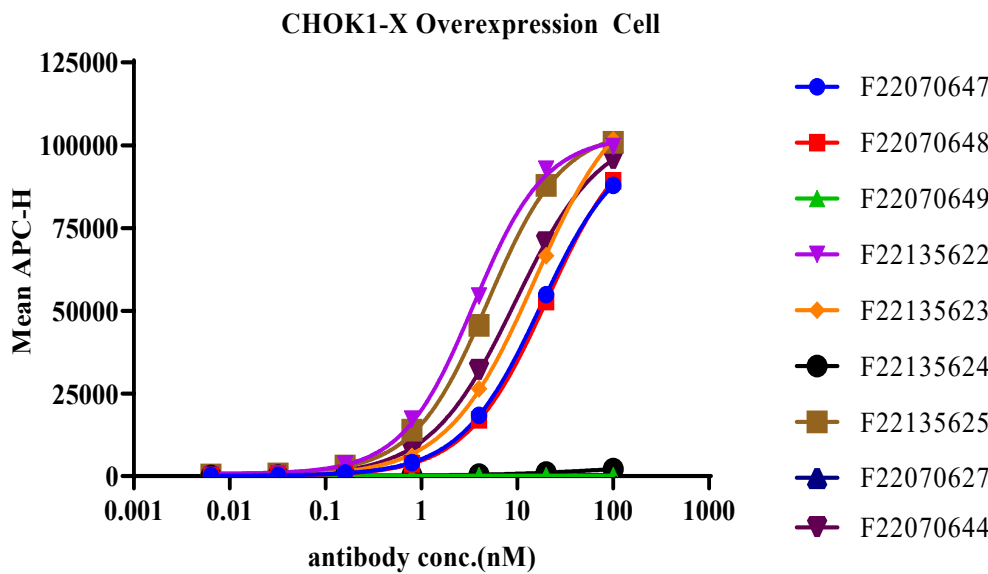
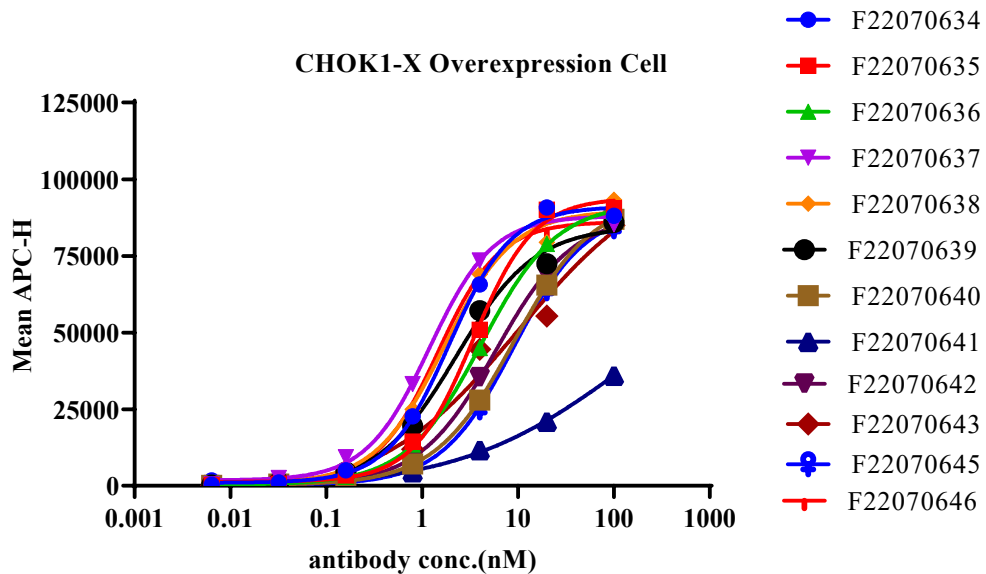
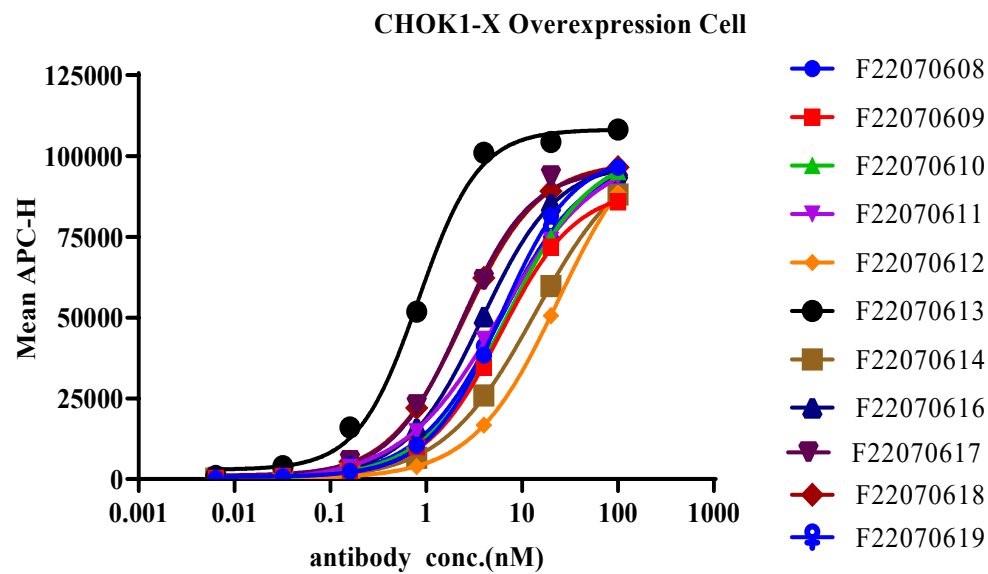
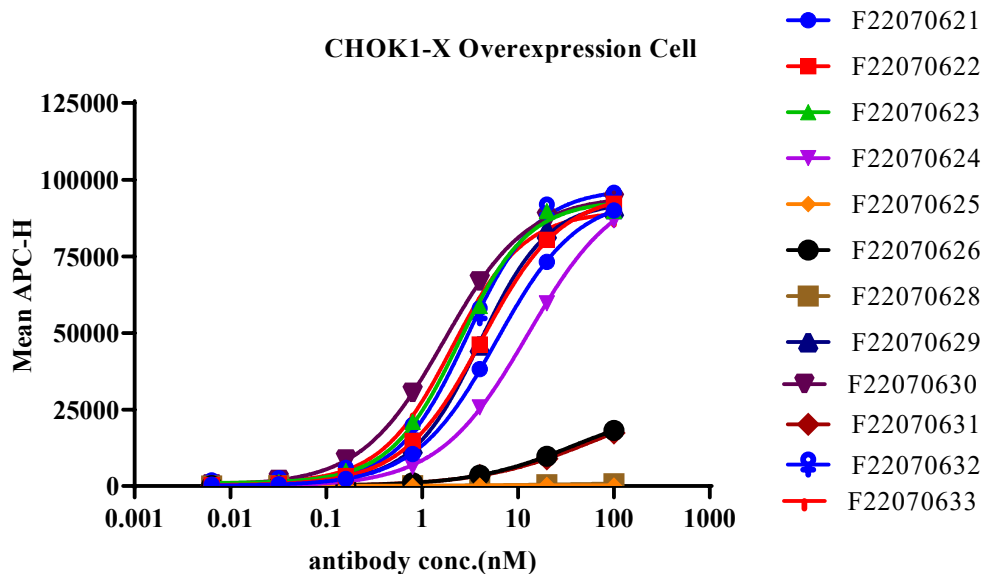


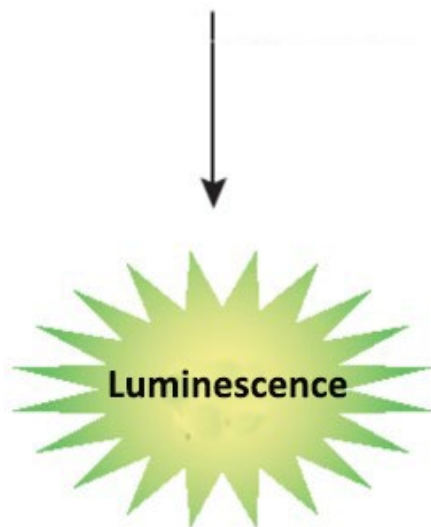
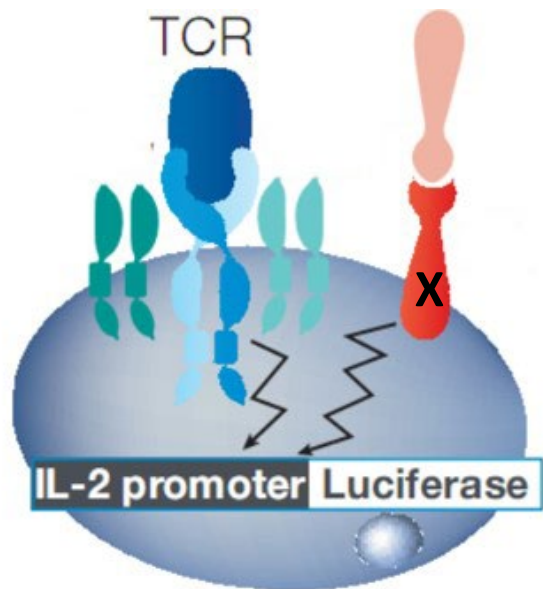
Antibody Characterization

CELL-BASED BINDING ASSAY BY FLOW CYTOMETRY

54 VHH antibodies were examined by flow cytometry against CHO-K1/X overexpression cell.

43 of 54 VHH Antibodies Bound against CHO-K1/X Cell



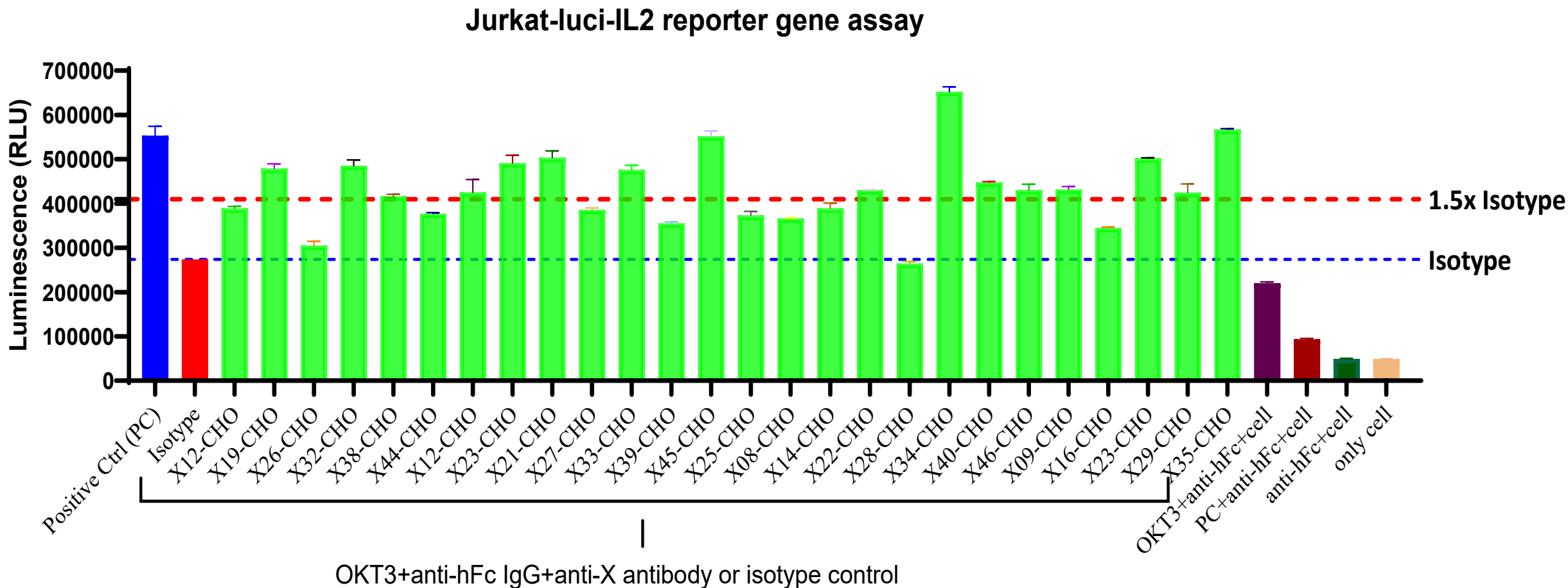


Antibody Characterization

AGONIST ACTIVITY ASSAY

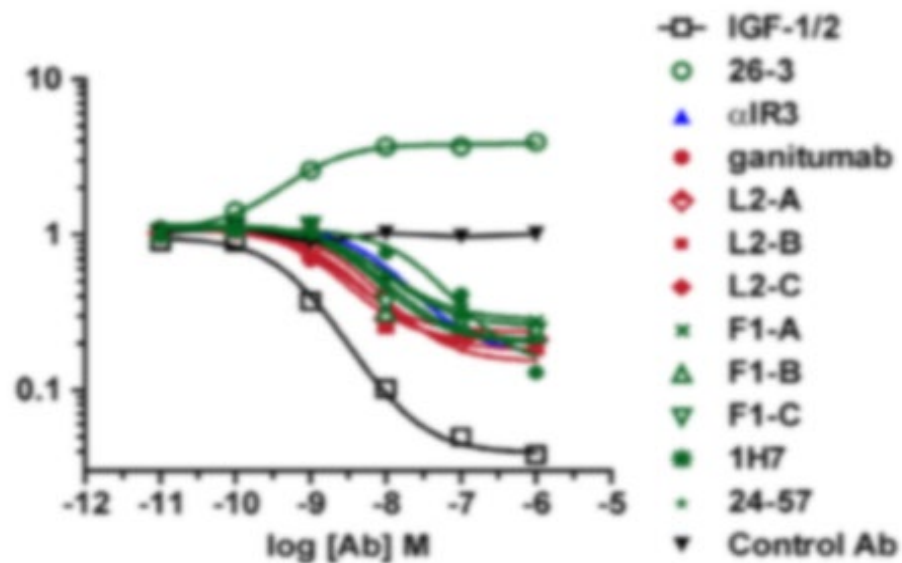
53 VHH antibodies were subjected to agonist activity assay with Jurkat-luci-IL2 reporter system.

31 of 53 Hits Showed Agonist Activity



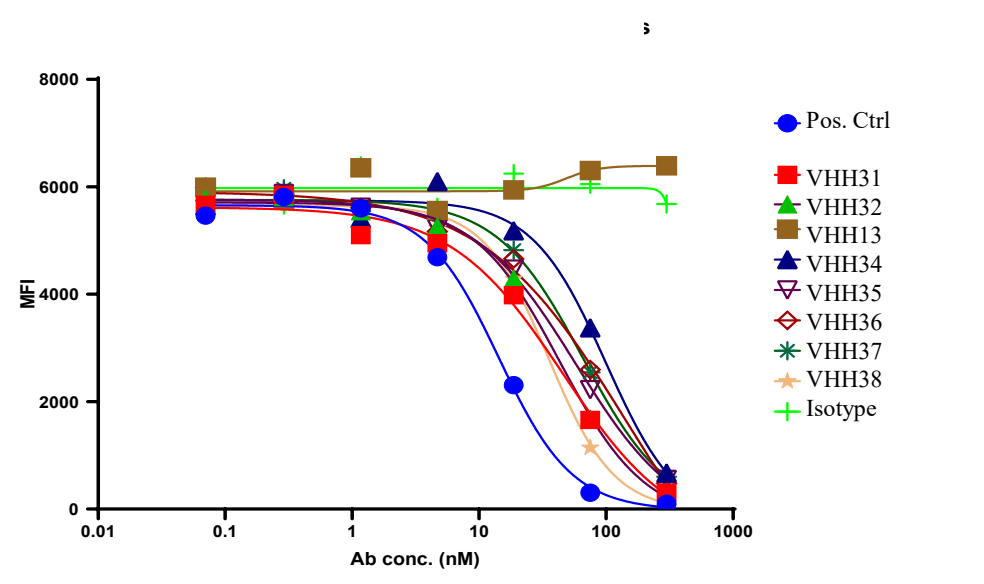
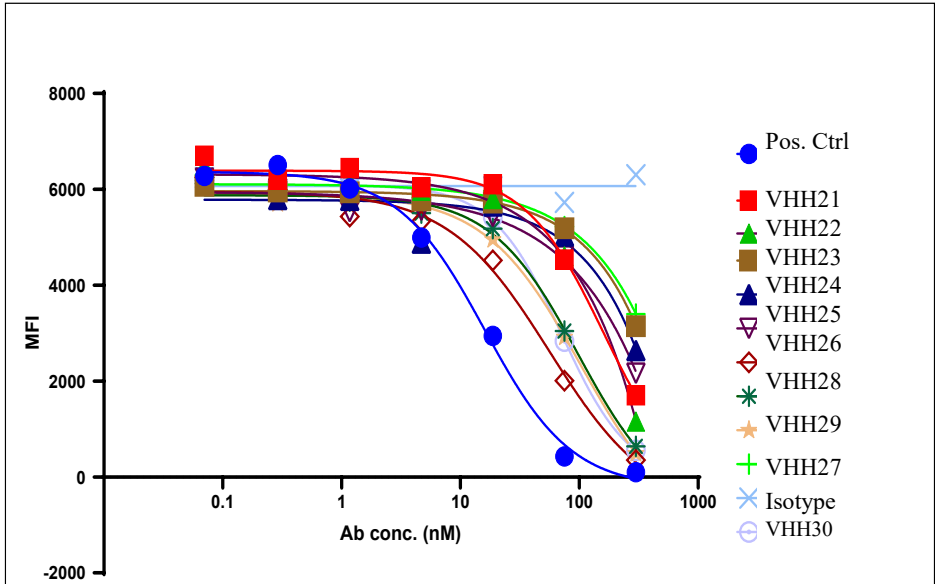
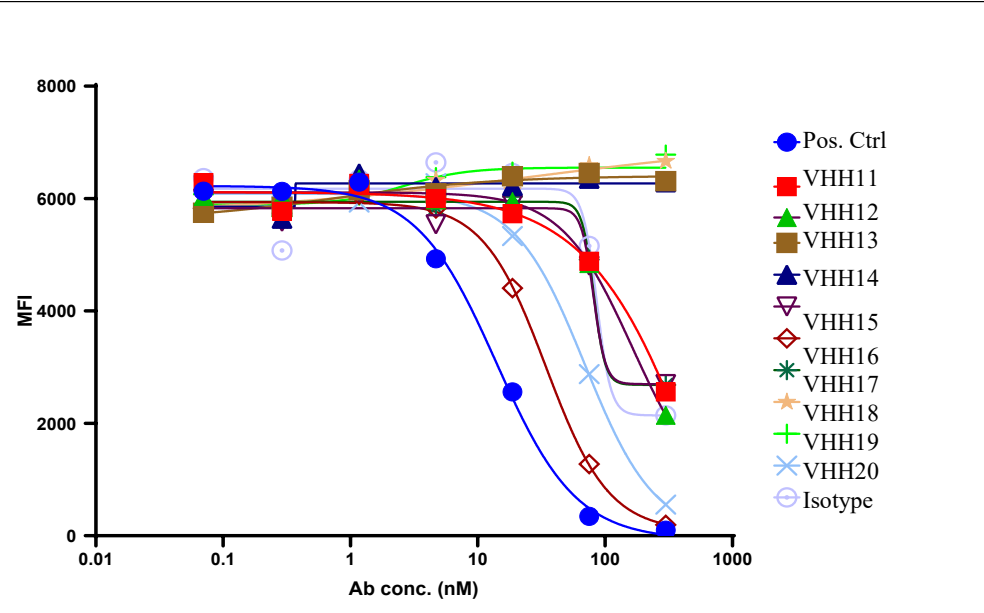
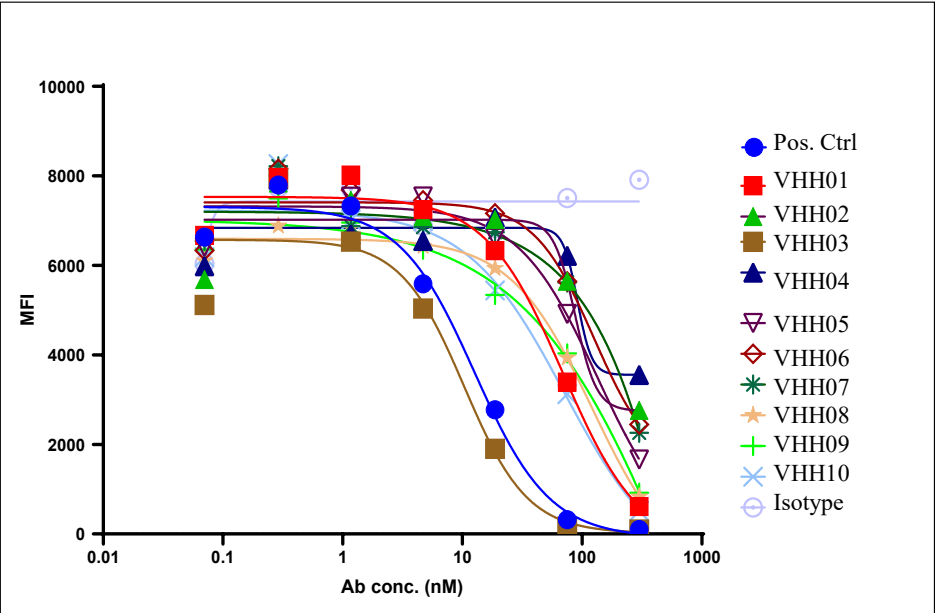
Antibody Characterization

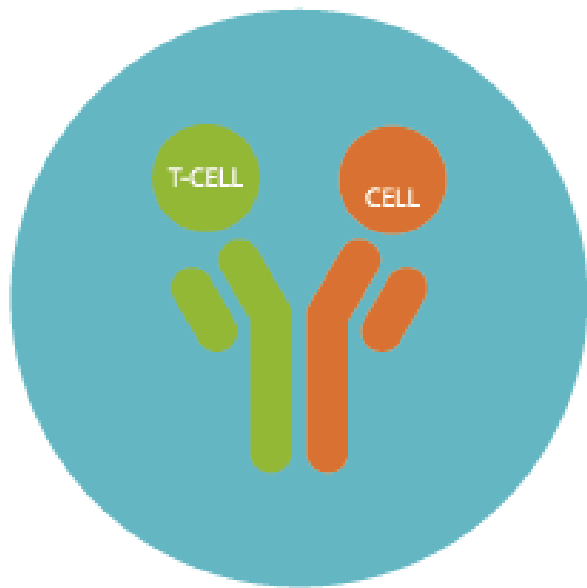
LIGAND BLOCKING ASSAY



51 VHH antibodies were subjected to blocking assay to determine the ability of VHH-hFc to block interaction between ligands and cell membrane-bound Antigen X.

44 of 51 VHH Antibodies Showed Blocking Effect



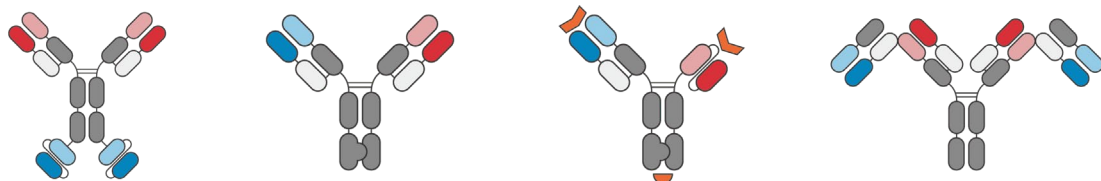


Antibody Application

BISPECIFIC ANTIBODIES

After VHH antibodies are screened, characterized and optimized to meet the requirements, they are ready for applications, such as the construction of bispecific antibodies.

Construction of Common Formats of Bispecific Antibodies



IgG-scFv

Knobs-into-holes

Y-body

FIT-Ig



Cross MAB

Ortho-Fab IgG

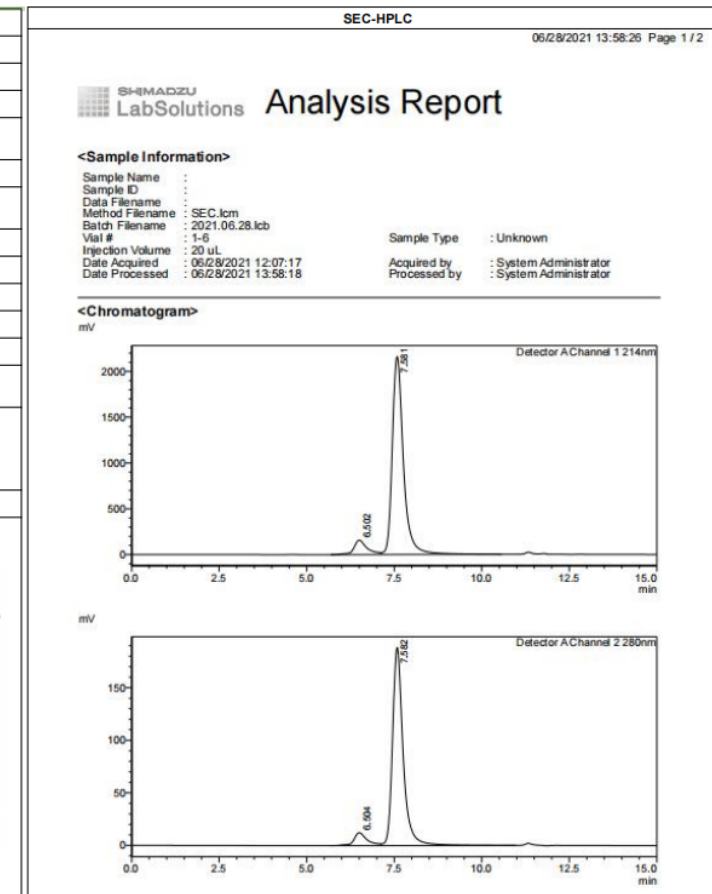
DVD-Ig

bi-Nanobody

BiTE

CH CL V_AH V_AL V_BH V_BL

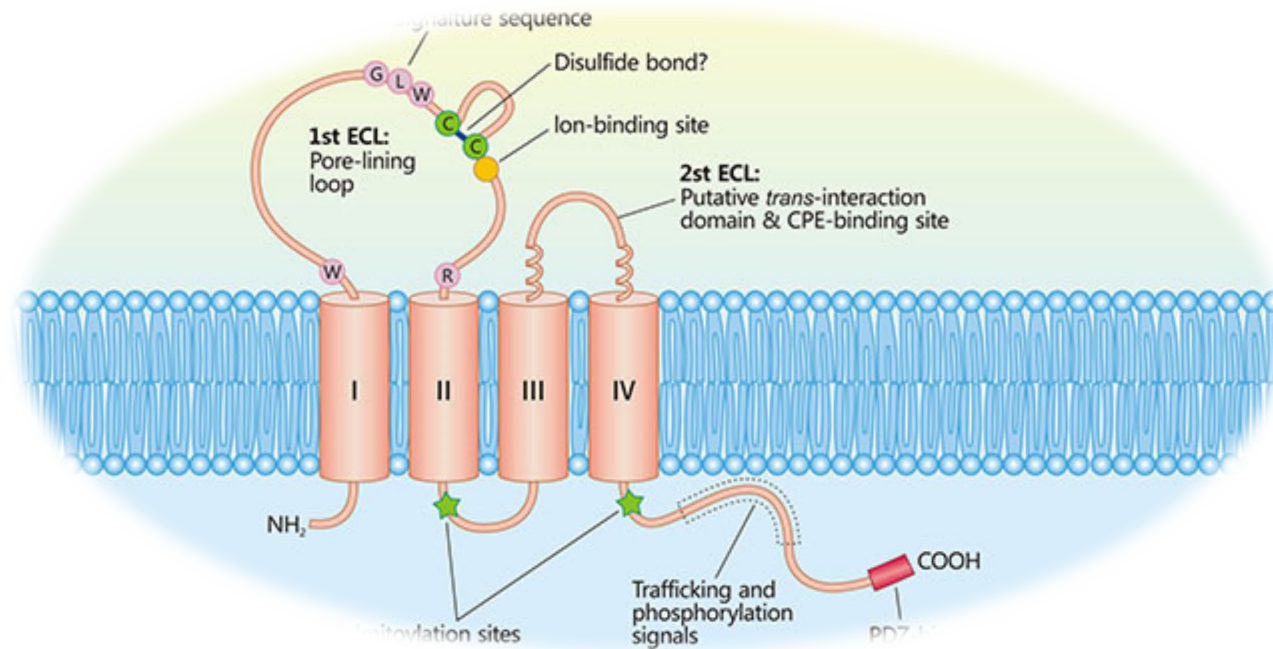
CERTIFICATE OF ANALYSIS			
Name		Label Type	Human IgG1-Kappa
Project ID		Host	HEK293
Delivery Amount	86.42mg	Lot. No.	
Buffer	10mM NaAc-HAc , pH5.2	Expression yield	43.3mg/L
Delivery format	Liquid	Concentration	4.69mg/ml
Molecular characterization	The predicted MW is 74/23Kda and the experimental MW is about 70-100/25-35 kDa in SDS-PAGE under reducing condition.		
QC Results			
Test Items	Specifications	Results	
Purity	SDS-PAGE under reducing conditions.	>95%	
	SEC-HPLC test.	92.476%	
Endotoxin	LAL test.	<1EU/mg	
Storage	sterile filtered, no preservatives.The product should be stored at -20°C or lower upon receipt, and avoid repeated freeze-thaw cycles.		
	Storage condition suggestion: 1. 2°C to 8 °C for 2 weeks under sterile conditions; 2. -20°C for 3 months under sterile conditions; 3. -70°C for 36 months under sterile conditions.		
SDS-PAGE			
R N-R M 150 50 25 M 230kDa 150 100 70 50 25 20 15 10 LaneM: Marker LaneR: Reducing LaneN-R: Non-Reducing			



Challenge 1. Transmembrane Targets

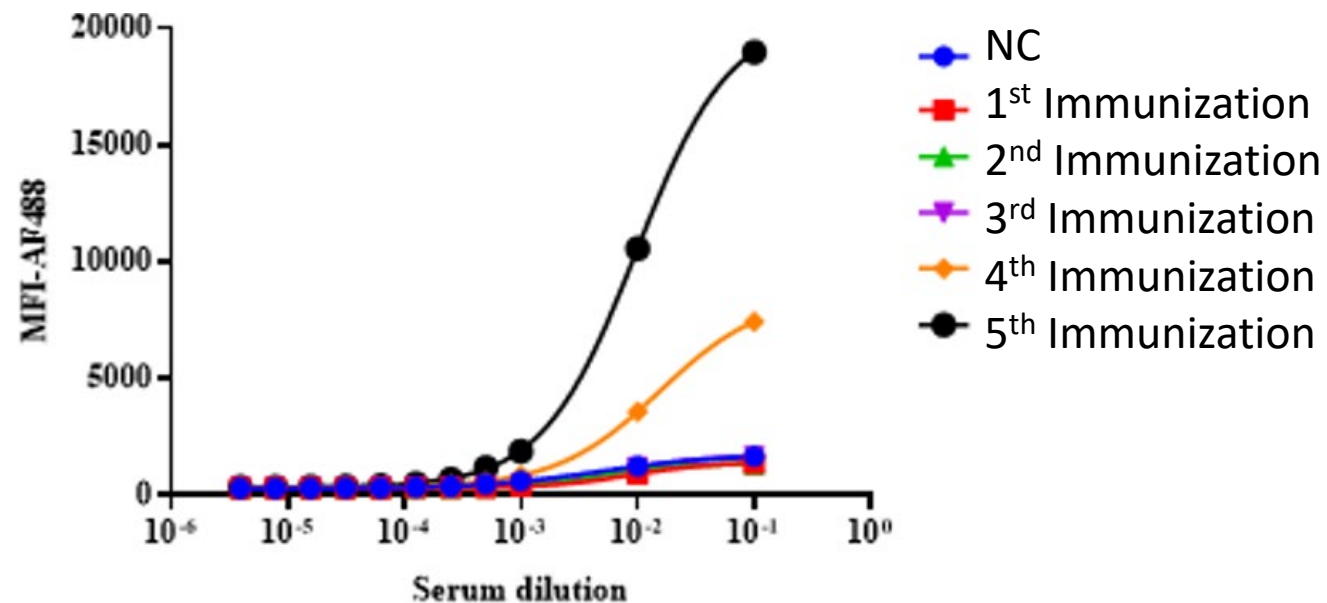


What if it is difficult to prepare soluble protein as antigen?



Human Claudin 18.2 Case

Antigen	Immunization
DNA encoding Claudin 18.2	1, 2
CHO-K1-Claudin 18.2	3, 4, 5



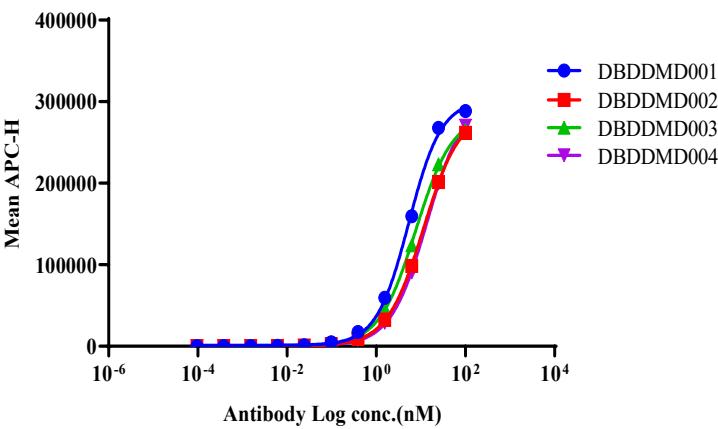
Cell Panning using CHO-K1-Claudin 18.2

Cell panning	Input (CFU/ml)	Output	Output/Input
1	2.00E+12	9.00E+07	4.50E-05
2	1.33E+12	2.10E+08	1.58E-04
3	2.07E+12	4.20E+08	2.03E-04

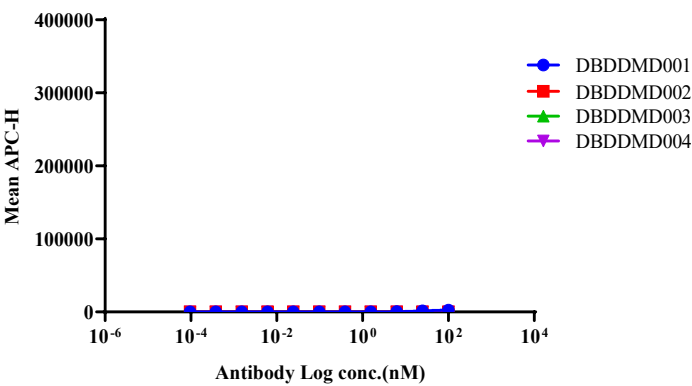
4 VHH Antibodies Specifically Bound Claudin 18.2 But Not 18.1

	Selected Clones	Positive Clones	Positive%	Unique Sequences
0635-Human C2-1CP	88	2	2.27%	1
0635-Human C2-2CP	88	6	6.82%	2
0635-Human C2-3CP	88	14	15.91%	10

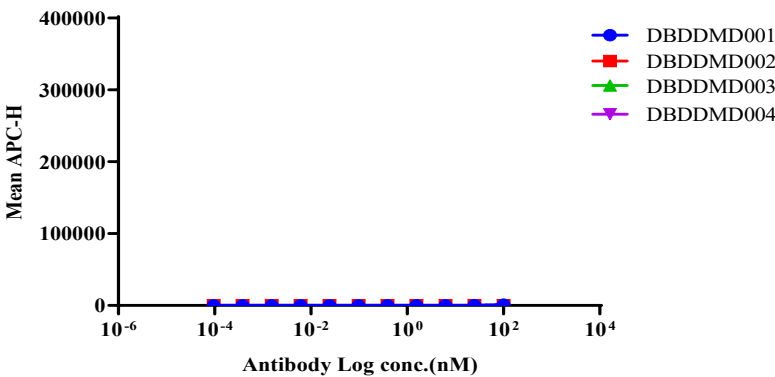
293T (Claudin 18.2)



293T (Blank)



293T (Claudin 18.1)



Challenge 2. Naïve Phage Display Library



Naïve phage display lib. instead of alpaca immune antibody lib.



300 Alpacas' PBMC



**phage display
& production**



Naïve Phage Display Library
Library Size: 10^{12}

Monoclonal Phage ELISA Screening after Liq. Phase Panning

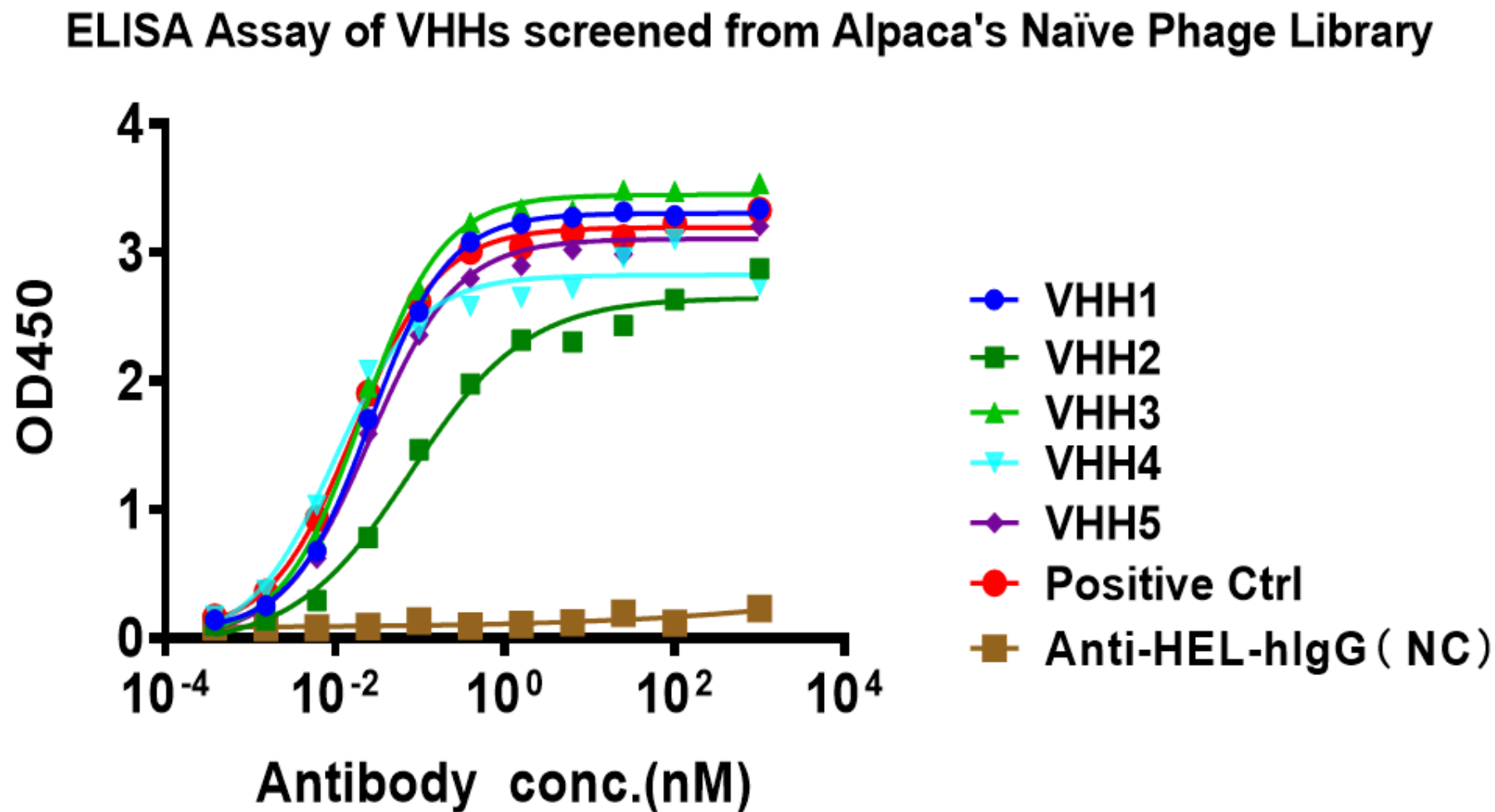
Plate ID	Total colnes	OD450 > 0.5	Ratio	OD450(BSA) > 0.1	Ratio	OD450 > 0.5&OD450(BSA)<0.1	Ratio
X/his -1LP	88	6	6.8%	6	6.8%	0	0.0%
X/his -2LP	88	29	33.0%	0	0.0%	29	33.0%
X/his -3LP	88	72	81.8%	1	1.1%	71	80.7%

	Total clones	X-specific binder	X-specific binder /total clone	Unique seq.	Unique seq. /total clones
X/his -LP	264	100	37.8%	18	6.82%

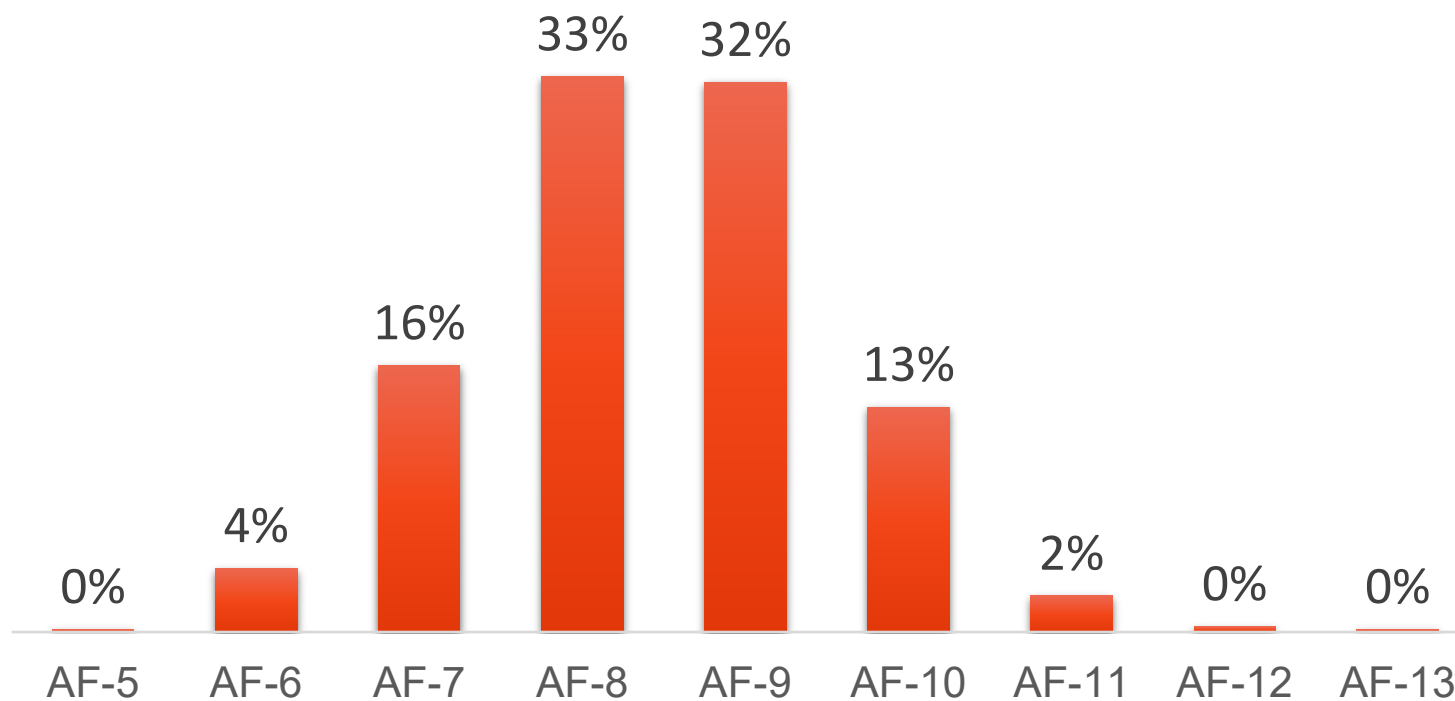
100 positive clones identified, resulting in **18** unique sequences,
followed by VHH antibody express & characterization.

ELISA Binding Assay of Top 5 VHH Antibodies

Antibody	EC50
VHH1	0.02569
VHH2	0.07843
VHH3	0.02072
VHH4	0.009848
VHH5	0.02563
Positive Ctrl	0.01688
Anti-HEL-hIgG (NC)	~ 1.335e+15



Affinity Distribution of 615 Delivered VHH sequences

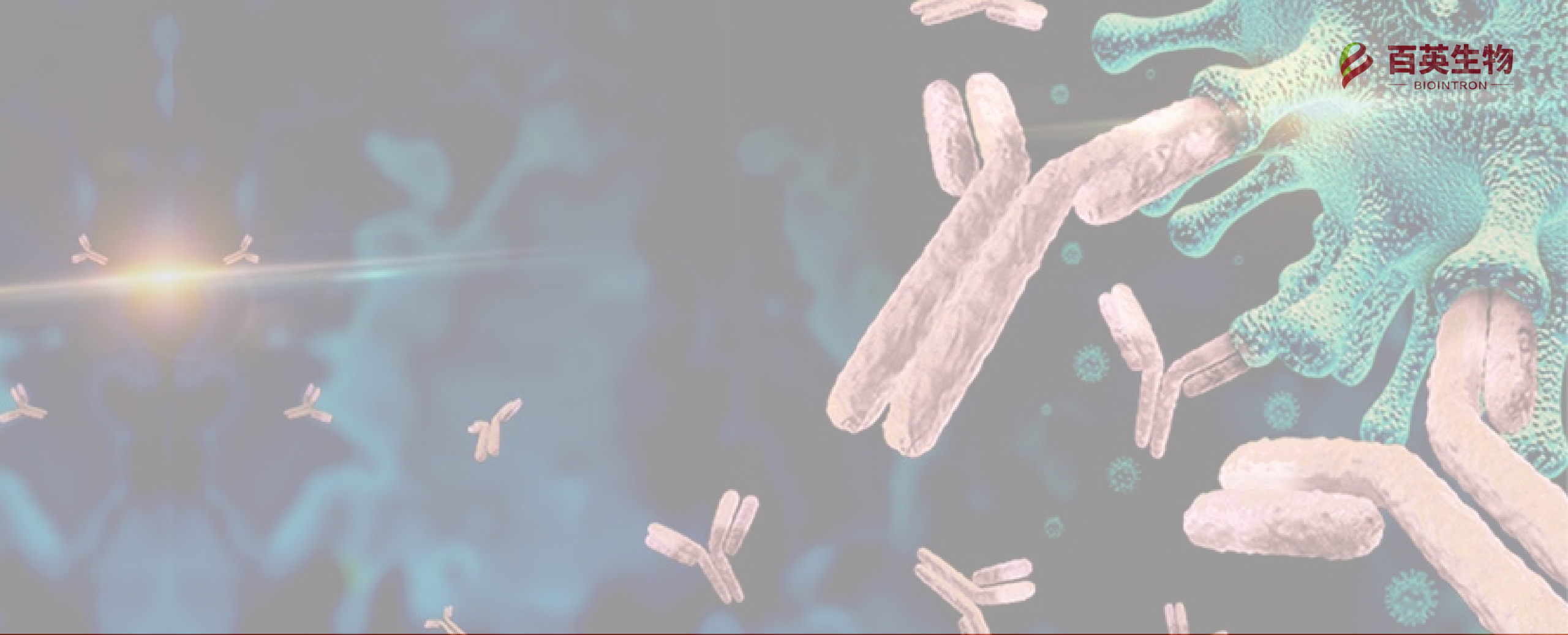


Data from 615 unique sequence of VHH

Total number of VHH from different targets with an affinity of 10^{-8} M or better

Total number of VHH from different targets (615 unique sequence)

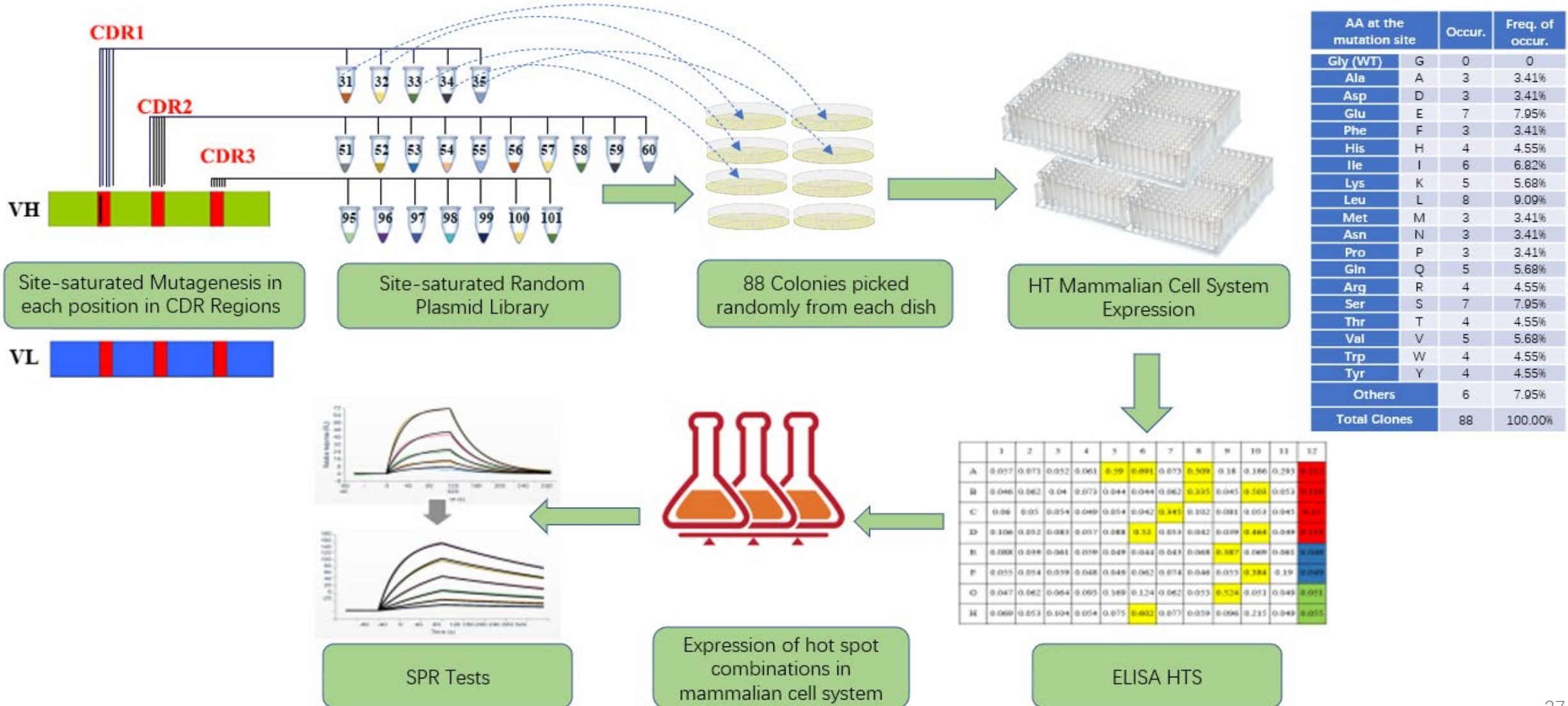
= 80%

The background features a 3D illustration of several Y-shaped antibodies in light blue and yellow, floating in a dark blue space. On the right side, there is a large, detailed illustration of a virus with a green, textured surface and multiple protruding spikes. A bright yellow light source is visible on the left, creating a lens flare effect.

FCMES-AM

Affinity Maturation Platform for Antibody Optimization

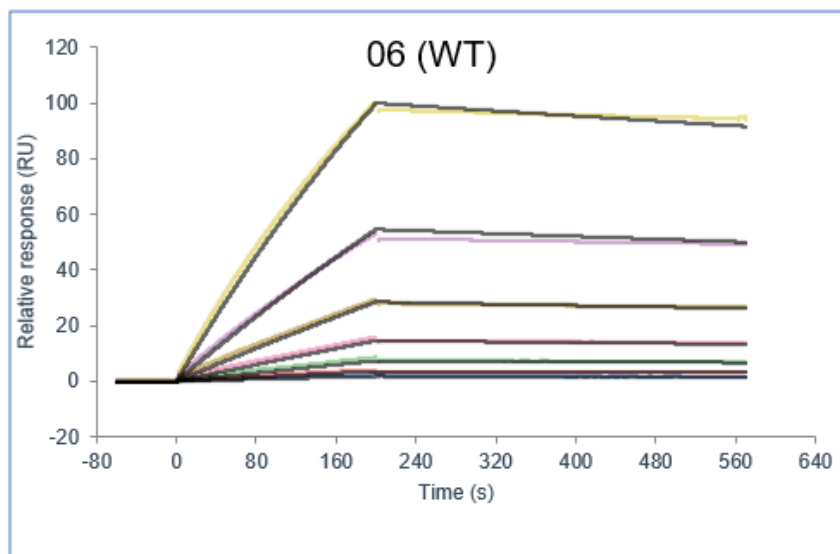
Full Coverage Mammalian Expression System For Affinity Maturation



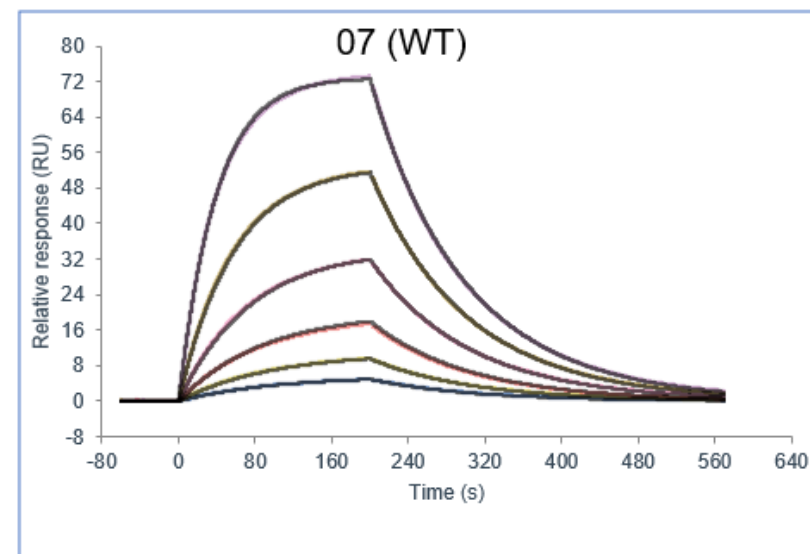
Challenge - Nanobodies



Possible to improve low-affinity nanobodies?
Possible to improve K_{on} or K_{off} specifically?



2.50×10^{-8} M

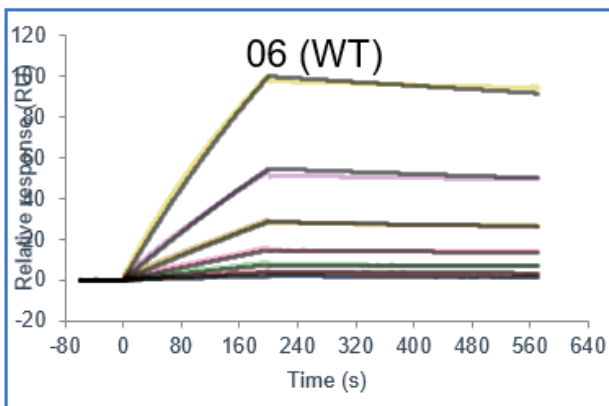


3.03×10^{-8} M

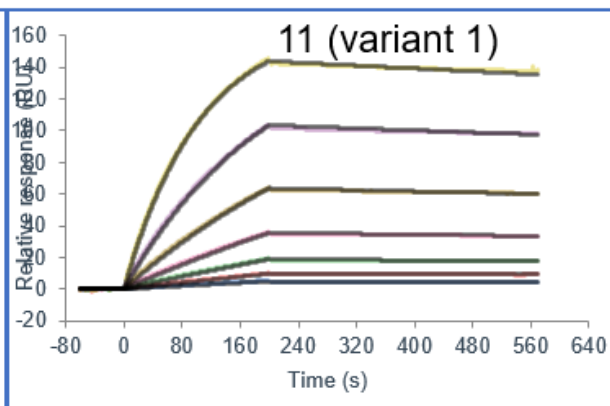
Case 1. VHH (K_{on} improved)

	AA position	Original AA	Mutated AA	OD450 (mutant)	OD450 (parental)
06 (VHH)	32	*	Y	0.434	0.143
	52	*	D	0.851	0.143
	105	*	E	0.482	0.143
	109	*	D	0.512	0.143
	111	*	D	0.419	0.143

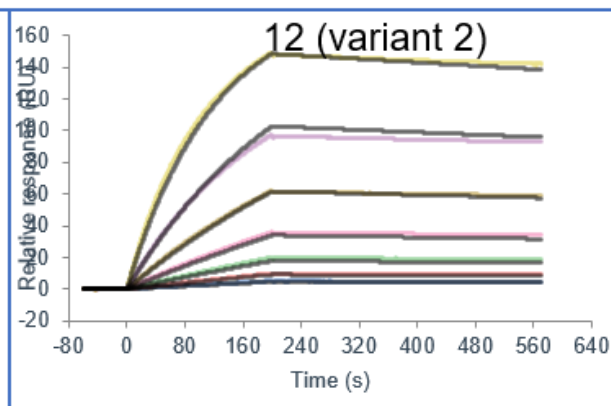
Ligand	k_a (1/Ms)	k_d (1/s)	KD (M)	Increased fold
11 (variant 1)	4.76E+04	1.66E-04	3.49E-09	7.16
12 (variant 2)	4.09E+04	1.89E-04	4.61E-09	5.42
16 (variant 3)	5.37E+04	1.57E-04	2.93E-09	8.53
06 (WT)	9.42E+03	2.36E-04	2.50E-08	1



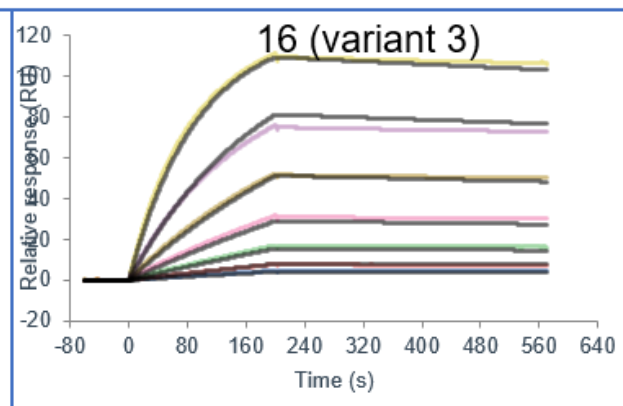
Parental



Affinity 7-fold ↑



Affinity 5-fold ↑

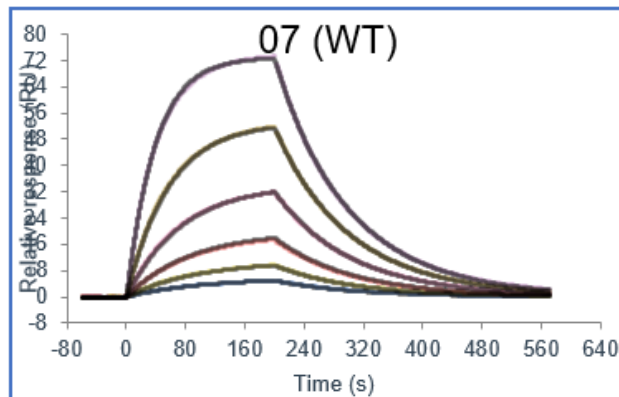


Affinity 8-fold ↑

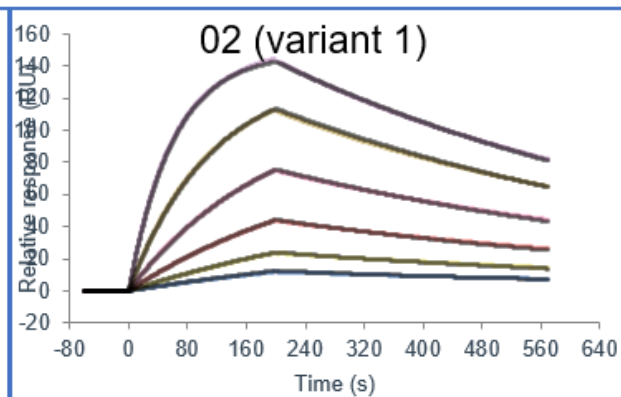
Case 2. VHH (K_{off} reduced)

	AA position	Original AA	Mutated AA	OD450 (mutant)	OD450 (parental)
07 (VHH)	40	*	A	0.363	0.134
	59	*	Q	1.647	0.173
	106	*	I	0.957	0.173
	108	*	T	0.543	0.173

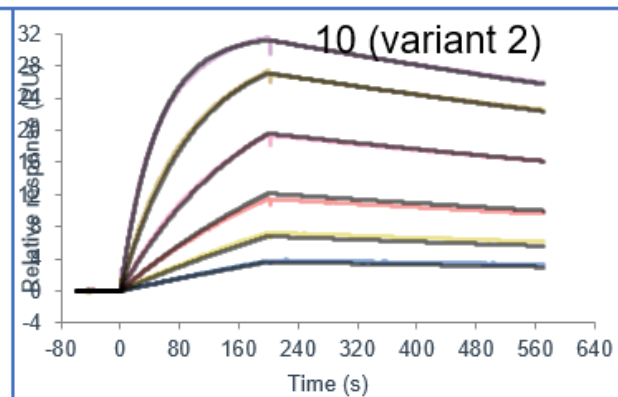
Ligand	k_a (1/Ms)	k_d (1/s)	KD (M)	Increased fold
02 (variant 1)	3.09E+05	1.55E-03	5.01E-09	6.05
10(variant 2)	3.96E+05	5.22E-04	1.32E-09	22.95
11(variant 3)	3.47E+05	5.48E-04	1.58E-09	19.18
07 (WT)	3.73E+05	1.13E-02	3.03E-08	1.00



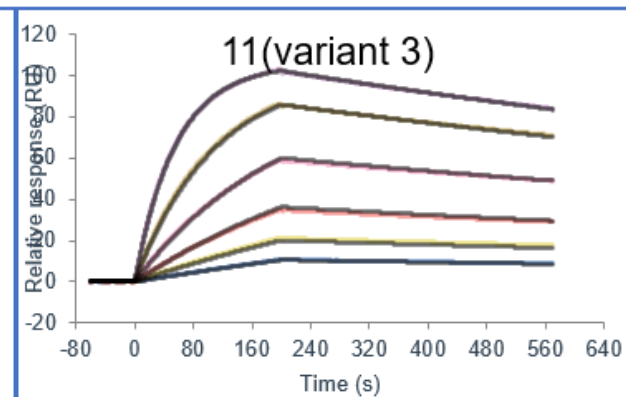
Parental



Affinity 6-fold ↑

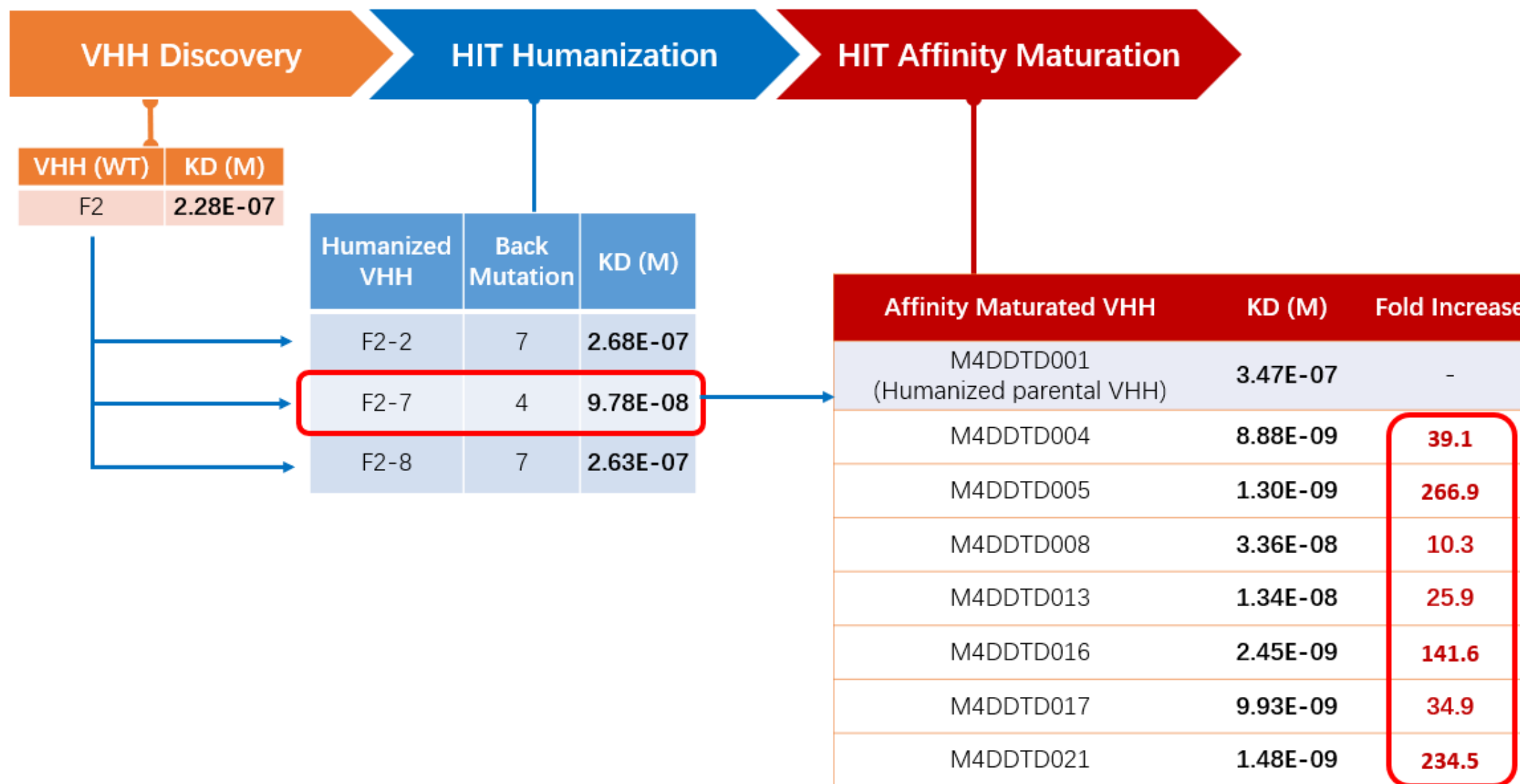


Affinity 23-fold ↑



Affinity 19-fold ↑

Case 3. VHH Affinity Maturation after Humanization

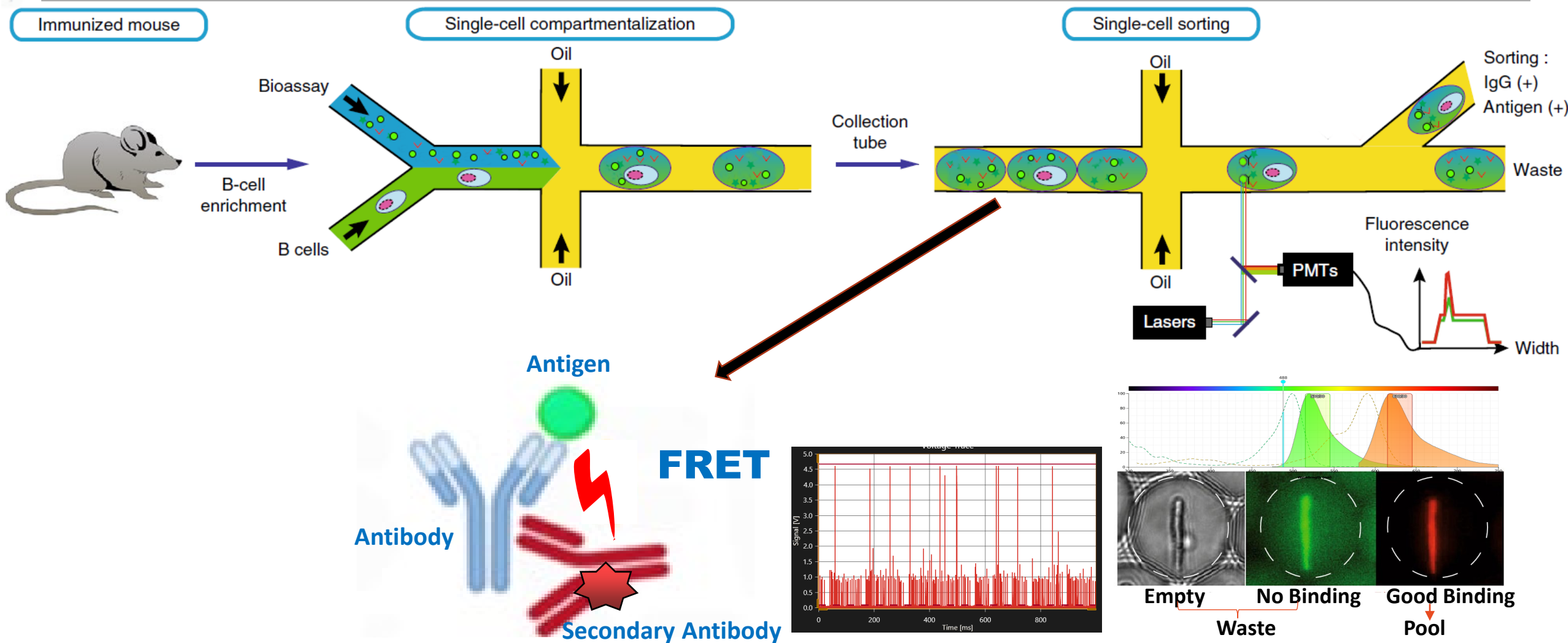




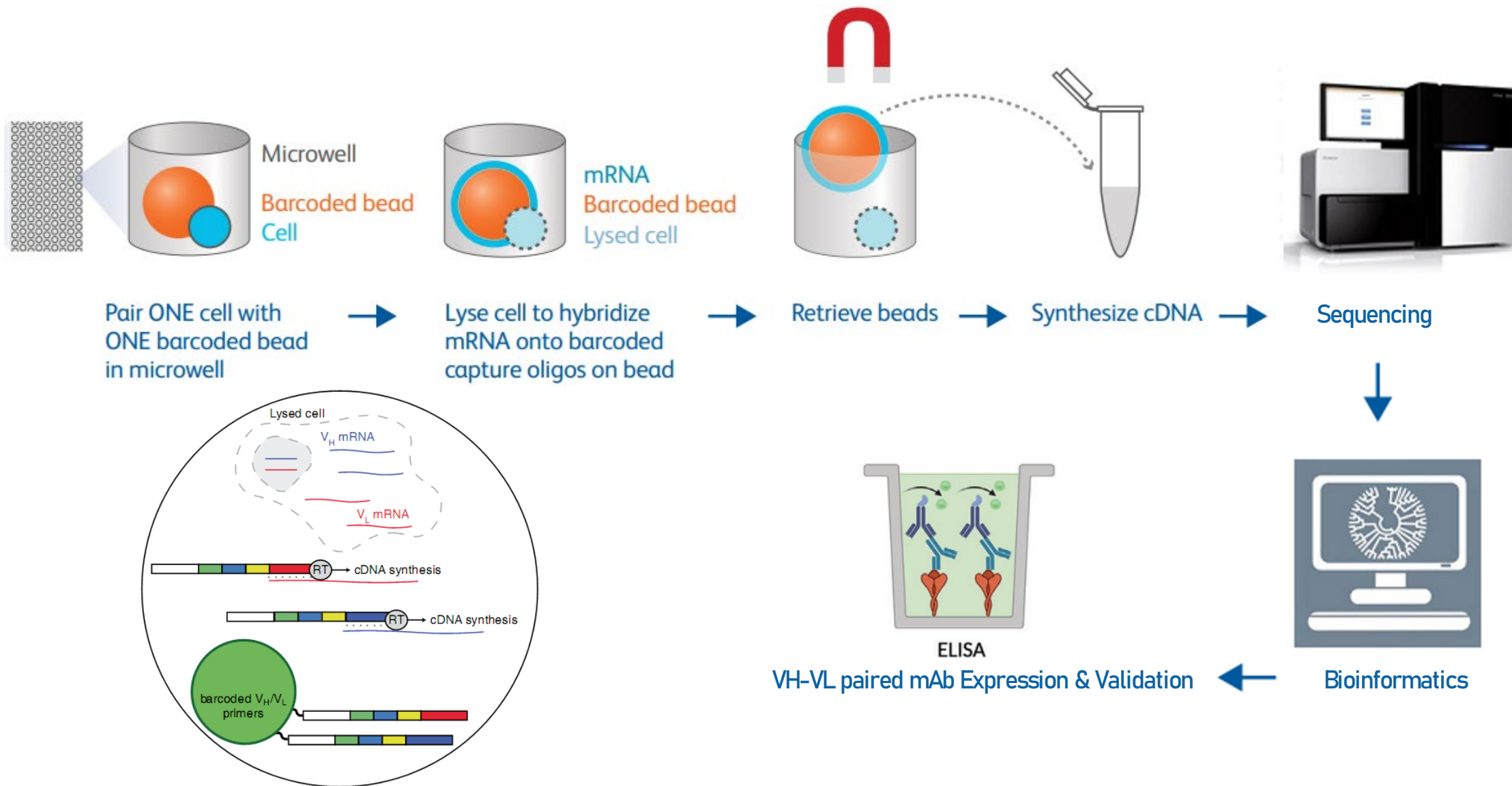
Single B Cell Platform

Ultra-fast Antibody Sorting Platform

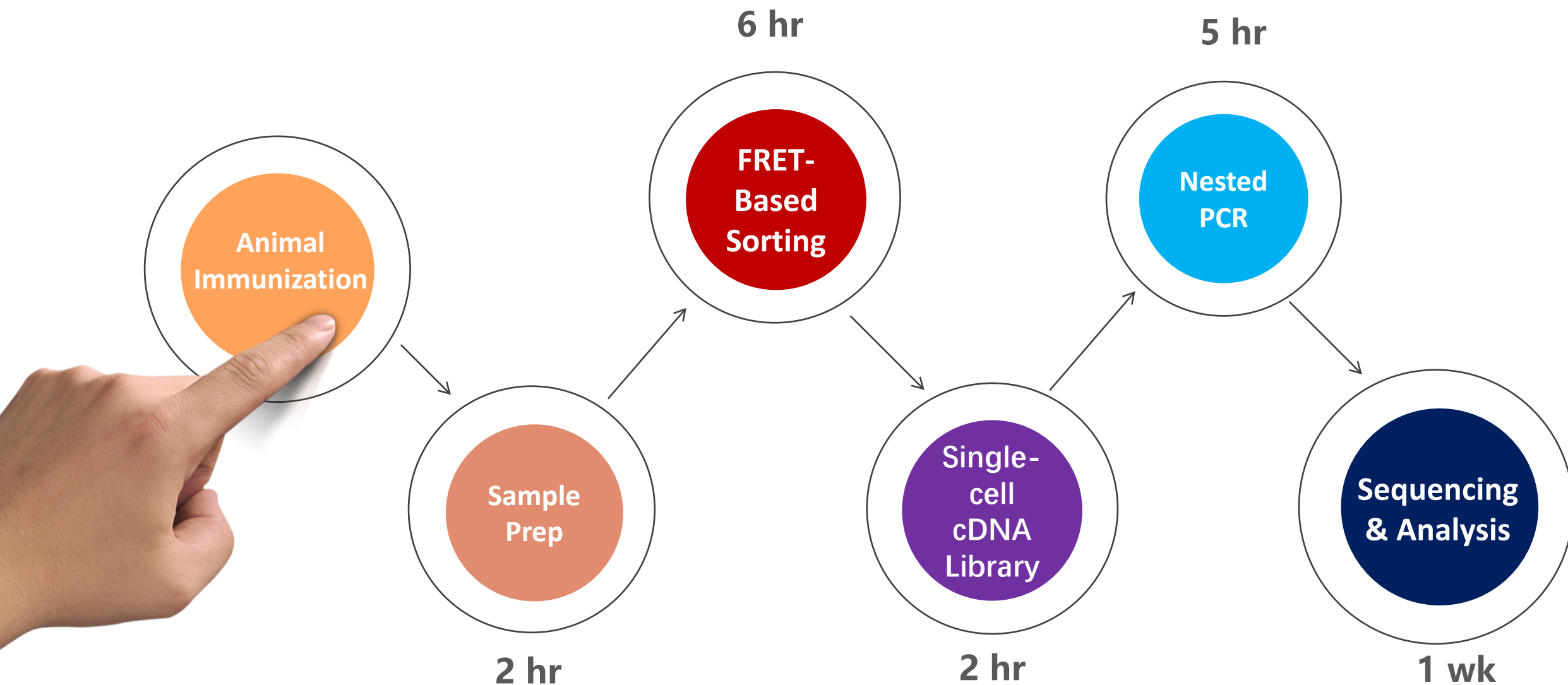
Single B Cell Sorting



Single B Cell Analysis & Validation



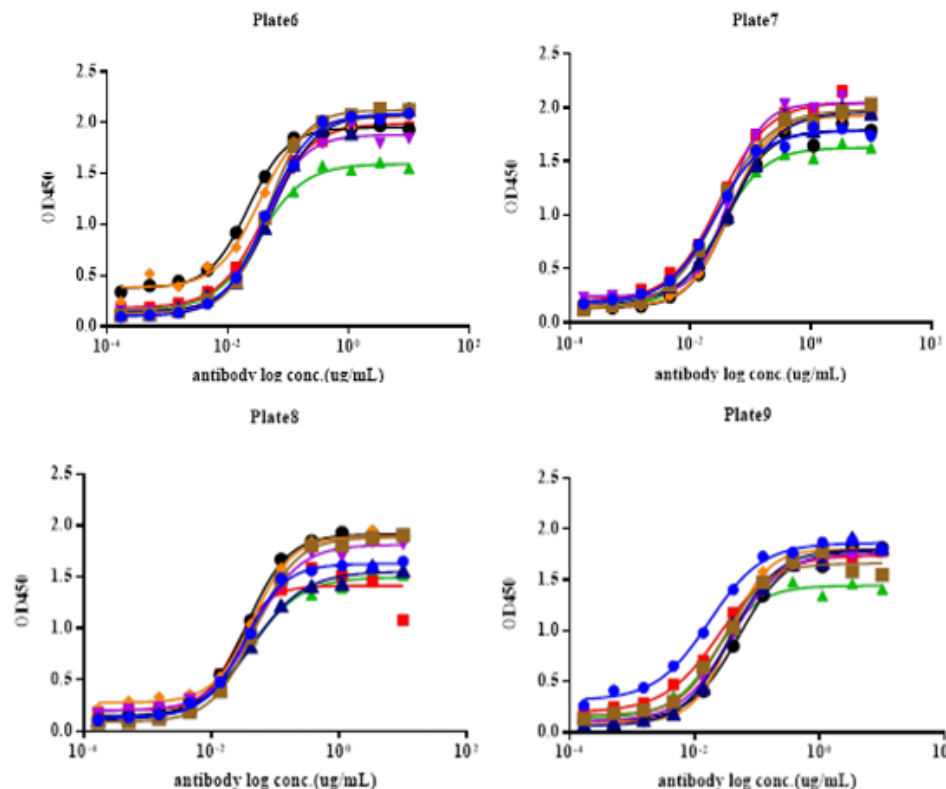
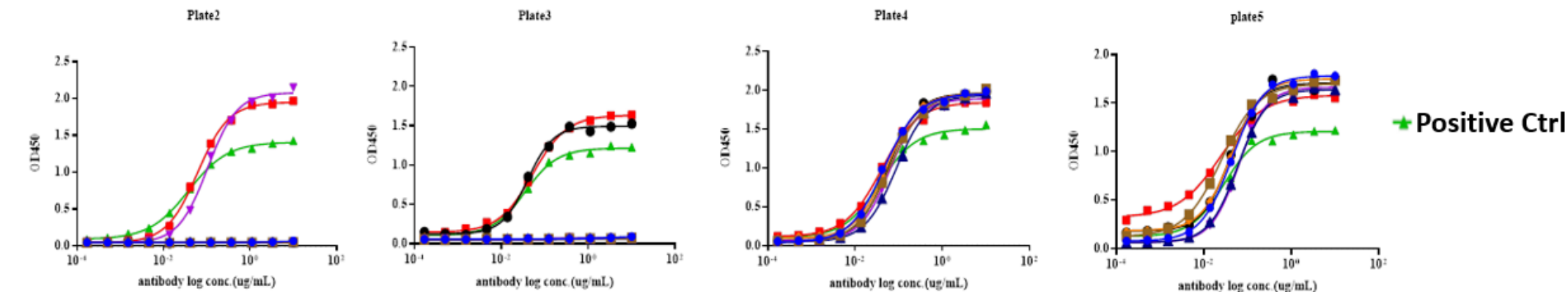
Single B cell Antibody Discovery



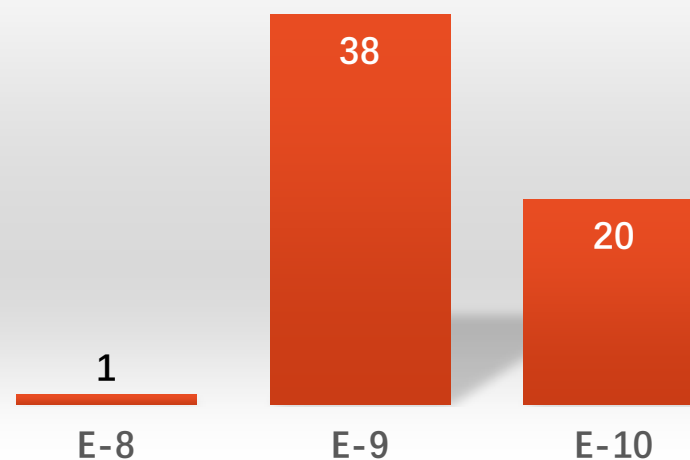
Paired Heavy & Light Chains

Unique Barcode	Locus	FWR1	CDR1	FWR2	CDR2	FWR3	CDR3	FWR4
AACCGCCTC.ATGAGTTAC.AAATGGAGG	Cluster5 TTCTACAA IGH	F01 97.874	TTCTACAA/N	TTTACTGATGGA		AGTAGTTAGAC		GPPELVKPGA
AACCGCCTC.ATGAGTTAC.AAATGGAGG	Cluster6 AACTGGCT IGK	F01 100	ACTGGCTTD	TGTAAG/AGGCA		ACGTAGTAAGAI		NHVCBGE
AACGTGATT.TAGTCTTGA.CTATTAGCC	Cluster9 GATGAGCT IGH	F01 98.148	GATGACTTT	TCACAA/CAGGA		TCCGACGGGAC		GPPELVKPGA
AACGTGATT.TAGTCTTGA.CTATTAGCC	Cluster2 CAAAGTCT IGK	F01 100	GTCTCCAA/P	CAGTTCTGCAAG		TCACATGCTCAI		PLSCLSVLEI
ACAAGGATC.ACCAAATG.AGTTGCATC	Cluster1 GCATCCAC IGK	F01 97.368	TGCATCCAI	GTAGCAC/CAGG		TCATAGCACIAI		CSWLCRRT
ACAAGGATC.ACCAAATG.AGTTGCATC	Cluster5 TACAATCA IGH	F01 100	TACAATCGI	TTACCA/CTGGA		CATATAGGTAAC		AAELVRSQA
ACACACAAA.AGGAGGCGC.TGTCATCA	Cluster2 ACTTCAAC IGH	F01 94.643	ATGACTTC/I	TCACAA/GAAA		TCCGACGGGAC		GPPELVKPGA
ACACACAAA.AGGAGGCGC.TGTCATCA	Cluster4 CTTGGAAC IGK	F01 92.5	CTTGGAA/G	ACTAGC/CAGG		TCAGTTATCTGA		TSLASLGD
ACCAAGGAC.AATCAGTTT.ATATTGTAA	Cluster3 CTTCTTAC IGH	F01 100	ACTTCTAC/I	TTTACTCATGG		AGTAGCTAGACI		SELVKNPGAS
ACCAAGGAC.AATCAGTTT.ATATTGTAA	Cluster8 CTGGGCT IGK	F01 95.852	CCTGGGCT/P	AGCTC/AGCCA		ACTCTCACAATC		ATTSASLGEI
AGAAGCACT.TTCCATTGA.CAACCTCCA	Cluster9 AGTCTATC IGK	F01 100	AGTCTATC/I	TTGGCA/CAAAI		TAATAGCTGGAC		NLSVSPGER
AGAAGCACT.TTCCATTGA.CAACCTCCA	Cluster5 TTCTACAA IGH	F01 97.874	TTCTACAA/I	TTTACTGATGGA		AGTAGCTAGCC		GPPELVKPGA
AGCACACAG.TAGGGATAC.CAATAGGGT	Cluster4 TTCTACAA IGH	F01 100	TTCTACAA/N	TTTACTGATGGA		AGTAGCTAGACI		GPPELVKPGA
AGCACACAG.TAGGGATAC.CAATAGGGT	Cluster10 GAGTCTAT IGK	F01 100	GAGTCTAT/Y	TTGGCA/CAAAI		TAATAGCTGGAC		NLSVSPGER
AGCACACAG.TTCATTGA.CAACCTCCA	Cluster1 AGTCTATC IGK	F01 100	AGTCTATC/I	TTGGCA/CAAAI		TAATAGCTGGAC		NLSVSPGER
AGCACACAG.TTCATTGA.CAACCTCCA	Cluster2 TTCTACAA IGH	F01 100	TTCTACAA/N	TTTACTGATGGA		AGTAGCTAGACI		GPPELVKPGA
AGCCCAATC.ACITTAAC.TGAACGACAA	Cluster2 TTCTACAA IGH	F01 100	CTTTCTACAY	TTTACTGTGGAA		CAGTAGCTAGACI		GPPELVKPGA
AGCCCAATC.ACITTAAC.TGAACGACAA	Cluster4 ACATCCAA IGK	F01 100	SCATCCAA/I	ACATCTCAGGA		C/GGGAGATZAI		TILAVSLGQI
ATGTAATGG.ACCAGGTGT.ATCAGTCT	Cluster1 ACTACAAT IGK	F01 100	ACTACAATIG	TCACCA/CTGGA		ACTATGGTAAC		AAELVKNPA
ATGTAATGG.ACCAGGTGT.ATCAGTCT	Cluster4 CTGGGCT IGK	F01 100	CCTGGGCTT/I	TGTTCTC/CAGG		CTATCGTTCCAI		IMASLGEI
CAAACCGCC.TCGTTAGCA.GAACGACAA	Cluster6 CSAGGTAT IGH	F01 95.918	CCGAGCTE	TTCACTCTGGA		CATGGGACCCT		CAEMARPG
CAAACCGCC.TCGTTAGCA.GAACGACAA	Cluster6 TTCCAAAC IGK	F01 100	TTTCCAAAC/I	AGTAATCAGGO		CAACATGTTCAI		CLSVSLGD
CAGCAAGAT.TTCCATTGA.GGTGAGTTA	Cluster9 AGTCTATC IGK	F01 100	AGTCTATC/I	TTGGCA/CAAAI		TAATAGCTGGAC		NLSVSPGER
CAGCAAGAT.TTCCATTGA.GGTGAGTTA	Cluster5 TTCTACAA IGH	F01 97.874	TTCTACAA/I	TTTACTGATGGA		AGTAGCTAGCC		GPPELVKPGA
CTACAGAAC.TACTAGTCA.CGTCTAGGT	Cluster1 CAAACTG IGK	F01 91.428	AAACTGG/K	AAGTTA/CAGG		TACTGATCAI		NITAA/SPGQ
CTACAGAAC.TACTAGTCA.CGTCTAGGT	Cluster2 TTCTACAA IGH	F01 100	CTTTCTACAY	TTTACTGCCATGA		ACAGCTAGTACI		GPPELVKPGA
GACGGATTA.AGATAGTTC.TGTATGCGA	Cluster9 ACCTATAT IGK	F01 100	ACCTACTATG	TCAGGT/CAGAG		GTGATTTCAC		TGLVKNPGG
GACGGATTA.AGATAGTTC.TGTATGCGA	Cluster2 TTCTGAGT IGK	F01 100	CTTCTGAGT	TTGGCA/GAAC		TAGCATCAACAI		RAISVESRR
GACGGATTA.AGCGACACC.AAGCCTTCT	Cluster9 ACTTTACA IGK	F01 92.108	CTTTACAC/Y	ATTAGCCACAI		TGTAAACCTNA		TSLASLGI
GACGGATTA.AGCGACACC.AAGCCTTCT	Cluster6 CTACAAC IGH	F01 97.874	TTCTACAA/I	TTTACTGATGGA		AGTAGCTAGCC		SELVKNPGAS
GACGGATTA.TTCCATTGA.GAACGACAA	Cluster9 AGTCTATC IGK	F01 100	GAGTCTAT/Y	TTGGCA/CAAAI		TAACAGCTGGAC		NLSVSPGER
GACGGATTA.TTCCATTGA.GAACGACAA	Cluster4 TTCTACAA IGH	F01 100	TTCTACAA/N	TTTACTGATGGA		AGTAGCTAGACI		GPPELVKPGA
GAGCCAATA.CACCCAAAG.CAACGATCT	Cluster9 CTACAAC IGH	F01 100	CTACAACCG	TTTACTGATGGA		AGTAGCTAGACI		GPPELVKPGA
GAGCCAATA.CACCCAAAG.CAACGATCT	Cluster3 GCCTTCT IGK	F01 94.737	TTGGCTTCT	AAGTTCTCAGG		CTGTGGTTAGCI		NMSASPEK
GAGCCAATA.GAGTGGCAA.ACAAACTTT	Cluster1 CTACAAC IGH	F01 100	CTACAACCG	TTTACTGATGGA		AGTAGCTAGACI		GPPELVKPGA
GAGCCAATA.GAGTGGCAA.ACAAACTTT	Cluster3 CTACTGIG IGK	F01 97.059	CCTACTGGI	GTGAA/CAGG		CAACAGTACTAI		CRMSVGC
GAGTACATT.TACAGGATA.TGCATAGTA	Cluster2 CCTGGGCT IGK	F01 93.939	CTGGGCT/I	TGTAAGCCAGG		CTAGTAACGAI		IMASLGE
GAGTACATT.TACAGGATA.TGCATAGTA	Cluster6 TTCTACAA IGH	F01 100	TTCTACAA/N	TTTACTGATGGA		AGTAGCTAGACI		GPPELVKPGA
GCACTGTCA.AGCGACACC.CTAAGCTTC	Cluster2 ACTTGGAT IGK	F01 100	TGCATCCAI	GTAGCAC/CAGG		TTGCACTTTAIC		TQASMSVC
GCACTGTCA.AGCGACACC.CTAAGCTTC	Cluster7 TCATCAAC IGH	F01 97.874	CTTTCTACAY	TTTACTGTGGAA		AGTAGCCAGCC		SELVKNPGAS
GCACTGTCA.AGCGACACC.CTAAGCTTC	Cluster10 TCCAAAC IGK	F01 100	TTCCAAACD	CAGTTA/CTGGG		ACACATCAICAI		NLSCLSALEI
GGCAAGCAA.CACCCAAAG.ACAAACTTT	Cluster9 CTACAAC IGH	F01 100	CTACAACCG	TTTACTGATGGA		AGTAGCTAGACI		GPPELVKPGA
GGCAAGCAA.CACCCAAAG.ACAAACTTT	Cluster3 ATTAACAAT IGK	F01 93.794	ATTACACTV	ATTAGCCAGAT		CTACGCTTGN		TSLASLGC
TCCAGTCTGA.GTGTGTCGA.CAACCTCCA	Cluster5 CTATCTCT IGK	F01 100	AGCCTATCL	TTGGC/GAACAI		TTATACCTGGAC		NLSVSPGER
TCCAGTCTGA.GTGTGTCGA.CAACCTCCA	Cluster4 CTTCTTAC IGH	F01 100	ACTTCTAC/N	TTTACTGATGGA		AGTAGCTAGACI		SELVKNPGAS
TCCAGTCTGA.GTGTGTCGA.CAACCTCCA	Cluster9 AGTCTATC IGK	F01 100	AGTCTATC/I	TTGGCA/CAAAI		TAATAGCTGGAC		NLSVSPGER
TCCAGTCTGA.GTGTGTCGA.CAACCTCCA	Cluster4 TTCTACAA IGH	F01 100	TTCTACAA/N	TTTACTGATGGA		AGTAGCTAGACI		GPPELVKPGA
TGGCTCAGA.CACCCAAAG.CAACGATCT	Cluster9 CTACAAC IGH	F01 100	CTACAACCG	TTTACTGATGGA		AGTAGCTAGACI		GPPELVKPGA
TGGCTCAGA.CACCCAAAG.CAACGATCT	Cluster3 GCCTTCT IGK	F01 94.737	TTGGCTTCT	AAGTTCTCAGG		CTGTGGTTAGCI		NMSASPEK
TGTACCTTA.TTCATTGA.CAACCTCCA	Cluster9 AGTCTATC IGK	F01 100	AGTCTATC/I	TTGGCA/CAAAI		TAATAGCTGGAC		NLSVSPGER
TGTACCTTA.TTCATTGA.CAACCTCCA	Cluster2 TTCTACAA IGH	F01 97.874	TTCTACAA/N	TTTACTGATGGA		AGTAGCTAGACI		GPPELVKPGA

Case: High Affinity PD-1 Antibodies Identified

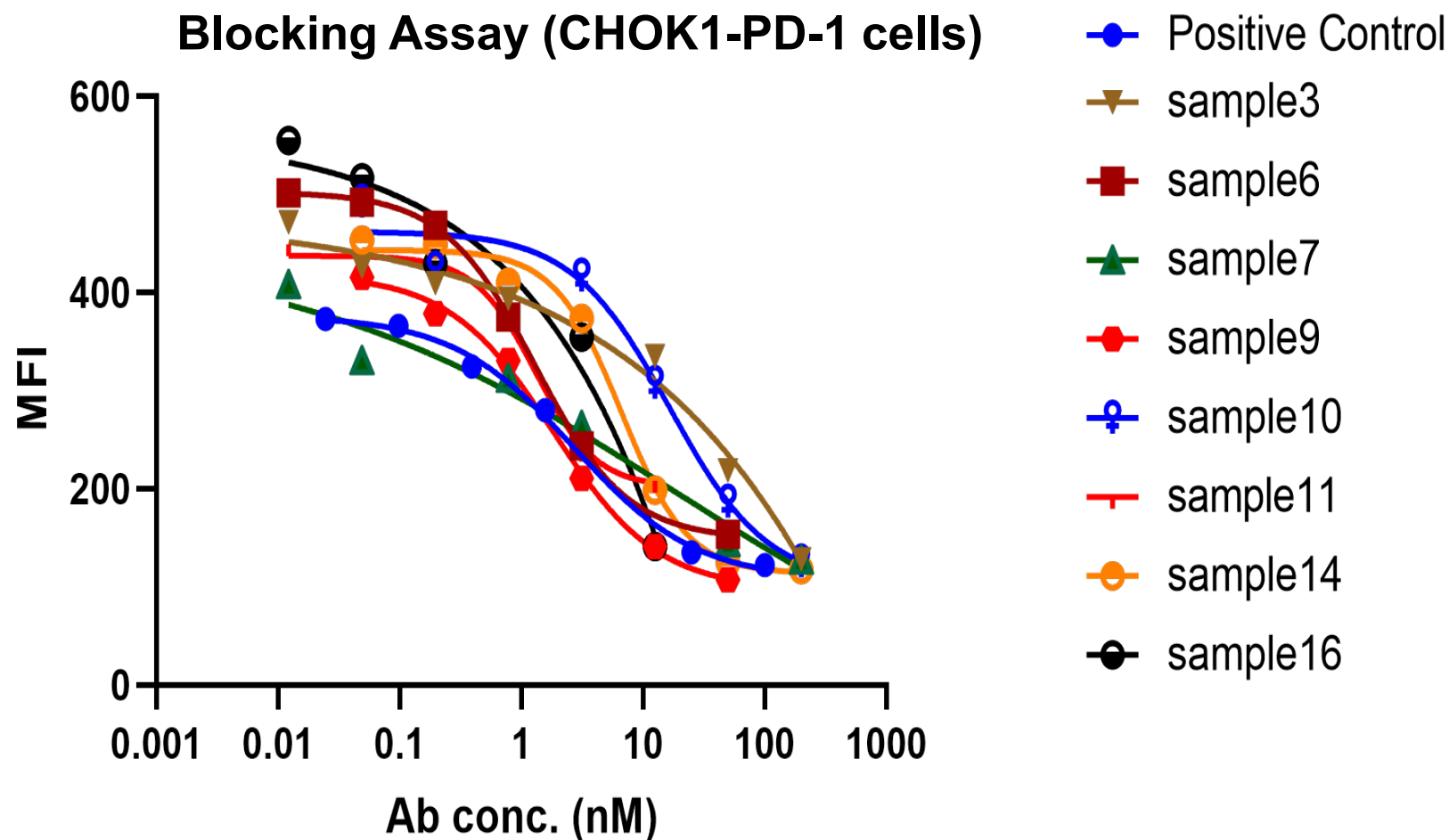


Affinity Distribution



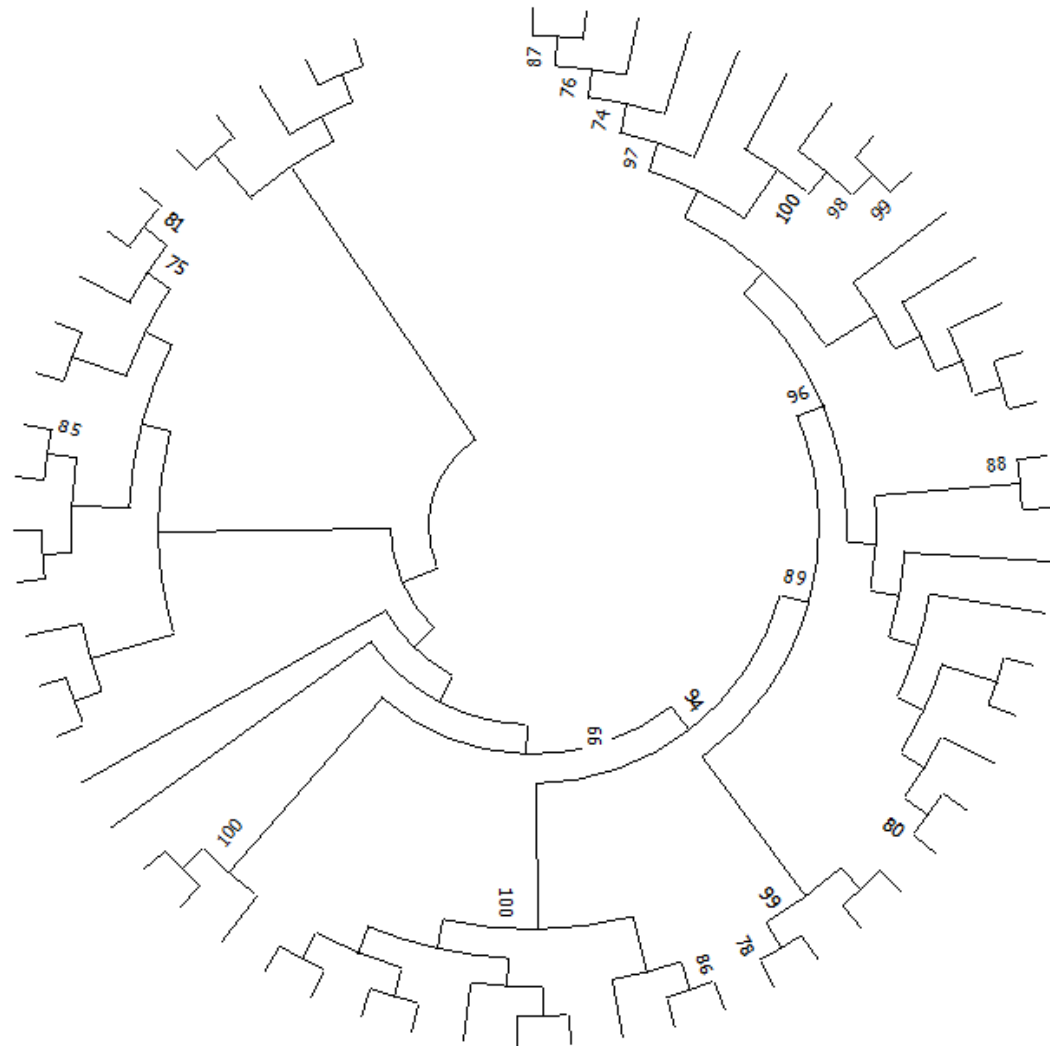
Antigen PD-1 → 59/62 positive

8 PD-1 Antibodies with Blocking Effect Identified



Blocking: 8 positive

ase: HT





Thank You!

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