



TECHday 2024

Co-hosted with InterSystems

November 15, 2024 – Boston – InterSystems Global Headquarters

Welcome

Today, we'll uncover how AI is not just transforming but revolutionizing competitive strategies in this fast-paced landscape.

Powering the ability to decode complex datasets, seamlessly integrate diverse data sources, and gain insights at a depth never before possible.

Agenda

TECHday
2024
Co-hosted with InterSystems

Intro

AI

Streamlining
Antibody Discovery:
Integrating Data for
Smarter Candidate
Selection

Wet lab

In Vivo Discovery
Meets *In Silico*
Scalability

Disruptive
Dialogue
Session

Fireside chat

Partners

TECHday
2024
Co-hosted with InterSystems

Thank you





IpA



BioStrand

a subsidiary of IPA

LENS^{ai}TM

Streamlining Antibody Discovery:
Integrating Data for Smarter Candidate Selection

Universal Foundation AI model for life sciences

TECHday
2024

Co-hosted with InterSystems

Core challenges in drug discovery: The first principles perspective

LENS^{ai}[™] was developed to address three key industry issues

1. Fragmented data and slow discovery processes

Siloed data handling causing delays and increased costs



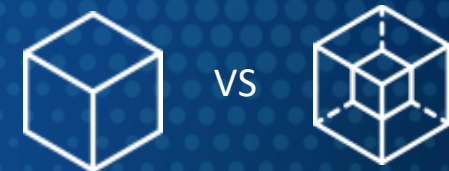
2. The Information Integration Dilemma (IID)

Expanding omics data creates isolated datasets, limiting integration and insight extraction



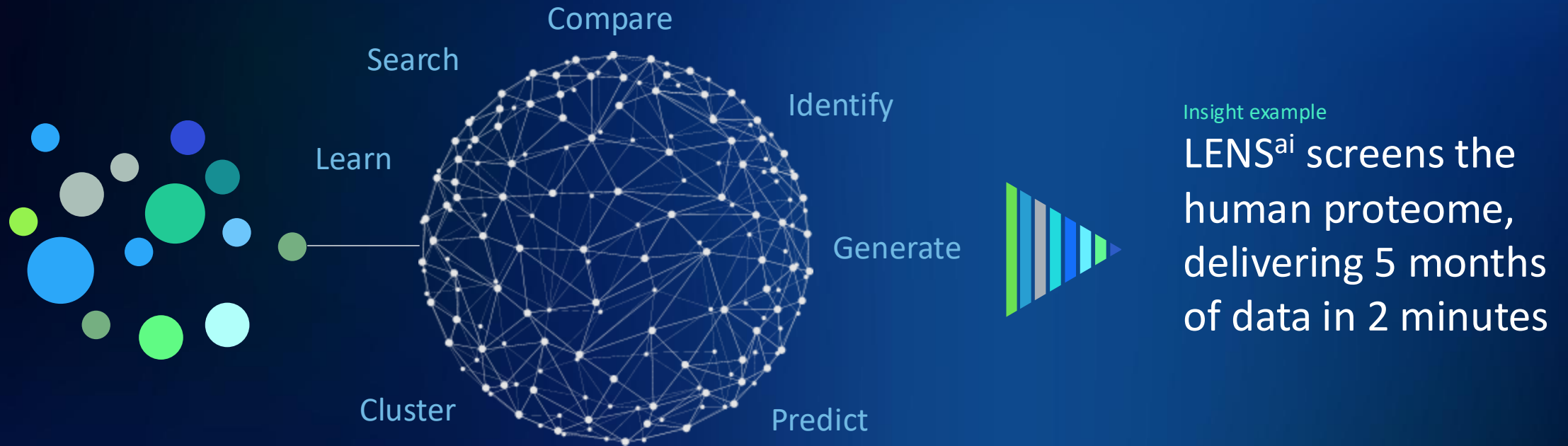
3. Lack of transparency in AI-driven predictions

Many AI platforms operate as black boxes, limiting interpretability and reliability



Data granularity meets data integration

LENS^{ai} powered by patented Hyft[®] Technology



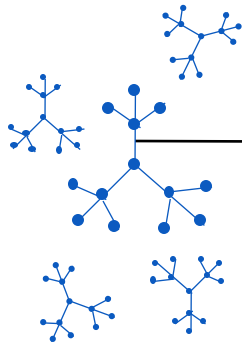
Technology engineered for speed, precision, and limitless scalability.

Welcome to LENS^{ai}: a Foundation AI Model for multiscale biological data integration

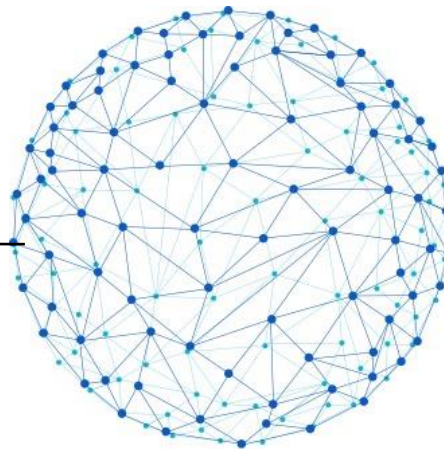


A transformative foundation model designed for the integration of complex, multiscale biological data

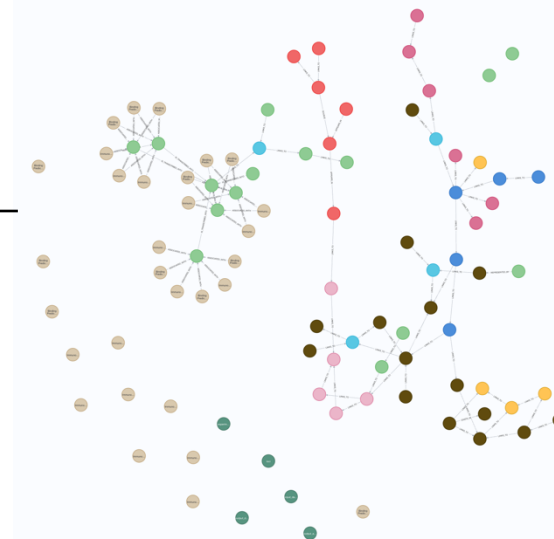
Vast number of novel data points



Pre-Integrated Data



Application ready connections



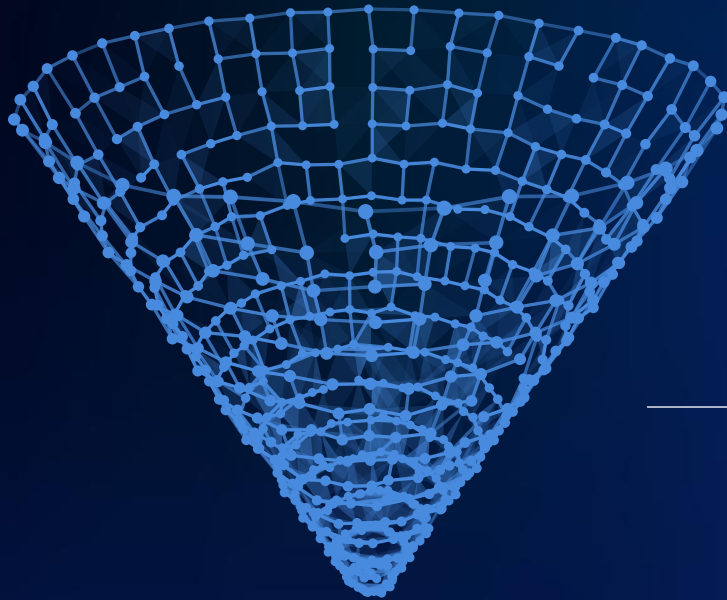
Overview

- Contract (5)
- Immunogenicity (30)
- Resource (6)
- Set_Members (1)
- rdfs (60)
- Named_set_of_Ordered_lists_of_nucleotides (1)
- Named_set_of_Unstructured_Texts (1)
- Named_Set_of_Ordered_Lists_of_AA (1)
- Ordered_Lists_of_AA (1)
- Data_Sources (1)
- Molecules (1)
- Macromolecules (1)
- Small_Molecules (1)
- Complex_of_Molecules (1)
- Environment_Contexts (1)
- Appearances (1)
- Parsing_Methods (1)
- Hyfts (1)
- AA_Sequences (1)
- Atoms (1)
- Residue_AA (1)
- Translation_Frames (1)
- DNA_Sequences (1)
- Complex_Structures (1)
- Single_Molecule_Structures (1)
- Protein_Chain_Isoform_Structures (1)
- Small_Molecule_Structures (1)
- Polypeptides (1)
- Proteins (1)
- Protein_Chains (1)
- Protein_Chain_Isoforms (1)
- Protein_Chain_Isoform_Variants (1)
- mRNAs (1)
- Pre-mRNAs (1)
- Gene_Products (1)
- RNA_Splicing_Mechanisms (1)
- Genes (0)
- DNA_Fragments (1)
- Sequencing_Reads (1)
- Codons (1)
- Nucleotides (1)
- Ordered_Lists_of_Nucleotides (1)
- Positions_of_the_Domain (1)
- Reference_Classifications (1)
- Classification_Items (1)
- Classification_Annotations (1)
- Documents (1)
- NI_Path (1)
- NI_Relations (1)

Show 10 more | Show all

Antibody Discovery and Development

Data-driven down selection



End-to-End Analysis



Target

Target Analysis

- Antigen Modeling & Design
- Epitope Prediction

- Epitope Specificity



Discovery

Hit Selection

- NGS Data Processing
- Hit Expansion

- Epitope Binning



Leads

Candidate Characterization

- Epitope Mapping
- Developability
- Off-target Screening

Lead Optimization

- Immunogenicity Screening
- Affinity Maturation
- De-risk Engineering
- pH Optimization
- Humanization

+ Many microservice tools and technologies

Target Analysis:

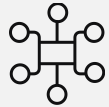
Optimize clinical success at project onset

Target

LENS^{ai} Target Analysis
Antigen Modeling & Design
Epitope Prediction
Epitope Specificity

Input

Omic Sequence Data



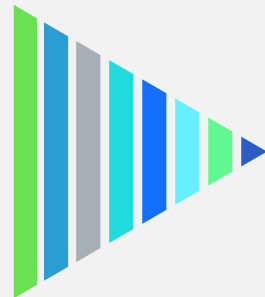
Structural Models



Text Data



LENS^{ai}



Output

Target Selection Criteria



Disease causality

Druggability

Toxicity

Novelty

Target Insights



Benefits

- Commoditize all data types (sequence, structure, function) at inception of discovery workflow
- Gain insights from historical data and utilize external data sources effectively
- Create the first entry point for system-based-screening through data feedback loop

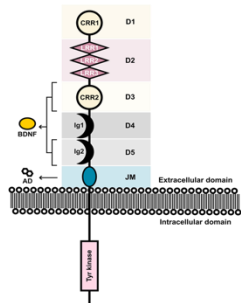
LENS^{ai} Protein Structure Prediction

Modeling complex targets: from high-throughput to detailed refinements

Structural Modeling

●●● Target | Discovery | Leads

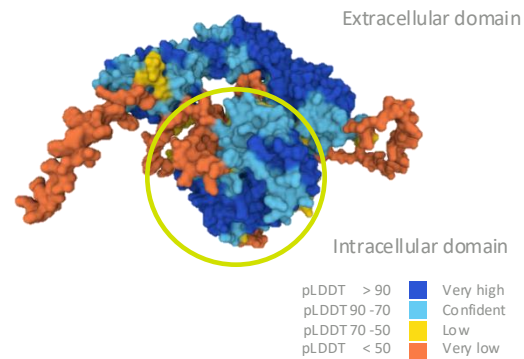
Target is a multi-domain, heavily glycosylated protein



Alpha Fold

Modeling of the EC domain of target

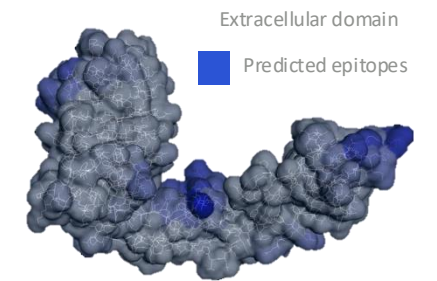
In various regions of the protein, AlphaFold structure prediction shows low to very low model confidence.



Epitope prediction

Using our target model as an input

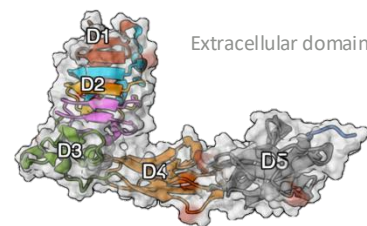
Using AI based epitope prediction tools, we define potential binding areas on the antigen. We combine predicted epitopes with known epitopes in our final model.



Template-based

Modeling of the EC domain of target based on family member model

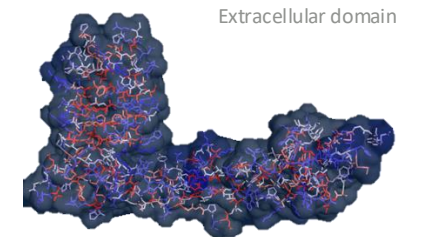
family member model (resolution X-ray diff 1.84 Å) has the largest coverage and a seq. identity of 37.8% with respect to target EC.



Multimer & Complex Proteins

Molecular dynamics-based workflows

Utilizing physics-based engines to model atomic interactions and to estimate stability of multimeric protein complexes.



LENS^{ai} Hit Expansion Analysis

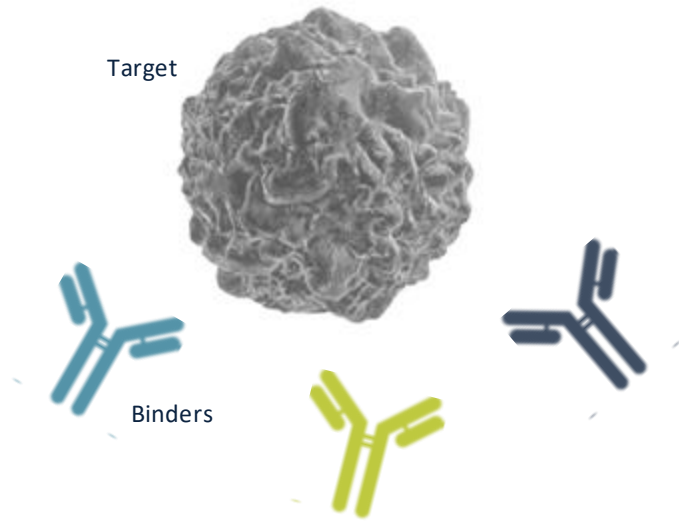
Selection and prioritization of diverse antibody sequences

Discovery

LENS^{ai} Hit Selection
Hit Expansion: Optimizing diversity through multi-modal strategy

Input

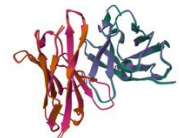
NGS antibody repertoire & functional seed antibodies



LENS^{ai}

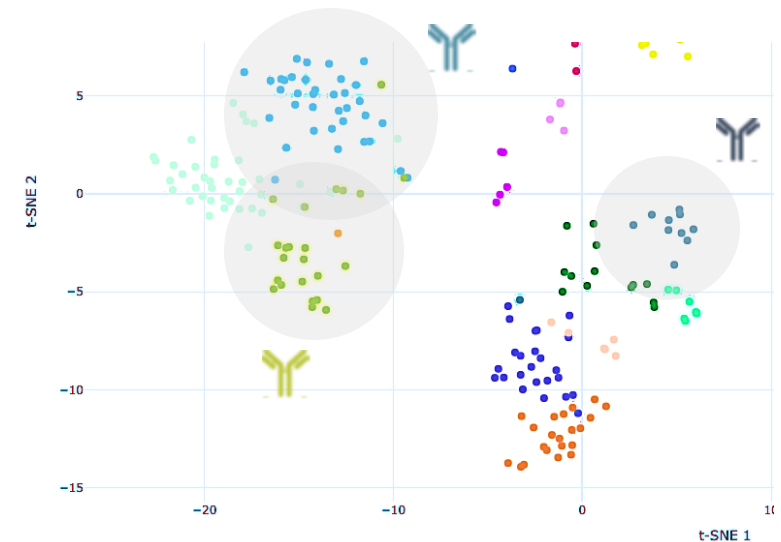
Multi-dimensional analysis

```
Q L V E S G G G L V Q  
O M T Q S P S S L S A  
O L V E S G G G L V K  
I O M T Q T T S L S C  
V L P Q G G S L R L S C  
V L T Q S S P G T V L A R  
Q L Q S S G T V L A R  
V S T Q S P A I M S A
```



Output

Additional clusters of functional clones



LENS^{ai} Hit Expansion pipeline is an end-to-end workflow built to extract all relevant hits for downstream analysis.

Epitope Binning:

More-informed early triaging of lead candidate panel

Discovery

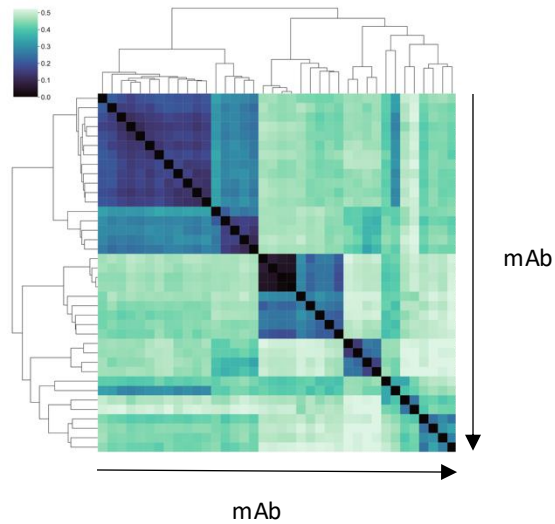
LENS^{ai} Hit Expansion
Epitope Binning

Input

Combination of sequence and structural features to identify main bins

Antibody sequence input:

- from single cell sequences up to full immune repertoires
- target-agnostic



Output

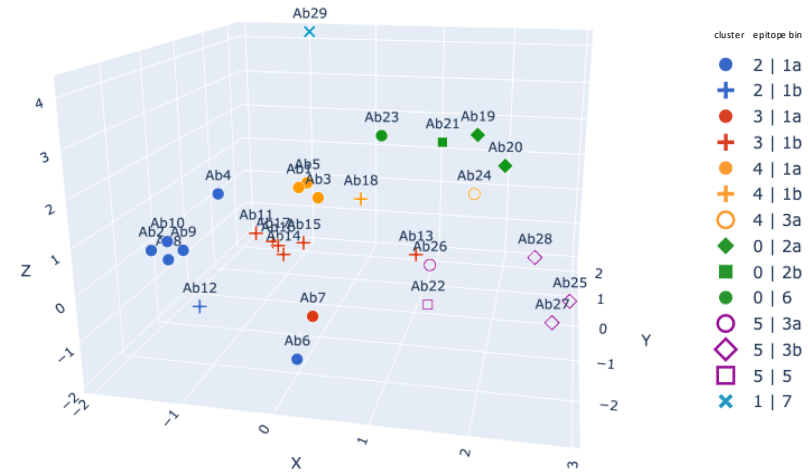
Integration of physics-based engines and advanced target modeling for high granularity

Resolving larger bins and sub-bins: Cohen's Kappa score

cluster -> bin **0.93***

bin -> cluster **0.84**

* [-1 to 1]; [>0.8 = perfect agreement]



LENS^{ai} Epitope Binning relies on a hybrid prediction engine for optimal results without the need for physical material

Epitope Mapping: Informed lead selection

Leads

LENS^{ai} Candidate Characterization Epitope Mapping

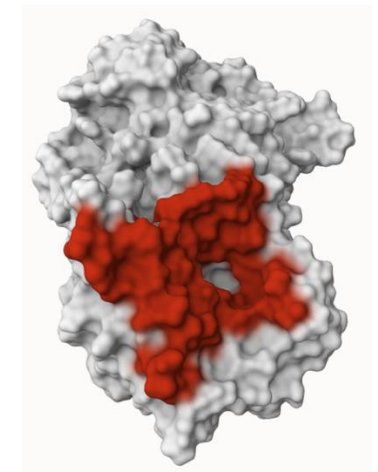
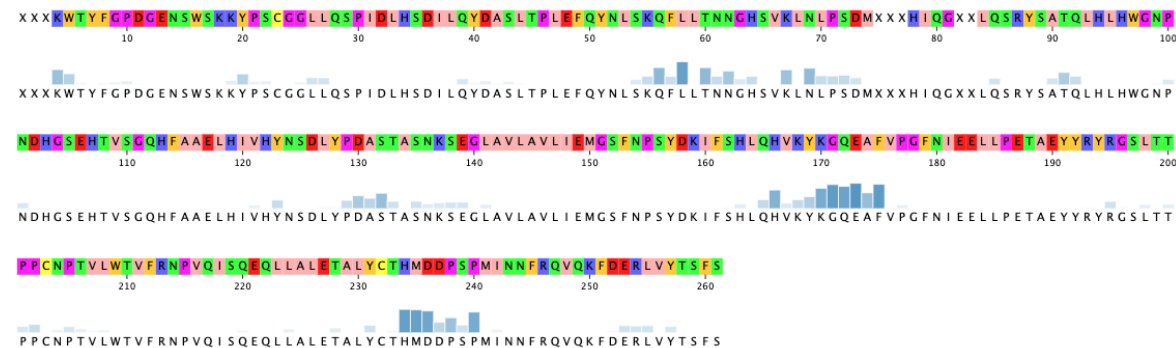
Input

Amino acid sequences
of hits or candidates



Output

Multi-feature-based Epitope Mapping:
Based on syntactical-, structural profiling and, atomic interactions to enable affinity propagation clustering. Function driven information package to select potential lead candidates.



Immunogenicity & Developability profiling:

Compare your antibodies against a database of all therapeutic antibodies

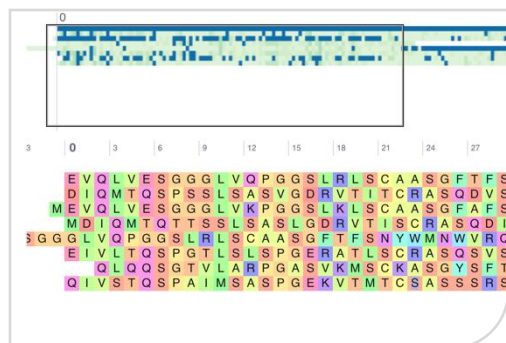
○● Leads

LENS^{ai} Lead Optimization
Immunogenicity Screening
Affinity Maturation

De-risk Engineering
pH Optimization
Humanization

Input

Amino acid sequences of lead candidates

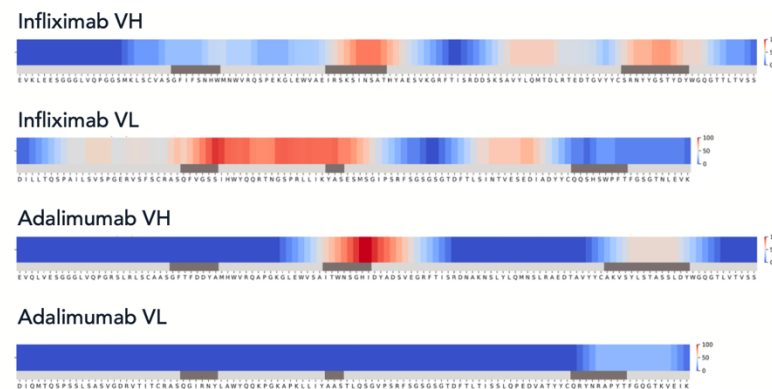


Output

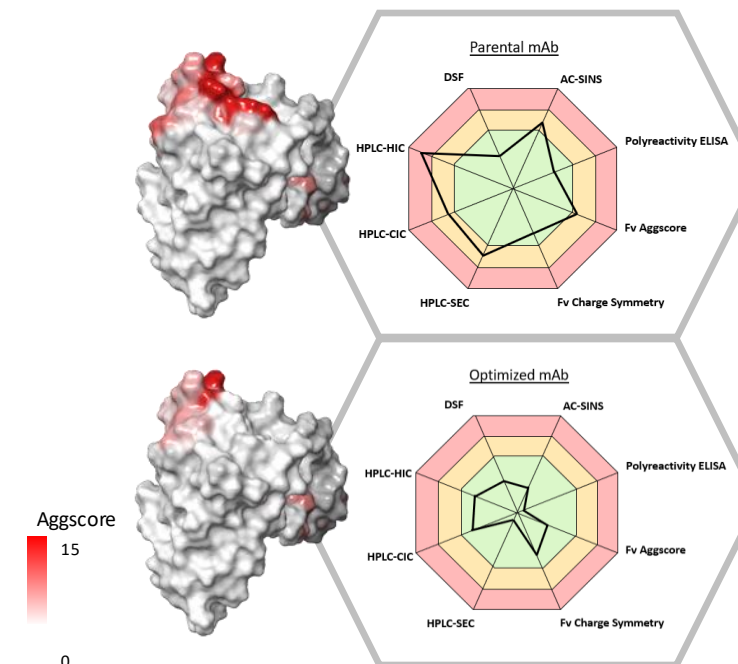
Multi-parameter optimization to create therapeutic leads

Analyse candidates to gain 360-degree insight in developability and immunogenicity profiles to guide engineering. Easily humanize and optimize candidates to become leads.

Immunogenic heat maps illustrating hotspots

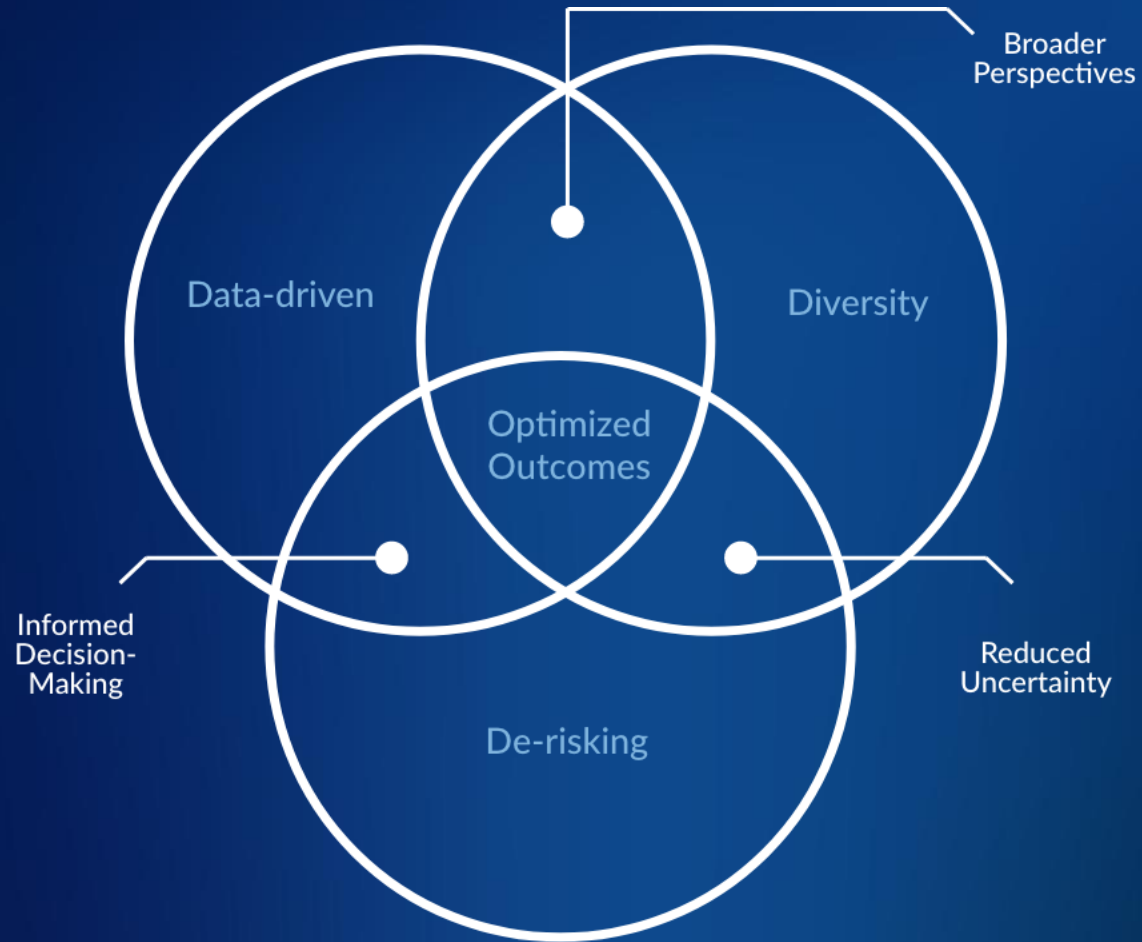


Developability profile radar chart of a parental mAb and an optimized humanized variant. Data is relatively ranked towards the red/orange/green flag areas of the clinical benchmark mAb library.



Data granularity meets data integration

Powering rational, data-driven drug design, enabling critical decisions early in the process and driving faster, more precise paths to clinical success.



“You pioneered discovery insights that previously could not be solved”

LENS^{ai} Integrated Intelligence Platform

In action:

TECHday
2024

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DEMO

Shaping the Future of Rational Drug Discovery with **First Principles Thinking**

Thank you for joining us on this journey through LENS^{ai}'s.

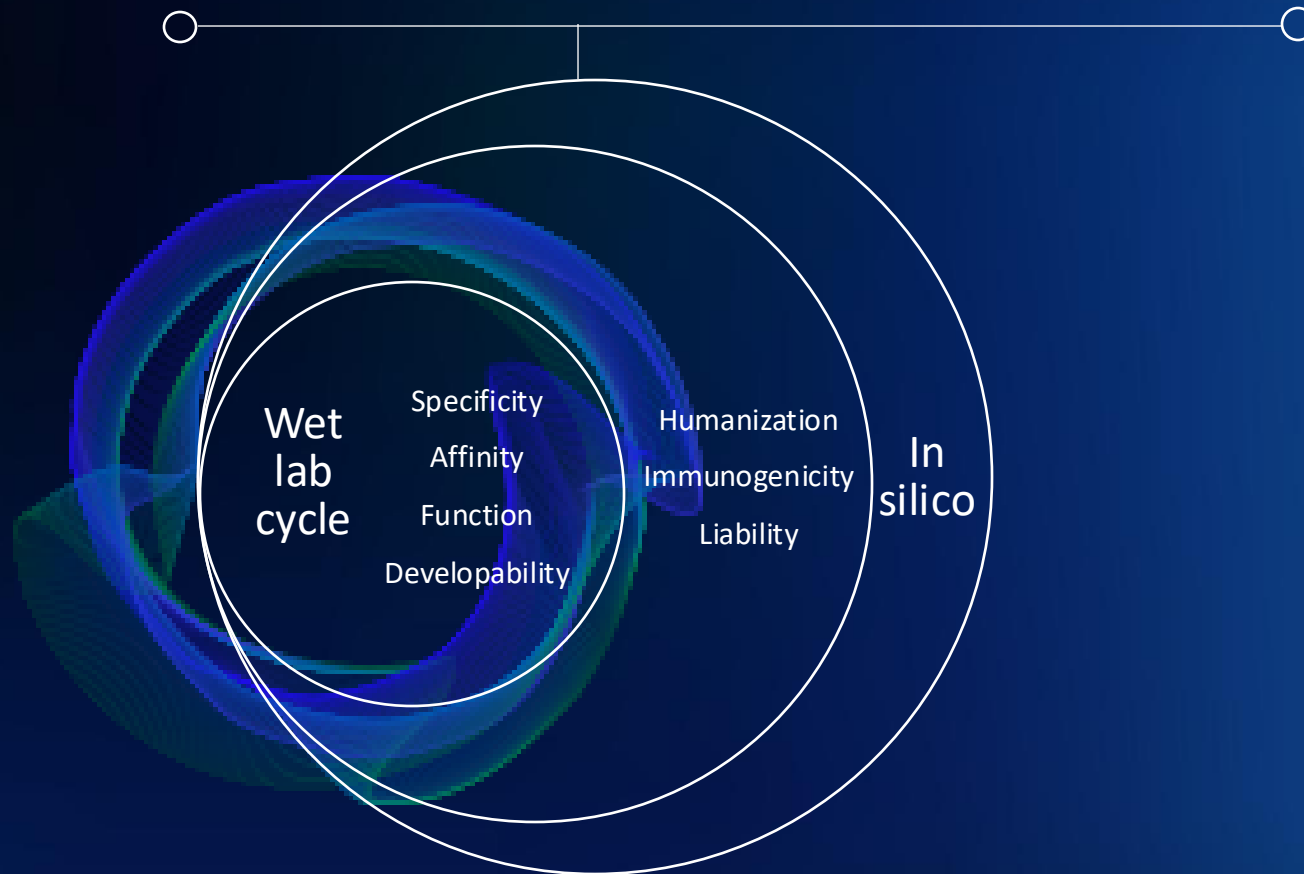
- Built for transparency and ultra scalability
- Reshaping drug discovery with a comprehensive suite of tools
- Accelerating research and optimizing costs for a streamlined process
- Driving breakthroughs that set new standards in therapeutic advancement

In Vivo Discovery Meets *In Silico* Scalability

Intersection of phenotypically rich
B cell Select[®] discovery and
multidimensional, high-throughput
LENS^{ai}[™] applications

Integration of infinitely scalable and accurate multi-modal *in silico* methods to exhaustively mine functional B cell repertoires

Fully-integrated therapeutic end-to-end lead generation workflow

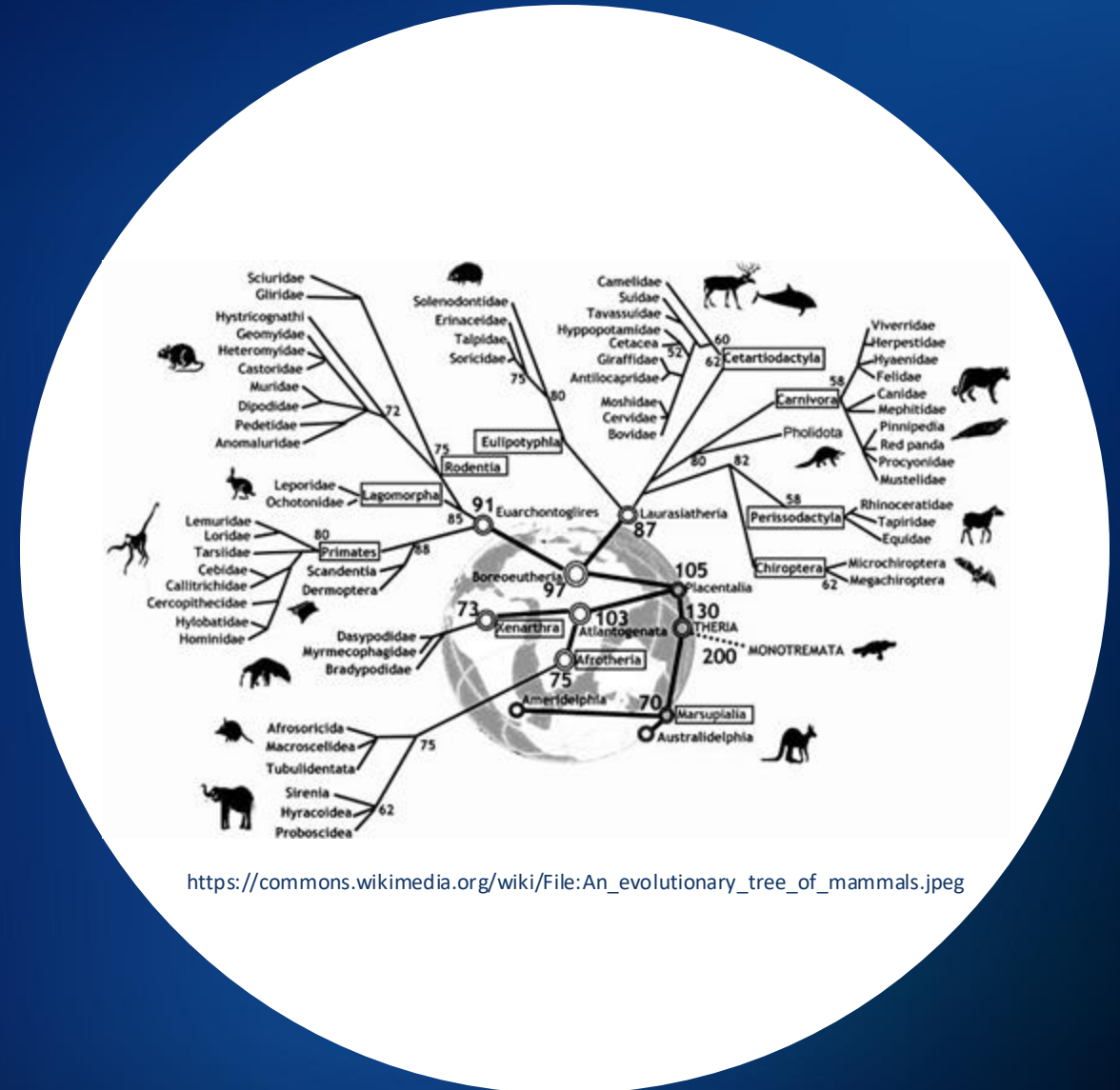


Key Benefits:

- Diversity-driven discovery design
- Early-stage identification of (functional) lead candidates
- Integration of high-throughput *in silico* methods to fully harness the functional B cell repertoire
- Decision support for de-risking/optimization to increase clinical suitability

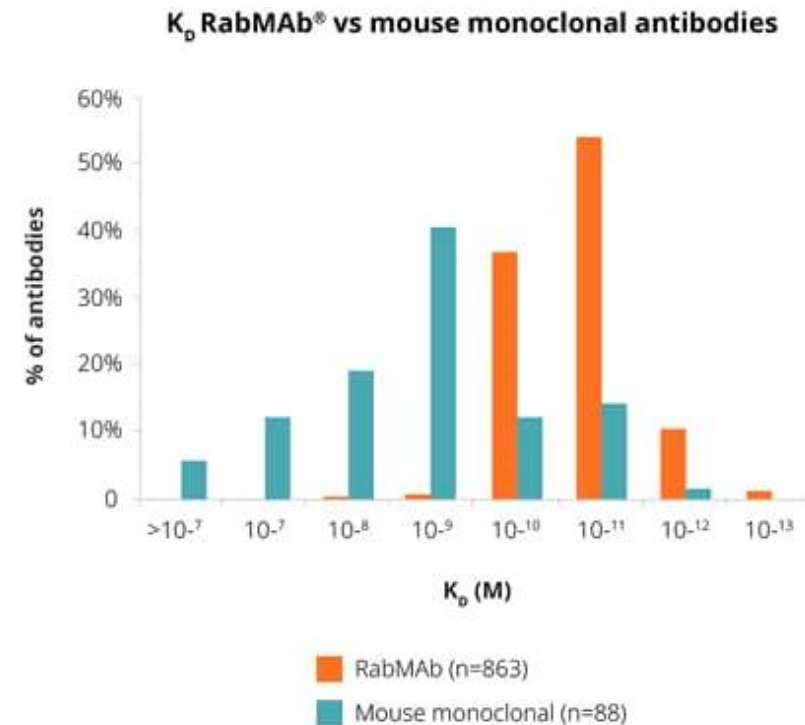
What about rabbit antibodies?

- Phylogenetically distinct from rodents
- Higher B cell diversity:
 - outbred
 - gene conversion



What about rabbit antibodies?

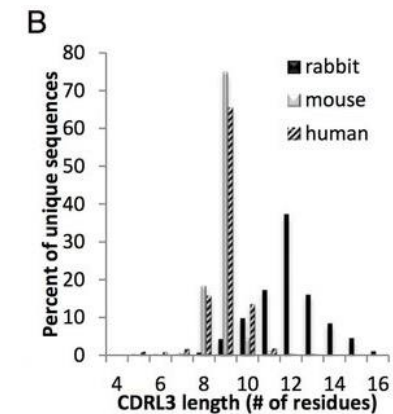
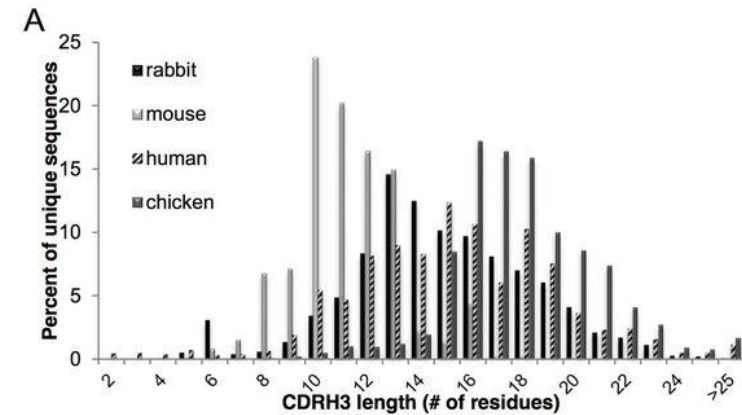
- High affinity (sub-nM) with exquisite specificity



<https://www.abcam.co.jp/primary-antibodies/kd-value-a-quantitative-measurement-of-antibody-affinity>

What about rabbit antibodies?

- CDRH3 length is closer to human than is mouse
- Greater diversity in light chain sequence compared with human/mouse



Lavinder *et al.* PLOS One (2014).

What about rabbit antibodies?

- 2 approved humanized rabbit mAbs as therapeutics (8 more in clinical trials)
- At least 11 approved for diagnostics



Rabbit Antibody Discovery at IPA

Superiority of Rabbit B Cell Select[®]

IPA's proprietary Rabbit B cell Select[®] workflow success

- a versatile solution that is unmatched in the industry, with a >98% program success rate in therapeutics, anti-drug/anti-id and diagnostics.

IPA discovers rabbit anti-LILRB2 antibody for OncoResponse

- This molecule has entered Ph1/2 as a best-in-class anti-LILRB2 to reverse macrophage-mediated immunosuppression in cancer patients.

OncoResponse progresses dual-blockade antibody to IND studies

- Second molecule from IPA collaboration campaign cross-reacts with LILRB1 and 2 as a dual-blockade antibody, potentially enhancing efficacy.

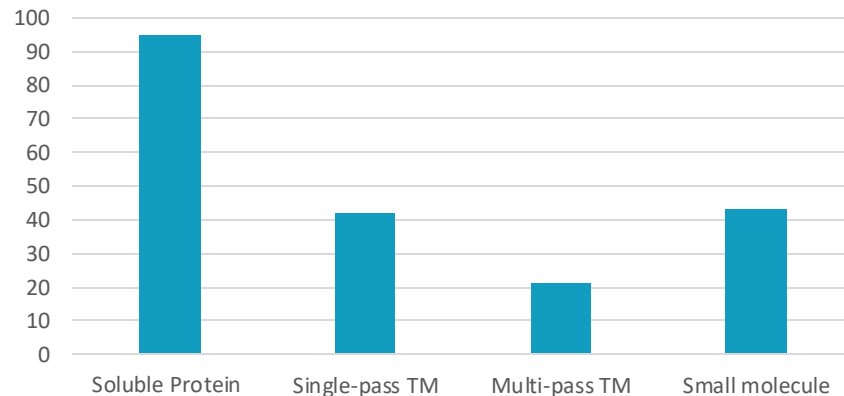
Rabbit B cell Select[®]

Industry leading success rate with high quality, diverse output

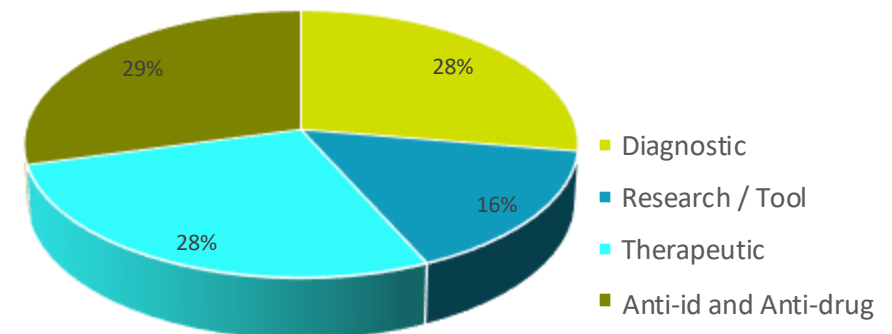
Rabbit B Cell Select program overview

207 Number of projects since 2019

Target type since 2019



Total antibody end-use since 2019



Rabbit B cell Select[®] workflow

Versatility and efficiency (~500-fold higher efficiency than hybridoma)



Pre-Phase

Target Validation:
QC of immunogen prior to immunization

Target Validation

QC by ELISA, Octet[®]

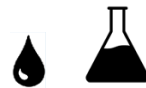


Phase I

Immunization:
28-day immunization

Immunization:

Short timeline



Phase II

PBMC isolation:
30 mL whole blood (no sacrifice required)
B cell enrichment:
Proprietary antigen specific enrichment
B cell culture and primary screen:
40x 96-well plates

Test Bleed:

- ELISA: Immunogen
- ELISA: Off-target
- Flow cytometry (multiplexed)



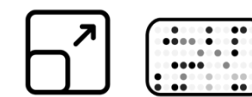
Phase III

Molecular cloning and sequencing: in sets of 48 lead candidates based on primary screening data

Secondary screening:
Sequence confirmation and further testing of sets of 48 recombinant lead candidates

1st Screening (B cell supernatant):

- ELISA: Human Target
- ELISA: Off-target
- ELISA: Cyno Target
- Flow cytometry (multiplexed)
- Octet[®]:
 - In-solution binding
 - Competition
 - Off-rate ranking



Phase IV

Recombinant expression and purification:
in sets of 48 clones

Tertiary testing:
Testing of purified material

2nd / 3rd Screening (Recombinant)

- ELISA: Target
- ELISA: Off-target scaffold
- Flow cytometry (multiplexed)
- Octet[®]:
 - In-solution binding
 - Competition/epitope bin
 - kinetics

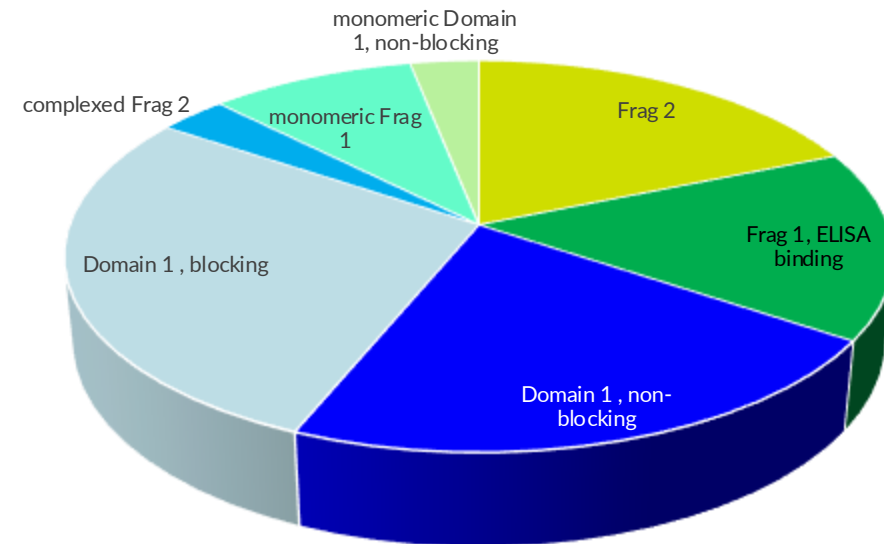
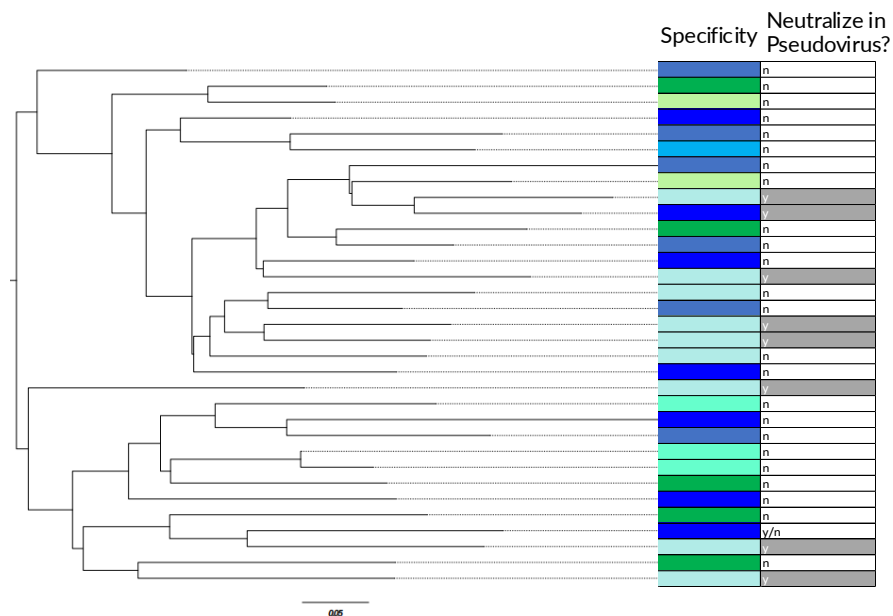
The B cell Select[®] advantage

Phenotypically rich, multilayer screening uncovers functional clones at an early stage

Case study: Infectious Disease program

Generating diverse output while screening for potent function

Immunogens	Screening Methods	Cloning Efficiency	Bins
Frag 1, Full protein complex	ELISA, Octet HTX	38/48 (79%)	7



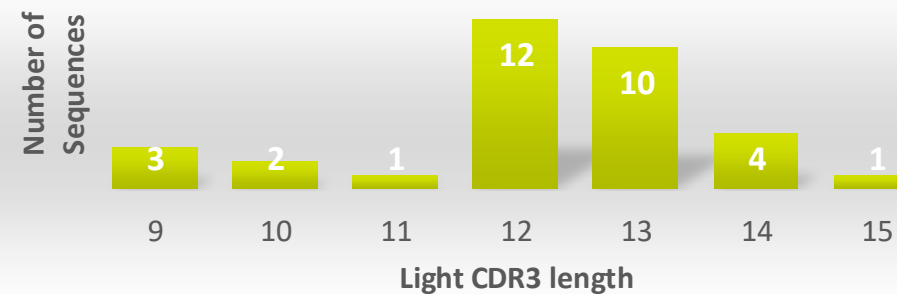
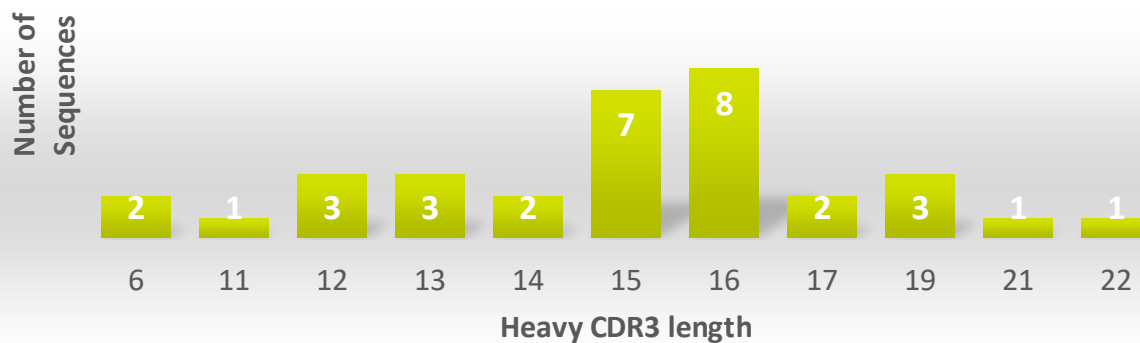
The B cell Select[®] advantage

Clonal diversity of functional leads identified due to high efficiency workflow

Case study: Infectious Disease program

Germline Usage

4 IGHV, 9 IGHD and 5 IGHJ,
14 IGKV and 1 IGKJ

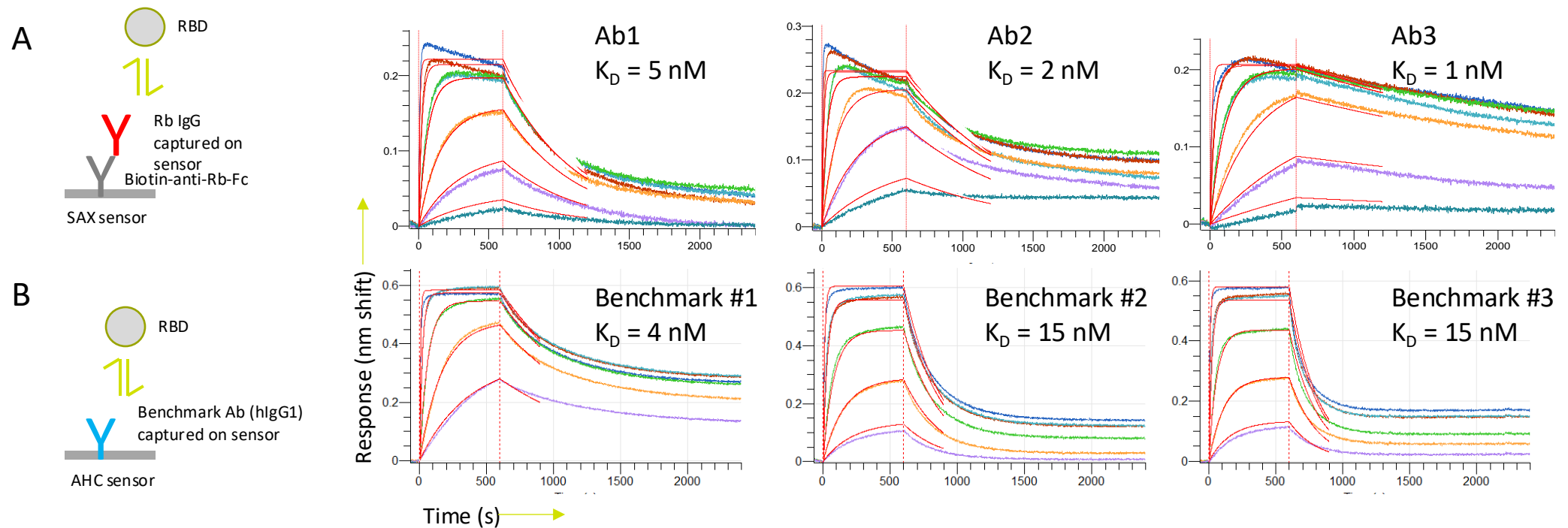


The B cell Select[®] advantage

Superior affinity of identified leads negates the need for costly downstream engineering

Case study: Infectious Disease program

Functional characterization – benchmarked against clinically relevant / commercially available antibodies



LENS^{ai} Hit Expansion Analysis

Mining complete repertoires to extract ALL relevant clones

Discovery

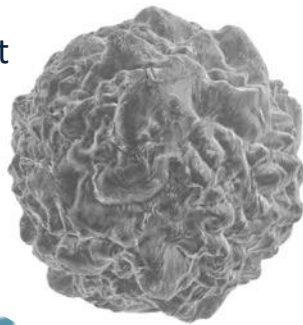
LENS^{ai} Hit Selection

Hit Expansion: Phage display, B-cell, and Hybridoma output as *seed* sequences

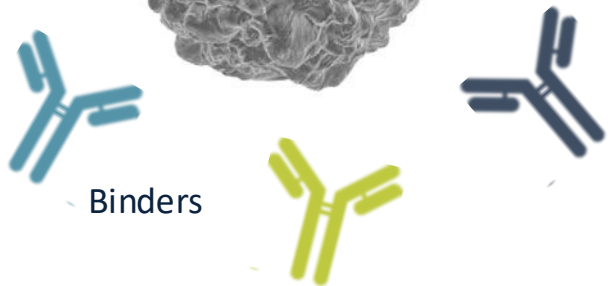
Input

Wet lab lead candidates

Target



Binders



LENS^{ai}

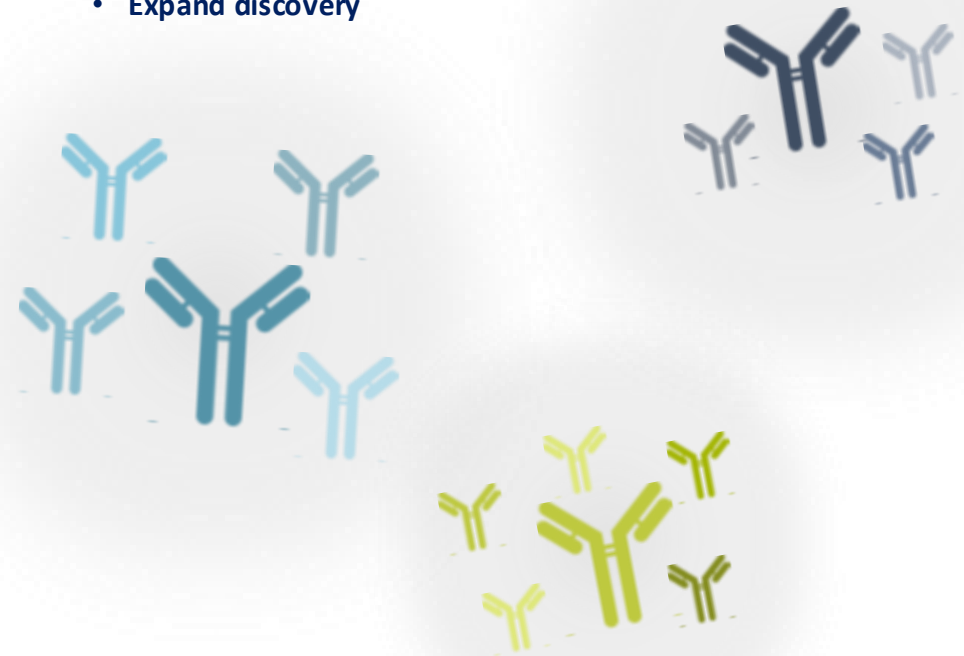
Binders

NGS
Repertoire

Output

Hit expansion

- Multi-modal analyses to retrieve additional hits
- Expand discovery



LENS^{ai} Hit expansion pipeline is an end-to-end workflow built to extract all relevant hits for downstream analysis.

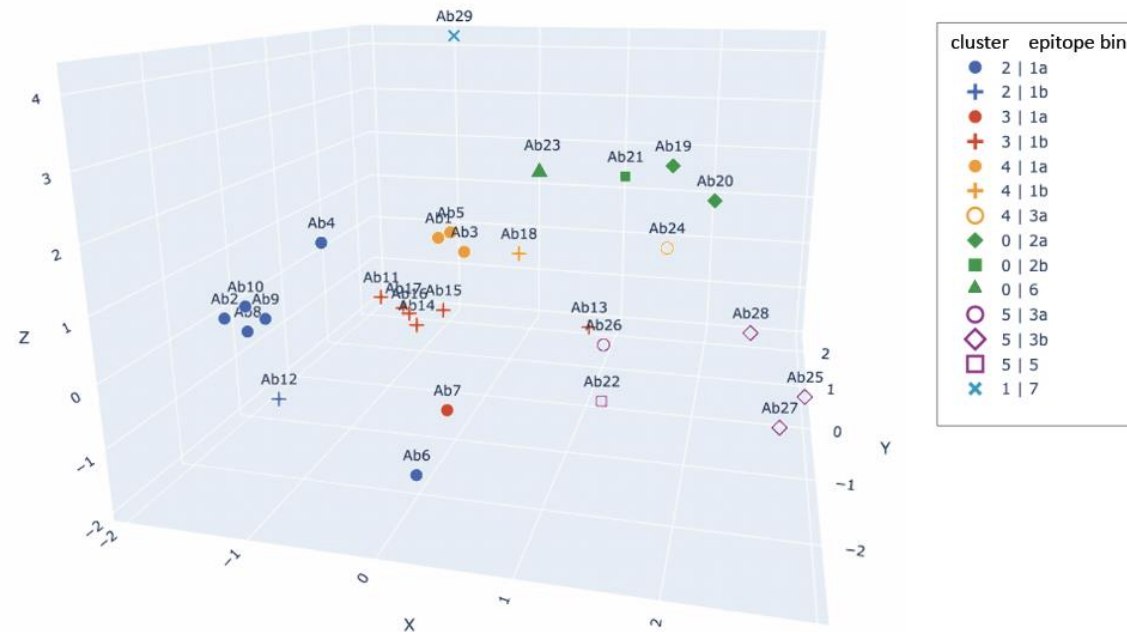
LENS^{ai} Epitope Binning

An infinitely scalable clustering tool without the need for physical material

Integration of physics-based engines and advanced target modeling enables clustering of clones from sequences alone

LENS^{ai} sequence and structure-based epitope binning

- Highly scalable clustering of antibody sequences based on predicted target binding region
- Rapid and early-stage epitope landscape profiling of large panels of hits
- No need for physical material



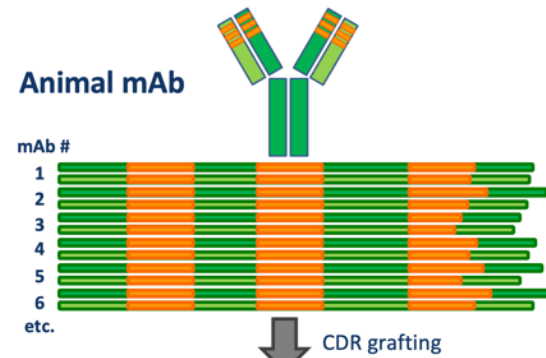
Rapid high-throughput over >5,000 candidates

Immunogenicity Screening: De-risking lead candidates

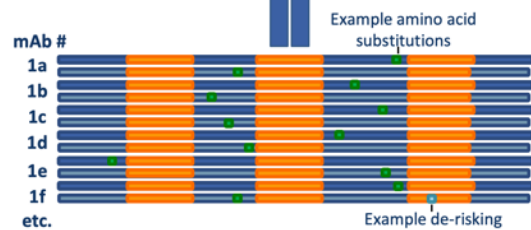
Highly scalable *in silico* risk assessment during humanization of top leads

Input

Non-human lead sequences

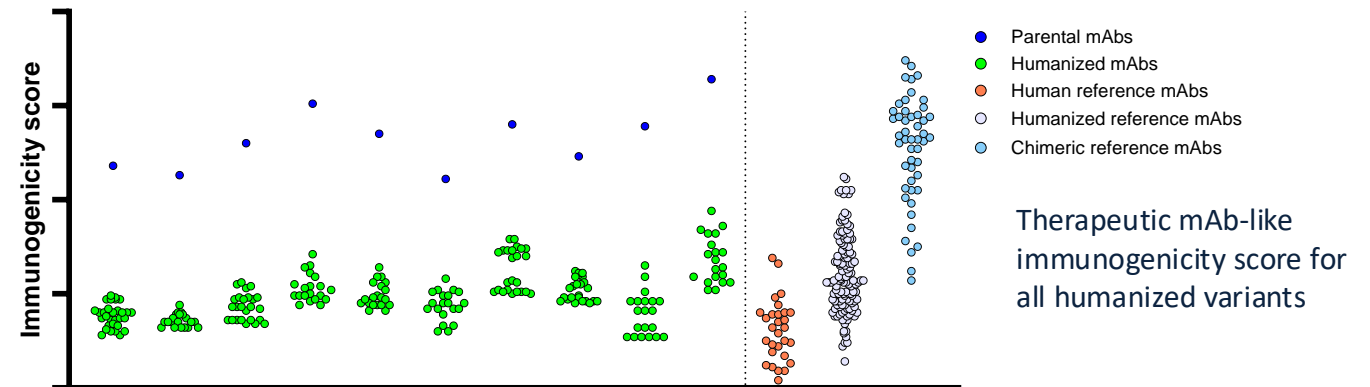


Humanized mAb

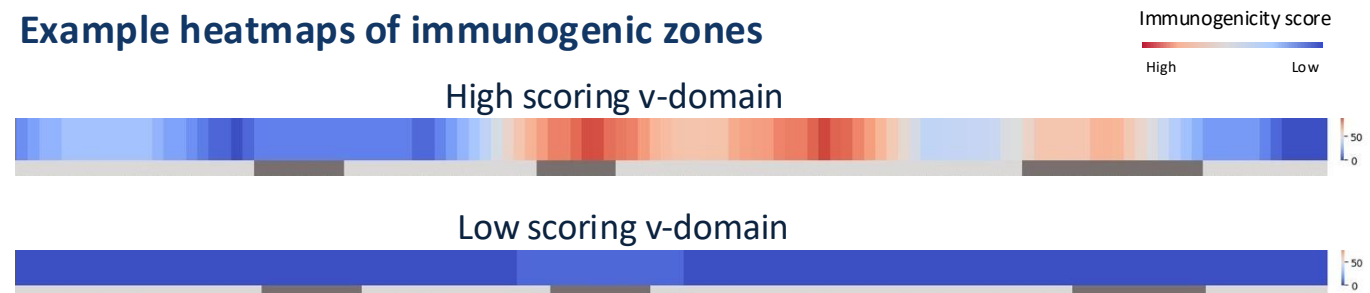


Output

Multiparametric humanization design to derisk therapeutic candidates

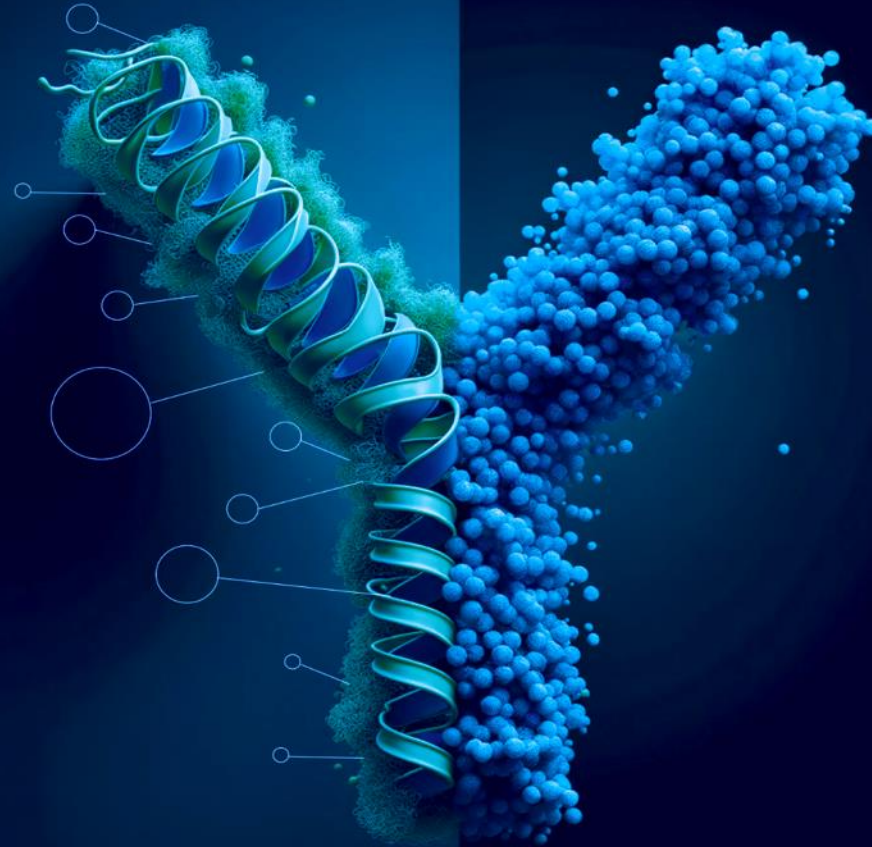


Example heatmaps of immunogenic zones



Advanced antibody technologies: speed + quality

In today's ever-evolving clinical landscape, uniting the industry-leading *in vivo* mAb discovery platform that harnesses the unmatched power of nature with the scalability of *in silico* methods **amplifies therapeutic lead generation.**





BioStrand
a subsidiary of IPA

Disruptive Dialogue Session

Dirk Van Hyfte + Jeff Fried

TECHday
2024
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IpA



BioStrand
a subsidiary of IPA

Data granularity meets data integration

Bridging the gap between disparate data
and discovery, transforming complexity
into clarity for a future where innovation
and precision drives every breakthrough

Disclosures

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