Click.mAb.

Multi-Agent AI Antibody Design Platform Enterprise Solution

Design antibodies against a defined epitope in one click.
Generative AI for every antibody discovery program.

- Advanced Generative Algorithms
- Natural Language Interaction
- Multi-Agent Collaboration
- Online Team Collaboration

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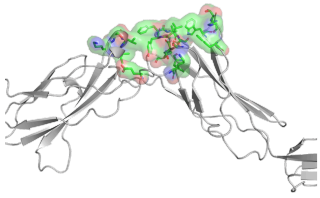
About Clickmab

Clickmab is focused on AI-driven antibody design. Built on proprietary large models, extensive proprietary antibody data, and a multi-agent architecture, the Click.mAb. platform supports antibody discovery and engineering optimization across the full R&D workflow for biopharmaceutical teams.

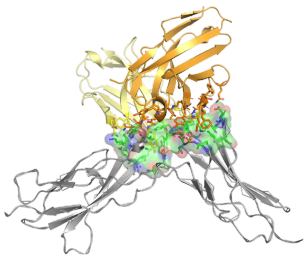


Antigen Epitope

User-defined functional region

Click.mAb.

Generative AI Platform



De Novo–Designed Antibodies

Fully human antibodies with a common light chain

TECHNICAL ADVANTAGES

Proprietary Wet-Lab Data

High-quality proprietary data from our in-house wet labs supports accurate, reliable model training.

World-Leading AI Algorithms

Proprietary, world-leading AI antibody design algorithms enable precise, efficient design.

AI Agent Technology

AI agents enable end-to-end automation across antibody discovery workflows.

Cross-Disciplinary Expertise

An interdisciplinary team of AI experts, structural biologists, antibody engineers, and wet-lab scientists.

CORE TEAM

AI Algorithms

Leading expertise in AI algorithms, protein language models, and structure prediction.

Structural Biology

Deep understanding of protein structure, biophysics, and molecular interaction mechanisms.

Antibody Engineering

Extensive hands-on experience in therapeutic antibody discovery and optimization.

Wet-Lab Team

Our in-house wet-lab team enables rapid feedback between computational design and experimental validation.

Precision Antibody Design: AI Breaks Key R&D Bottlenecks

R&D CHALLENGES

Difficult epitopes remain hard to target

Conventional discovery favors immunodominant surfaces, so effective antibodies against cryptic or conserved epitopes are hard to obtain.

Antibody optimization is slow

Humanization, affinity maturation, and developability work rely on repeated trial and error, consuming time and resources.

R&D productivity remains a challenge

Long timelines, high attrition, and risk at critical milestones limit the gains from experience-based screening alone.

SOLUTIONS

Targeted Epitopes · Controlled Antibody Design

01 De Novo Antibody Design

Generate new antibodies directly against a defined epitope without animal immunization, enabling rational design guided by the desired function.

02 Epitope Prediction

When multiple binders are available, use epitope predictions to prioritize those most likely to have the desired function. Fewer candidates enter functional testing, reducing costs and timelines.

03 Scientific Writing & Reporting

Draft target assessments, literature analyses, patent invention disclosures, and project summaries to save research time.

Efficient Antibody Engineering · Shorter R&D Timelines

04 CDR Diversity Engineering

Expand CDR diversity from a parent antibody to generate high-quality variant sequences ready for library construction and screening.

05 Affinity Maturation

Use AI-predicted antigen–antibody complex structures to identify synergistic mutations and improve affinity with small, focused libraries.

06 Antibody Humanization

Search a broad human framework library using AI structure prediction to preserve CDR–framework interactions. Achieve higher humanness with no back-mutations and shorter turnaround times.

07 Nanobody Humanization

Use accurate AI structure prediction and stepwise back-mutation design to improve humanness while aiming to retain affinity, with better candidate selection, lower experimental costs, and shorter timelines.

08 Developability Assessment

Assess risk across aggregation, chemical modifications, humanness, polyreactivity, and viscosity (mAbs) or thermostability (VHHs) to help teams compare and prioritize candidates.

De Novo Antibody Design

Generate new antibodies directly against a defined epitope without animal immunization, enabling rational design guided by the desired function.

REFERENCE PRICE
18,888 credits

ESTIMATED TIME
48 hours

INPUT Target structure + epitope definition

COMPUTATIONAL WORKFLOW

01 **Define Target Epitope**

02 **Predict Compatible Frameworks**

03 **Generate CDR-H3**

04 **Score Across Multiple Criteria**

05 **Export Design Report**

CORE TECHNICAL ADVANTAGES

✓ **Structure-Constrained Framework Selection**
Select frameworks that fit the target epitope's geometry as starting scaffolds for de novo design.

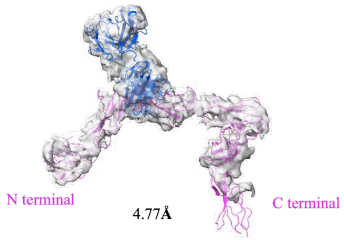
✓ **Generative AI CDR-H3 Design**
Generate new CDR-H3 sequences beyond template libraries and variants of existing binders.

✓ **Multidimensional Scoring & Selection**
Rank and filter candidates using model predictions and structural features to improve the quality of initial designs.

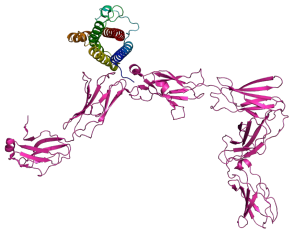
✓ **Traceable Design Reports**
Export candidate sequences and traceable design reports for library construction and screening.

CASE STUDY

De novo design against a challenging functional epitope yielded seven BLI-confirmed binders with K_D values of 10^{-7}–10^{-9} M. Two blocked natural ligand binding and inhibited STAT3 phosphorylation in cell-based assays. Cryo-EM confirmed the binding epitope of P211858.



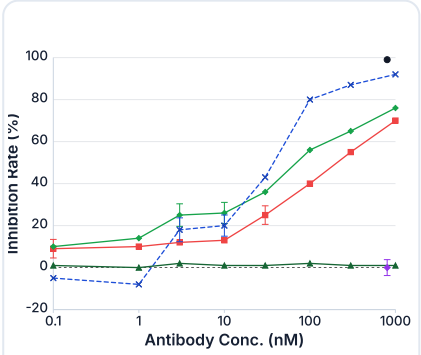
Cryo-EM epitope validation



Epitope Prediction Results

ANTIBODY	KD (M)	KA (M^{-1} S^{-1})	KD (S^{-1})
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 Binding Affinity

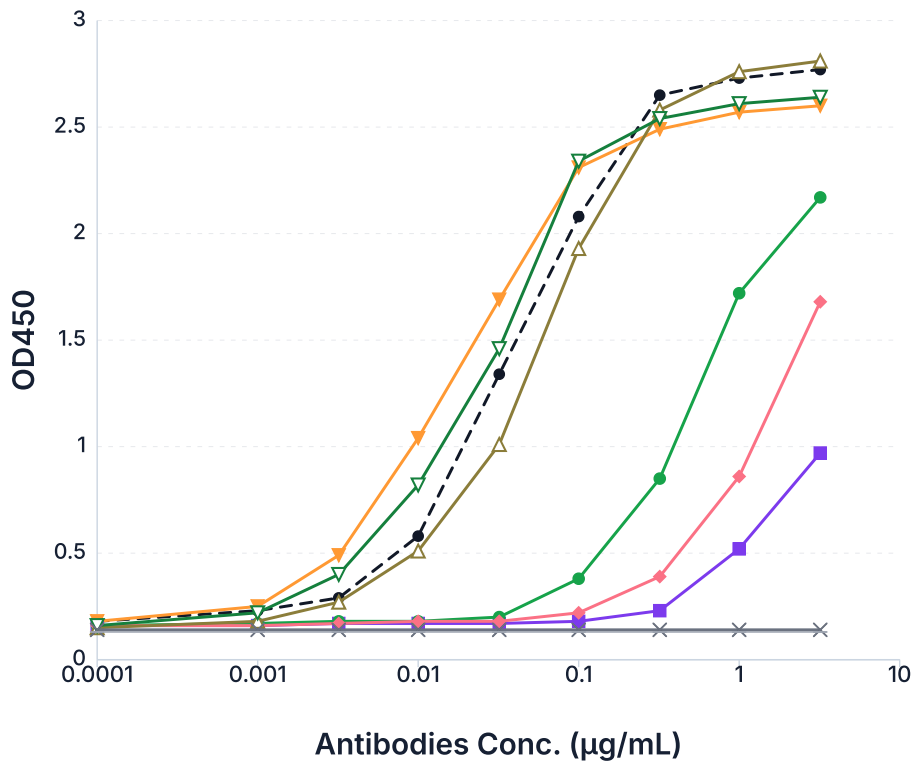


SAMPLES	IC50(NM)
P211858	159.5
P211859	68.30
Positive ctrl	12.53

Inhibition of STAT3 Phosphorylation

Experimental Validation (Continued)

BINDING ACTIVITY ASSAY



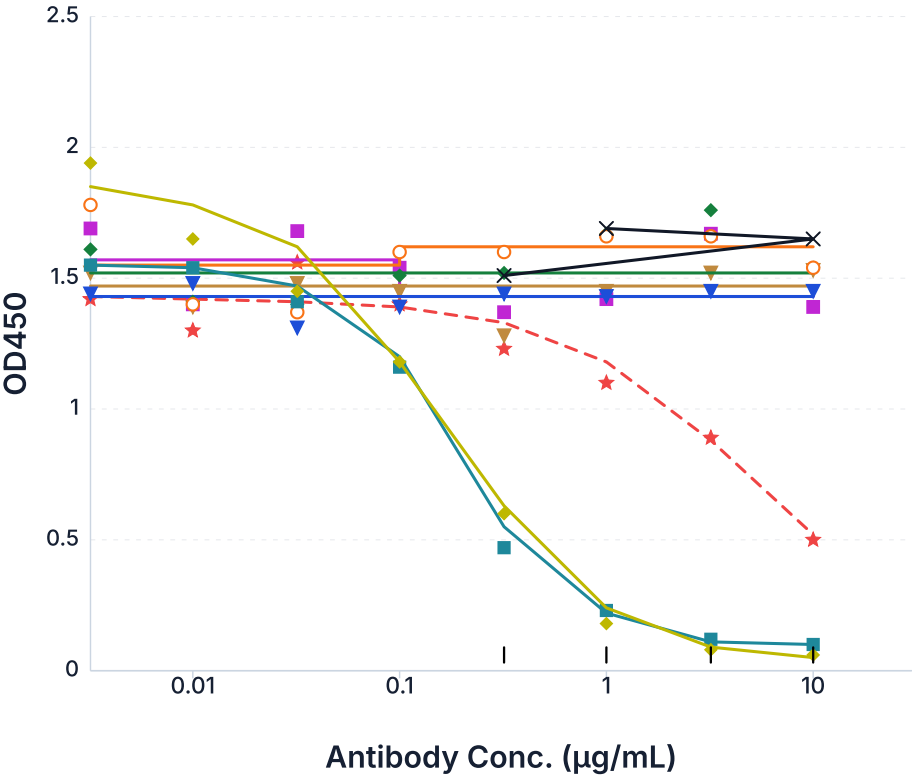
LEGEND

- 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

LIGAND 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

Epitope Prediction

INSPIRE-SEEN uses an antigen structure and antibody sequences to predict conformational epitopes for screening and differentiated design. Top-ranked patch accuracy increases from 50% to 78% (+28 percentage points). Predictions take 10–20 minutes at approximately one-hundredth the cost of conventional experiments.

REFERENCE PRICE
Free

ESTIMATED TIME
20 min

INPUT Antigen structure + antibody sequences

COMPUTATIONAL WORKFLOW

01 **Provide Antigen & Antibody Data**

02 **Partition Surface Patches**

03 **Predict Affinity Scores**

04 **Select the Best Patch**

05 **Report Epitope Residues**

CORE TECHNICAL ADVANTAGES

✓ **High Accuracy, Continuous Improvement**
Top-ranked patch accuracy improves by 28 percentage points over AlphaFold-Multimer (50% → 78%). The model is continually refined using extensive in-house cryo-EM data.

✓ **Rapid, Low-Cost Prediction**
Get results in 10–20 minutes at 0.1–1% of the cost of conventional wet-lab experiments.

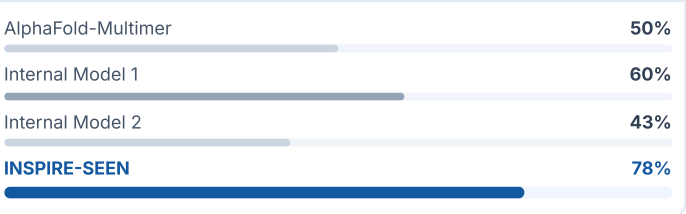
CASE STUDIES

Case 1: On a test set of 110 known epitopes, INSPIRE-SEEN achieved 78% top-ranked patch accuracy, versus 50% for AlphaFold-Multimer. Patch classification metrics are shown separately below.

Patch Classification Metrics

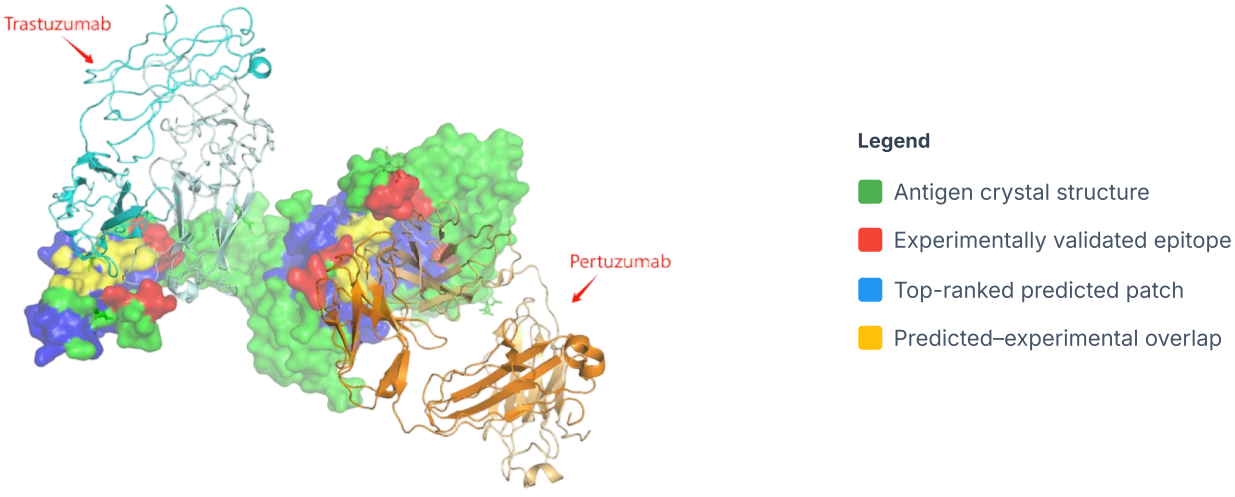
MODEL	RECALL	PRECISION	AUROC	AUPRC
AlphaFold-Multimer	0.40	0.43	0.65	0.48
Internal Model 1	0.42	0.52	0.72	0.55
Internal Model 2	0.27	0.34	0.58	0.37
INSPIRE-SEEN	**0.52**	**0.55**	**0.71**	**0.60**

Top-Ranked Patch Accuracy



Case 2: HER2 with trastuzumab / pertuzumab — predicted epitopes closely match the binding sites

Using the HER2 crystal structure and antibody sequences, INSPIRE-SEEN predicts epitope patches that overlap the experimentally determined epitopes and distinguish the binding sites of trastuzumab and pertuzumab.



Scientific Writing & Reporting

Turn public evidence and project records into structured target assessments, literature analyses, invention disclosures, and project summary reports.

INPUT Target names, PDF papers, patent-application data, or project data

COMPUTATIONAL WORKFLOW

01 Define the Objective

02 Gather Relevant Sources

03 Organize and Evaluate Evidence

04 Draft a Structured Document

05 Review and Refine

CORE CAPABILITIES

Target Research

Assess target biology, disease relevance, druggability, epitopes, and the competitive landscape.

DELIVERABLE

A target assessment with cited sources, opportunities, risks, and research priorities for project discussion.

Literature Analysis

Analyze a PDF paper's research question, methods, findings, and the evidence behind its conclusions.

DELIVERABLE

A structured paper analysis linking findings to figures and tables, with limitations and research implications.

Invention Disclosure

Organize molecular designs, inventive features, methods, results, and sequence information.

DELIVERABLE

A draft for inventor and patent counsel review, with VH/VL, CDR, and SEQ ID records and information gaps identified.

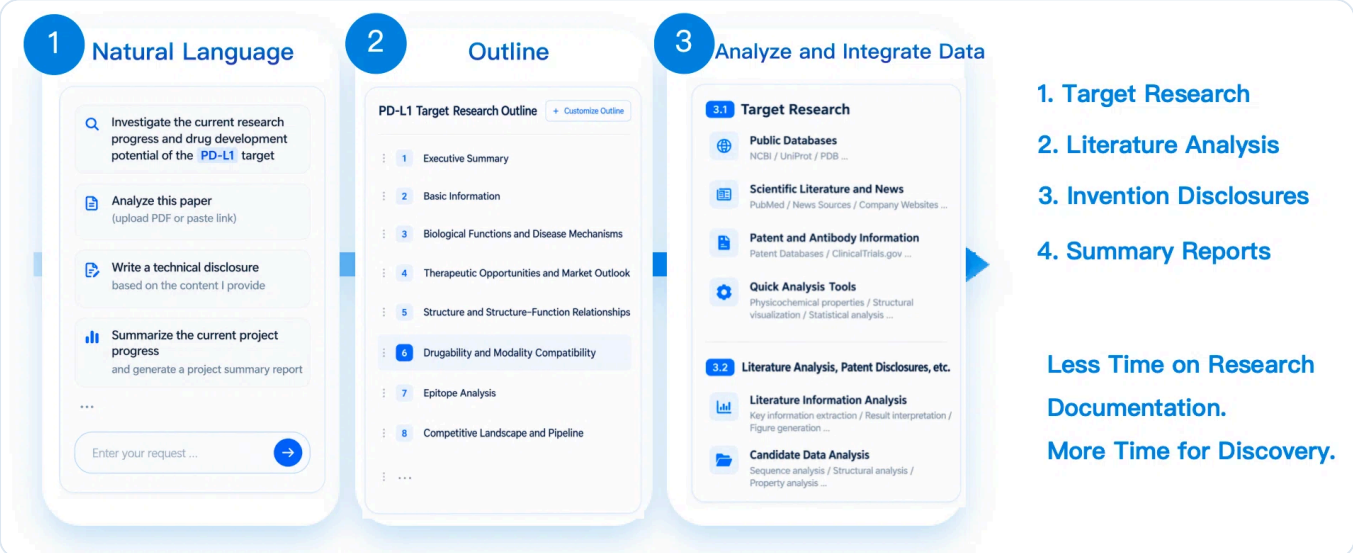
Project Summary Reports

Consolidate objectives, design iterations, computational analyses, experimental results, and decisions.

DELIVERABLE

A summary of progress, key findings, open questions, and next steps for review and handover.

WORKFLOW PREVIEW



CDR Diversity Engineering

CDRs largely determine antibody specificity and affinity. AI-guided structural design explores sequence space while retaining stability and affinity, creating smaller, higher-quality variant libraries with broader sequence diversity and the same target function.

REFERENCE PRICE
12,888 credits

ESTIMATED TIME
2 hours

INPUT Antibody sequence; antigen sequence or complex structure as required

COMPUTATIONAL WORKFLOW

01 **Provide Sequences or Complex Structure**

02 **Identify CDRs Across Numbering Schemes**

03 **Predict and Optimize Structure**

04 **Saturation Mutagenesis & Energy Scoring**

05 **Export Candidate Library & Report**

CORE TECHNICAL ADVANTAGES

✓ **Structure-Guided Mutation Design**
Evaluate mutations in 3D, identify antigen-contact residues and residues that support the structure, and focus the search on promising substitutions.

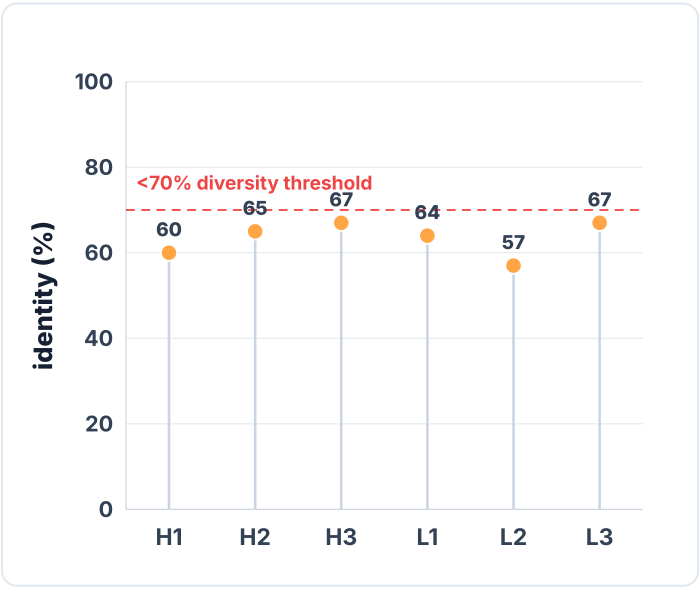
✓ **Intelligent Sequence-Space Sampling**
Guide sequence sampling with physicochemical properties and evolutionary information. Protect or include selected sites and adjust N- or C-terminal boundaries.

✓ **Multiple Numbering Schemes**
Support Kabat, Chothia, IMGT, AHo, and the ALL union mode for compatibility with diverse databases and publications.

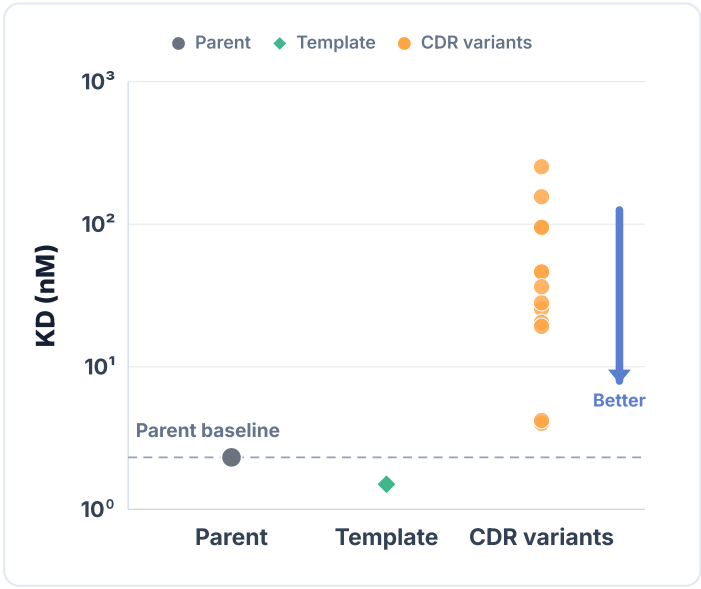
✓ **Sequence and Structure Workflows**
Use automated modeling from sequences, or start from a complex structure for more precise energy calculations and site-specific analysis.

CASE STUDY

A Trop2 antibody was diversified so that each heavy- and light-chain CDR had less than 70% identity to its parental counterpart. Expression, purification, and biophysical testing showed that two candidates retained more than half the parental affinity, 11 reached at least half the parental expression yield, and several showed higher SEC-HPLC purity than the parent.



A CDR Sequence Identity to Parent (all below 70%)

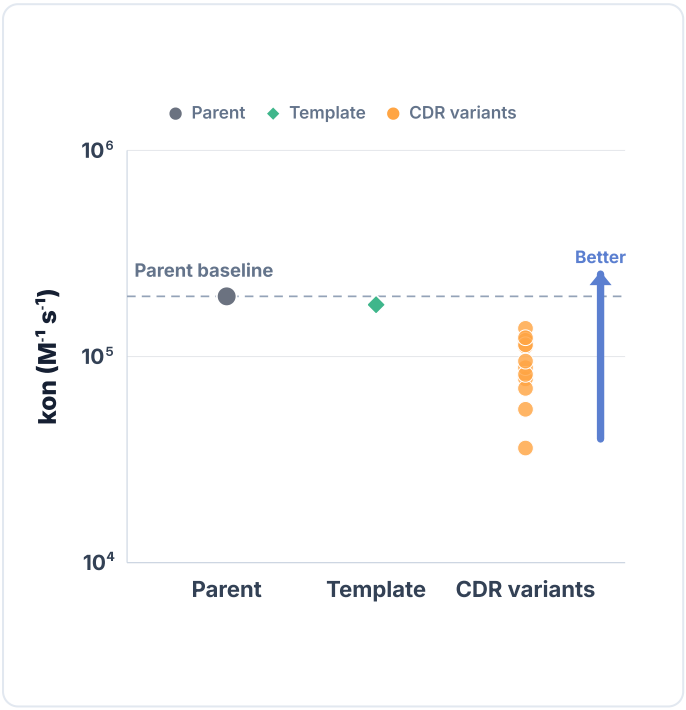


B Binding Affinity, KD (nM; lower is better)

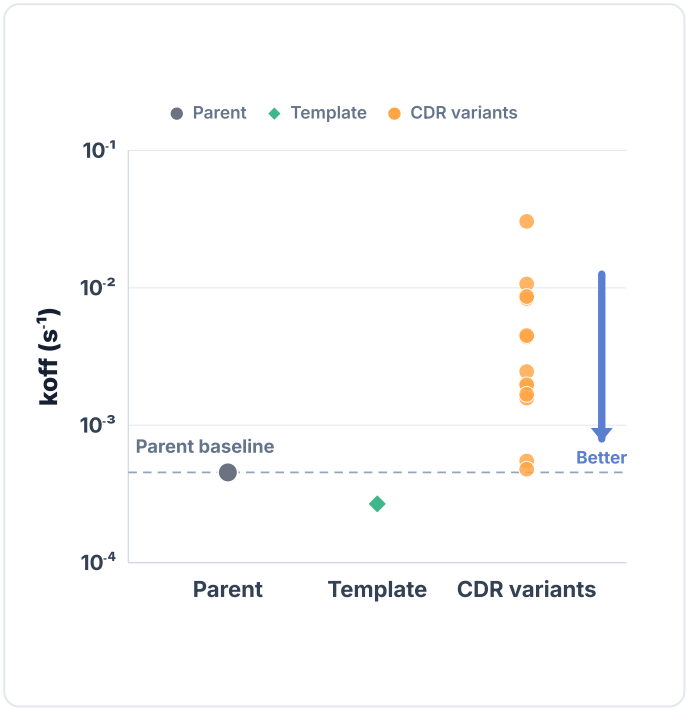
CDR Diversity Engineering

Kinetics (kon / koff), expression yield, and purity compared across the parent, template, and diversified candidates (n = 13).

CASE STUDY (CONTINUED)



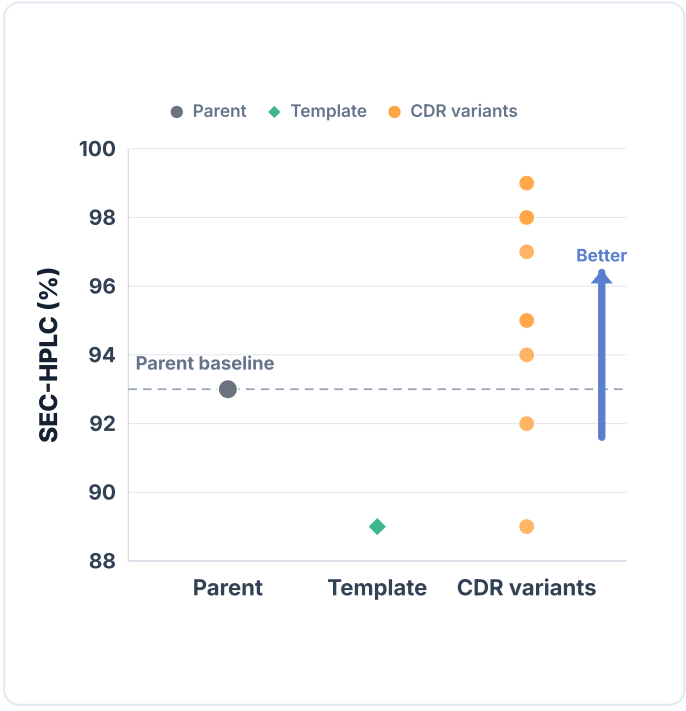
C Association rate, kon (M^{-1} s^{-1}; higher is better)



D Dissociation rate, koff (s^{-1}; lower is better)



E Expression yield (mg; higher is better)



F SEC-HPLC purity (%; higher is better)

Affinity Maturation

Analyze AI-predicted antigen–antibody complex structures to identify synergistic mutations and improve affinity using small, focused libraries.

REFERENCE PRICE
9,888 credits

ESTIMATED TIME
3 hours

INPUT Antigen and antibody sequences, or complex structure with chain IDs; epitope constraints

COMPUTATIONAL WORKFLOW

01 **Provide Antigen & Antibody Sequences**

02 **Predict Structure with AI**

03 **Analyze Mutations with AI**

04 **Select Mutation Sites**

05 **Build Multiple Sublibraries**

CORE TECHNICAL ADVANTAGES

✓ **Integrated Multi-Model Mutation Assessment**
Assess mutations using protein language models, inverse-folding models, and complex structures, considering sequence evolution, structural contacts, and residue compatibility.

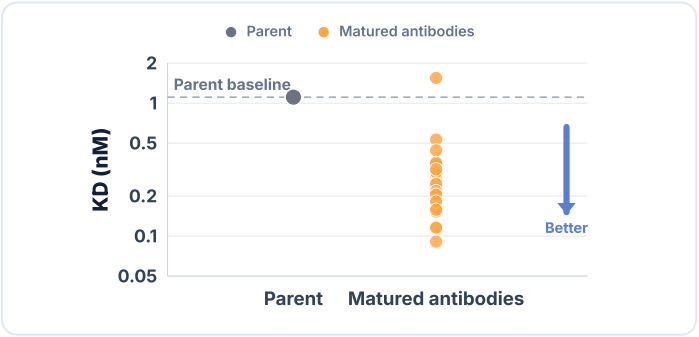
✓ **Structure-Driven Affinity Optimization**
Identify sites that may improve binding from AI-predicted complex structures, rather than relying on empirical selection or large-scale random screening.

✓ **Synergistic Mutations & Intelligent Ranking**
Use hyperparameter optimization and spatial cooperativity analysis to identify synergistic mutation combinations and prioritize candidate sites.

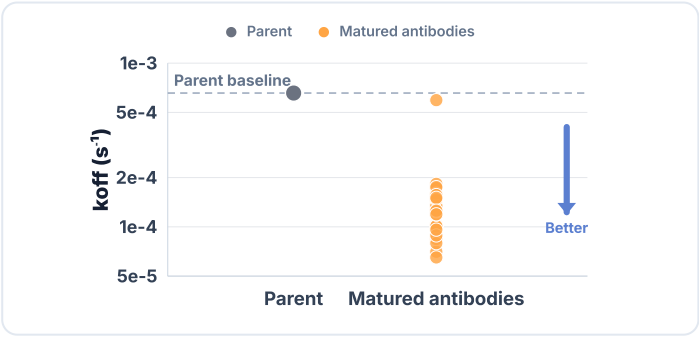
✓ **Automated Compact Sublibrary Design**
Build compact sublibraries around selected framework and CDR mutations to reduce unproductive experiments. Export structures, scores, and risk annotations.

CASE STUDY

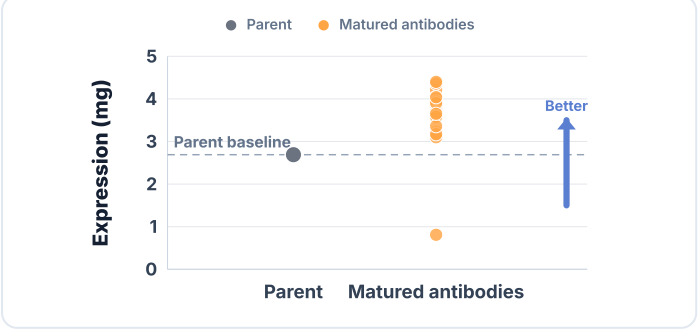
A focused light-chain library yielded 32 affinity-matured variants. Most had more than threefold higher affinity; the best K_D fell from 1.11 to 0.091 nM. Expression exceeded the parent in 31 of 32 samples, and most had SEC-HPLC purity above 90%.



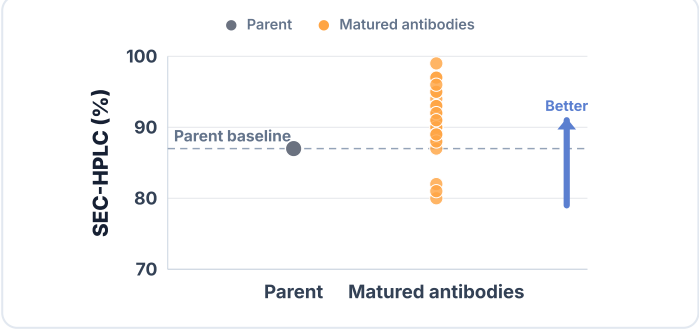
Binding Affinity, KD (nM; lower is better)



Dissociation Rate, koff (s^{-1}; lower is better)



Expression Yield (mg; higher is better)



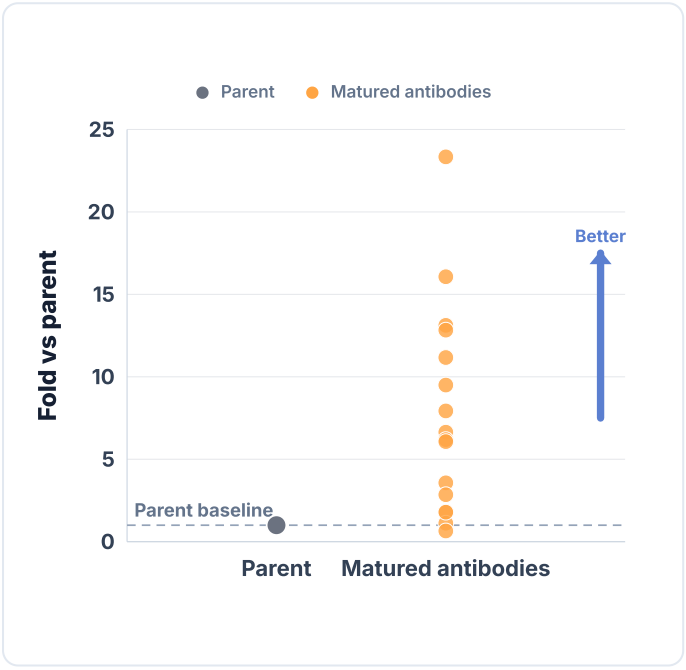
SEC-HPLC Purity (%; higher is better)

Affinity Maturation · Additional Case

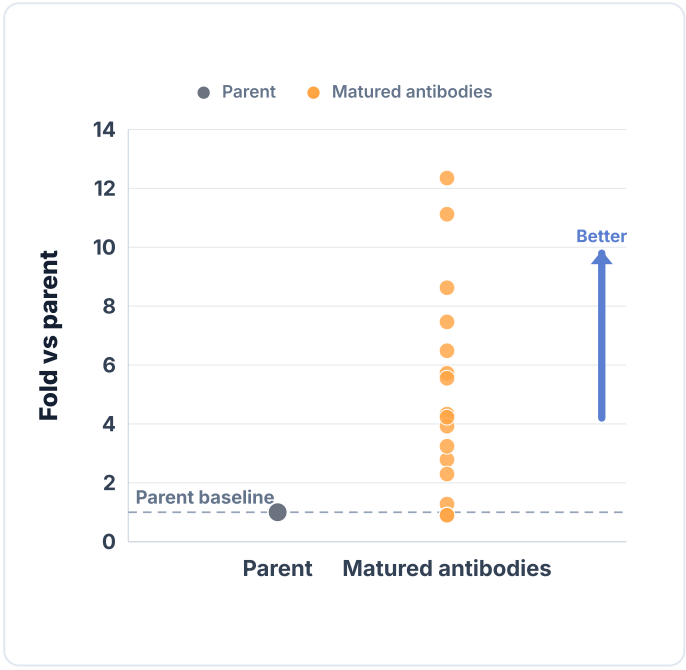
Coordinated heavy- and light-chain optimization improved the best candidate's affinity by 23.3-fold over the parent.

CASE STUDY

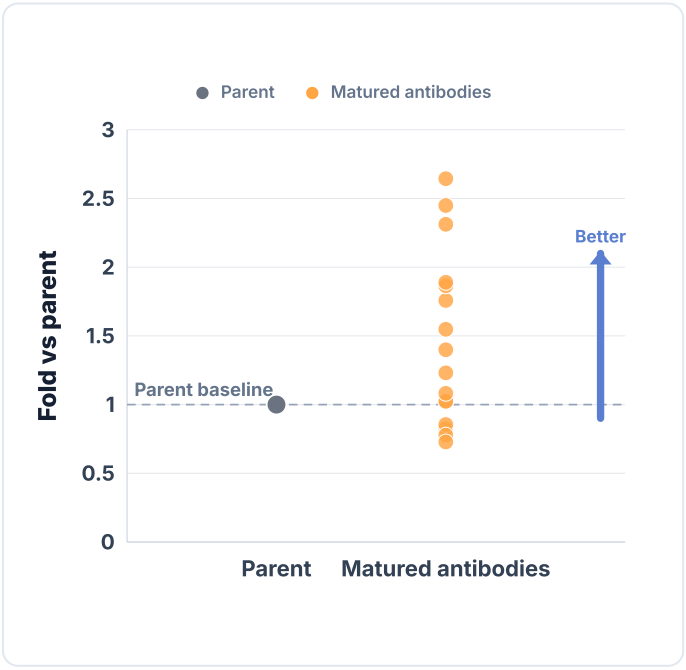
Sixteen affinity-matured antibodies were evaluated following coordinated heavy- and light-chain design. Relative to the parent (C48 = 1), most showed improved affinity, dissociation kinetics, and association kinetics. The best affinity improvement was 23.3-fold, with an approximately 12.4-fold reduction in k_{off}. Several candidates also exceeded parental expression.



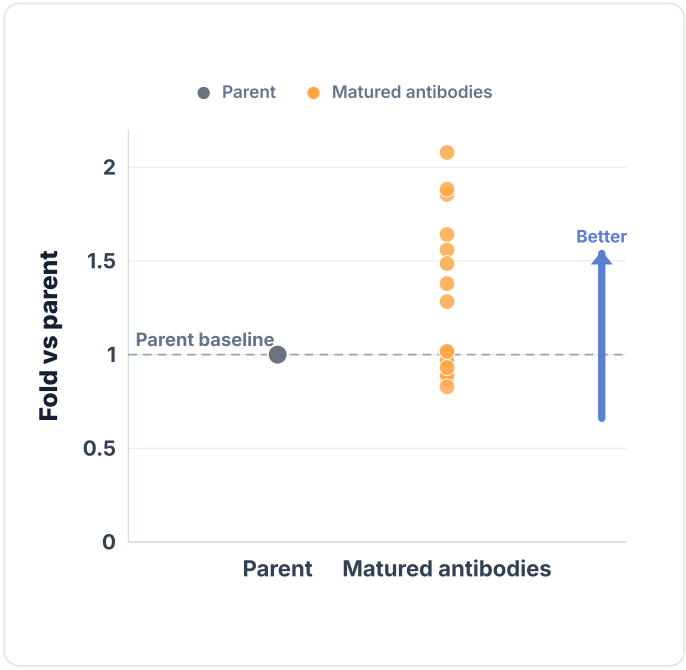
Fold Improvement in Affinity (higher is better; n = 16)



Fold Reduction in koff (higher is better; n = 16)



Fold Increase in kon (higher is better; n = 16)



Relative Expression (parent = 1; n = 16)

Antibody Humanization

Combine a broad human framework library with AI structure prediction to select optimal frameworks while preserving CDR–framework interactions, achieving higher humanness without back-mutations and with shorter turnaround times.

REFERENCE PRICE
2,888 credits

ESTIMATED TIME
4 hours

INPUT Parental VH and VL sequences

COMPUTATIONAL WORKFLOW

01 **Provide Parental mAb Sequences**

02 **Generate Framework Library with AI**

03 **Graft CDRs onto Frameworks**

04 **Score and Select with AI**

05 **Export Report**

CORE TECHNICAL ADVANTAGES

✓ **Intelligent Framework Matching**
Search beyond closely related human frameworks, using structural compatibility to select scaffolds that support the parental CDRs.

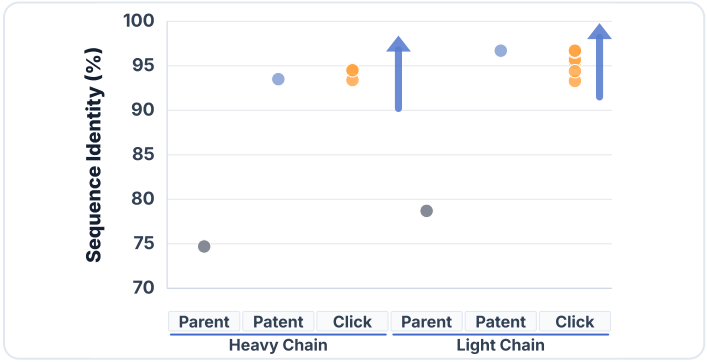
✓ **Structure-Driven Affinity Retention**
Evaluate CDR–framework interactions in AI-predicted 3D structures to improve the likelihood of retaining affinity after humanization.

✓ **No Back-Mutations Required**
Combine structural compatibility with intelligent human framework selection to obtain high-quality candidates without back-mutations.

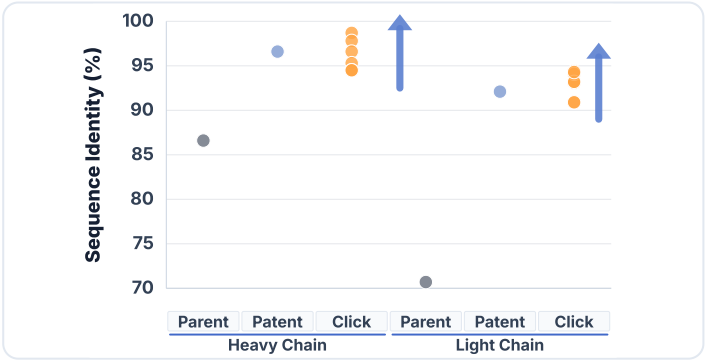
✓ **Multidimensional Candidate Selection**
Score, cluster, and select candidates based on humanness, stability, and predicted biophysical properties.

CASE STUDY

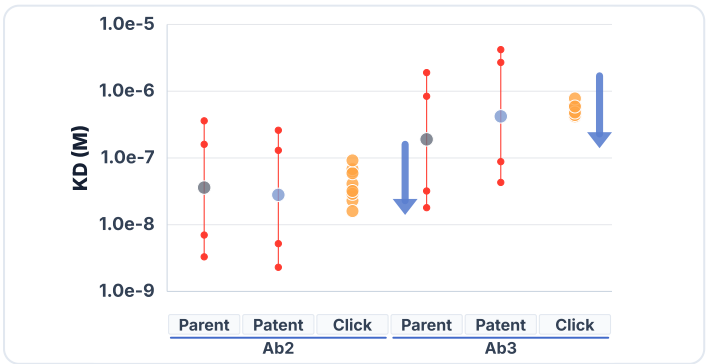
Two murine antibodies, Ab2 and Ab3, were humanized for an international pharmaceutical client. For each parent, 10 designs yielded at least one variant that outperformed the patent-reported comparator. Human sequence identity was 90–95%.



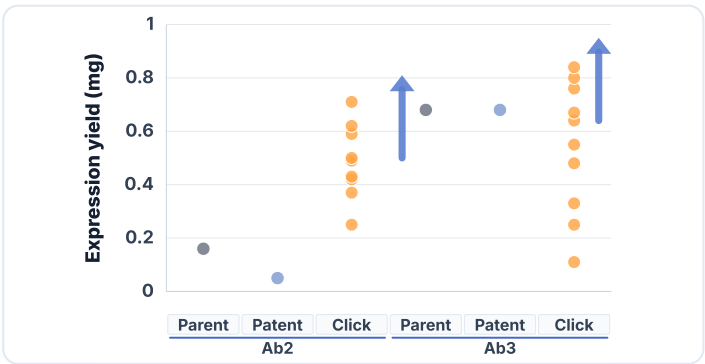
Human Sequence Identity (Ab2)



Human Sequence Identity (Ab3)



Binding Affinity



Expression (4 mL system)

Nanobody Humanization

Combine accurate AI structure prediction with stepwise back-mutation design to improve humanness while aiming to retain affinity. Structural analysis of key residues guides candidate selection, lowers experimental costs, and shortens development timelines.

REFERENCE PRICE
2,888 credits

ESTIMATED TIME
30 min

INPUT Parental VHH sequence

COMPUTATIONAL WORKFLOW

01 **Provide VHH Sequence**

02 **Model Structure with AI**

03 **Select Human Frameworks**

04 **Optimize Grafting at Key Sites**

05 **Score Across Multiple Criteria**

06 **Export Report**

CORE TECHNICAL ADVANTAGES

✓ **Dedicated Framework Selection**
Select human germline frameworks suited to single-domain humanization and capable of supporting VHH CDRs.

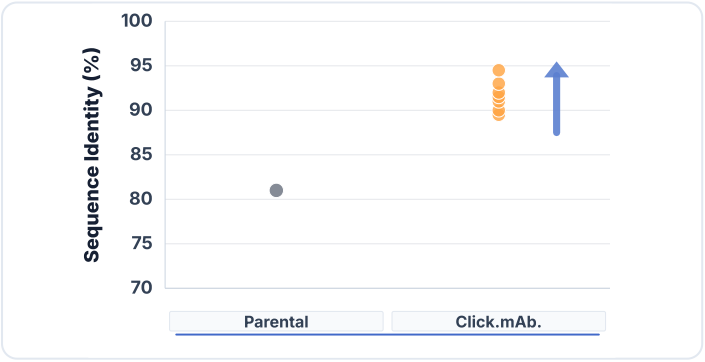
✓ **Stepwise Key-Residue Back-Mutations**
Refine back-mutations at framework–CDR interfaces, Vernier regions, and core structural residues to balance function with high humanness.

✓ **VHH-Specific Site Optimization**
Assess how VHH-specific framework residues, the DE loop, and key structural sites affect conformation, expression, and stability.

✓ **Multidimensional Risk & Property Assessment**
Rank and recommend sequences using humanness, structural stability, physicochemical properties, and potential risk sites.

CASE STUDY

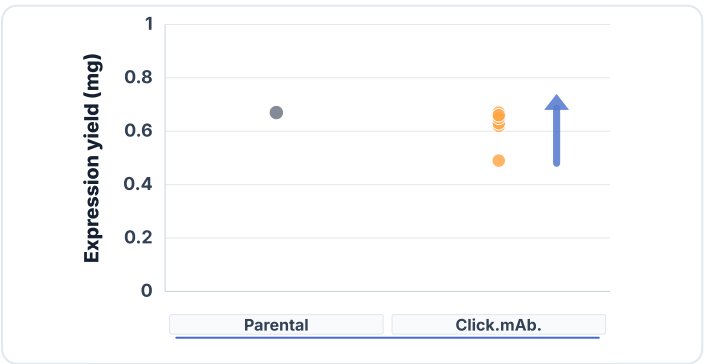
Seven humanized VHH sequences were recommended, with 89–94% human sequence identity. Four showed improved affinity, and most retained parental expression levels. All had SEC-HPLC main-peak purity above 90% and low aggregate levels, suggesting no major impairment of expression or basic physicochemical properties.



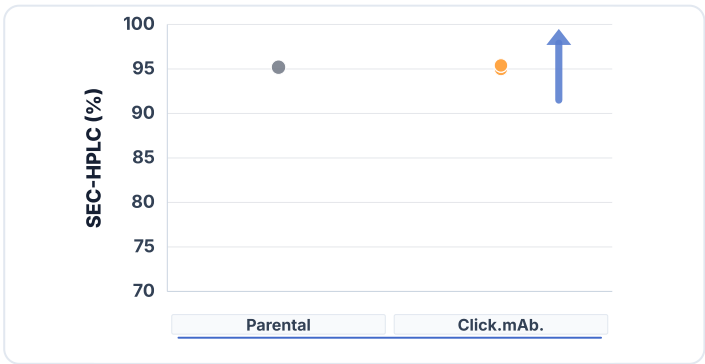
Human Sequence Identity



Binding Affinity



Expression Yield



SEC-HPLC Purity

Developability Assessment

Assess developability risk across aggregation, chemical modifications, humanness, polyreactivity, and viscosity (mAbs) or thermostability (VHHs), with quantitative metrics to compare and prioritize candidates.

REFERENCE PRICE
5 credits / Ab

ESTIMATED TIME
5 min / Ab

INPUT mAb VH/VL sequences or a VHH sequence

COMPUTATIONAL WORKFLOW

01 **Provide Antibody Sequences**

02 **Predict Antibody Structure**

03 **Analyze by Antibody Type**

04 **Calculate Metrics & Flag Risks**

05 **Display Assessment Report**

ASSESSMENT DIMENSIONS

FOUR SHARED DIMENSIONS mAb + VHH

Aggregation
SEC screening pass probability, developability index (DI), and surface hydrophobic patch score (PSH).

Chemical Liabilities
Potential oxidation and deamidation sites, reported by residue and position.

Humanness
OASis percentile relative to a human antibody reference set.

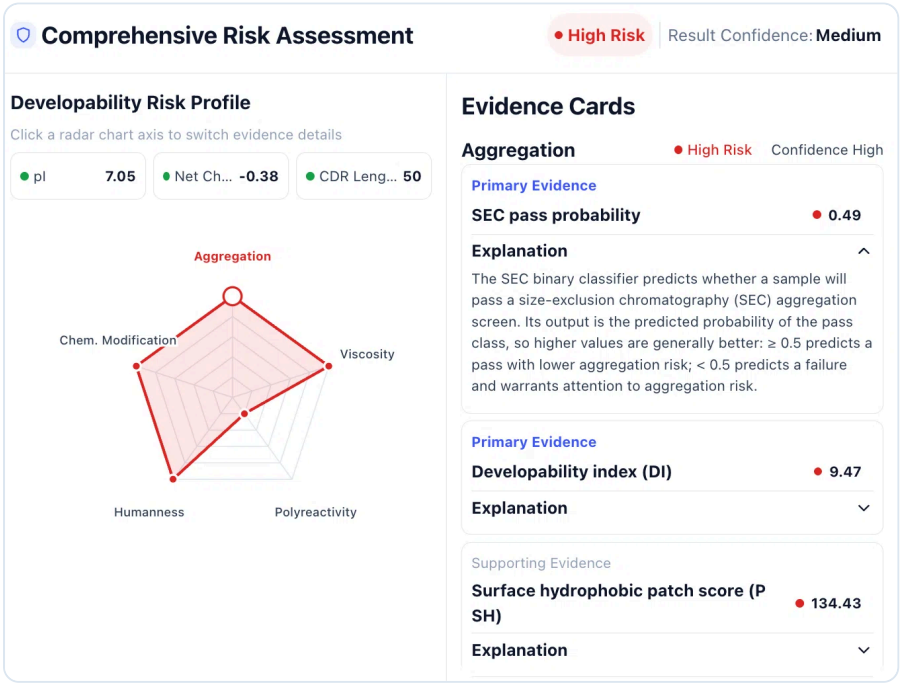
Polyreactivity
PSR classification probability and positive patch charge (PPC).

MOLECULE-SPECIFIC FIFTH DIMENSION

mAb **Viscosity**
DeepViscosity prediction probability, SFvCSP, and Fv surface charge.

VHH **Thermostability**
TEMPRO-predicted melting temperature (T_m, °C).

EXAMPLE REPORT



Report Excerpt

Five-Dimension Risk Radar with Aggregation Metrics

Intelligent Interaction & Multi-Agent Collaboration

Describe your research goals in natural language. AI agents coordinate core algorithms and lightweight tools as needed, so you can focus on scientific judgment.

NATURAL LANGUAGE INTERACTION

Replace Manual Steps with Conversation Drive AI Without Coding

Describe your R&D needs in natural language. The platform interprets intent, selects algorithms, orchestrates workflows, and returns results without coding or manual parameter setup.

"Design antibodies against a PD-L1 epitope involved in immune evasion."

"Goal confirmed: target a functional PD-L1 epitope involved in immune evasion. Next: ① Confirm the PD-L1 UniProt sequence → ② Retrieve the PD-L1 / PD-1 complex → ③ Identify key interacting residues and functional epitopes → ④ Design antibodies de novo..."

MULTI-AGENT COLLABORATION

Four Specialist Assistants Coordinated, Autonomous Decisions

A shared orchestration engine brings four specialist assistants together in a single exchange.

Antibody Design Assistant

Understand research needs, run tools, and generate reports with expert guidance.

Visualization Assistant

Display 3D structures, potential risk sites, and design reports for intuitive interpretation.

Risk Assessment Assistant

Assess humanness, aggregation, chemical stability, and other developability risks.

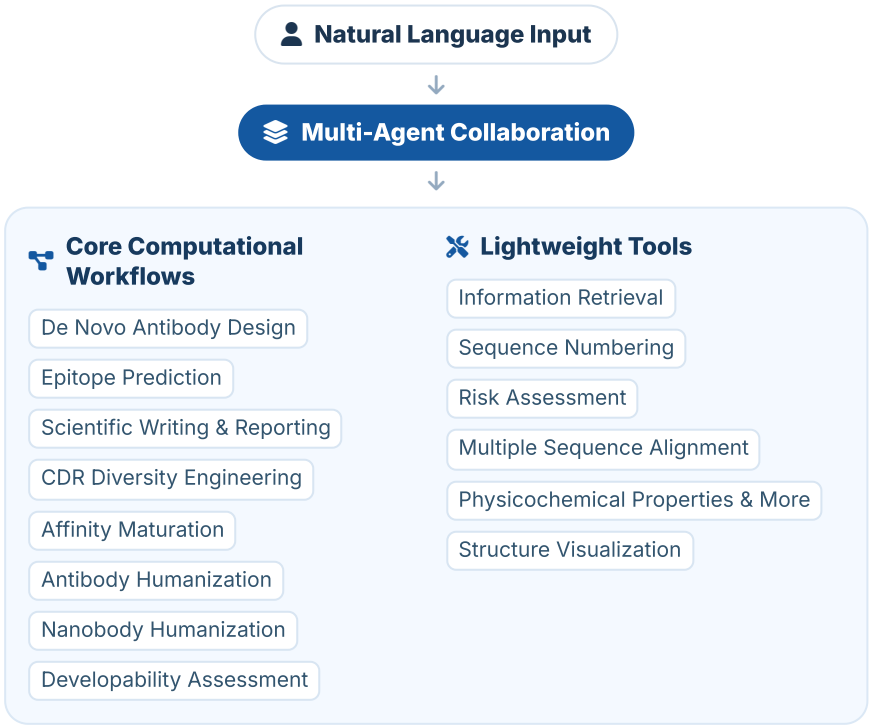
Next-Step Advisor

Recommend and prioritize next steps based on the available data.

INTELLIGENT ORCHESTRATION ARCHITECTURE

Core Computational Workflows + Lightweight Tools

Assistants combine core computational workflows and lightweight tools into a task-specific sequence of actions.



Project Management for Team Collaboration

Bring AI capabilities and project management into a shared R&D workspace, turning individual tools into reusable team infrastructure.

PARALLEL PATHS

Explore Design Paths in Parallel; Trace Decisions

Automatic Design-Path Archiving

Explore multiple design strategies within one project. Branches and decision history are archived automatically for review and comparison.

INDIVIDUAL EXPLORATION → TEAM DISCUSSION

Connect Individual Exploration with Team Collaboration

AI Assistance at Every Step

AI assistants provide immediate sequence analysis, literature retrieval, and design recommendations during individual exploration and team review.

AUTOMATIC KNOWLEDGE CAPTURE

Retain Expertise as a Team Asset

Automatic Project Knowledge Capture

Project documents, computational results, and discussions are captured automatically in a shared knowledge base, giving the team a common foundation for decisions.

Review, Trace, and Hand Over

Keep methods, results, and decisions traceable throughout the project and ready for handover.

Retain research experience as reusable team knowledge.

Collaboration Workspaces

Shared workspaces for industry and academic research teams.

Contact Us for a Quote ›

Enterprise Edition | Education Edition

- ✓ Shared Team Credits
- ✓ Online Team Collaboration
- ✓ Unlimited Lightweight Tools
- ✓ Dedicated Support & Training

Three Ways to Partner With Us

Access our AI platform, co-develop antibody programs, or build AI into your own R&D workflows.

01 AI Antibody Design Platform

Self-service or dedicated deployment

Online Platform

Access Click.mAb. online for target research, antibody design, optimization, and assessment.

Private Deployment

Deploy Click.mAb. in a dedicated cloud environment with isolated data storage and access controls to support security, compliance, and knowledge retention.

02 Antibody R&D Services

AI design, expert support, and wet-lab validation

Joint Development

Co-develop antibody programs with shared goals, AI design, experimental validation, and agreed milestones.

Integrated Design & Wet-Lab Validation

Connect AI design, library screening, expression, and affinity testing. Receive candidate molecules and complete experimental results.

03 FDE R&D Engineering Services

AI capabilities built into your workflows

Build internal AI R&D capabilities through tailored workflows, AI agents, tool integration, and platform development.

WHY WORK WITH US?

- **Technical Expertise**
- **Flexible Engagement**
- **Data Security**
- **Expert Service Team**

HOW WE WORK

01 **Discovery**
Align on goals.

02 **Solution Design**
Define the plan.

03 **Delivery**
Execute the project.

04 **Ongoing Support**
Review and refine.

Contact Us

Partner with us to redefine antibody R&D through generative AI and advance the discovery of next-generation innovative medicines.

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Platform Updates

User Community

Business Inquiries

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

Partnership Inquiries

Scan the QR code or email us to discuss an integrated solution.

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