



Ab Studio Inc.

your partner for therapeutic antibody development

www.antibodystudio.com

Development of Novel Therapeutic Antibodies via Computational Design

*by Yue Liu, Ph.D.
Ab Studio Inc.*

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Unique feature of Ab Studio Inc.

A novel biotech platform company with promising therapeutic antibody programs

We have invented the following three novel platforms via computational design:

- 1) “Imbalanced” bispecific antibody platform
- 2) “Serial” internalization antibody platform
- 3) “Catalytic” antibody platform

We deeply believe in the “quality by design” concept and wish our work can help addressing unmet clinical needs.



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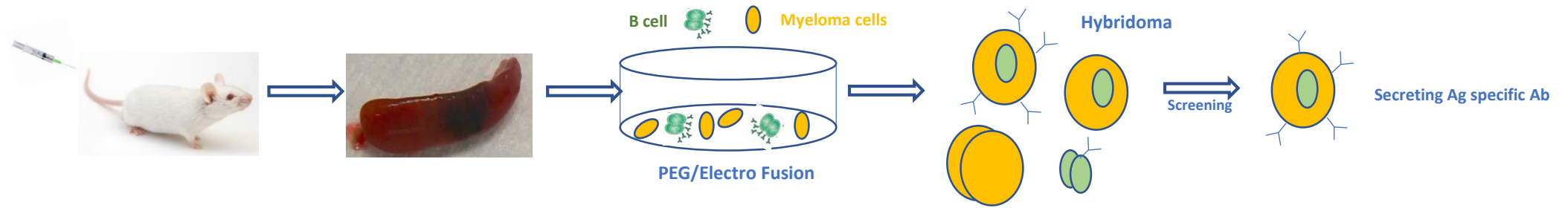
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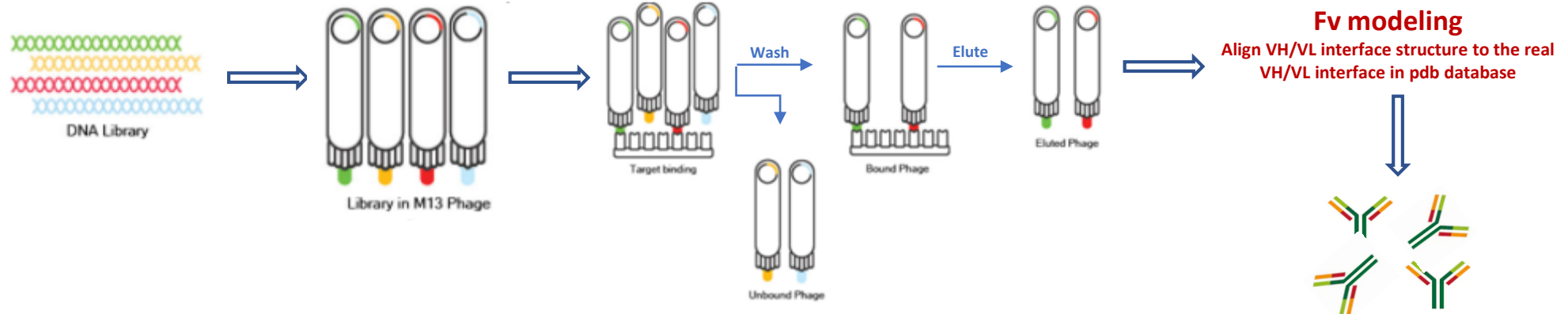
Introduction of Ab Studio's novel therapeutic antibody discovery platforms

Basic technologies:

Platform I- Hybridoma



Platform II- Phage display





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Hybridoma + Computational Design:

- 1) Apply computer aided modeling to identify epitopes exposed on 3D surface of antigen
- 2) Based on target biology, 3D information and bioinformatics (such as cross-species homology), design and apply appropriate strategy for immunization
- 3) Based on target biology and target protein structure, design and apply high throughput binding assay, functional assay and epitope bin assay to screen the best functional antibody
- 4) Align the sequences of several “best functional antibodies” to get “best developable antibodies” by screening candidates with: high “human score” + less immunogenicity epitopes + less PTMs



Unique features for phage display technology:

- 1) In house developed 10e9 human naïve ScFV phage library with a restriction enzyme site between VH and VL. Therefore, VH and VL can be replaced separately (suitable for common light chain screening)
- 2) Leading phage screening not only based on antigen binding ability pre and post heating, but also based on ScFV seqs' other develop-ability features. **After building up a Fv model structure, we study**
 - **Aggregation surface on Fv model**
 - **PTMs on Fv model**
 - **Immunogenicity epitopes inside ScFV sequence**
 - **“Naturalness” of VH/VL interface by aligning the query ScFV’s VH/VL interface to that of real 3D antibody structures in the pdb database**



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Antibody Humanization and Optimization

We balance:

Humanization percentage

CDR Immunogenicity

Antigen binding affinity

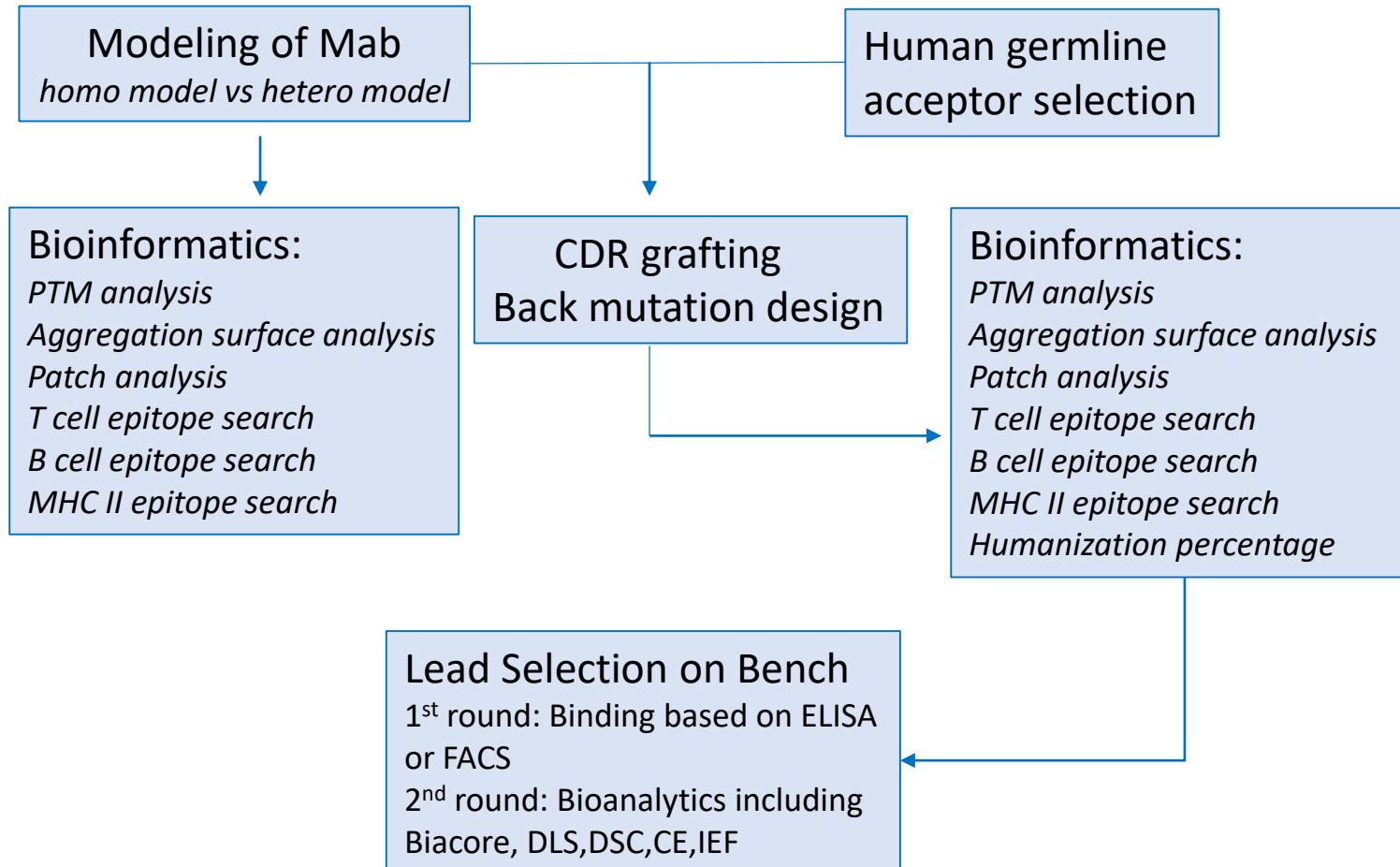
Antibody expression level

Aggregation potential

Antibody stability

Heterogenicity

Workflow of Antibody Humanization and Optimization



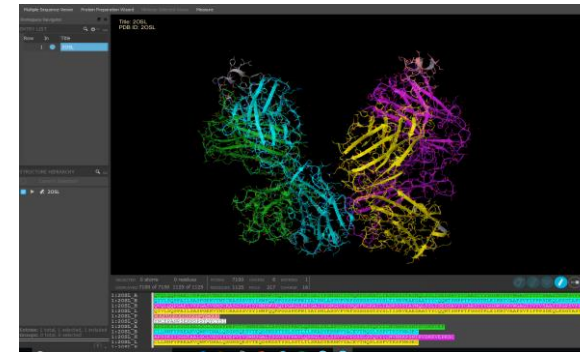


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Molecular Modeling and 3D Surface Analysis



Protein Surface Analyzer

Use structure from: Workspace Analyze Settings...

Patch Browser Aggregation Reactive Residues Properties

Highly Surface Exposed Patch Residues

Arg Cys Trp Tyr Deulfide bond

Deamidation site Glycosylation site Proteolysis site Oxidation site

Minimum side chain accessibility: 20.0%

Residue	Patch	Side Chain Accessibility	Disul.	Deam.	Glyc.	Prot.	Oxid.
A:TYR101	3	36.7%					X
B:TYR48	3	22.1%					X
Q:ASN176	4	53.5%		X			
A:ASN55	4	36.6%		X			
B:ARG24	6	49.5%					
A:ARG43	6	39.2%					
	6	60.8%					

List patch type: Positive Negative Hydrophobic Only selected patches

Export...

Protein Surface Analyzer

Use structure from: Workspace Analyze Settings...

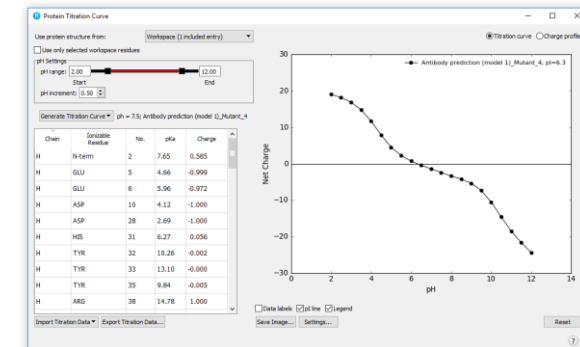
Patch Browser Aggregation Reactive Residues Properties

Residue Aggregation Profiles

Residue	Topo	Patch	Size (Å ²)	Score	Contribution (cal/mol)	Zygg	Agg	Side Chain Accessibility
Q:PRO178	N/A	1	57.2	44.005	12.77	-2.236	-0.476	54.3%
Q:SER177	N/A	1	57.2	44.005	8.65	-2.624	-0.630	30.2%
A:TYR101	N/A	2	36.6	17.008	9.93	-0.208	0.266	36.7%
A:GLY104	N/A	2	36.6	17.008	7.08	0.638	-0.142	89.0%
A:LYS74	N/A	3	650.1	736.249	120.23	-1.114	-0.678	43.4%
A:GLN1	N/A	3	650.1	736.249	117.57	-0.503	-0.115	68.4%
A:LYS23	N/A	3	650.1	736.249	89.25	-0.297	-0.190	38.6%
A:GLM3	N/A	3	650.1	736.249	35.91	-0.503	-0.144	40.0%

List patch type: Positive Negative Hydrophobic Only selected patches

Export...





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Immunogenicity Epitope Scan

The screenshot displays the Ab Studio software interface for an immunogenicity epitope scan. The main window shows two protein chains: 2OSL:L, 2OSL:B (left) and 2OSL:H, 2OSL:A (right). The analysis tracks include:

- Features - Author annotations
- Disulfide
- Modifications - SUMOylation
- B-cell epitopes - DNASTAR
- MHC II epitopes - Sette
- Antigenicity - Jameson-Wolf
- Antigenicity - Welling
- T-cell epitopes - AMPHI
- T-cell epitopes - Rothbard-Taylor

The right-hand panel shows the 'Immunogenicity' settings, which are currently checked for:

- Antigenicity
- B-cell epitopes (DNASTAR)
- MHC II epitopes (Sette)
- T-cell epitopes

The bottom panel shows the 'LIGHT CHAIN OF THE RITUXIMAB FAB FRAGMENT (2OSL:L)' with the amino acid sequence: Q I V L S Q S P A I L S A S P G E K V T M T C R A S S S V S Y I H W F Q Q K P G S S P K P W I Y A T S N L A S G V P V R F S G S G S G T S Y S L T I S R V E A E D A A T Y Y C Q Q W T S N P P T F G G G T K L E I K R T V A. A ruler below the sequence indicates positions from 10 to 110.



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Novel platform 1:

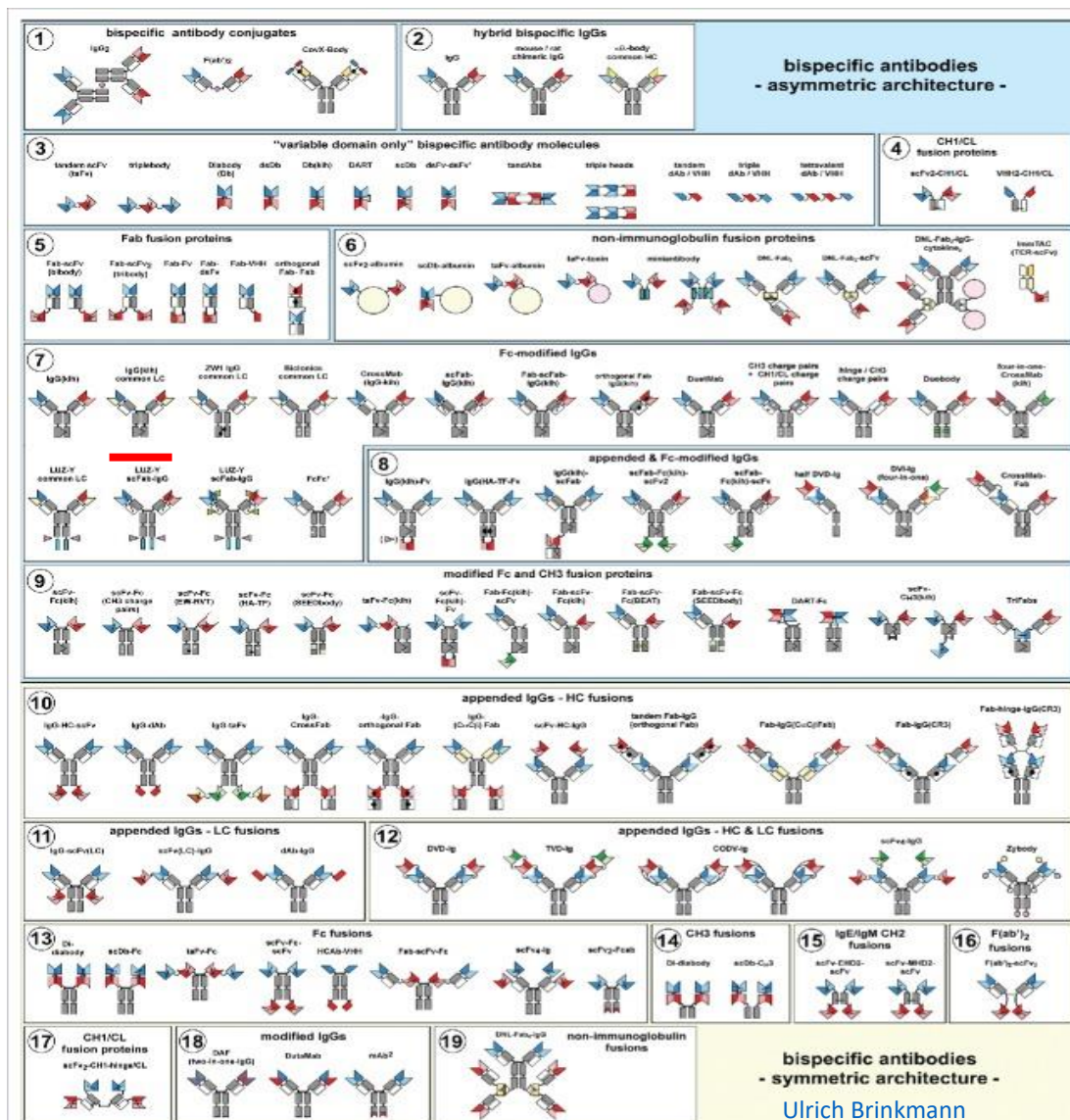
Imbalanced Bispecific Antibody Technology Platform



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https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5297537/

Only a few platforms meet the following criterias:

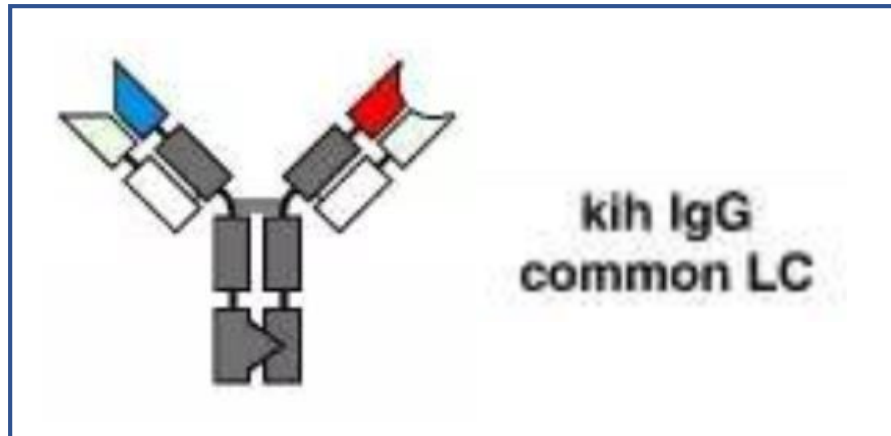
- 1) Free to operate
- 2) No extra immunogenicity and developability concerns
- 3) No PKPD concerns

“Knob into hole” + Common LC format is an one meets the above criterias

Imbalanced Bispecific Antibody Technology Platform

What is an imbalanced bispecific antibody?

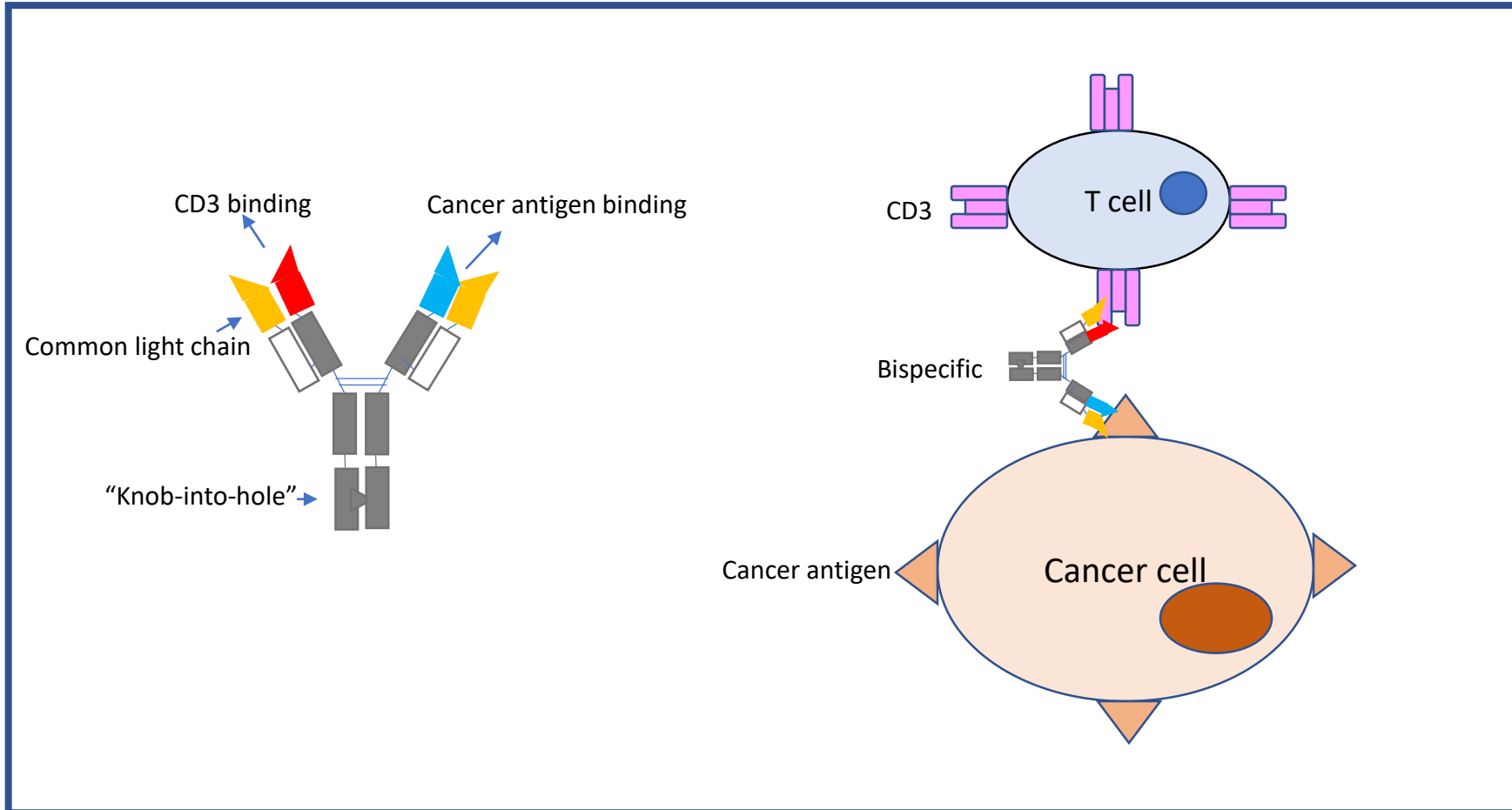
- A “Knob-into-hole plus common LC” version allowing two arms to have very different binding affinity to each one’s own antigen (natural IgG structure and half life).



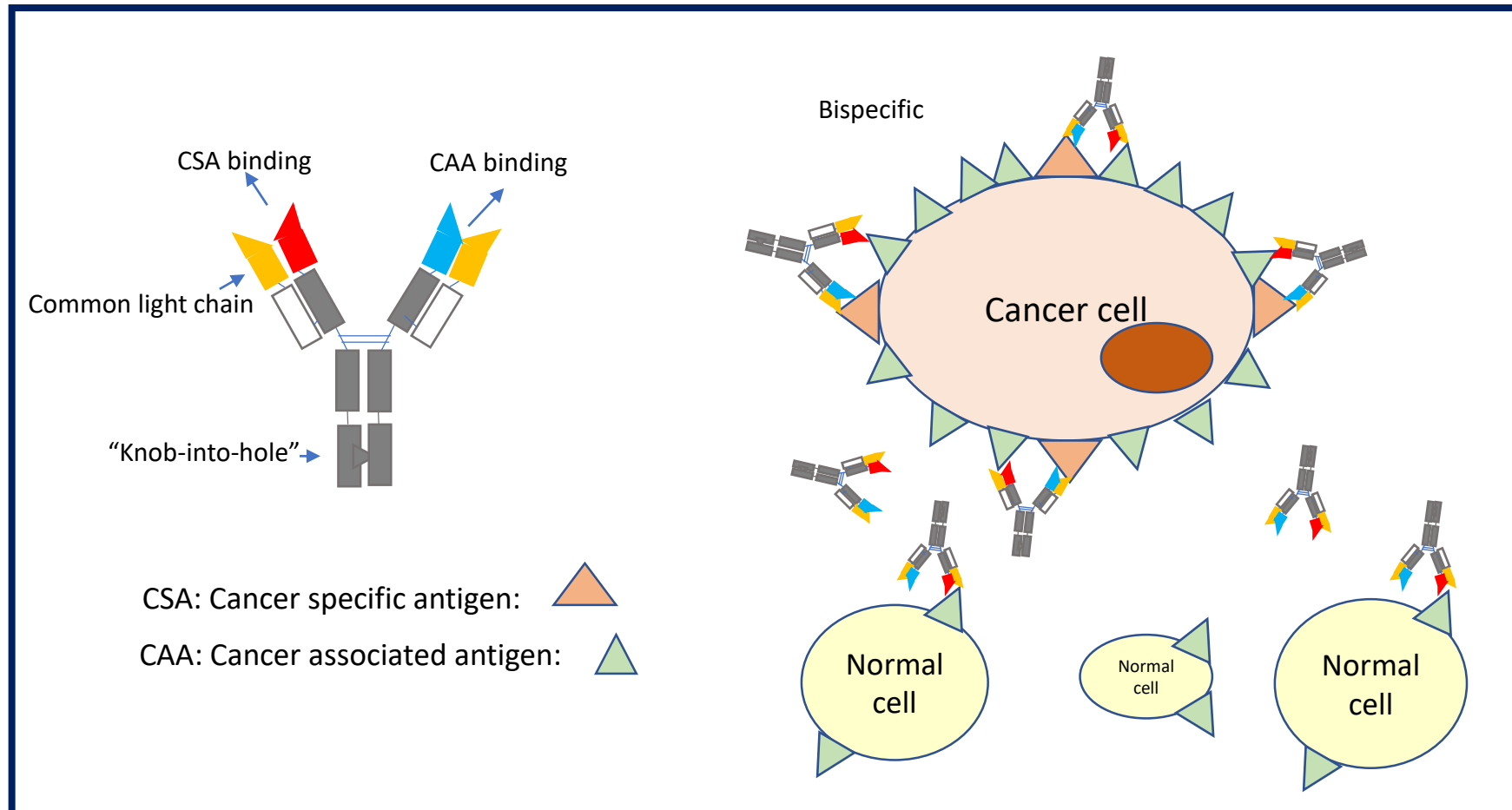
Why “imbalanced”?

- Imbalanced binding affinity is required for some bispecific therapeutic antibodies’ Mechanism of Action.

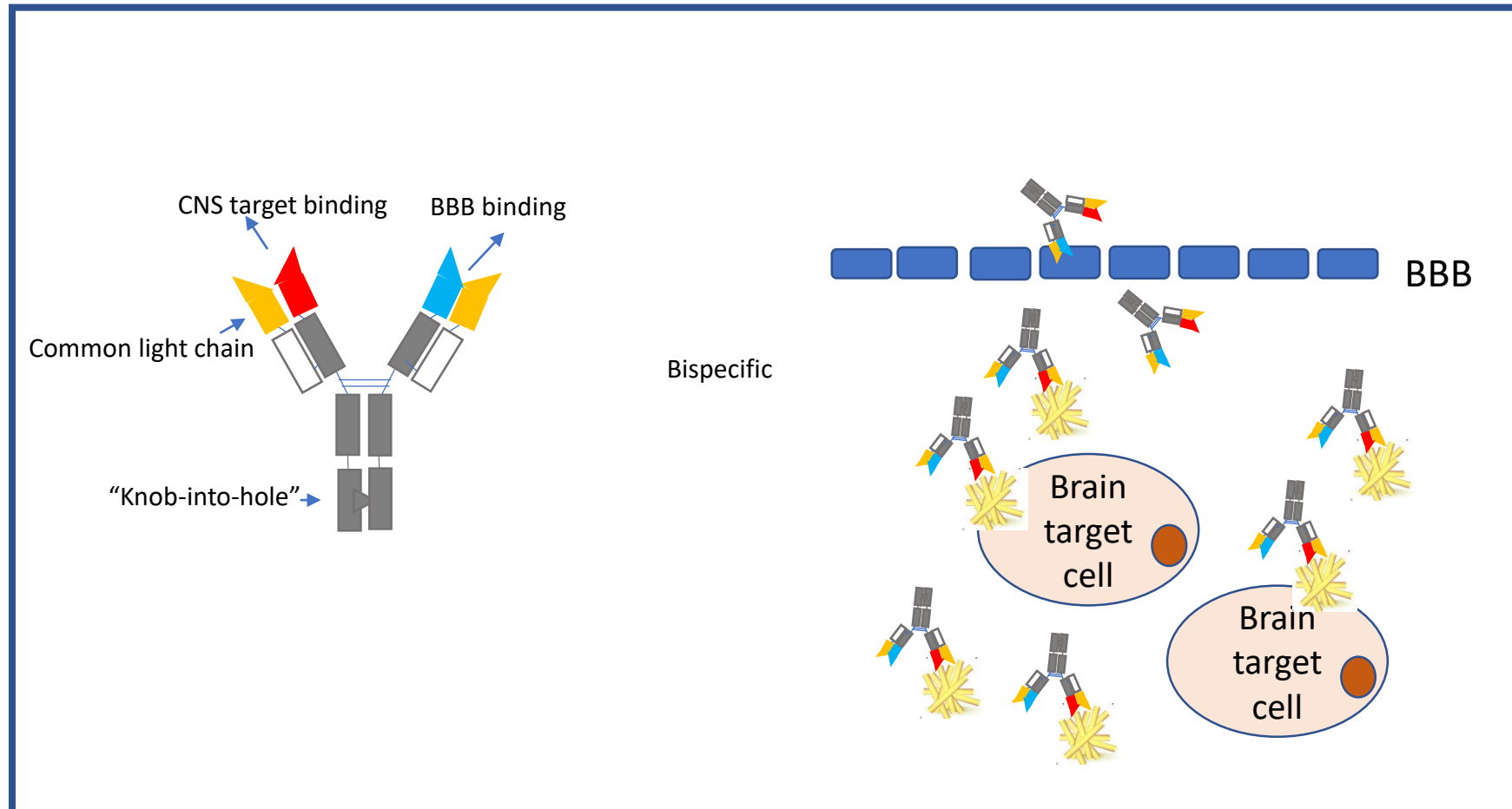
Bispecific involves a CD3 binder



Bispecific against a CSA (cancer specific antigen) and a CAA (cancer associated antigen)



Bispecific against one target for CNS and another target on BBB





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How “imbalanced bispecific antibodies” are made at Ab Studio?

(‘A’ is the corresponding high affinity arm and ‘B’ is the corresponding low affinity arm)

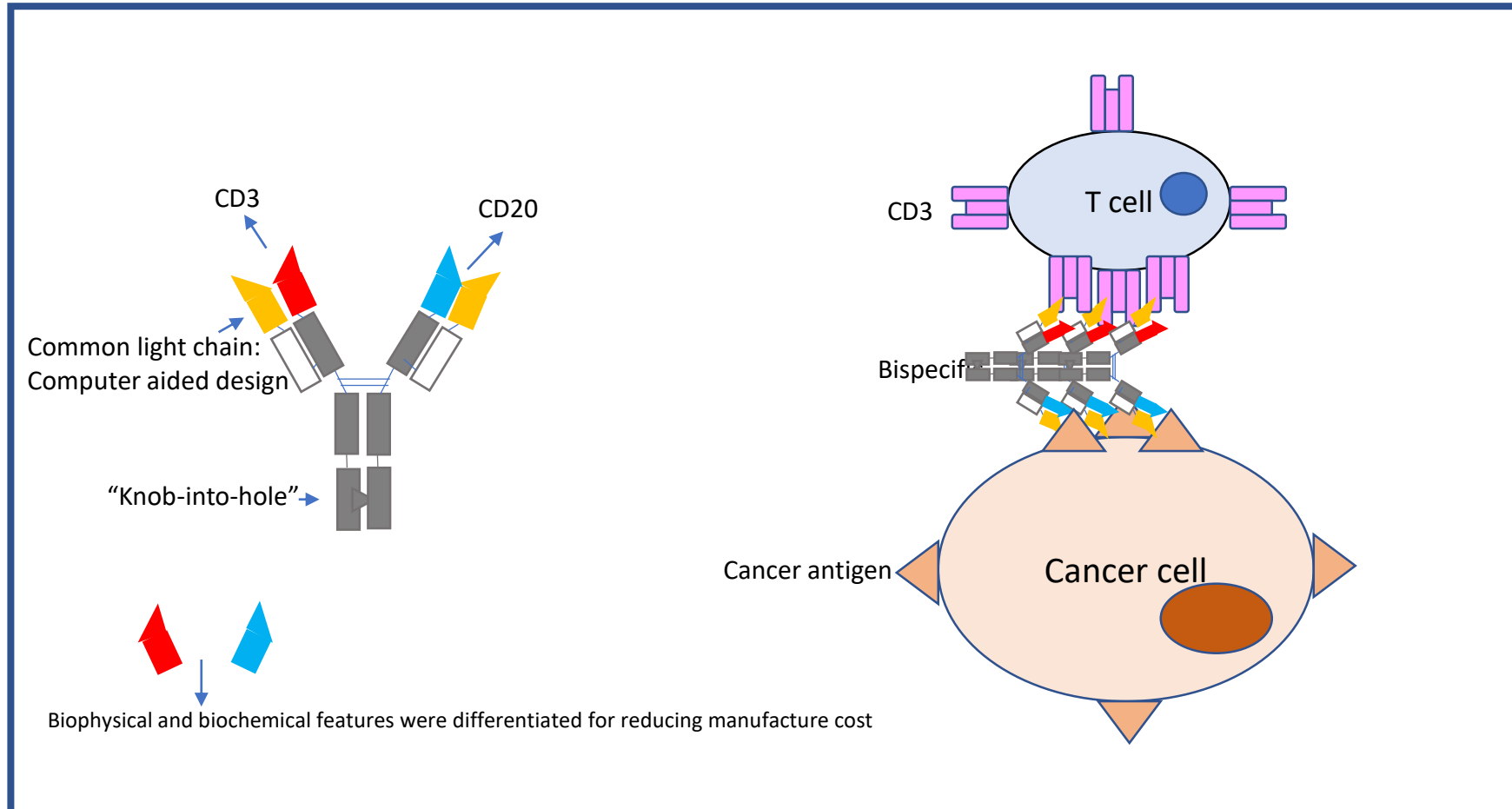
VL Design:

- 1) If VL-A and VL-B light chain homology >80%, design a VL-C based on VL-A via computer aided design: Maintain VH-A/VL-C’s affinity as close as that of VH-A/VL-A, allow VH-B/VL-C to have reduced affinity compared to VH-B/VL-B
- 2) If VL-A and VL-B light chain homology <80%, construct phage ScFV library:
VHs of the ScFV library are human germline VH library
VLs of the ScFV library are VL-A and its mutants derived from error prone PCR at less than 20% of mutation frequency

VH Design:

Use computer aided design to differentiate the biochemical and biophysical features of VH-A and VH-B in order to isolate ‘AB’ better from ‘AA’ and ‘BB’

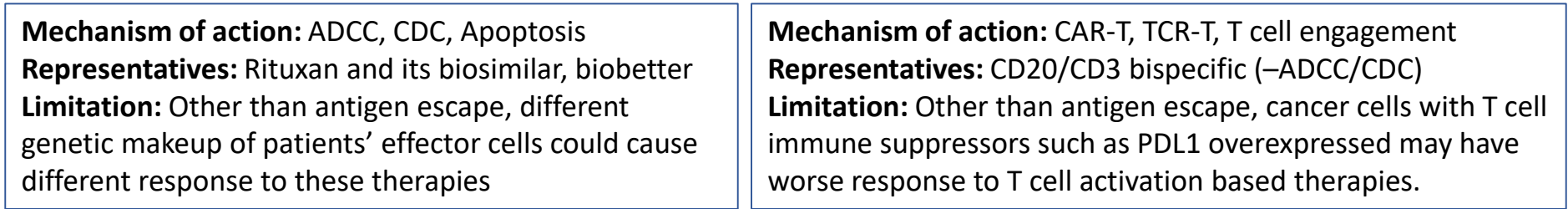
Case Study: CD20/CD3 Bispecific



Difference to other CD20/CD3 bispecific: ADCC/CDC effector function is maintained



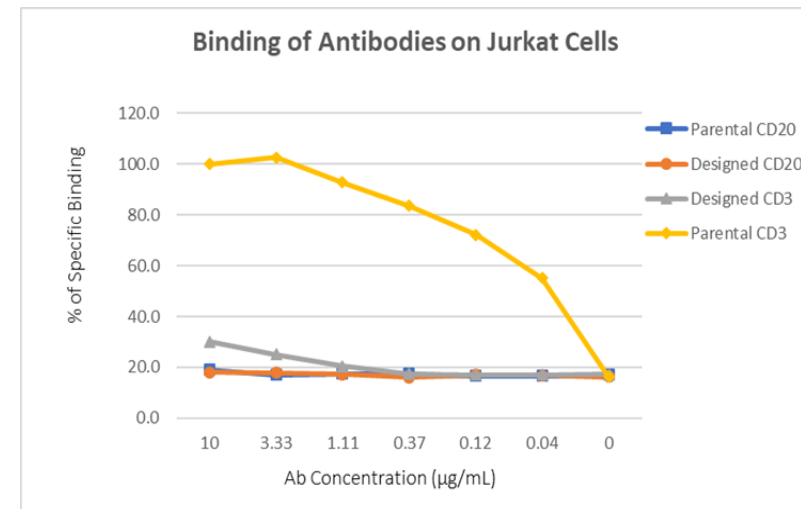
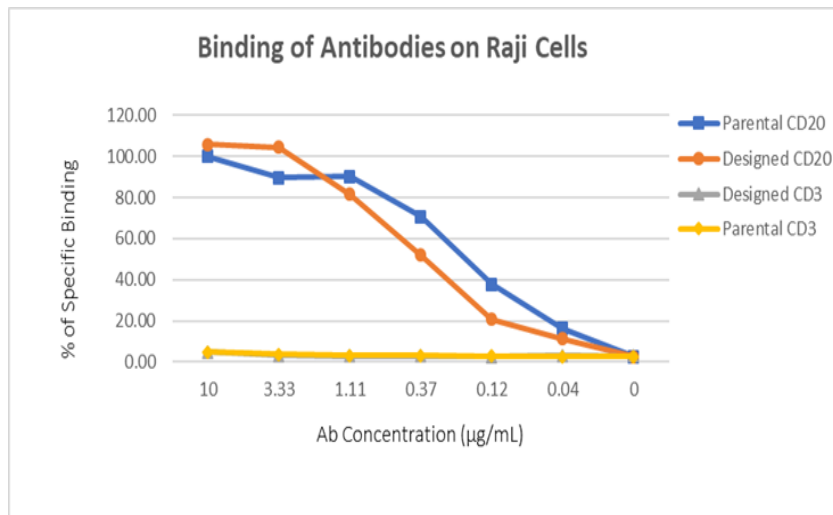
Current CD20+ Cancer Immuno-Therapy



Novel “imbalanced” CD20/CD3 based cancer therapy

By making a CD20/CD3 bispecific antibody with CD3 binding affinity significantly reduced, we hope to “safely” maintain the effector function and reduce cytokine storm. Therefore, the novel “imbalanced” CD20/CD3 bispecific would have all mechanisms as described above.

Binding Ability of Designed Abs Compared to That of Parental Abs



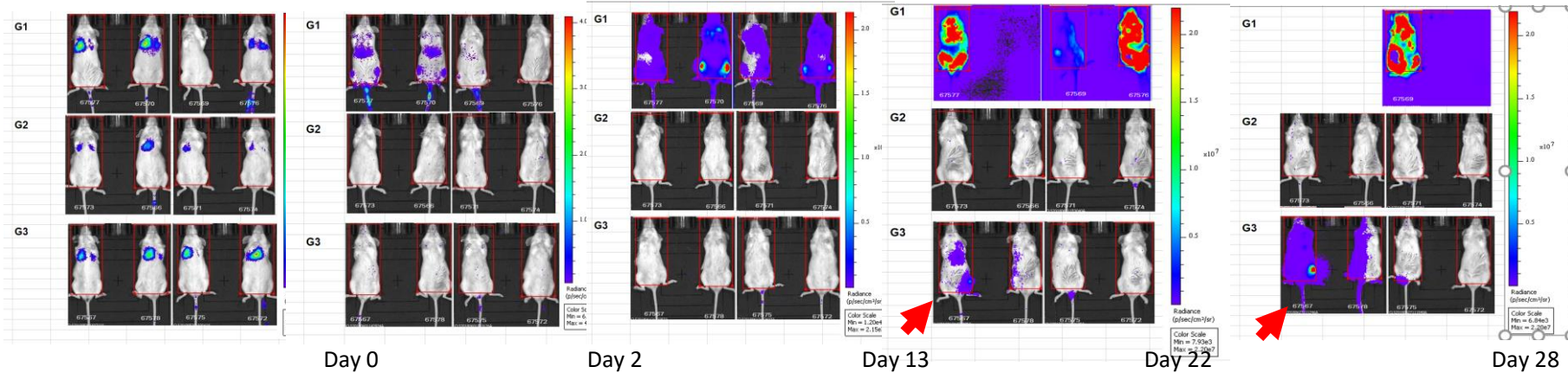
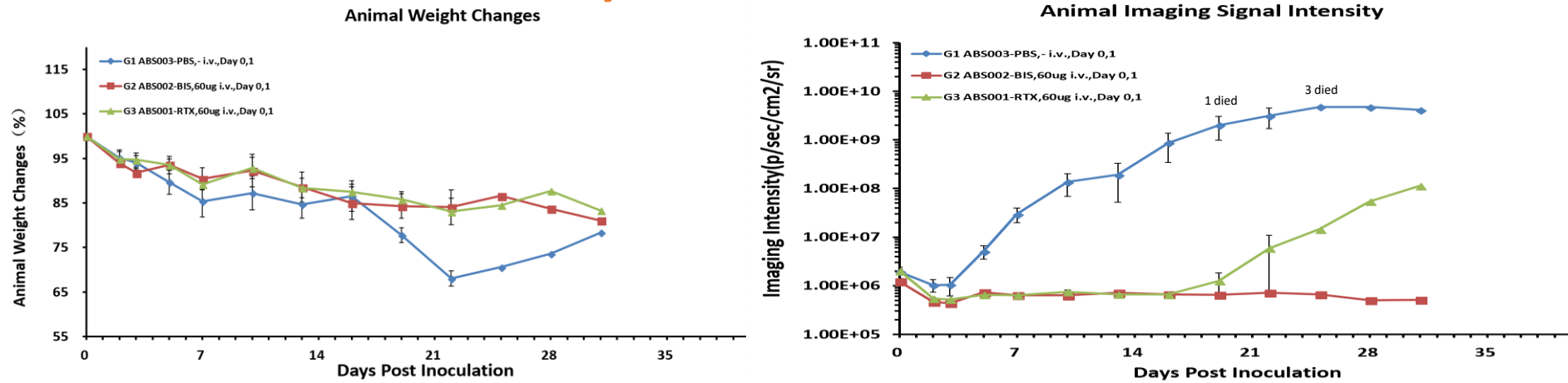
After computational design, CD20 homodimer (hole-hole) IgG contains designed VH sequence and common VL sequence showed similar binding capacity for CD20 compared to that of parental CD20 IgG while CD3 homodimer (knob-knob) IgG contains designed VH sequence and common VL sequence showed significant reduced binding capacity for CD3 compared to that of parental CD3 IgG



CD20/CD3 “Imbalanced” BsAb has Good Efficacy and Safety *in vitro*

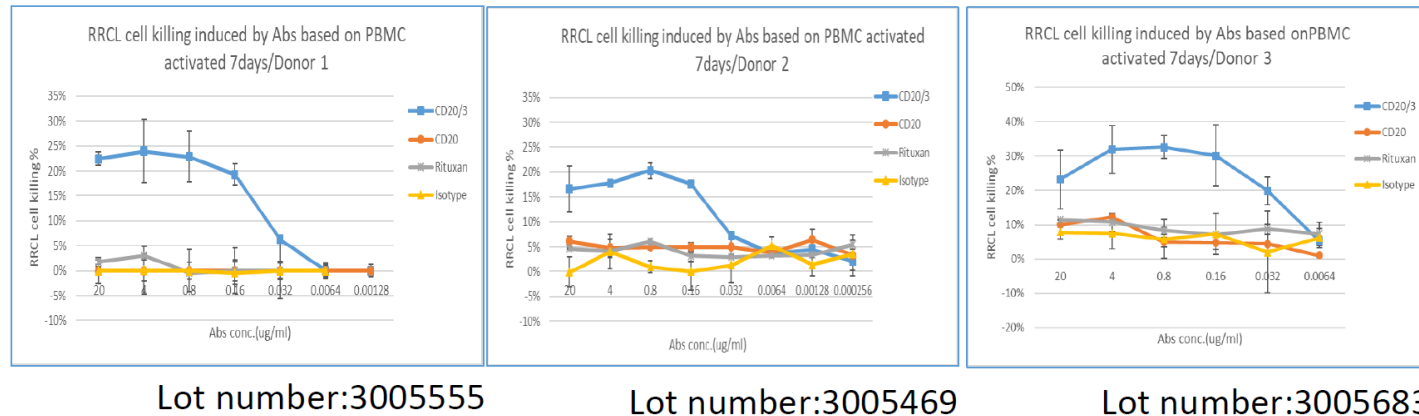
	Efficacy Assay			Safety Assay			
	ADCC on Raji cell	CDC on Raji cell	T cell killing on Raji cell	ADCC on Jurkat	CDC on Jurkat	T cell killing on Jurkat	T cell depletion from PBMC
Isotype Control	-	-	-	-	-	-	-
Rituxan	++	++	-	-	-	-	-
CD20 homodimer	++	++	-	-	-	-	-
CD20/CD3 BsAb	+ / ++	+	+++	-	-	- / +	-
Raji cell: CD20+/CD3- NHL tumor cell							
Jurkat cell: CD20-/CD3+ T cell tumor cell							

CD20/CD3 “Imbalanced” BsAb has better Tumor Killing Potency than Rituxan *in vivo*



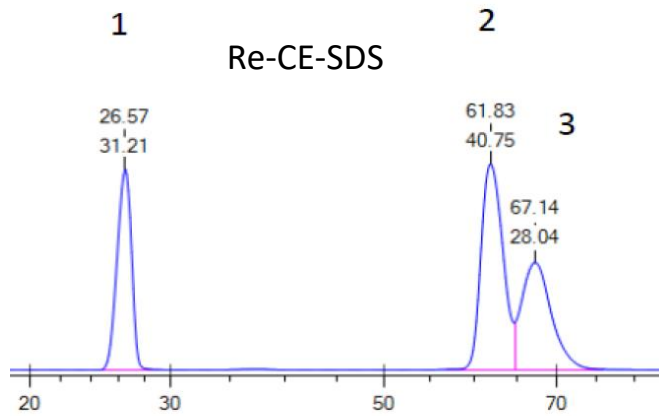
Day 0: IV injection with “Abs/PBS + Raji-Luc cell + human PBMC”, first imaging: 15min post injection. **G1: PBS, G2: BsAb, G3: Rituximab**

Rituxan Resistant Raji Cell (RRCL) can be Efficiently Killed by Imbalanced CD20/CD3 BsMab Abs and PBMC with T cell Pre-activated for 7 days



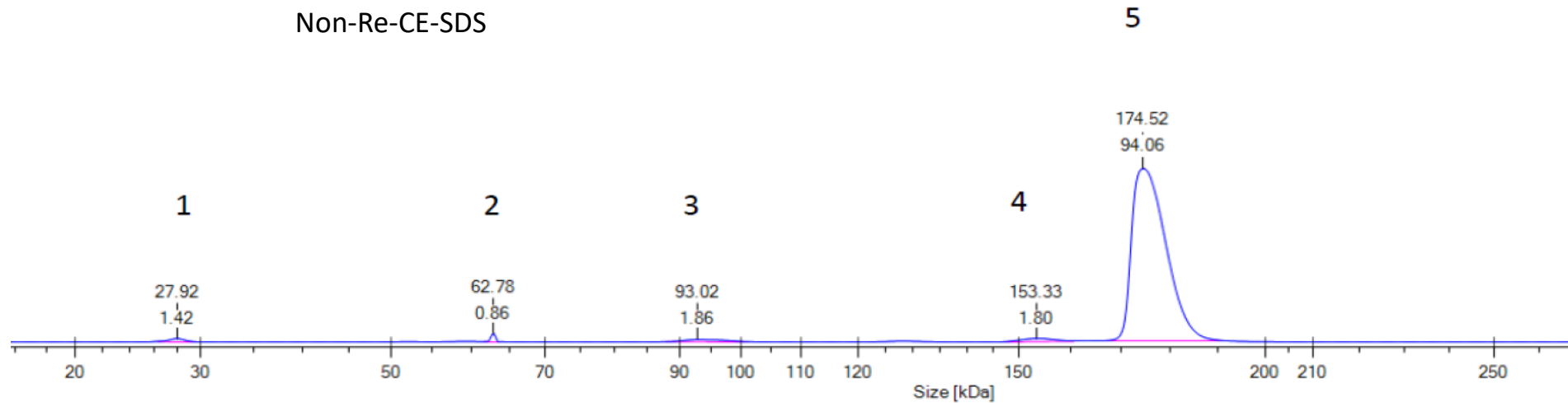
Furthermore, We studied the most important question: Whether Rituxan resistant cancer can be treated by Imbalanced CD20/CD3 BsMab.

CD20/CD3 “Imbalanced” BsAb has good Developability



Temperature (°C)	DSF				SLS	
	Tm1	Tm2	Tm3	Tm4	Tagg 266	Tagg 473
	66.0	80.1	86.7		70.9	71.2

DLS	Peak #	Mode Diameter (nm)	Mass (%)	PDI
20 °C	Pk1	10.15	100	0.177
	Pk2			
	Pk3			





Summary:

1) Computational designed Imbalanced CD20/CD3 BsMab has good efficacy, safety and developability *in vitro* and in animal model.

Item	m Ab	CAR-T	Bispecific Ab	Imbalanced Bispecific Ab
Efficiency of killing tumor	+	+++	++/+++	++
Cytokine storm	N/A	++	++	N/A
Mechanism	ADCC, CDC, Apoptosis	T cell	T cell	T cell engagement, ADCC, CDC
Dosage	High	N/A	Low	Low
Large-scale production	Yes	Personalized production, 3-4weeks, high cost	Yes	Yes

2) This imbalanced CD20/CD3 BsMab has potential to treat Rituxan resistant, difficult to treat and relapsed CD20+ cancer (unmet clinical needs, fast track for filing IND).



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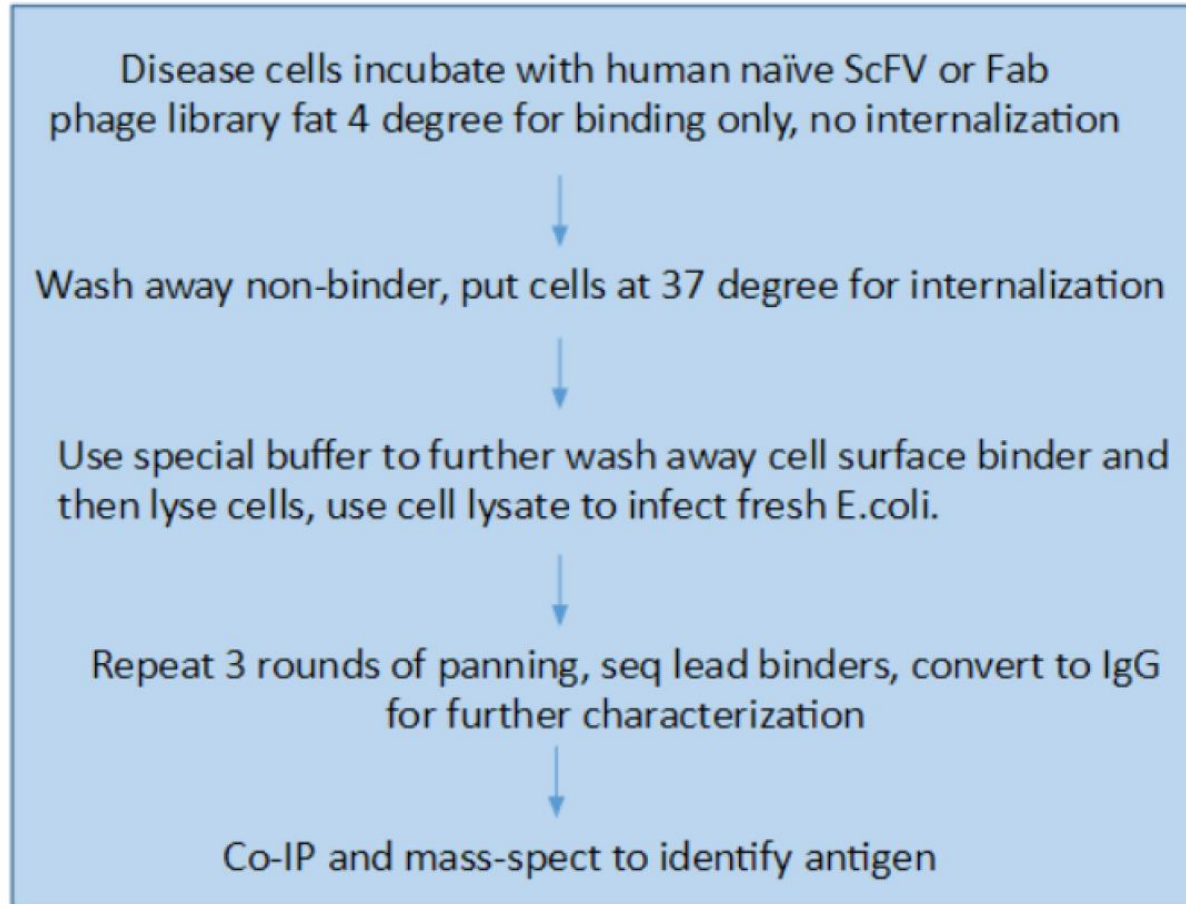
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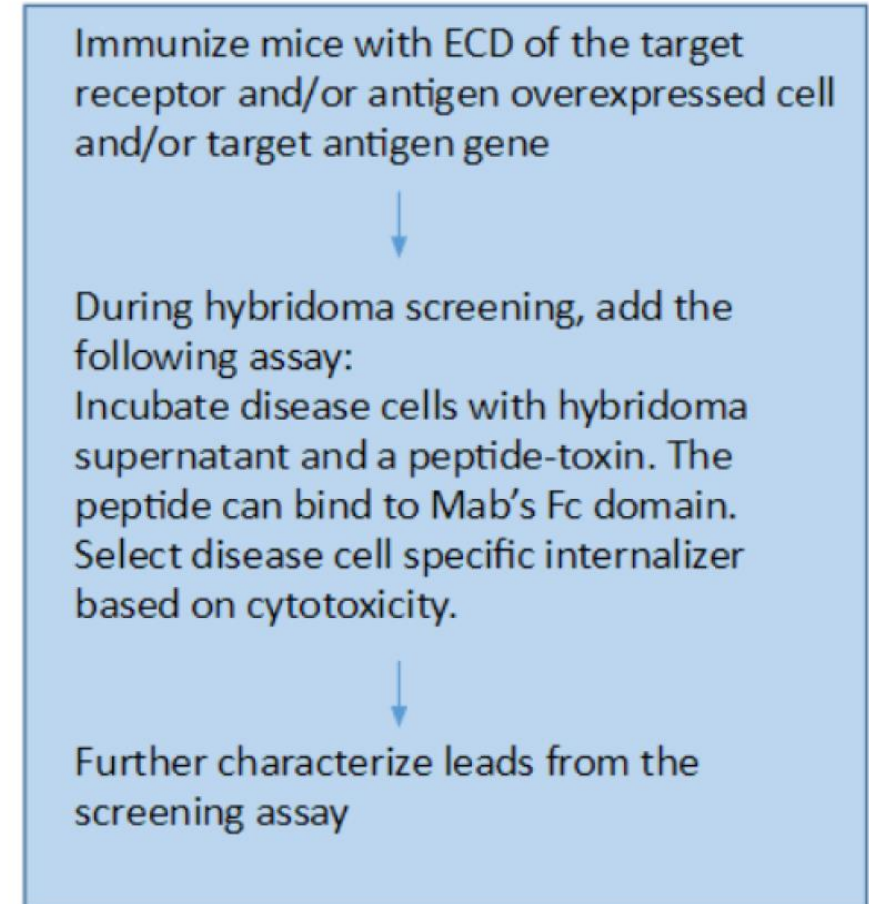
Development and Screening of Therapeutic Antibodies with Internalization Potential



Start from unknown target antigen

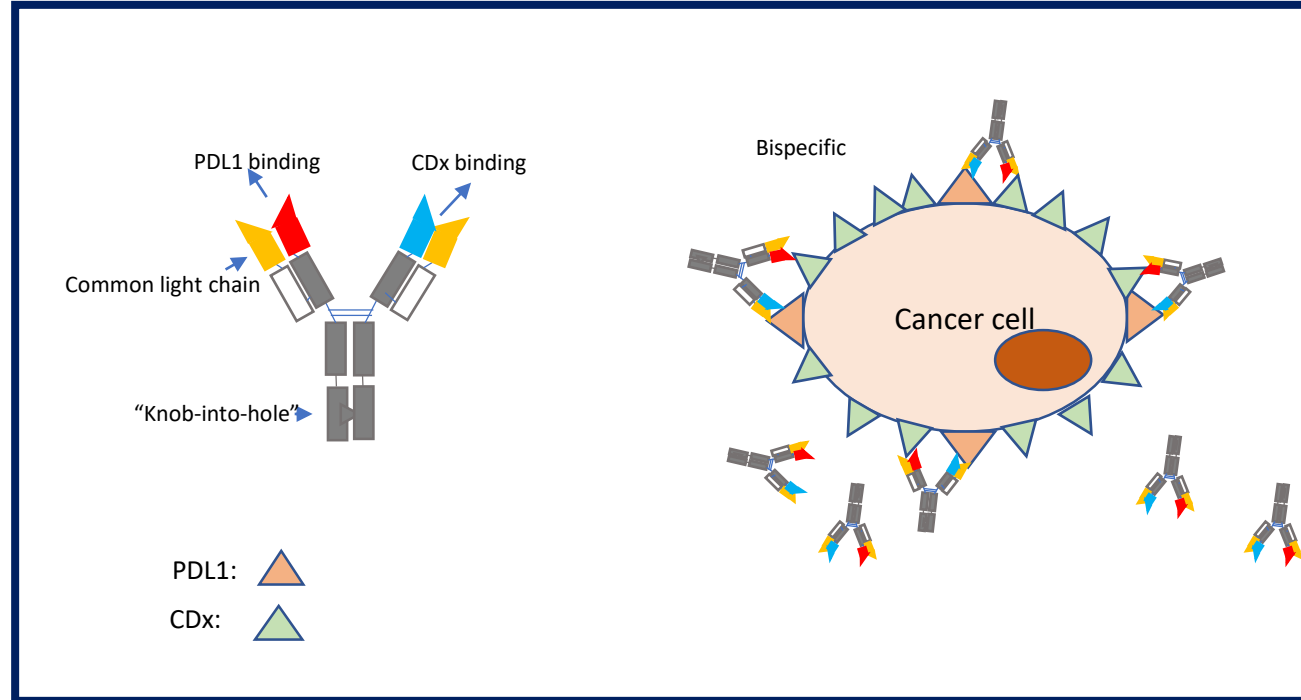


Start from known target antigen



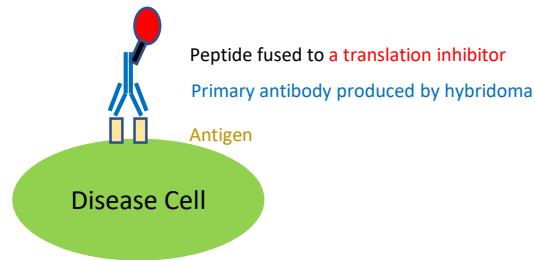
- Computer aided design for serial reduced internalization
- In house developed high-throughput screening assay

Case Study : PDL1/CDx Bispecific Antibody with Internalization Potential



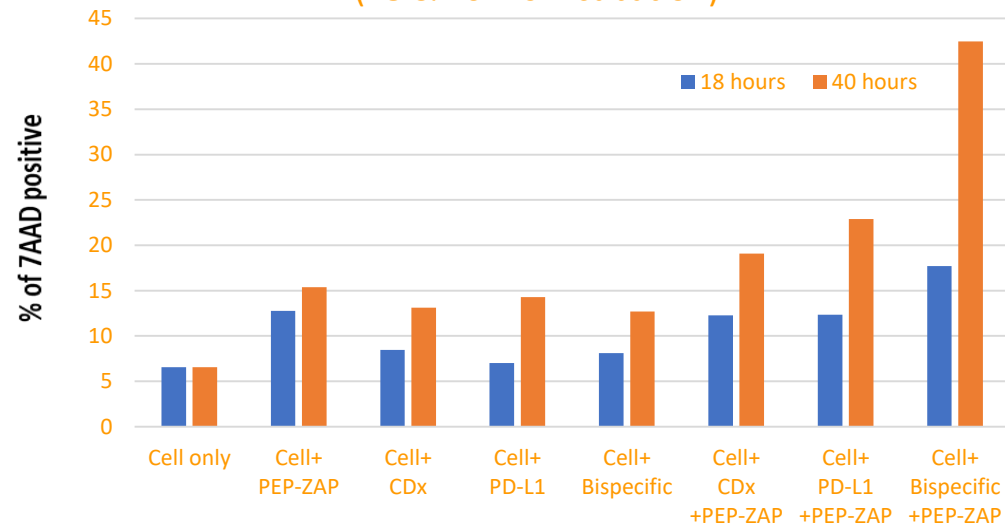
PDL1/CDx Bispecific Antibody Induces more Cell Death than PDL1 and CDx Homodimer in the Presence of Pep-ZAP

How PEP-ZAP works?



Pep-ZAP is a Fc binding peptide conjugated to a translation inhibitor protein, cell death is the readout of antibody internalization

PEP-ZAP Mediated Cell Death of Target Cancer Cell (18 & 40 hrs incubation)





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Biological Significance:

This imbalanced bispecific may induce target cancer cell death at three different levels

- 1) Blocking PD1/PDL1 interaction
- 2) Induce PDL1 internalization
- 3) When conjugated to a drug, kill target cancer cells as an Antibody drug conjugate

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Thank you very much!