Click.mAb.

Multi-Agent AI Antibody Design Platform

Enterprise Solution

One click to de novo design epitope-specific antibodies
Generative AI empowering every antibody discovery project

- Cutting-Edge Generative AI
- Natural Language Interaction
- Multi-Agent Collaboration
- Team Collaboration Online

PRESENTED BY
Click.mAb Biotech

VERSION
2026.03

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Contents

ALGORITHM CAPABILITIES

Precision Antibody Design: AI Algorithms Breaking Key Bottlenecks

From challenging epitopes to engineering optimization, core algorithm capabilities cover the entire R&D pipeline.

R&D CHALLENGES

Antibody R&D Is Moving Toward Precision Design, Yet Key Bottlenecks Remain

Difficult Epitopes Hard to Target

Traditional methods tend to hit immunodominant regions; obtaining effective antibodies against cryptic, conserved, or otherwise challenging epitopes remains difficult.

Long Optimization Cycles

Humanization, affinity maturation, and developability optimization rely on multiple rounds of trial-and-error, consuming significant time and resources.

Difficulty in Improving R&D Efficiency

Long timelines, high attrition rates, and risk concentrated at critical nodes — relying solely on experience-based screening can no longer meet the industry's need for speed.

SOLUTIONS

SCENARIO ALPHA

Target Specific Epitopes Enable Controllable Antibody Design

01/ Epitope-Specific De Novo Antibody Design / *DE NOVO DESIGN*

Without animal immunization, directly generate novel antibodies targeting specific epitopes from scratch, enabling function-driven rational design.

02/ Epitope Prediction / *EPITOPE PREDICTION*

When multiple binders are obtained, perform epitope-based pre-screening to select those most likely to exhibit target function, reducing downstream validation cost.

SCENARIO BETA

Efficient Engineering Optimization Dramatically Shorten R&D Cycles

03/ Affinity Maturation / *AFFINITY MATURATION*

AI-predicted complex structures analyze spatial residue synergy, identify cooperative mutation sites, and improve affinity through a "1+1>2" strategy.

04/ Antibody Humanization / *ANTIBODY HUMANIZATION*

Leveraging large-scale human framework libraries and AI structure prediction to match optimal frameworks, precisely preserving CDR-framework interactions without back-mutations.

05/ Nanobody Humanization / *NANOBODY HUMANIZATION*

Customized humanization strategies for the unique nanobody framework, balancing humanness and stability while retaining the small molecular weight advantage.

DE NOVO DESIGN

Epitope-Specific De Novo Antibody Design

Without animal immunization, directly generate novel antibodies targeting specific epitopes from scratch, enabling function-driven rational design

COMPUTATIONAL PIPELINE

Specify Target Epitope → Predict Suitable Framework → Generate CDRH3 → Affinity Scoring → Output Report

Core Technical Advantages

Structure-Constrained Framework Selection
Screen candidate frameworks based on spatial features of the target epitope for downstream de novo design.

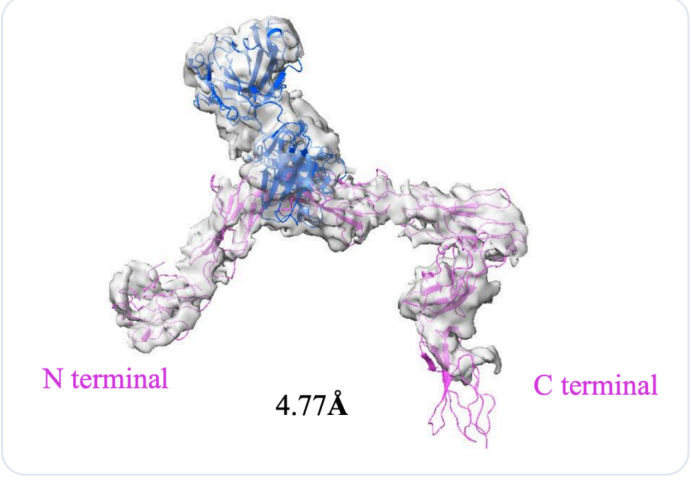
Generative AI-Designed CDRH3
De novo CDRH3 design via generative models, breaking template library limitations and expanding sequence space.

Multi-Dimensional Scoring & Screening
Combining model predictions and structural features to rank candidates, improving first-round output quality.

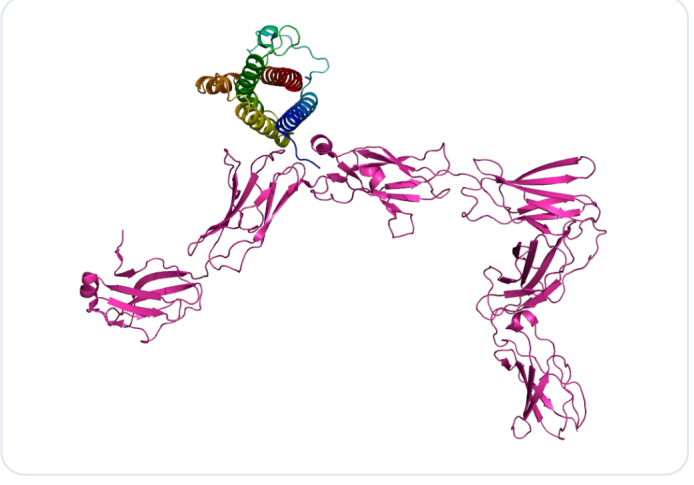
End-to-End Traceable Reports
Output sequences, scored rankings, and reports for team review and downstream decisions.

CASE STUDIES

Case 1: De novo design targeting a challenging functional epitope yielded 7 BLI-validated positive antibodies (KD 10E-7–10E-9 M); 2 blocked natural ligand binding with STAT-3 phosphorylation inhibition at cellular level; cryo-EM confirmed the precise epitope of P211858



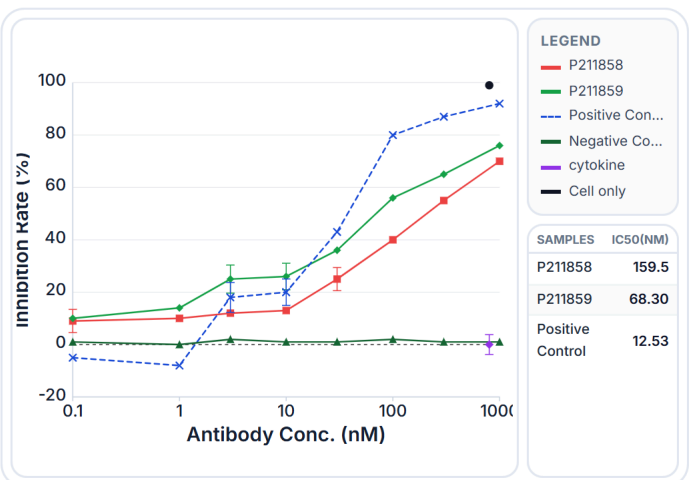
Cryo-EM Epitope Verification



Epitope Prediction Results

ANTIBODY	KD (M)	KA (1/MS)	KD (1/S)
P95531	**7.10E-07**	2.01E+04	1.43E-02
P211853	**1.03E-07**	1.39E+04	1.43E-03
P211854	**7.60E-09**	8.50E+04	6.46E-04
P211855	**9.62E-08**	9.14E+03	8.79E-04
P211856	**7.04E-08**	9.20E+03	6.48E-04
P211857	**9.35E-08**	9.46E+03	8.84E-04
P211858	**5.87E-09**	9.68E+04	5.68E-04
P211859	**3.97E-09**	1.70E+05	6.75E-04

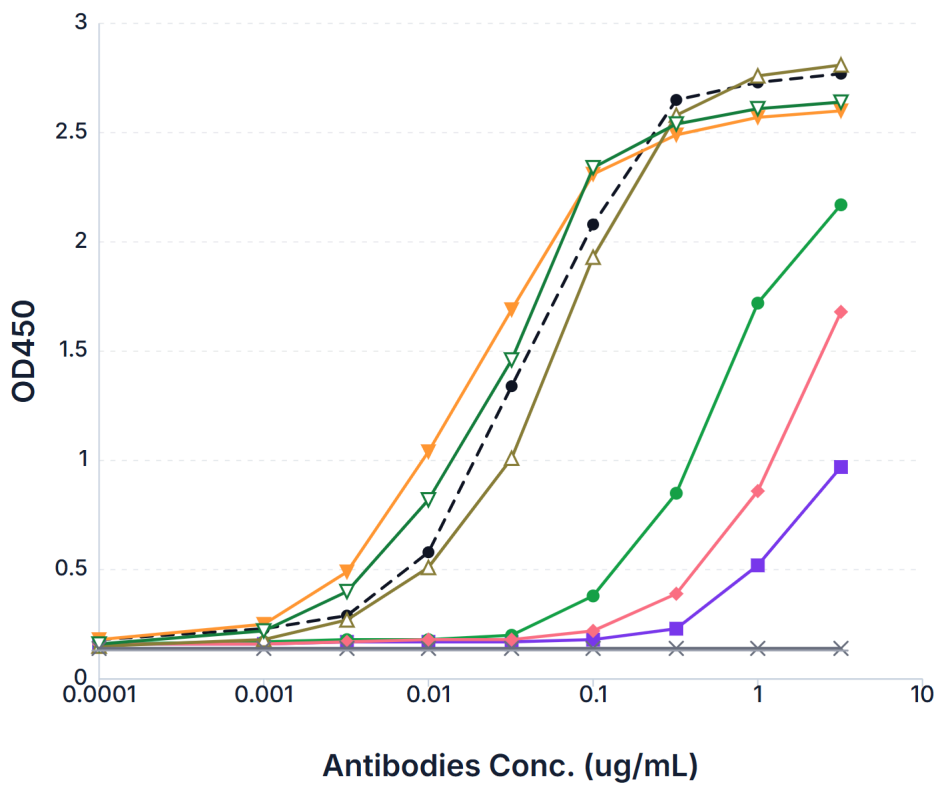
BLI Affinity Measurement Results



STAT-3 Phosphorylation Inhibition Activity

Case 1: Obtained 2 antibodies with ligand-blocking activity

BINDING ASSAY

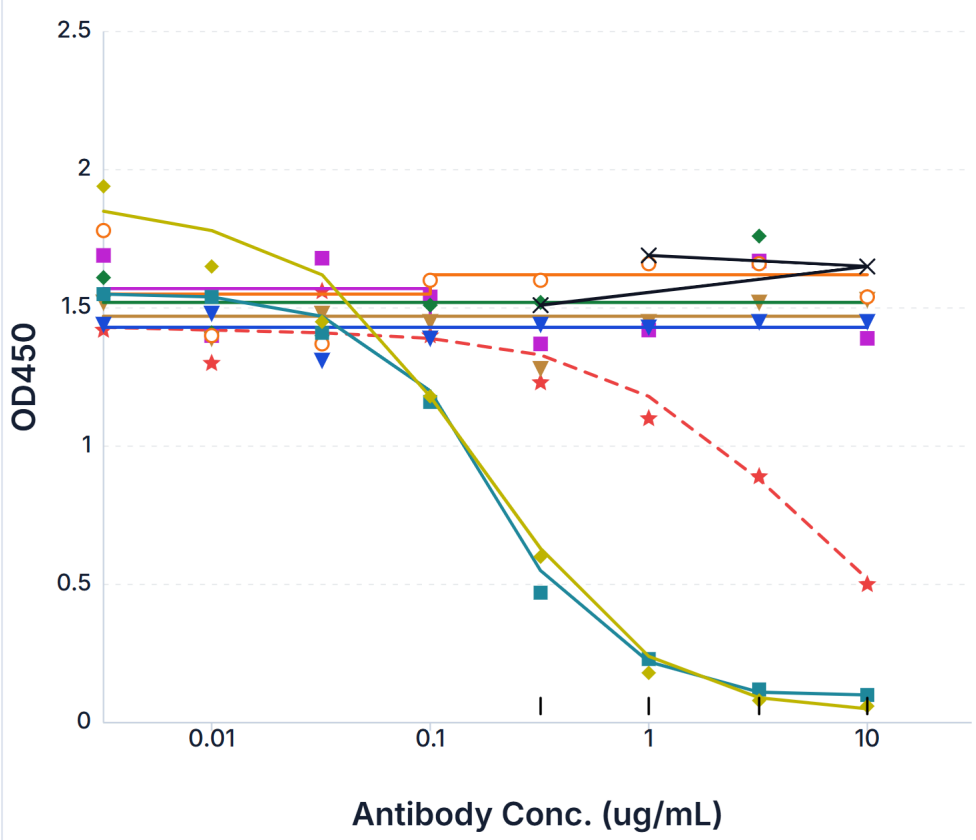


LEGEND
- P95531 (PC)
- P211854
- P211855
- P211856
- P211857
- P211858
- P211859
- NC (IPI)
- BC (1% PBSM)

EC50

SAMPLE	VALUE
P95531 (PC)	0.04748
P211854	0.02238
P211855	1.319
P211856	0.6156
P211857	2.490
P211858	0.06618
P211859	0.03155

BLOCKING ASSAY

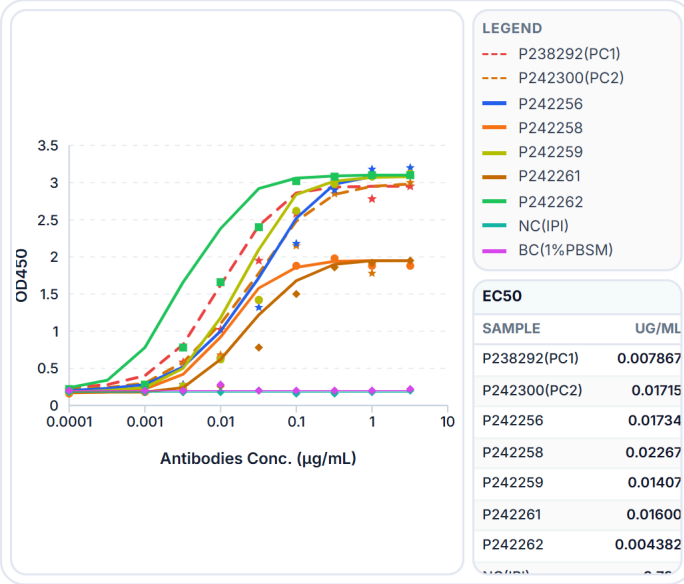


LEGEND
- P95531 (PC)
- P211853
- P211854
- P211855
- P211856
- P211857
- P211858
- P211859
- NC (IPI)
- BC (1% PBSM)

EC50

SAMPLE	VALUE
P95531 (PC)	9.840
P211853	~ 0.2025
P211854	~ 0.000
P211855	~ 1.004e+029
P211856	~ 0.000
A083 (P211857)	~ 0.1119
P211858	0.2076
P211859	0.1756

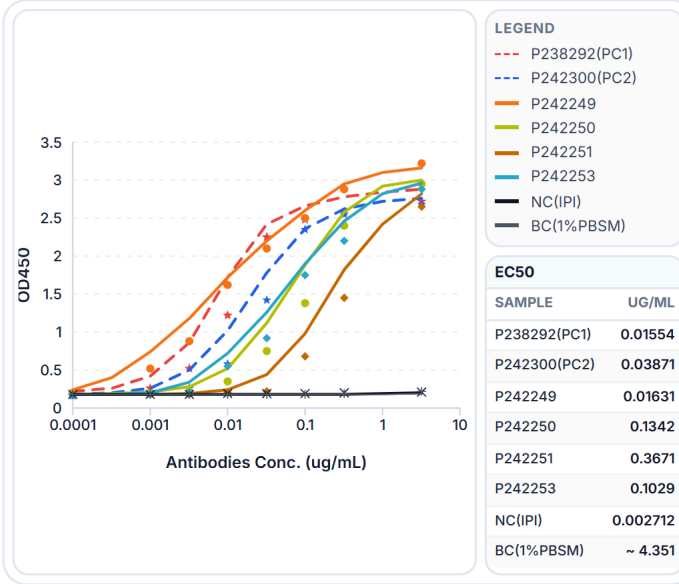
Case 2: Obtained 11 antibodies with BLI-measured KD = 10E-6 to 10E-8 M; one showed comparable cellular functional activity to positive control



EC50

SAMPLE	UG/ML
P238292(PC1)	0.007867
P242300(PC2)	0.01715
P242256	0.01734
P242258	0.02267
P242259	0.01407
P242261	0.01600
P242262	0.004382

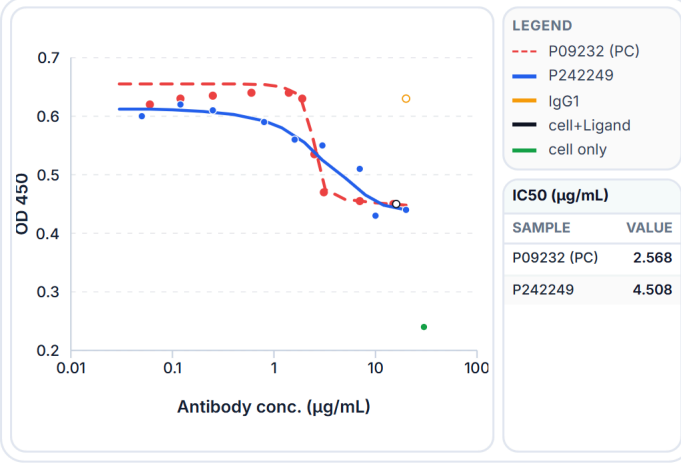
Binding Assay



EC50

SAMPLE	UG/ML
P238292(PC1)	0.01554
P242300(PC2)	0.03871
P242249	0.01631
P242250	0.1342
P242251	0.3671
P242253	0.1029
NC(IPI)	0.002712
BC(1%PBSM)	~ 4.351

Binding Assay



IC50 (μg/mL)

SAMPLE	VALUE
P09232 (PC)	2.568
P242249	4.508

Phosphorylation Inhibition Assay (SUN-16)

ANTIBODY NO.	KD (M)	KA (1/MS)	KD (1/S)
P238292 (PC1)	**1.37E-07**	2.40E+05	3.28E-02
P242300 (PC2)	**2.64E-09**	1.13E+06	2.98E-03
P242249	**4.63E-06**	1.94E+04	9.01E-02
P242250	**7.40E-06**	1.14E+04	8.41E-02
P242251	**6.38E-06**	9.52E+03	6.08E-02
P242253	**2.90E-06**	4.67E+04	1.36E-01
P242256	**1.10E-04**	5.86E+03	6.42E-01
P242258	**4.75E-06**	3.73E+04	1.77E-01
P242259	**3.38E-07**	3.11E+05	1.05E-01
P242261	**1.13E-04**	3.46E+03	3.91E-01
P242262	**1.91E-08**	1.05E+06	2.00E-02
P246176	**9.48E-07**	2.68E+05	2.54E-01

BLI Affinity Measurement Results

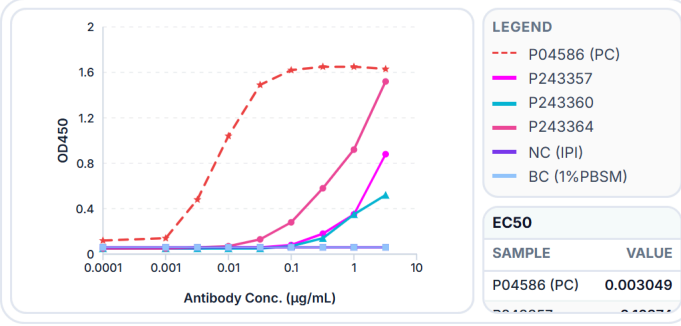
Case 3: Obtained 4 antibodies (KD 10E-7–10E-8 M); 3 showed inhibitory function with no concentration-dependent effect

ANTIBODY NO.	KD (M)	KA (1/MS)	KD (1/S)
P04586 (PC)	**1.47E-12**	2.61E+05	3.83E-07
P243357	**1.82E-08**	4.13E+04	7.52E-04
P243360	**2.31E-07**	1.60E+03	3.70E-04

BLI Affinity Results (1)

ANTIBODY NO.	KD (M)	KA (1/MS)	KD (1/S)
P243364	**2.10E-08**	5.27E+03	1.11E-04
P246188	**1.46E-07**	2.25E+03	3.29E-04

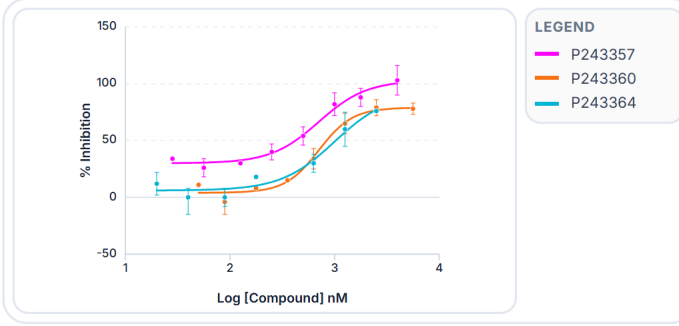
BLI Affinity Results (2)



EC50

SAMPLE	VALUE
P04586 (PC)	0.003049

Binding Assay



Enzyme Assay

Case 4: AI de novo designed antibodies for an ADC target; 3 AI-designed antibodies showed binding activity; A091 competed with specified epitope antibody; expression, purity, and internalization IC50 comparable to benchmark

ANTIBODY NO.	KD (M)	KA (1/MS)	KDIS (1/S)
BM Ab	**8.16E-10**	3.37E+05	2.75E-04
A011	**5.35E-08**	3.24E+05	1.73E-02

BLI Affinity Screening (1)

ANTIBODY NO.	KD (M)	KA (1/MS)	KDIS (1/S)
A091	**1.31E-08**	7.61E+05	1.00E-02
A098	**9.74E-07**	1.11E+04	1.08E-02

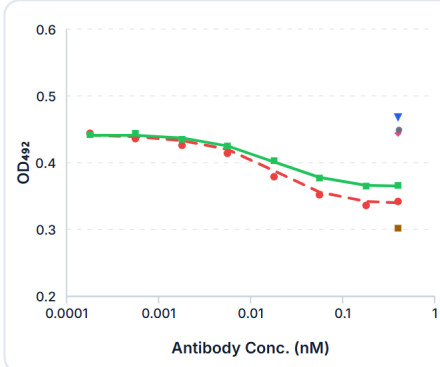
BLI Affinity Screening (2)

Ab2 \ Ab1	Epitope Ab	A091
Epitope Ab	**1.05%**	**2.7%**

Criteria:

- Self-reaction signal <20%, system control
- Inhibition <20%, full competition
- 20% < inhibition <70%, partial competition
- Inhibition >70%, no competition

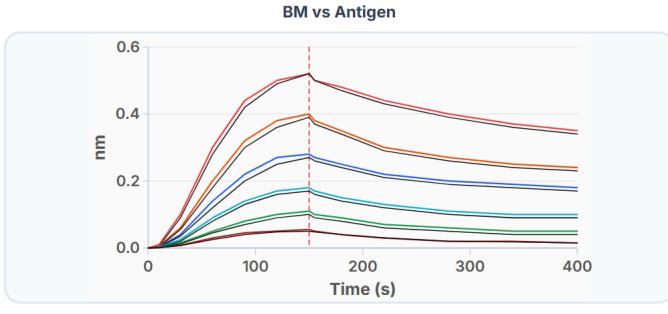
Epitope Binning — A091 Competes with Target Epitope

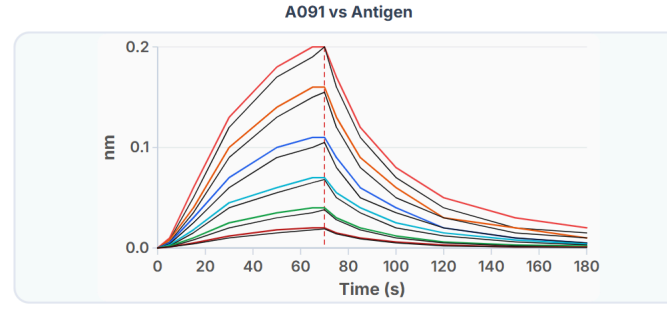


IC50 (nM)	
SAMPLE	VALUE
A091	0.01399
BM Ab	0.01029

Internalization Assay (NCI-N87, Fab-ZAP)

ANTIBODY NO.	KD (M)	KA (1/MS)	KDIS (1/S)	FULL R^2
BM Ab	**2.44E-09**	1.82E+05	4.44E-04	0.99
A091	**2.40E-08**	6.08E+05	1.46E-02	0.98

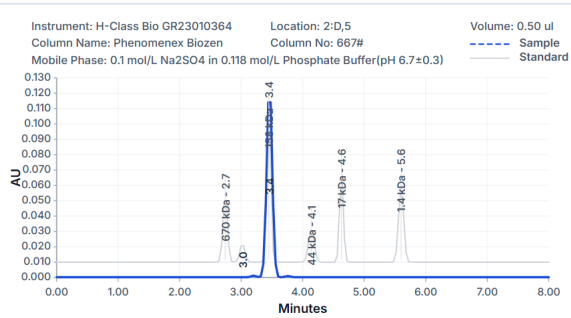




BLI Kinetics Fitting

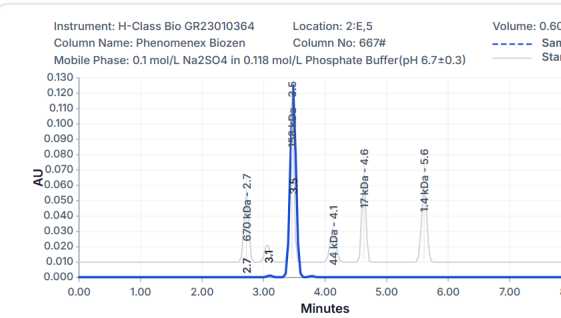
ANTIBODY NAME	CONC. (MG/ML)	CE-SDS (%)	SEC-HPLC (%)	TOTAL (MG)
BM Ab	4.69	>95	98	**3.28**
A091	5.48	>95	>99	**3.84**

Sample name: BM Ab



	RT	Height	Width (sec)	Area	AreaPercentage
1	3.0	210.8	16.4	2390.6	0
2	3.4	127583.3	57.4	786158.7	>99

Sample name: A091



	RT	Height	Width (sec)	Area	AreaPercentage
1	2.7	156.2	7.9	802.1	0
2	3.1	1152.1	28.8	13376.7	2
3	3.5	124280.3	54.1	750249.8	98

Recombinant Expression Verification — CHO-S 10mL Scale

Affinity Maturation

AI-predicted complex structures analyze spatial residue synergy, identify cooperative mutation sites, and improve affinity through a "1+1>2" strategy.

COMPUTATIONAL PIPELINE

Input Antigen-Antibody Sequences → **AI Structure Prediction** → **AI Mutation Analysis** → **Mutation Site Selection** → **Build Multiple Sub-Libraries**

Core Technical Advantages

Multi-Model Fusion Mutation Evaluation
Integrating protein language models, inverse folding models, and complex structure analysis to evaluate mutations across multiple dimensions.

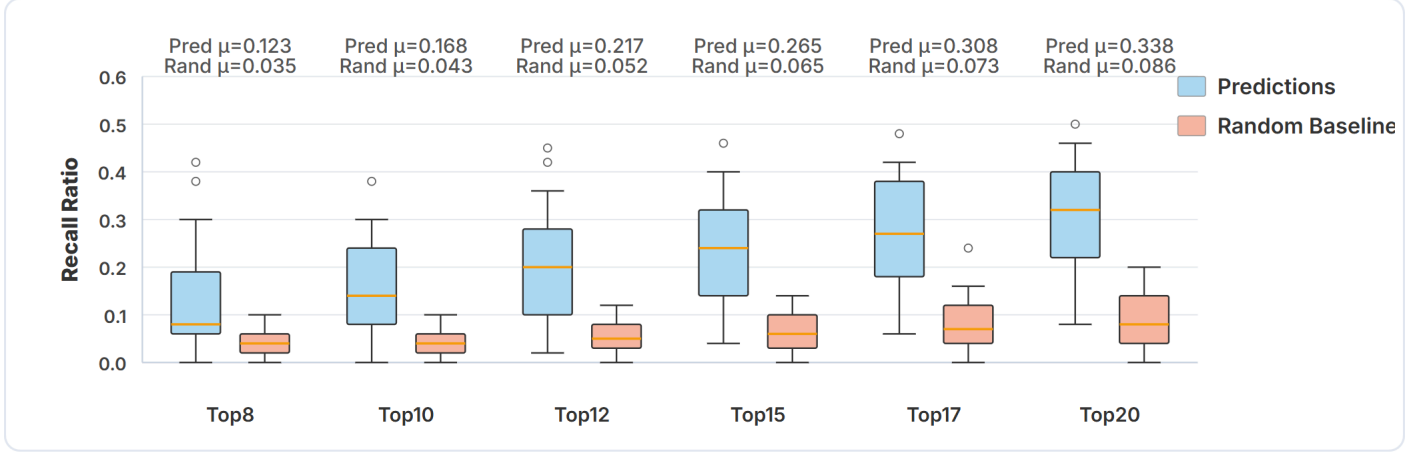
Cooperative Mutation Mining & Ranking
Spatial synergy analysis discovers "1+1>2" mutation combinations and prioritizes candidate sites.

Structure-Driven Affinity Optimization
Identifying key binding-enhancing sites based on AI-predicted 3D complex structures, replacing experience-based random scanning.

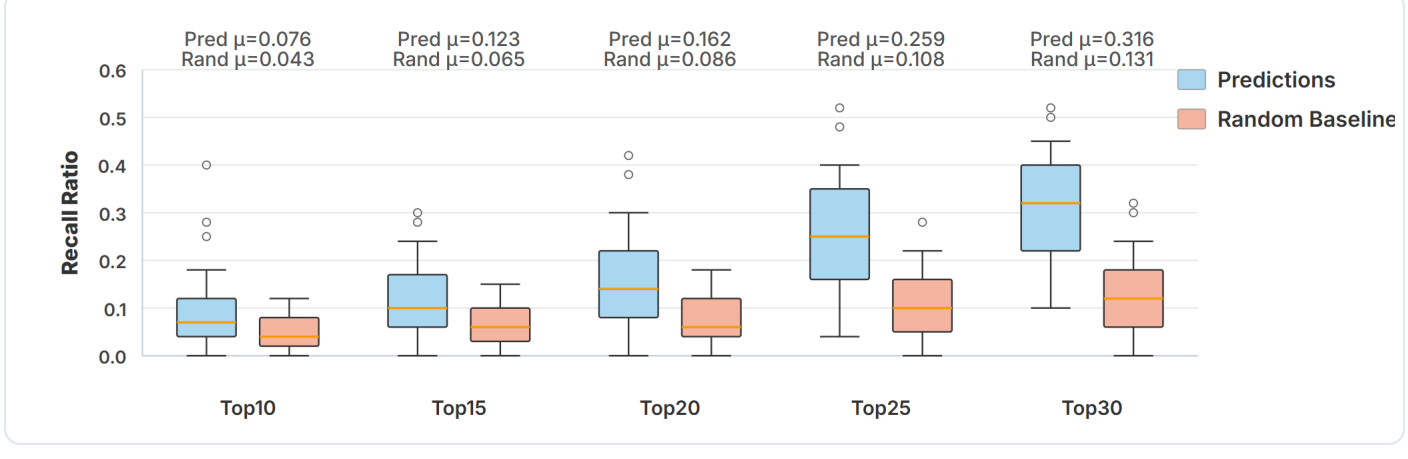
Automated Compact Sub-Library Design
Auto-generating compact sub-libraries around preferred mutations with comprehensive reports including structures, scores, and risk annotations.

CASE STUDIES

Case Study: Collected affinity maturation data from patents for site validation; site hit rate far exceeded random mutagenesis



SAPROT API — Position Recall Comparison



ESMIF API — Position Recall Comparison

Antibody Humanization

Leveraging large-scale human framework libraries and AI structure prediction to match optimal frameworks, precisely preserving CDR-framework interactions without back-mutations.

COMPUTATIONAL PIPELINE

Input Parental mAb Sequence → **AI-Generated Framework Library** → **Graft CDRs to Framework** → **AI Model Scoring & Screening** → **Output Report**

Core Technical Advantages

Intelligent Framework Matching
Breaking traditional similar-framework limitations, screening candidates from a larger human framework space that better support parental CDRs.

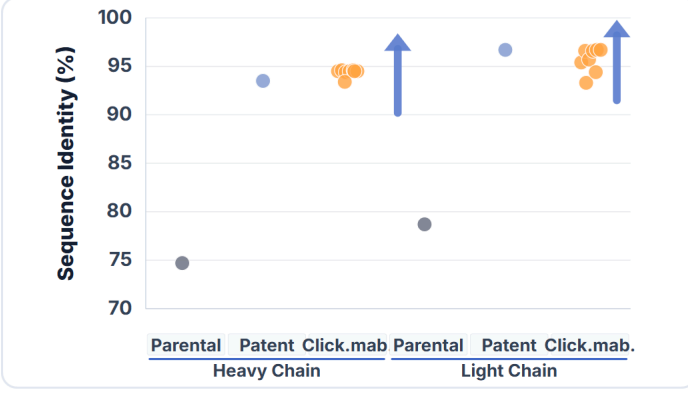
Structure-Driven Affinity Preservation
Evaluating CDR-framework interactions based on AI-predicted 3D structures to maintain affinity after humanization.

No Back-Mutations Required
High-quality candidates obtained without back-mutations through structural compatibility and intelligent framework screening.

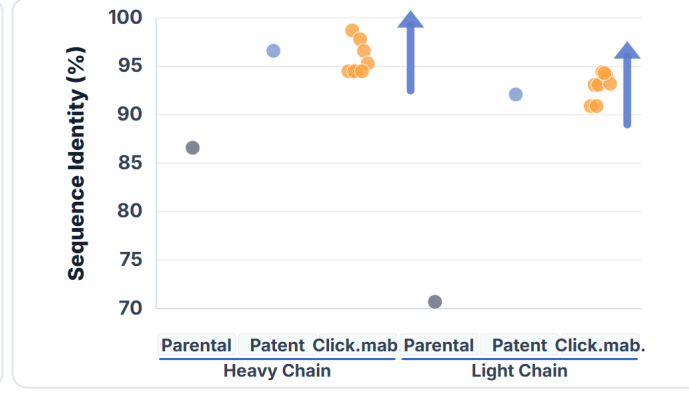
Multi-Dimensional Screening
Scoring by humanization degree, stability, and biophysical properties to output superior recommendations.

CASE STUDIES

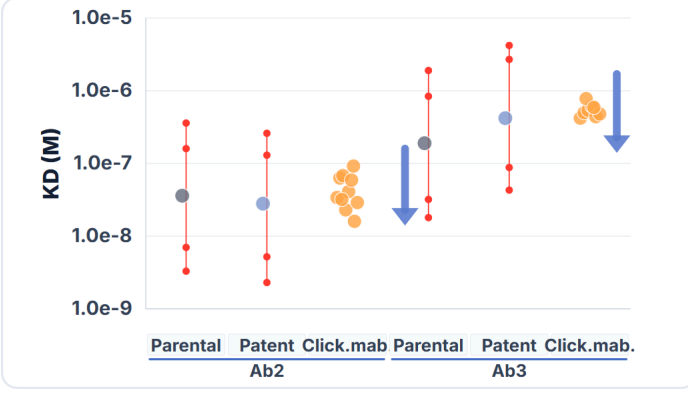
Case Study: A North American client selected 20 manual humanization projects for blind testing; the platform generated 400 highly humanized sequences; the project with the largest manual/AI divergence was chosen for wet-lab validation — high humanization did not sacrifice affinity



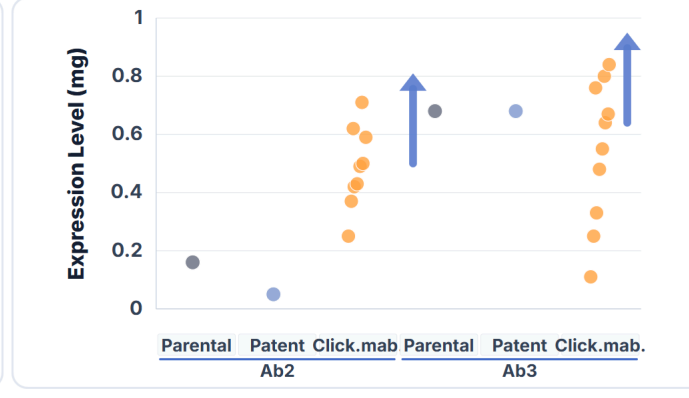
Humanization Degree (Ab2)



Humanization Degree (Ab3)



Affinity



Expression Level (4mL System)

Nanobody Humanization

AI high-precision structure prediction and stepwise back-mutation design evaluate key residue roles, preserving affinity while improving humanization degree with lower experimental costs.

COMPUTATIONAL PIPELINE

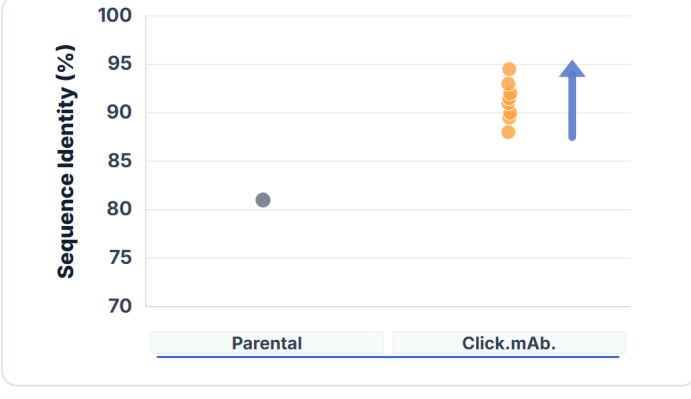
Input VHH Sequence → **AI Structure Modeling** → **Human Framework Screening** → **Key Site Optimized Grafting** → **AI Multi-Dimensional Scoring** → **Output Report**

Core Technical Advantages

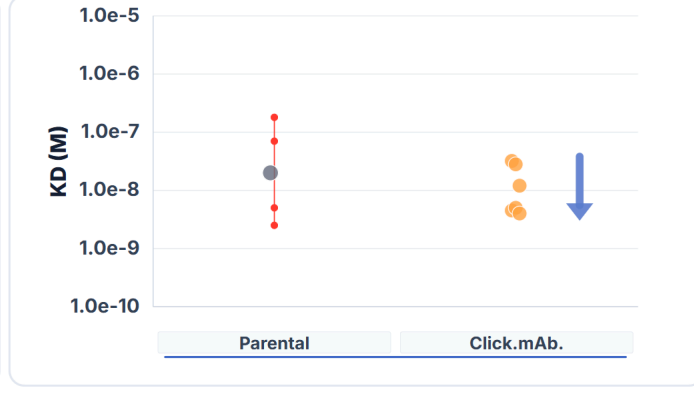
- **Dedicated Framework Selection**
  Tailored for VHH humanization, screening human germline frameworks best suited to support VHH CDRs.
- **Unique Site Optimization**
  Focusing on VHH-specific framework residues, DE Loop, and key structural sites affecting conformation and stability.
- **Progressive Back-Mutation Design**
  Stepwise optimization around framework-CDR interface, Vernier zone, and core residues, balancing function with humanness.
- **Multi-Dimensional Risk Assessment**
  Scoring by humanization degree, structural stability, physicochemical properties, and risk sites.

CASE STUDIES

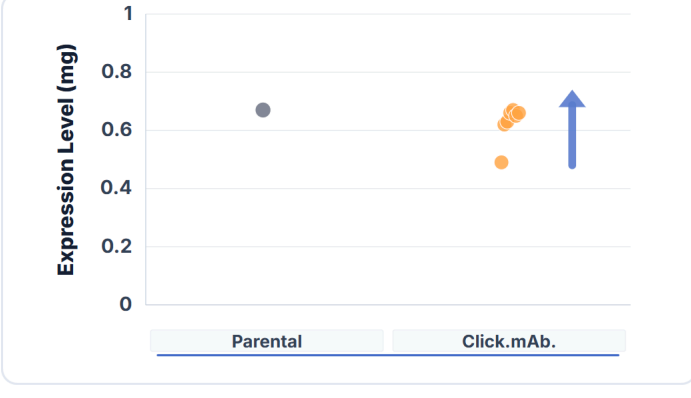
Case Study: 7 humanized sequences recommended, achieving 89–94% humanization; 4 showed improved affinity, >80% had expression comparable to parental, all with >90% purity — balancing activity, expression, and developability



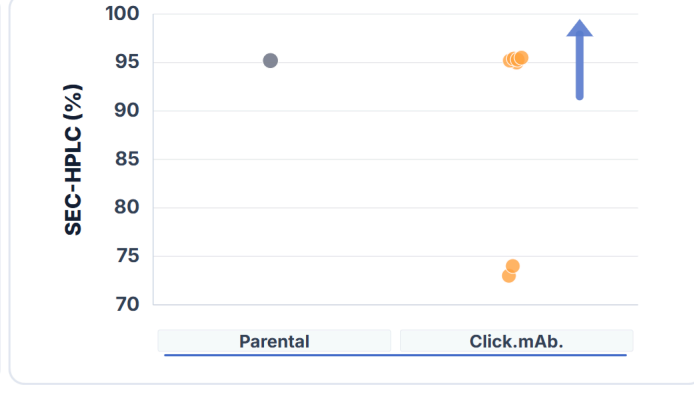
Humanization Degree



Affinity



Expression Level



Purity

CHALLENGES

AI Antibody Design Is Evolving Rapidly, Yet Effective Adoption Remains a Challenge

Antibody R&D has entered an era of high complexity and multi-technology integration. AI tools are proliferating, yet translating scientific intent into computational results efficiently still faces significant obstacles.

TOOL & COMPLEXITY EXPLOSION

TOOL EXPLOSION

Rapid Tool Growth Ever-Rising Complexity

From structure prediction and epitope analysis to affinity maturation and humanization, each step involves numerous tools. Researchers must jump between fragmented tool chains and manually link them.

Too Many Tools

Dozens of tools for de novo design, structure prediction, risk assessment, etc. are scattered everywhere, lacking a unified entry point

Thousands of Parameter Combinations

Each tool has its own parameter system; different combinations have a huge impact on results, making it hard for scientists to master them all

Difficult Pipeline Orchestration

From optimization to de novo design, different tasks require entirely different tool combinations and chaining logic

HIGH BARRIER TO ENTRY

HIGH BARRIER

Cross-Domain Knowledge Overlap Extremely High Learning Cost

Using AI tools efficiently requires multidisciplinary backgrounds in structural biology, antibody engineering, and computational biology. A single-domain expert can hardly navigate the entire workflow alone.

Cross-Domain Knowledge

Structural biology, antibody engineering, pharmacology/toxicology, CMC development — knowledge barriers stacked upon barriers

Extremely High Learning Cost

Each tool has its own interface and operational logic; onboarding takes long and team training costs are high

Difficult Intent Translation

Scientists must manually translate research intent into tool operations; a gap exists between scientific questions and computational tasks

Computational Resource Barrier

Complex models require substantial computing power; environment configuration and resource scheduling add extra burden

CORE CONTRADICTION

Scientific Intent & Project Needs

Researchers focus on biological questions and clinical goals

≠

Tool Operation & Computational Execution

Tools require programming, parameter configuration, and pipeline orchestration

Scientists need an AI research partner that understands their intent and autonomously plans and executes tasks

INTELLIGENT INTERACTION

Intelligent Interaction & Multi-Agent Collaboration

No need to learn complex toolchains \u2014 drive professional capabilities with natural language. Multi-agent collaboration, with core algorithms and lightweight tools orchestrated on demand, letting researchers focus on scientific judgment.

NATURAL LANGUAGE INTERACTION

NATURAL LANGUAGE

Replace Operations with Conversation
Zero-Barrier AI Access

Researchers describe R&D needs in natural language; the platform automatically parses intent, selects algorithms, orchestrates pipelines, and outputs results.

"Design antibodies targeting the PD-L1 immune escape epitope"

"Target confirmed: design antibodies around the PD-L1 immune escape functional epitope.
Preparing to execute: ① Confirm PD-L1 UniProt sequence → ② Retrieve PD-L1 / PD-1 complex structure → ③ Identify key interacting residues and functional epitope → ④ Perform epitope-based de novo design..."

MULTI-AGENT COLLABORATION

MULTI-AGENT SYSTEM

Four Specialized Assistants
Autonomous Collaborative Decision-Making

Each AI assistant has independent capabilities, coordinated by a collaboration engine, completing tasks within a single conversation turn.

Antibody Design Assistant

Understands requirements, invokes tools, outputs reports, and provides professional advice and support for researchers.

Visualization Assistant

3D structures, risk sites, design reports \u2014 intuitively presenting computational results.

Risk Assessment Assistant

Multi-dimensional assessment of developability risks including humanness, aggregation, and chemical stability.

Next-Step Advisor

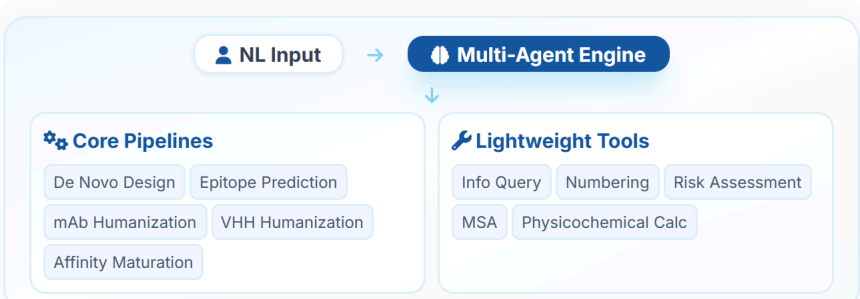
Providing next-step recommendations and pathway prioritization based on current data.

SMART ORCHESTRATION ARCHITECTURE

SMART ORCHESTRATION

Core Pipelines
+ Lightweight Tools

Unifies algorithm pipelines and lightweight tools; AI assistants auto-orchestrate call chains per task.



REAL-WORLD R&D COMPLEXITY

Real-World R&D Projects Involve Tools, Collaboration & Decisions

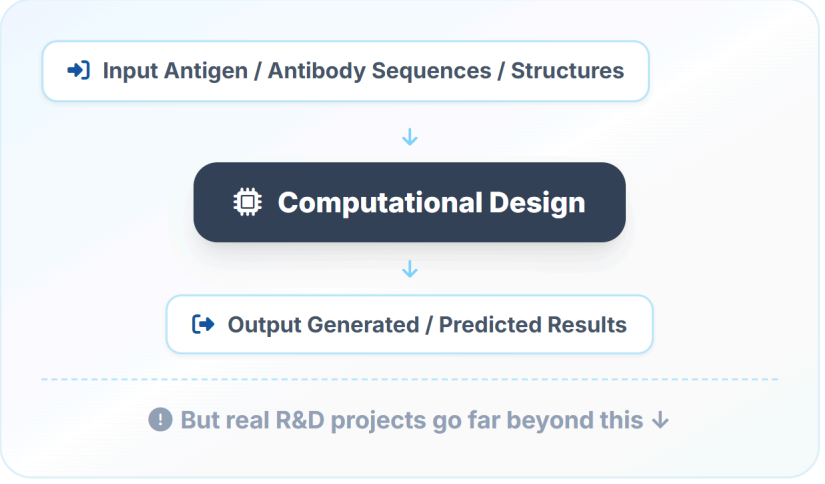
Real antibody R&D projects go far beyond one or a few computations. From strategy exploration and data integration to team collaboration and knowledge transfer, every step demands more from tools.

COMPUTATION IS JUST THE STARTING POINT

BEYOND COMPUTATION

Computation Is Just Step One
Project Management Is the Complete Picture

Input sequences/structures, run design to generate results — but this is merely the starting point. Pathway decisions, data aggregation, team consensus, and knowledge accumulation are all still needed.



REAL-WORLD CHALLENGES

Multi-Pathway Exploration

The same target often requires parallel design pathways, but parameters and intermediate results from each pathway are scattered across different tools and files, making unified management and cross-comparison impossible \u2014 decisions can only be made through manual aggregation.

Multi-Source Heterogeneous Data

Computational predictions, experimental measurements, literature research, external databases — data is scattered across different systems in various formats; correlation analysis relies mostly on manual assembly, making it error-prone and easy to miss critical information.

Team Sharing & Consensus

Computation, experiment, and engineering teams each look at their own data, lacking unified project context; team members are frequently out of sync on progress and rationale, keeping communication costs high.

Knowledge Accumulation & Transfer

Which pathways worked, which parameters were effective, why key decisions were made — this experience mostly stays in personal memory; when personnel change, project knowledge is lost, and subsequent teams must start from scratch.

Proper tool and project integration helps improve R&D efficiency and quality

However, most existing AI tools focus on single computation tasks, lacking systematic support for multi-pathway management, data integration, team collaboration, and knowledge transfer

PROJECT-LEVEL COLLABORATION

Project-Level Management for Team Collaboration

Deeply integrating algorithm capabilities with organizational management, upgrading from personal tools to team-level R&D infrastructure for continuous accumulation and reuse of R&D assets.

PARALLEL PIPELINES

PARALLEL PIPELINES

Push Multiple Pipelines in Parallel
Decision Rationale Always Traceable

Automatic Design Pipeline Archiving

Multiple design pipelines can be pursued simultaneously; all branches are automatically archived, historical rationale is clear, and can be traced at any time.

INDIVIDUAL EXPLORATION → TEAM DISCUSSION

EXPLORE → DISCUSS

Link Independent Validation & Collaborative Progress

AI Assistant Always Available

Whether in personal exploration or team review, the AI assistant is always ready, providing instant support for analysis, literature search, and recommendations.

AUTOMATED KNOWLEDGE ACCUMULATION

KNOWLEDGE ACCUMULATION

Knowledge Stays with the Team Accumulated as Team Assets

Automatic Project Knowledge Base Aggregation

Materials, results, and discussion records are automatically aggregated into the knowledge base; the team works from the same info, eliminating silos.

Reviewable · Traceable · Transferable

The entire project process is reviewable, traceable, and transferable. R&D experience becomes sustainable, reusable team assets.

Project-Level Collaboration Capabilities at a Glance

Parallel Pipelines
Branch Archiving · Metric Comparison

Explore First, Discuss Later
Personal Validation · Team Review

Automated Knowledge Accumulation
Unified Knowledge Base · Zero Loss

AI Always Available
Every Step · Always Ready

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De Novo Design Report Example

De Novo Antibody Design Report for Specific Epitope Target

Report Summary

	Description	Summary
Epitope Patch Confirmation	Confirm epitope structure for antibody generation	You selected 4H1S-B_0 as the epitope patch for antibody design.
Epitope Patch V-Gene Matching	Use AI models to identify antibody sequences with high binding probability to the given epitope patch	Selected 24 template antibody sequences from 7 germline types for antibody generation.
Antibody Generation	Based on the given epitope information, template antibodies that match will first be searched. Then, antibody sequences will be generated and evolved using internal antibody language models and affinity prediction models. Finally, antibody sequences of different scales will be obtained through clustering methods.	Finished generating antibody sequences of different scales, generated 891410 sequences for 1 million library.
Generated Antibody Summary	Analysis and overview of generated antibodies	Summarizes total antibody sequences across libraries, details distribution of germlines and CDRH3 lengths in largest library, provides amino acid distribution, and download links for different library sizes and template sequences.

Epitope Patch Confirmation

Based on provided information, we confirmed the target epitope patch 4H1S-B_0 for antibody binding. Details of the patch:

patchId	Patch Residue Numbers and Types
4H1S-B_0	100E;101V;102A;103H;104F;105M;106N;107A;108L;109R;110Y;111D;112A;113M;114A;115L;116G;117N;118H;119E;120F;121D;122N;123G;124V;125E;126G;127L;128I;129E;130P;131L;132L;133K;134E;135A;136K;137F;138P;139I;140L;154I;156G;157L;158Y;159L;182P;184L;185S;186N;187P;282A;283F;284G;287L;323D;324I;326K;327W;328R;329I;330K;331L;332D;335S;349S;34T;35N;36D;37V;38H;392G;395R;396S;39S;409E;40R;412A;413A;416P;417F;41L;42E;61V;80L;81L;82D;84G;85D;86Q;87Y;88Q;89G;90T;91I;92W;93F;94T;95V;96Y;97K;98G;99A

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De Novo Design Report Example

Epitope Patch V-Gene Matching

Internal AI models predict the template antibodies of following germlines have higher matching probability with this epitope, indicating better potential for successful antibody design. Each germline type may correspond to multiple antibody sequences. The V-Gene portions will be used for CDRH3 sequence generation. To reduce development risks, template antibody germlines are sourced from clinically-tested antibodies.

Germline Type
IGHV3-15
IGHV4-30
IGHV4-31
IGHV4-34
IGHV4-39
IGHV4-4
IGHV4-59

Antibody Generation

Based on the given template antibody sequences, antibody sequences will be generated using internal antibody language models and ranked using internal affinity prediction models. Subsequently, evolutionary algorithms will be employed for evolution screening and filtering of candidate antibody sequences. Finally, different scales of antibody sequences will be obtained through affinity prediction model scoring and clustering methods.
We generated, evolved and screened antibody sequences with CDRH3 lengths of 8, 10, 12, 14, and 16 residues this time.

After generation, risk site analysis was performed to remove CDRH3 sequences with high-risk elements.

Generated Antibody Summary

AI models generated and validated 891410 antibody sequences. Statistical analysis of sequence distribution across germline types, CDRH3 lengths, and amino acid composition:

Generated Antibody Sequence Distribution

Germline Type	CDRH3Len = 8	CDRH3Len = 10	CDRH3Len = 12	CDRH3Len = 14	CDRH3Len = 16
IGHV3-15	4360	16762	35343	41339	20776
IGHV4-30	2373	15553	40984	54124	27703
IGHV4-31	2772	14730	30201	41165	20707
IGHV4-34	5924	20566	44001	55001	27754
IGHV4-39	5310	14871	41502	54555	27359
IGHV4-4	4077	11714	32071	41141	20599
IGHV4-59	2987	15493	35197	41571	20825

Amino Acid Distribution for CDRH3Len = 8

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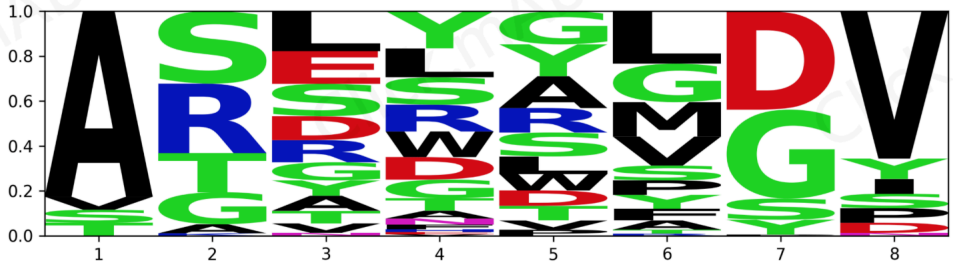
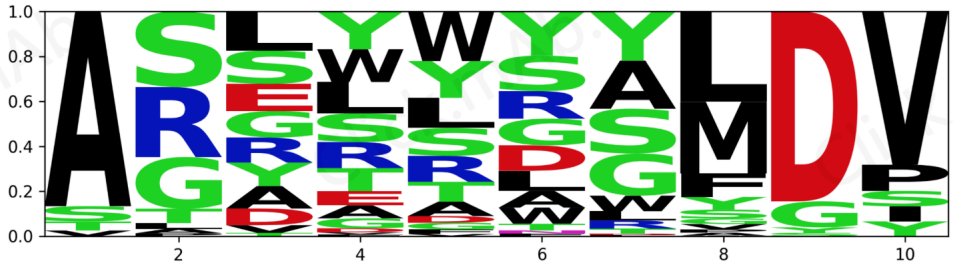
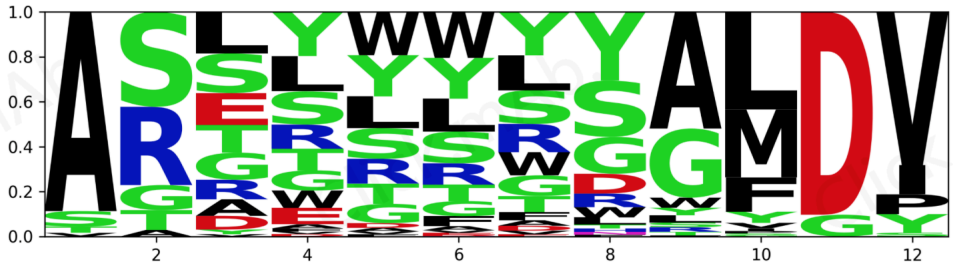
De Novo Design Report Example



Amino Acid Distribution for CDRH3Len = 10



Amino Acid Distribution for CDRH3Len = 12



Amino Acid Distribution for CDRH3Len = 14

Amino Acid Distribution for CDRH3Len = 16

De Novo Design Report Example

Download Generated Antibody Sequences

Download Generated Antibody Sequences (1 million)

Download Generated Antibody Sequences (200k)

Download Generated Antibody Sequences (10k)

- Notes:
  - Tables include: Sequence ID (ID), heavy chain sequence (sequence), heavy chain germline type (germline), CDRH3 sequence (CDRH3), CDRH3 length (CDRH3Len), and FWR4 sequence (JSeq).
  - All heavy chains share the same humanized light chain sequence: EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPTFGQGTKVEIK.
  - All heavy chain sequences in the table have the same FWR4 sequence, which is: WGQGTLVTVSS.

Download Template Germline Sequences

Download Germline Sequences

- Note:
  - Table includes germlineHseq column containing pre-CDRH3 germline sequences for antibody library construction.
  - The CDR1/2 in germline file will be hidden in the demo instance.

Report Conclusion

Through de novo antibody design, we identified 7 germline types comprising 24 template antibodies with high predicted binding probability to the target epitope patch. For each template, we generated antibodies with CDRH3 lengths of 8，10，12，14，16. Libraries of 10k, 200k, and 1 million sequences were created, containing 9582, 189226, and 891410 sequences respectively. You may select libraries of different sizes for construction and screening. Note that larger libraries generally yield higher screening success rates.

You can now proceed with antibody library construction and screening using the provided germline sequences, CDRH3 sequences, and FWR4 sequences to obtain antibodies binding to the target epitope.

Click.mAb.

Affinity Maturation Report Example

Antibody Affinity Maturation Report

1. Report Overview

This report provides a comprehensive affinity maturation design plan for the user-submitted antibody. We began with a systematic analysis of the input antibody sequence, including its Germline, CDR (Complementary Determining Region) sequences, and potential risk sites. Subsequently, we integrated **sequence-based** and **structure-based** computational design approaches to identify sites with a higher probability of improving antibody affinity. Based on this site information and internal interacting residue pairs, we designed multiple sub-libraries to maximize coverage of mutation sites while considering as many internal antibody interactions as possible. The core of this report prioritizes the recommended core mutation sites and provides a structure file and library visualization to aid in decision-making. Full mutation data is provided in both tabular format and as a downloadable CSV file to offer clear and reliable support for subsequent experimental validation.

2. Input Analysis

2.1. Basic Antibody Information

The following is the basic information of the antibody derived from the analysis of your input sequence or structure.

Information Type	Content
Heavy Chain Sequence	QVQLKESGPGLVAPSQSLSITCTVSGFSLASYGVHWVRQPPGKGLEWLGVIWTGGSTNYNSALMSRLSINRDNSKSQVFLKLNSLQTDDTAIYYCARDRGYGYGGFAYWGQGTLVTV(length : 117)
Light Chain Sequence	DIQMTQSPASLSASVGETVTITCRASENIYSYLAWYQHKQGKSPQLLVYNAKSLAEGVPSRFSGSGSGTQFSLKINSLQPEDFGSYYCQHHYGTPWTFGGGTKLE(length : 105)
Input Structure File	**PDB1**
Heavy Chain CDRs	CDR1: VSGFSLASYGVH, CDR2: WLGVIWTGGSTN, CDR3: ARDRGYGYGGFAY
Light Chain CDRs	CDR1: RASENIYSYLA, CDR2: LLVYNAKSLA, CDR3: QHHYGTPWT
Species Origin	mouse
Light Chain Germline	IGKV12-44*01
Heavy Chain Germline	IGHV2-9*02

2.2. Risk Site Analysis

Affinity Maturation Report Example

To ensure the antibody's developability, we have predicted potential chemically unstable sites (e.g., deamidation, oxidation) within the antibody sequence. These sites may affect the homogeneity and activity of the antibody during manufacturing or storage.

Chain	Sequence	Risk Summary
H	QVQLKESGPGLVAPSQSLSITCT VSGFSLASYGVHWVRQPPGKGL EWLGVIWTGGSTNYNSALMSRL SINRDNSKSQVFLKLNSLQTDDT AIYYCARDRGYGYGGFAYWGQG TLVTV	High: 0, Medium: 1, Low: 1
L	DIQMTQSPASLSASVGETVTITC RASENIYSYLAWYQHKQGKSPQ LLVYNAKSLAEGVPSRFSGSGSG TQFSLKINSLQPEDFGSYYCQHH YGTPWTFGGGTKLE	High: 0, Medium: 2, Low: 0

3. Recommended Mutation Sites & Visualization

We have combined both **sequence-based and structure-based** methods for affinity maturation design. The following are the core mutation sites recommended after a comprehensive evaluation:

Chain Type	Mutation Site	Mutation Region
H	**28S, 30A, 31S**	CDR1
H	**50V, 52W, 54G, 55G, 56S, 58N**	CDR2
H	**100G, 102G, 105G, 107A**	CDR3
H	**11L**	FWR1
H	**64M, 70N, 71R, 72D, 73N, 74S, 82L, 92I**	FWR3
L	**24R, 25A, 26S, 27E, 29I, 33L, 34A**	CDR1
L	**48V, 52K**	CDR2
L	**90H, 91H, 92Y, 93G**	CDR3
L	**37Q, 38H, 40Q**	FWR2
L	**56E, 70Q, 76N, 80P, 83F, 85S**	FWR3
L	**100G**	FWR4

3.1. Predicted Structure & Library Visualization

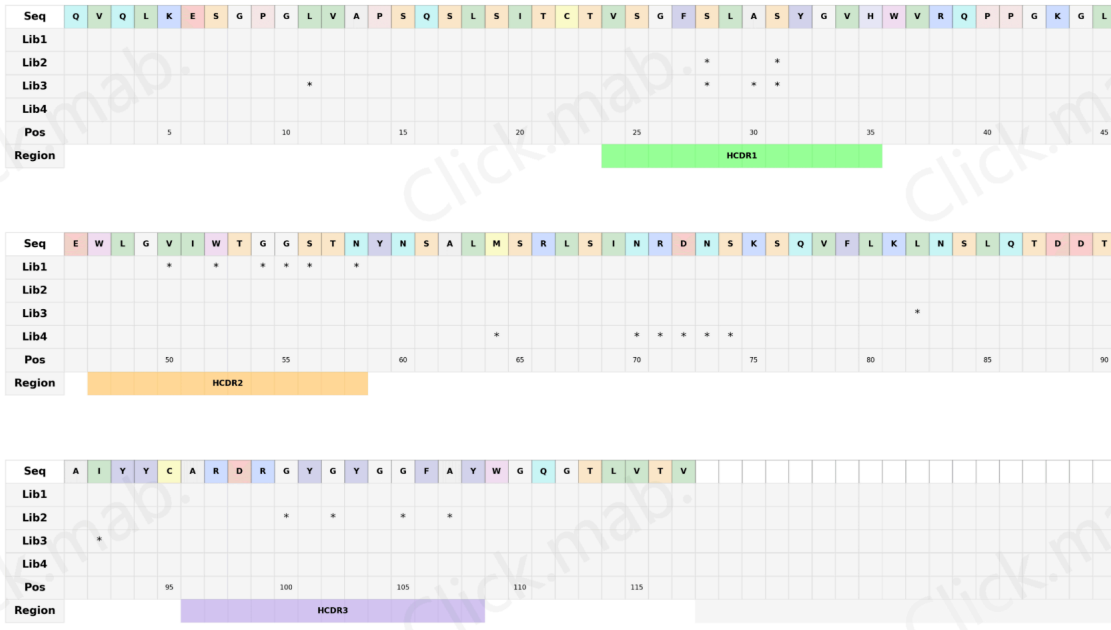
Affinity Maturation Report Example

To better understand the position and role of mutation sites in 3D space, we provide the antibody partial structure files and a visualization of each recommended sub-library.

Click here to download the antibody structure PSE file

Sequence Region Visualization Charts:

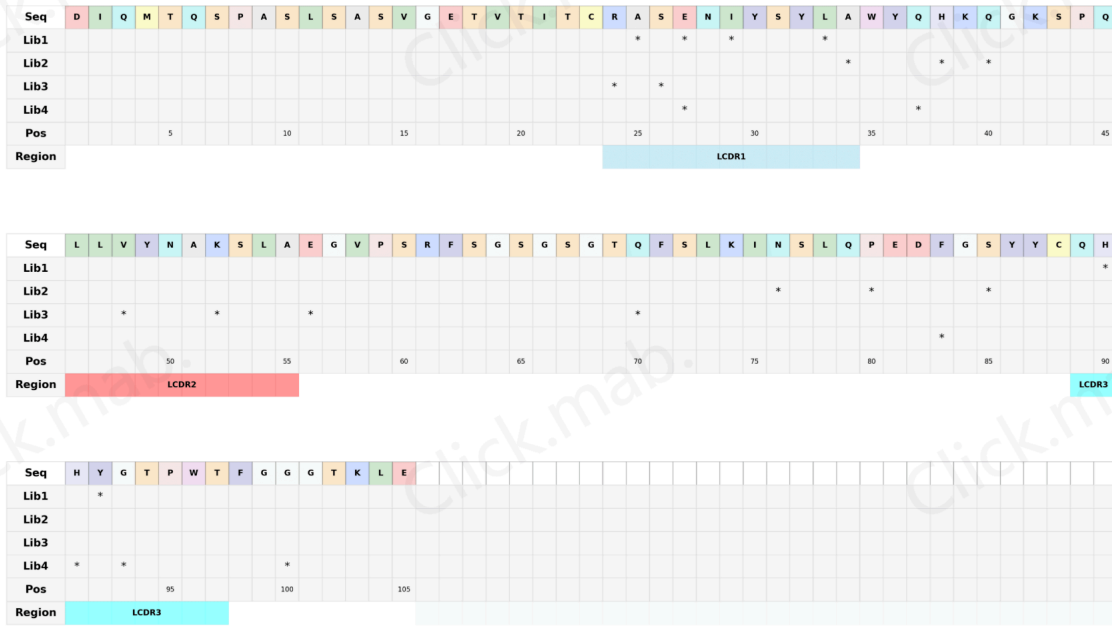
Heavy Chain Sub-library Mutation Site Distribution Map:



Light Chain Sub-library Mutation Site Distribution Map:

Affinity Maturation Report Example

2025/11/10 09:48 Antibody Affinity Maturation Report



4. Detailed Mutation Results & Data Download

4.1. Mutation Library Design Details

chainType	subLibID	mutPos	mutPosNum	mutRegionNum	interactNum	score
Heavy	H1	50V, 52W, 55G, 56S, 54G, 58N	6	2	6	14.800
Heavy	H2	28S, 31S, 100G, 102G, 105G, 107A	6	2	3	10.300
Heavy	H3	11L, 28S, 30A, 31S, 82L, 92I	6	3	2	8.600
Heavy	H4	64M, 70N, 71R, 72D, 73N, 74S	6	1	1	7.500
Light	L1	25A, 27E, 29I, 33L, 90H, 92Y	6	2	6	14.800

Affinity Maturation Report Example

chainType	subLibID	mutPos	mutPosNum	mutRegionNum	interactNum	score
Light	L2	34A, 38H, 40Q, 76N, 80P, 85S	6	2	1	7.300
Light	L3	24R, 26S, 48V, 52K, 56E, 70Q	6	3	1	7.100
Light	L4	27E, 37Q, 83F, 91H, 93G, 100G	6	3	0	5.600

4.2. Data Download

Click here to download all mutation results as a CSV file (Antibody_Analysis_results.csv)

5. Report Summary

This report provides a systematic affinity maturation design plan for the parent antibody.

- **Input Analysis:** We confirmed the antibody's basic information, identified the 6 CDR regions, and flagged potential risk sites.
- **Mutation Design:** Based on sequence and structure models, we have selected a series of high-potential mutation sites and provided a predicted structure file and library visualization to aid in decision-making.
- **Result Delivery:** The report provides core mutation sites, a complete list of mutation suggestions, and a downloadable CSV file for subsequent analysis and experimental design.

Based on the comprehensive evaluation, we have selected a total of **45** sites and designed **8** libraries, consisting of **4** heavy chain sub-libraries and **4** light chain sub-libraries. These designs cover a total of **20** antibody-antigen interactions, with **12** in the heavy chain and **8** in the light chain.

We recommend integrating these computational design results with your wet-lab platform to construct mutation libraries for screening, which will most efficiently lead to the discovery of candidate antibody molecules with significantly enhanced affinity.

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mAb Humanization Report Example

Antibody Humanization Computational Report

Report Overview

- This report provides the analysis results of the parental sequence, including its species, germline, highest sequence identity to the germline, and CDR sequences.
- In this antibody humanization process, two groups of humanized antibodies ("20 sequences" and "100 sequences") were generated through humanization computations and clustering using different methods.
- Due to space limitations, this report provides a detailed analysis of the "20 sequences" group only. The analysis of the "100 sequences" group is available for download as a separate file.
- The analysis of the "20 sequences" group includes sequence alignment between the humanized antibodies and the parental antibody for both the light and heavy chains, corresponding germline assignments for the light and heavy chains, the highest sequence identity with the IMGT germline (indicating the degree of humanization), and the results of risk site analysis.
- The sequence identity of the humanized VH sequences to their germline can reach up to 96%.
- The sequence identity of the humanized VL sequences to their germline can reach up to 96%.

Input Antibody Analysis

AbName	Test1
VH_Fv	EIQLQQTGPELVQPGASVKISCKASGYSFTDYIMVWVKQSHGKGLEWIGNINPYHGRTAYNLKFKGKAT LTVDKSSSTAFMQLNSLISEDSAVFYCVRKGYVEGGGLDYWGQGTSVIVS
VH_species	mouse
VH_germline	IGHV1-39*02
VH_germline _identity	89% (mouse)
HCDR1	ASGYSFTDYIMV
HCDR2	WIGNINPYHGRTA
HCDR3	VRKGYVEGGGLDY
VL_Fv	DIVLTQFPGSLAVSLGQRATISCKASQRVDYDGVSYMNWYQQKPGQPPKLLINAASDLESGIPARFSGT GSGTDFTLNIHPVEEEDAATYYCQQSNYDPWTFGGGTKLEIKRA
VL_species	mouse
VL_germline	IGKV3-4*01
VL_germline _identity	91% (mouse)
LCDR1	KASQRVDYDGVSYMN
LCDR2	LLINAASDLE
LCDR3	QQSNYDPWT

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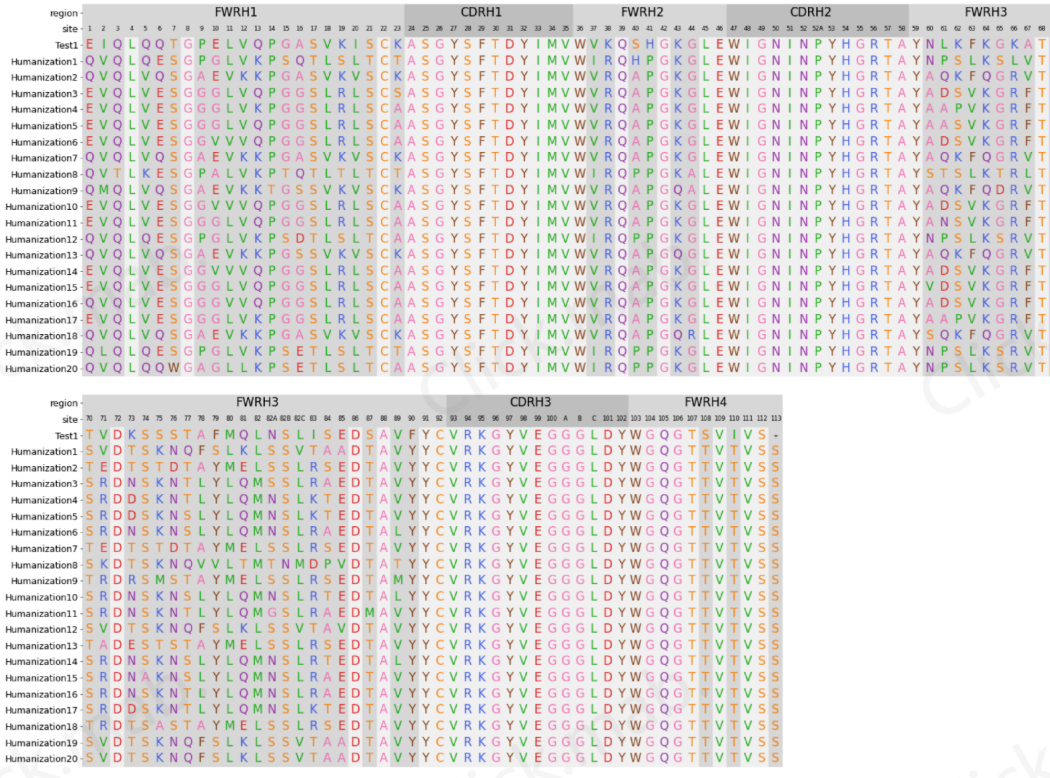
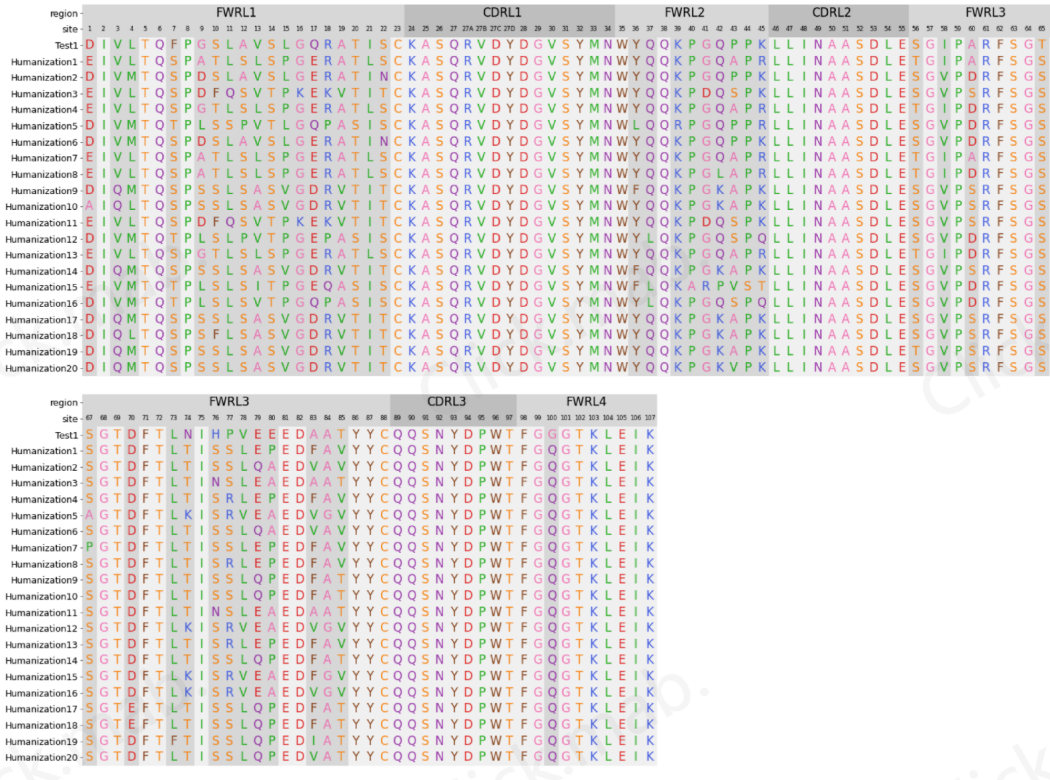
mAb Humanization Report Example

Humanized Antibody Results

Sequence Alignment of Heavy Chain Pre- and Post-Humanization



Sequence Alignment of Light Chain Pre- and Post-Humanization



mAb Humanization Report Example

Humanized Antibody Sequences

Each row in the table contains the optimally paired light and heavy chain sequences for the antibody. We do not recommend randomly matching the light and heavy chains. Generally, a lower HumanizedAbNumber indicates a superior humanized antibody (e.g., Humanization1 is preferred over Humanization2).

HumanizedAbNumber	Hseq	Lseq	VH-Germline	VL-Germline	VH-Identity	VL-Identity
Humanization1	QVQLQESGPGLVKPSQTLSLTCTASGYSFTDYIMVWIRQHPGKGLEWIGNINPYHGRTAYNPSLKSLVTISVDTSKNQFSLKLSSVTAADTAVYYCVRKGYVEGGGLDYWGQGTTVTVSS	EIVLTQSPATLSLSPGERATLSCKASQRVDYDGVSYMNWYQQKPGQAPRLLINAASDLETGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQSNYDPWTFGQGTKLEIK	IGHV4-31*01	IGKV3-11*01	95%	92%
Humanization2	QVQLVQSGAEVKKPGASVKVSCKASGYSFTDYIMVWVRQAPGKGLEWIGNINPYHGRTAYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYYCVRKGYVEGGGLDYWGQGTTVTVSS	DIVMTQSPDSLAVSLGERATINCKASQRVDYDGVSYMNWYQQKPGQPPKLLINAASDLESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSNYDPWTFGQGTKLEIK	IGHV1-24*01	IGKV4-1*01	95%	93%
Humanization3	EVQLVESGGGLVQPGGSLRLSCSASGYSFTDYIMVWVRQAPGKGLEWIGNINPYHGRTAYADSVKGRFTISRDNSKNTLYLQMSSLRAEDTAVYYCVRKGYVEGGGLDYWGQGTTVTVSS	EIVLTQSPDFQSVTPKEKVTITCKASQRVDYDGVSYMNWYQQKPDQSPKLLINAASDLESGVPSRFSGSGSGTDFTLTINSLEAEDAATYYCQQSNYDPWTFGQGTKLEIK	IGHV3-64D*06	IGKV6-21*01	93%	92%
Humanization4	EVQLVESGGGLVKPGGSLRLSCAASGYSFTDYIMVWVRQAPGKGLEWIGNINPYHGRTAYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCVRKGYVEGGGLDYWGQGTTVTVSS	EIVLTQSPGTLSLSPGERATLSCKASQRVDYDGVSYMNWYQQKPGQAPRLLINAASDLETGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQSNYDPWTFGQGTKLEIK	IGHV3-15*01	IGKV3-20*01	96%	92%
Humanization5	EVQLVESGGGLVQPGGSLRLSCAASGYSFTDYIMVWVRQAPGKGLEWIGNINPYHGRTAYAASVKGRFTISRDDSKNSLYLQMNSLKTEDTAVYYCVRKGYVEGGGLDYWGQGTTVTVSS	DIVMTQTPLSSPVTLGQPASISCKASQRVDYDGVSYMNWLQQRPGQPPRLLINAASDLESGVPDRFSGSGAGTDFTLKISRVEAEDVGVYYCQQSNYDPWTFGQGTKLEIK	IGHV3-72*01	IGKV2-24*01	96%	92%
Humanization6	EVQLVESGGVVVQPGGSLRLSCAASGYSFTDYIMVWVRQAPGKGLEWIGNINPYHGRTAYADSVKGRFTISRDNSKNSLYLQMNSLRAEDTALYYCVRKGYVEGGGLDYWGQGTTVTVSS	DIVMTQSPDSLAVSLGERATINCKASQRVDYDGVSYMNWYQQKPGQPPKLLINAASDLESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSNYDPWTFGQGTKLEIK	IGHV3-43D*03	IGKV4-1*01	95%	93%
Humanization7	QVQLVQSGAEVKKPGASVKVSCKASGYSFTDYIMVWVRQAPGKGLEWIGNINPYHGRTAYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYYCVRKGYVEGGGLDYWGQGTTVTVSS	EIVLTQSPATLSLSPGERATLSCKASQRVDYDGVSYMNWYQQKPGQAPRLLINAASDLETGIPARFSGSGPGTDFTLTISSLEPEDFAVYYCQQSNYDPWTFGQGTKLEIK	IGHV1-24*01	IGKV3D-11*01	95%	92%
Humanization8	QVTLKESGPALVKPTQTLTLTCTASGYSFTDYIMVWIRQPPGKALEWIGNINPYHGRTAYSTSLKTRLTISKDTSKNQVVLTMTNMDPVDTATYYCVRKGYVEGGGLDYWGQGTTVTVSS	EIVLTQSPATLSLSPGERATLSCKASQRVDYDGVSYMNWYQQKPGLAPRLLINAASDLETGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQSNYDPWTFGQGTKLEIK	IGHV2-70*10	IGKV3D-20*01	95%	92%
Humanization9	QMQLVQSGAEVKKTGSSVKVSCKASGYSFTDYIMVWVRQAPGQALEWIGNINPYHGRTAYAQKFQDRVTIT	DIQMTQSPSSLSASVGDRVTITCKASQRVDYDGVSYMNWFQQKPGKAPKLLINAASDLESGVPSRF	IGHV1-	IGKV1-	95%	93%

Click.mAb.

mAb Humanization Report Example

HumanizedAbNumber	Hseq	Lseq	VH-Germline	VL-Germline	VH-Identity	VL-Identity
Humanization19	QLQLQESGPGLVKPSETLSLTCTASGYSFTDYIMVWIRQPPGKGLEWIGNINPYHGRTAYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCVRKGYVEGGGLDYWGQGTTVTVSS	DIQMTQSPSSLSASVGDRVTITCKASQRVDYDGVSYMNWYQQKPGKAPKLLINAASDLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQSNYDPWTFGQGTKLEIK	IGHV4-39*01	IGKV1-33*01	95 %	96 %
Humanization20	QVQLQQWGAGLLKPSETLSLTCAASGYSFTDYIMVWIRQPPGKGLEWIGNINPYHGRTAYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCVRKGYVEGGGLDYWGQGTTVTVSS	DIQMTQSPSSLSASVGDRVTITCKASQRVDYDGVSYMNWYQQKPGKVPKLLINAASDLESGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQQSNYDPWTFGQGTKLEIK	IGHV4-34*01	IGKV1-27*01	93 %	93 %

Humanized Antibody Liabilities

HumanizedAbNumber	Chain	Sequence	Risk Summary
Humanization1	Hseq	QVQLQESGPGLVKPSQTLSLTCTASGYSFTDYIMVWIRQHPGKGLEWIGNINPYHGRTAYNPSLKSLVTISVDTSKNQFSLKLSSVTAADTAVYYCVRKGYVEGGGLDYWGQGTTVTVSS	High: 0, Medium: 1, Low: 0
Humanization1	Lseq	EIVLTQSPATLSLSPGERATLSCKASQRVDYDGVSYMNWYQQKPGQAPRLLINAASDLETGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQSNYDPWTFGQGTKLEIK	High: 2, Medium: 2, Low: 1
Humanization2	Hseq	QVQLVQSGAEVKKPGASVKVSCKASGYSFTDYIMVWVRQAPGKGLEWIGNINPYHGRTAYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYYCVRKGYVEGGGLDYWGQGTTVTVSS	High: 0, Medium: 1, Low: 0
Humanization2	Lseq	DIVMTQSPDSLAVSLGERATINCKASQRVDYDGVSYMNWYQQKPGQPPKLLINAASDLESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQSNYDPWTFGQGTKLEIK	High: 2, Medium: 2, Low: 1
Humanization3	Hseq	EVQLVESGGGLVQPGGSLRLSCSASGYSFTDYIMVWVRQAPGKGLEWIGNINPYHGRTAYADSVKGRFTISRDNSKNTLYLQMSSLRAEDTAVYYCVRKGYVEGGGLDYWGQGTTVTVSS	High: 0, Medium: 1, Low: 0
Humanization3	Lseq	EIVLTQSPDFQSVTPKEKVTITCKASQRVDYDGVSYMNWYQQKPDQSPKLLINAASDLESGVPSRFSGSGSGTDFTLTINSLEAEDAATYYCQQSNYDPWTFGQGTKLEIK	High: 2, Medium: 2, Low: 1
Humanization4	Hseq	EVQLVESGGGLVKPGGSLRLSCAASGYSFTDYIMVWVRQAPGKGLEWIGNINPYHGRTAYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCVRKGYVEGGGLDYWGQGTTVTVSS	High: 0, Medium: 1, Low: 0
Humanization4	Lseq	EIVLTQSPGTLSLSPGERATLSCKASQRVDYDGVSYMNWYQQKPGQAPRLLINAASDLETGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQSNYDPWTFGQGTKLEIK	High: 2, Medium: 2, Low: 1
Humanization5	Hseq	EVQLVESGGGLVQPGGSLRLSCAASGYSFTDYIMVWVRQAPGKGLEWIGNINPYHGRTAYAASVKGRFTISRDDSKNSLYLQMNSLKTEDTAVYYCVRKGYVEGGGLDYWGQGTTVTVSS	High: 0, Medium: 1, Low: 0
Humanization5	Lseq	DIVMTQTPLSSPVTLGQPASISCKASQRVDYDGVSYMNWLQQRPGQPPRLLINAASDLESGVPDRFSGSGAGTDFTLKISRVEAEDVGVYYCQQSNYDPWTFGQGTKLEIK	High: 2, Medium: 2, Low: 1

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mAb Humanization Report Example

The humanization analysis file for the “20” humanized antibody sequences

The humanization analysis file for the “100” humanized antibody sequences

Header in the Humanization Analysis File	Description
HumanizedAbNumber	The ID number of the humanized antibody
Hseq	The sequence of the humanized antibody’s heavy chain
Lseq	The sequence of the humanized antibody’s light chain
IMGT-VHGermline	The germline to which the antibody’s heavy chain sequence belongs, determined based on the IMGT database
IMGT-VLGermline	The germline to which the antibody’s light chain sequence belongs, determined based on the IMGT database
IMGT-VHIdentity	The sequence identity between the antibody’s heavy chain and the closest germline sequence in the IMGT database, representing the degree of humanization of the heavy chain
IMGT-VLIdentity	The sequence identity between the antibody’s light chain and the closest germline sequence in the IMGT database, representing the degree of humanization of the light chain

The detailed risk site information file for the “20” humanized antibody sequences
The detailed risk site information file for the “100” humanized antibody sequences

Header in the Risk Site Detail Information File	Description
HumanizedAbNumber	The ID number of the humanized antibody
Chain	Light chain or heavy chain
Name	Type of risk site
Motif	Amino acid sequence of the risk site
Positions	IMGT numbering of the amino acids in the risk site
Regions	Region where the risk site is located
Severity	Severity of the risk site’s impact on the antibody
Germline presence	Whether the risk site is present in the corresponding germline gene
Therapeutic presence	Percentage of therapeutic antibodies (INN-approved or in clinical trials) containing this risk site

Report Summary

1. We provide two sets of humanized antibody sequences: “20 sequences” and “100 sequences.” These sets were generated through clustering using different criteria and scoring methods.
2. Both sets (“20 sequences” and “100 sequences”) include information on their corresponding germline assignments for the heavy and light chains, the highest sequence identity with IMGT germline sequences (indicating the degree of humanization), and the results of risk site analysis. This information is available in the downloadable files.

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Nanobody Humanization Report Example

Antibody Humanization Computational Report

Report Overview

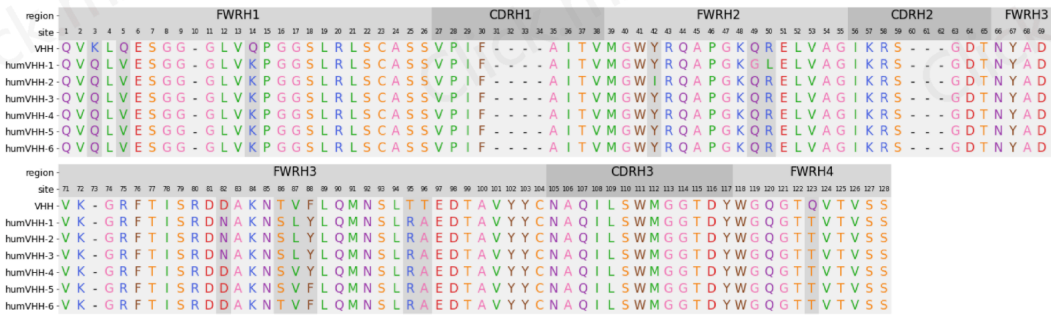
- This report provides a detailed analysis of the parental sequence, including its species, germline, the highest sequence identity to the germline, and the CDR sequences.
- During the antibody humanization process, we successfully generated 6 humanized antibody sequences using computational methods.
- The analysis of these humanized antibodies includes sequence alignment with the parental antibody, corresponding germline assignments, and the highest sequence identity with IMGT-FWR, which indicates the degree of humanization. Additionally, it includes the results of risk site analysis.
- The sequence identity of the humanized VHH sequences to their germline FWR regions can reach as high as 93%.

Input Antibody Analysis

AbName	VHH
Fv	QVKLQESGGGLVQPGGSLRLSCASSVPIFAITVMGWYRQAPGKQRELVAGIKRSGDTNYADSVKGRFTISR DDAKNTVFLQMNSLTTEDTAVYYCNAQILSWMGGTDYWGQGTQVTVSS
species	human
germline	IGHV3-64*04
germline_identity	81% (human)
CDR1	VPIFAITV
CDR2	IKRSGDT
CDR3	NAQILSWMGGTDY

Humanized Antibody Results

Sequence Alignment Pre- and Post-Humanization



Humanized Antibody Sequences

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Nanobody Humanization Report Example

Humanized VHHNumber	Sequence	Germline	IMGT-FWR-Identity
humVHH-1	QVQLVESGGGLVKPGGSLRLSCASSVPIFAITVMGWYRQAPGKGLELVAGIKRSGDTNYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCNAQILSWMGGTDYWGQGTTVTVSS	IGHV3-11*05	93%
humVHH-2	QVQLVESGGGLVKPGGSLRLSCASSVPIFAITVMGWIRQAPGKQRELVAGIKRSGDTNYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCNAQILSWMGGTDYWGQGTTVTVSS	IGHV3-11*05	92%
humVHH-3	QVQLVESGGGLVKPGGSLRLSCASSVPIFAITVMGWYRQAPGKQRELVAGIKRSGDTNYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCNAQILSWMGGTDYWGQGTTVTVSS	IGHV3-11*05	91%
humVHH-4	QVQLVESGGGLVKPGGSLRLSCASSVPIFAITVMGWYRQAPGKQRELVAGIKRSGDTNYADSVKGRFTISRDDAKNSVYLQMNSLRAEDTAVYYCNAQILSWMGGTDYWGQGTTVTVSS	IGHV3-11*05	89%
humVHH-5	QVQLVESGGGLVKPGGSLRLSCASSVPIFAITVMGWYRQAPGKQRELVAGIKRSGDTNYADSVKGRFTISRDDAKNSVFLQMNSLRAEDTAVYYCNAQILSWMGGTDYWGQGTTVTVSS	IGHV3-11*05	88%
humVHH-6	QVQLVESGGGLVKPGGSLRLSCASSVPIFAITVMGWYRQAPGKQRELVAGIKRSGDTNYADSVKGRFTISRDDAKNTVFLQMNSLRAEDTAVYYCNAQILSWMGGTDYWGQGTTVTVSS	IGHV3-11*05	87%

Humanized Antibody Liabilities

Humanized VHHNumber	Chain	Sequence	Risk Summary
humVHH-1	VHH	QVQLVESGGGLVKPGGSLRLSCASSVPIFAITVMGWYRQAPGKGLELVAGIKRSGDTNYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCNAQILSWMGGTDYWGQGTTVTVSS	High: 1, Medium: 3, Low: 1
humVHH-2	VHH	QVQLVESGGGLVKPGGSLRLSCASSVPIFAITVMGWIRQAPGKQRELVAGIKRSGDTNYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCNAQILSWMGGTDYWGQGTTVTVSS	High: 1, Medium: 3, Low: 1
humVHH-3	VHH	QVQLVESGGGLVKPGGSLRLSCASSVPIFAITVMGWYRQAPGKQRELVAGIKRSGDTNYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCNAQILSWMGGTDYWGQGTTVTVSS	High: 1, Medium: 3, Low: 1
humVHH-4	VHH	QVQLVESGGGLVKPGGSLRLSCASSVPIFAITVMGWYRQAPGKQRELVAGIKRSGDTNYADSVKGRFTISRDDAKNSVYLQMNSLRAEDTAVYYCNAQILSWMGGTDYWGQGTTVTVSS	High: 1, Medium: 3, Low: 1
humVHH-5	VHH	QVQLVESGGGLVKPGGSLRLSCASSVPIFAITVMGWYRQAPGKQRELVAGIKRSGDTNYADSVKGRFTISRDDAKNSVFLQMNSLRAEDTAVYYCNAQILSWMGGTDYWGQGTTVTVSS	High: 1, Medium: 3, Low: 1
humVHH-6	VHH	QVQLVESGGGLVKPGGSLRLSCASSVPIFAITVMGWYRQAPGKQRELVAGIKRSGDTNYADSVKGRFTISRDDAKNTVFLQMNSLRAEDTAVYYCNAQILSWMGGTDYWGQGTTVTVSS	High: 1, Medium: 3, Low: 1

The antibody humanization result files are available below. Please click to download and view.

The humanization analysis file for the humanized antibodies

Nanobody Humanization Report Example

Header in the Humanization Analysis File	Description
HumanizedVHHNumber	The ID number of the humanized antibody
Sequence	Nanobody sequence
Germline	The germline to which the antibody sequence belongs, determined based on the IMGT database
IMGT-FWR-Identity	The sequence identity between the humanized antibody FWR and the closest germline sequence in the IMGT database, representing the degree of humanization

The detailed risk site information file for the humanized antibodies

Header in the Risk Site Detail Information File	Description
HumanizedAbNumber	The ID number of the humanized antibody
Chain	Chain type
Name	Type of risk site
Motif	Amino acid sequence of the risk site
Positions	IMGT numbering of the amino acids in the risk site
Regions	Region where the risk site is located
Severity	Severity of the risk site's impact on the antibody
Germline presence	Whether the risk site is present in the corresponding germline gene
Therapeutic presence	Percentage of therapeutic antibodies (INN-approved or in clinical trials) containing this risk site

Report Summary

1. Through the humanization process, we have successfully generated 6 humanized antibody sequences.
2. Each humanized antibody sequence includes its corresponding germline assignment, the highest sequence identity with the IMGT germline (indicating the degree of humanization), and the results of risk site analysis. This information is available for download.

Start Your Next-Generation AI-Driven Antibody R&D Journey

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