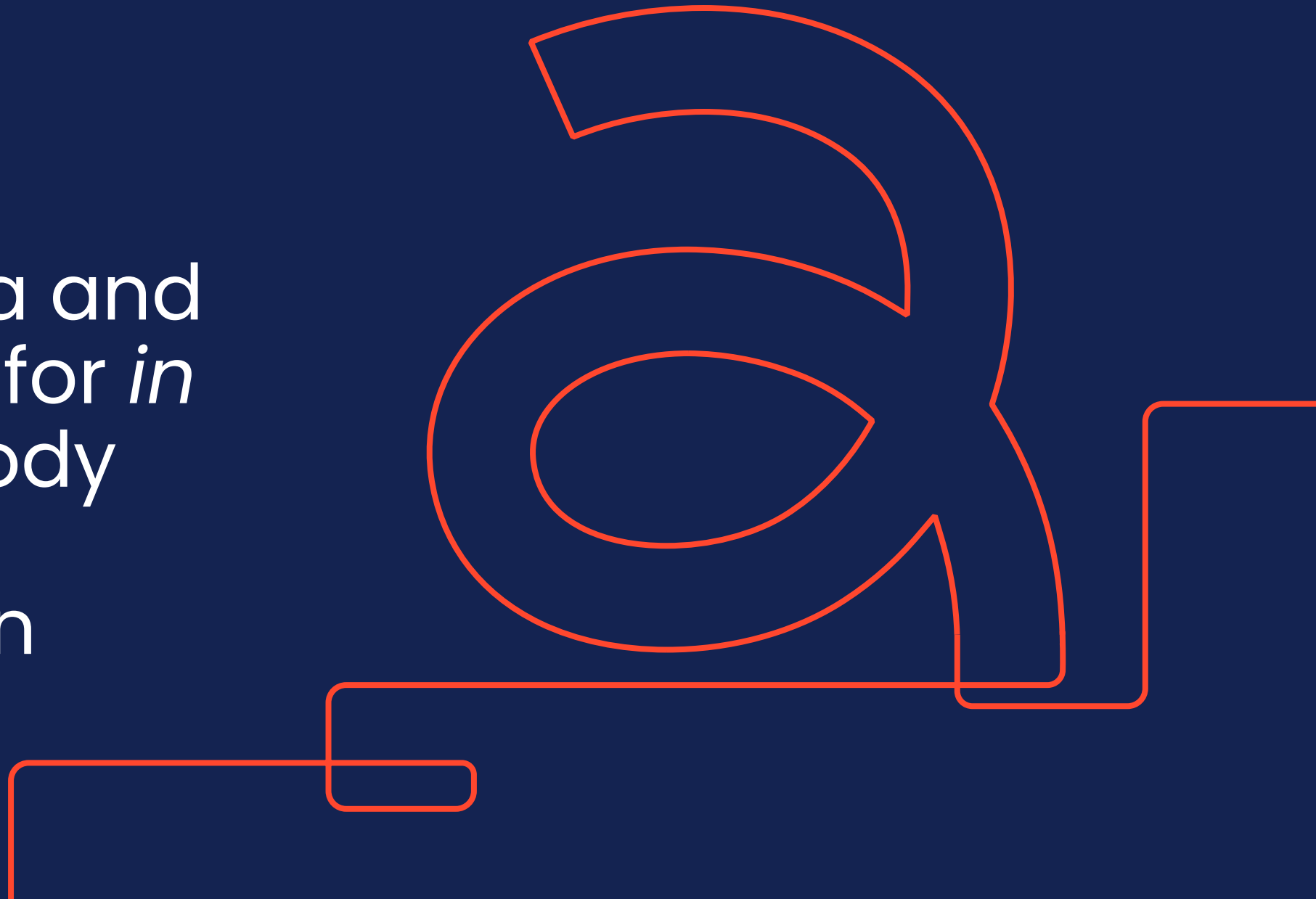
absci®

Absci's data and AI platform for *in silico* antibody design & optimization



March 22, 2022

Disclaimers

Forward-Looking Statements

Certain statements in this presentation that are not historical facts are considered forward-looking within the meaning of Section 27A of the Securities Act of 1933, as amended, and Section 21E of the Securities Exchange Act of 1934, as amended, including statements containing the words “will,” “may,” “anticipates,” “plans,” “believes,” “forecast,” “estimates,” “expects,” “predicts,” “advancing,” “aim,” and “intends,” or similar expressions. We intend these forward-looking statements, including statements regarding our strategy, future operations, future financial position, future revenue, research and technological development activities, efforts to scale fully in silico capabilities, growth plans, projected costs, prospects, plans and objectives of management, to be covered by the safe harbor provisions for forward-looking statements contained in Section 27A of the Securities Act and Section 21E of the Securities Exchange Act, and we make this statement for purposes of complying with those safe harbor provisions. These forward-looking statements reflect our current views about our plans, intentions, expectations, strategies, and prospects, which are based on the information currently available to us and on assumptions we have made. We can give no assurance that the plans, intentions, expectations, or strategies will be attained or achieved, and, furthermore, actual results may differ materially from those described in the forward-looking statements and will be affected by a variety of risks and factors that are beyond our control, including, without limitation, risks and uncertainties relating to the development of our technology; along with those risks set forth in our most recent periodic report filed with the U.S. Securities and Exchange Commission, as well as discussions of potential risks, uncertainties, and other important factors in our subsequent filings with the U.S. Securities and Exchange Commission. Except as required by law, we assume no obligation to update publicly any forward-looking statements, whether as a result of new information, future events, or otherwise.

Market and Statistical Information

This presentation also contains estimates and other statistical data made by independent parties and by us relating to market size and growth and other industry data. These data involve a number of assumptions and limitations, and you are cautioned not to give undue weight to such estimates. We have not independently verified the data generated by independent parties and cannot guarantee their accuracy or completeness.

Acknowledgements

I want to acknowledge the amazing Unlimiters

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Bob Albrecht
Jovan Cejovic

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Alexander Brown, PhD
Kelechi Fletcher

Legal Team:
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Thomas Wrona, PhD JD

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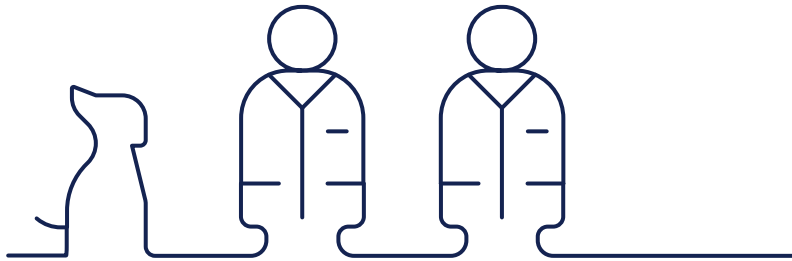
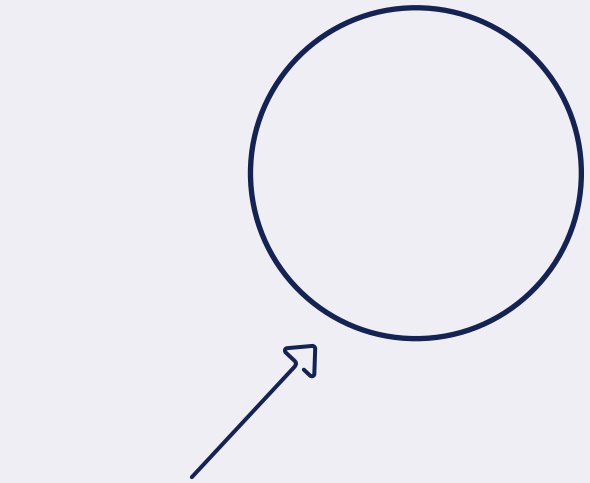


Biologic drug discovery is a complex combinatorial challenge

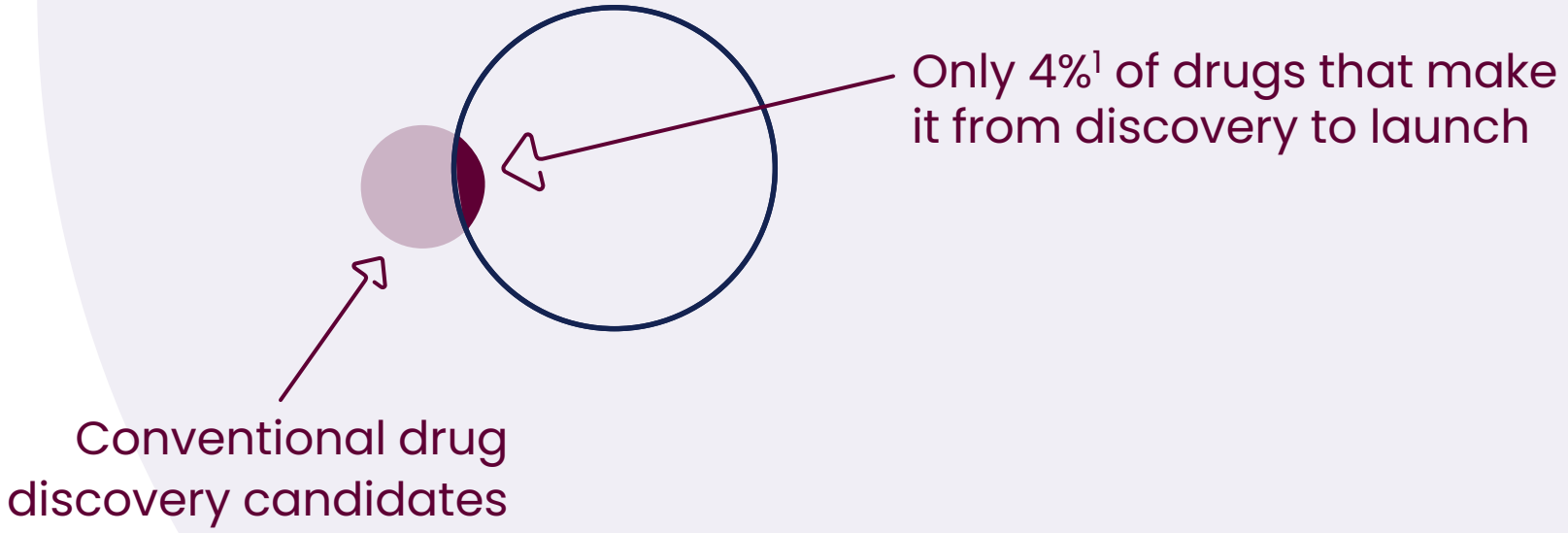
~20^{62} mAb CDR variants[1] *exceeds* **~10^{80}** atoms in the universe[2]

[1]Assuming 62 positions (6 unique CDRs of approximately 7-13 residues in length) to vary with 20 possible amino acids per position
[2]https://www.thoughtco.com/number-of-atoms-in-the-universe-603795

Biologic drug discovery fails too often



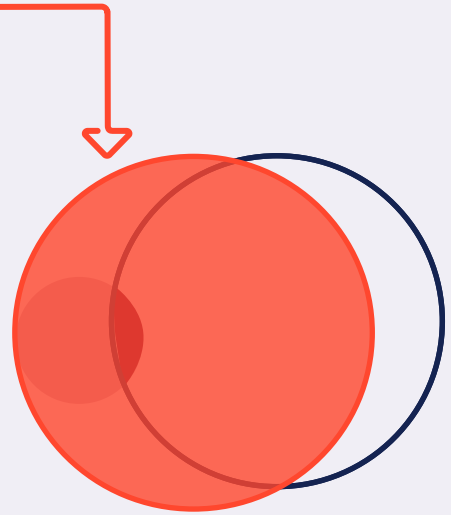
Biologic drug discovery fails too often



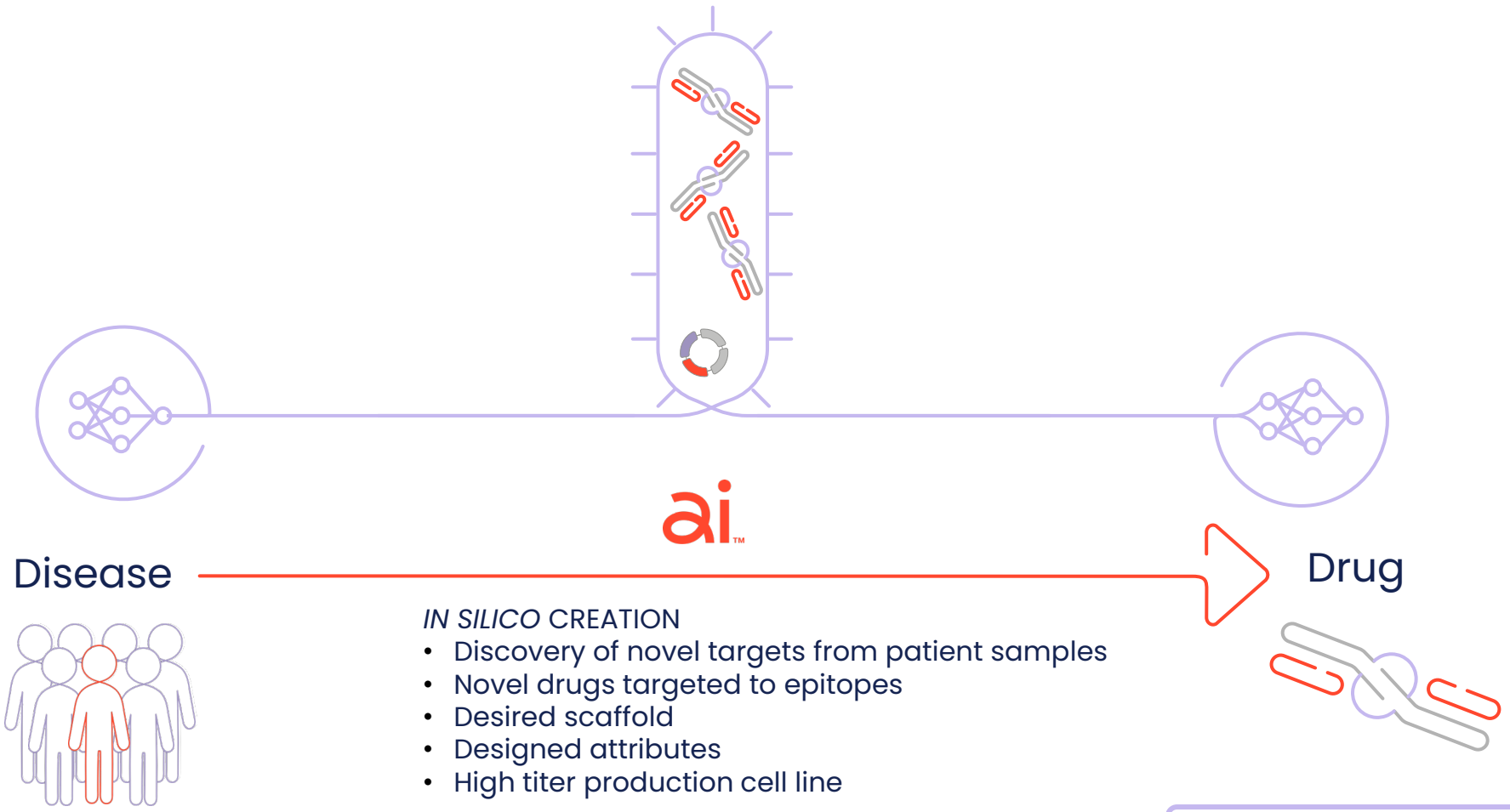
[1]Paul, S., Mytelka, D., Dunwiddie, C. et al. How to improve R&D productivity: the pharmaceutical industry's grand challenge. Nat Rev Drug Discov 9, 203–214 (2010).

Absci's mission – bring better drugs to patients

Proprietary wet lab data and AI enables Absci to explore **more** of the **right** sequences



A new reality – better drugs on demand



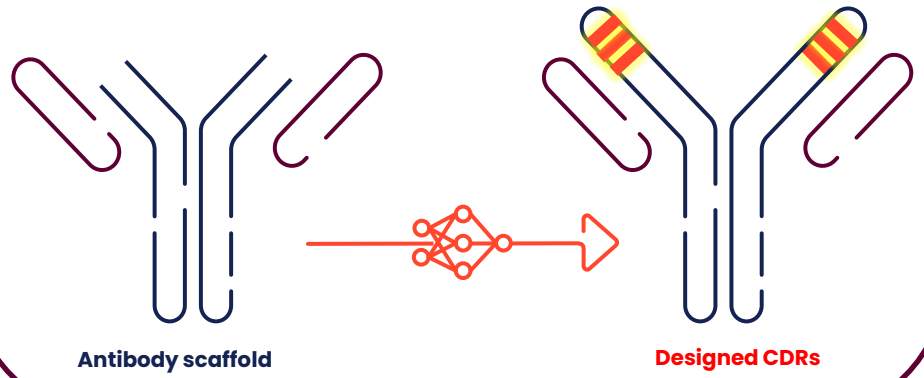
IN SILICO CREATION

- Discovery of novel targets from patient samples
- Novel drugs targeted to epitopes
- Desired scaffold
- Designed attributes
- High titer production cell line

Absci's AI models for *in silico* biologic drug design

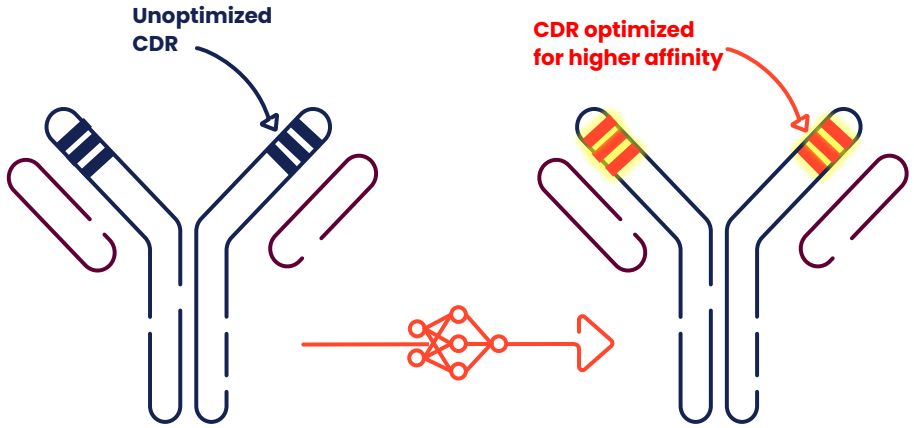
De Novo Discovery

In silico design of entire CDR3 in a specified scaffold to a never-before-seen antigen



Lead Optimization

In silico selection of amino acid identities within trastuzumab CDR3 to increase antibody affinity for antigen (Her2)



Absci's AI models for *in silico* biologic drug design

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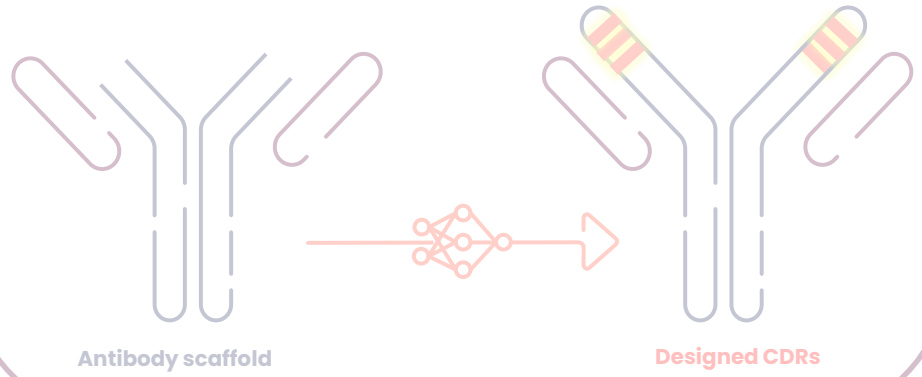

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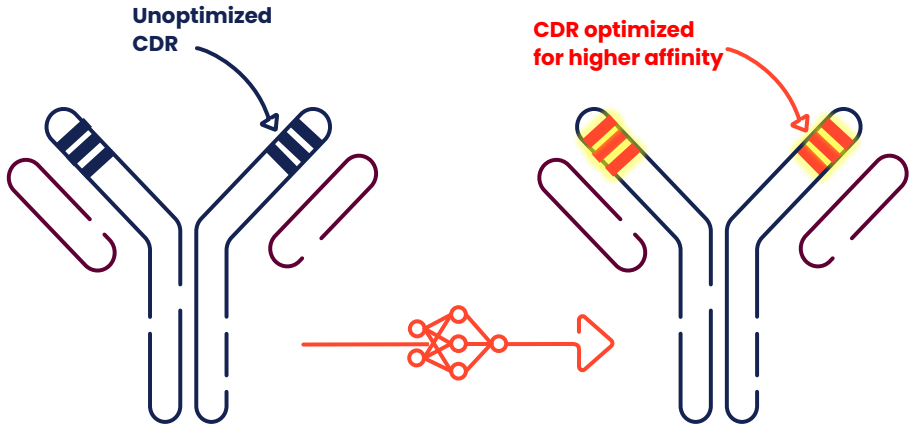


Enabling the future of AI-based drug discovery through data

SoluPro® strain

+

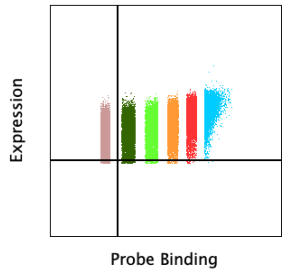
Library of molecule variants

+

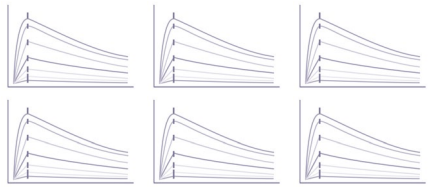
Folding & Expression Solutions library

billions of cells

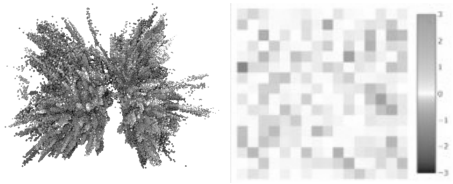
ACE Assay™ technology



High-throughput biophysical characterization



Denovium Engine™ platform,



AI-designed drug candidate

+

Manufacturing cell line

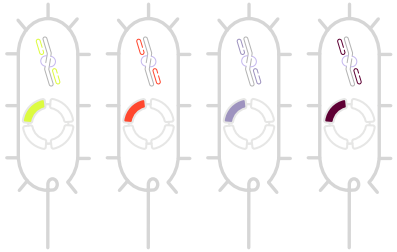
predict

ai™

learn

ACE Assay™ technology delivers ultra-high-throughput data on drug design

1. Strains expressing unique sequence variants



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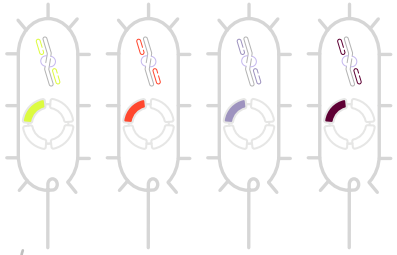
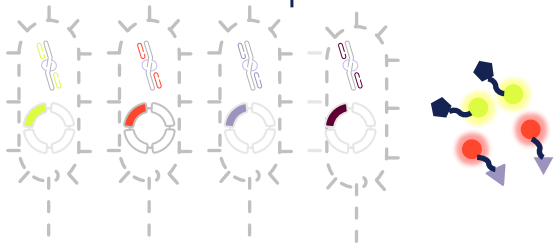


2. Fix and permeabilize cells and add labeled probes



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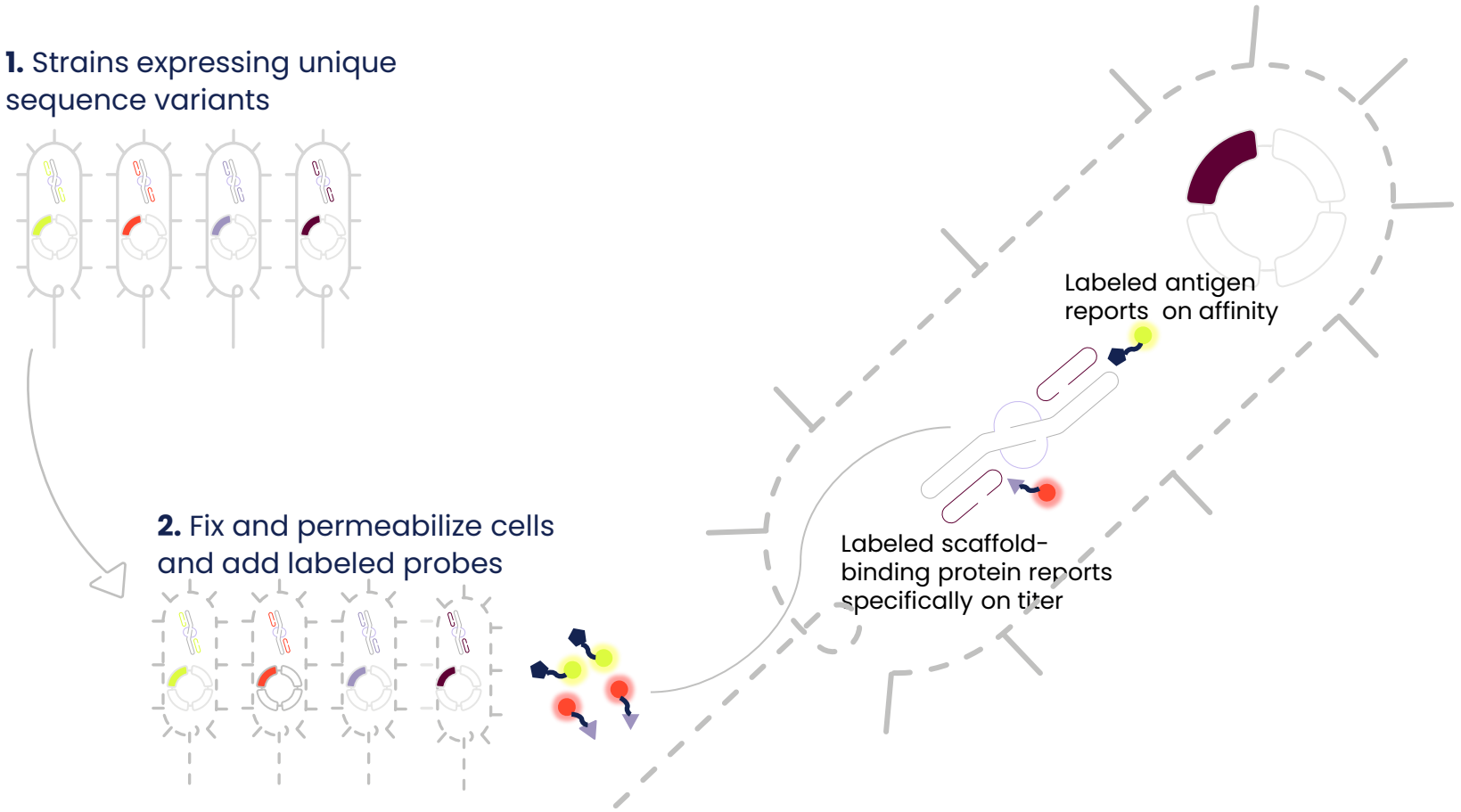

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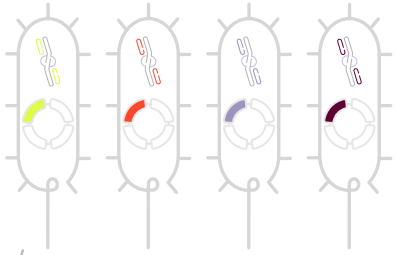

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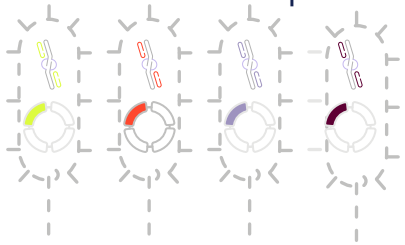
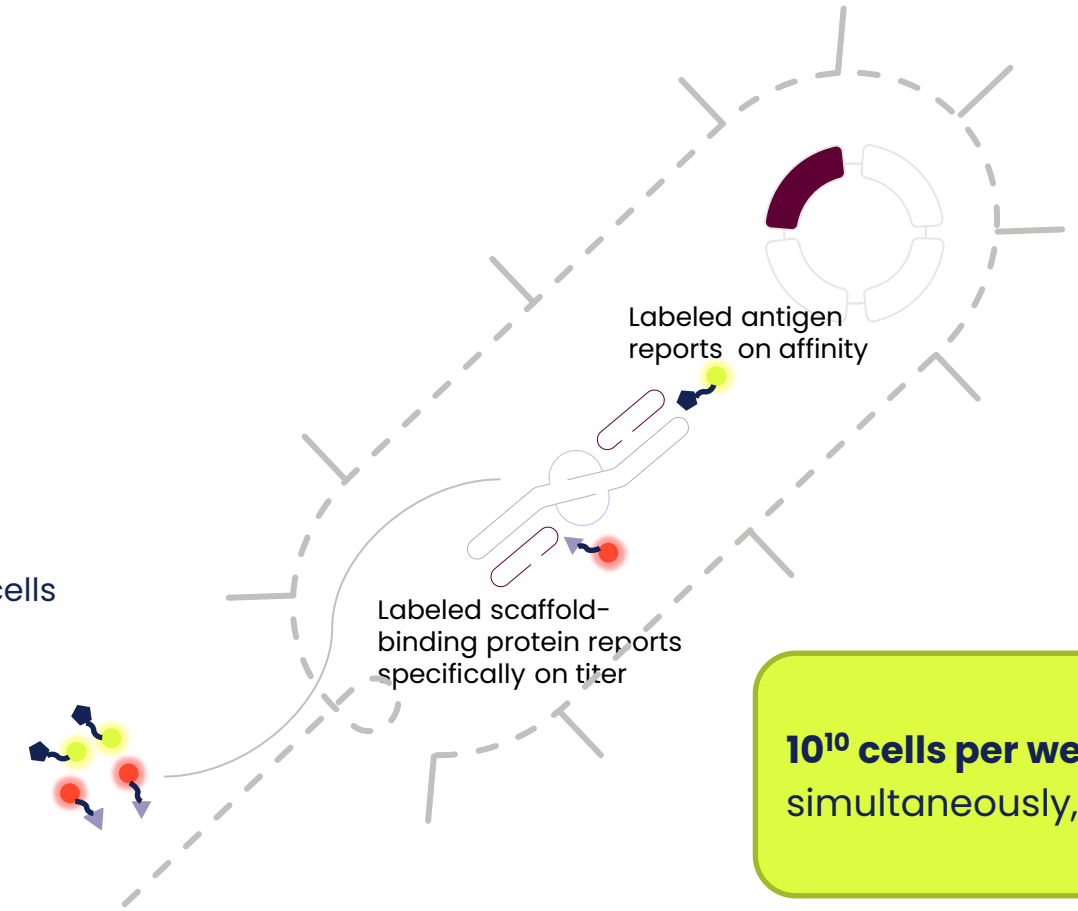
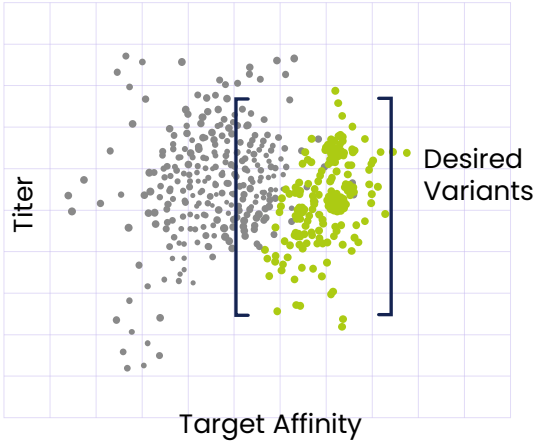




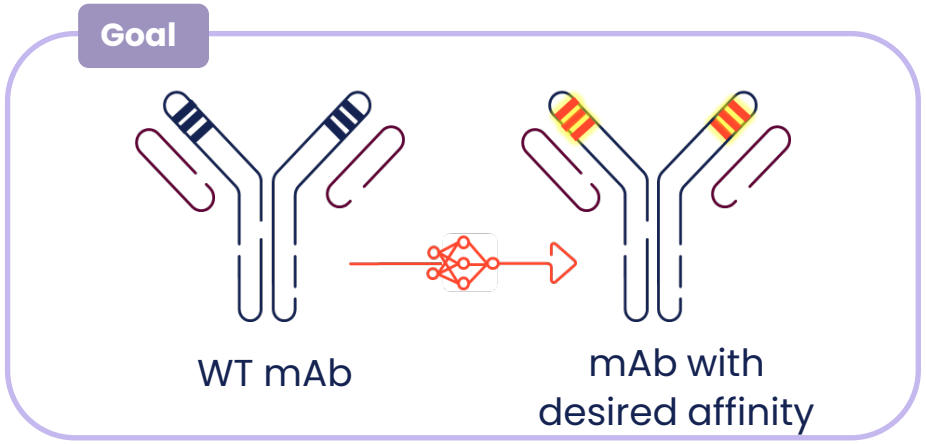
3. Screen and sort by flow cytometry

Representative ACE Assay™ data



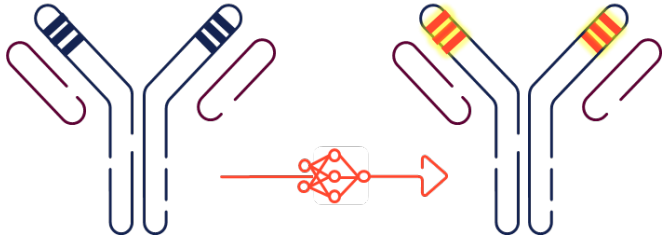
10^{10} cells per week for multiple parameters simultaneously, such as titer and affinity

Goal: Dial-in antibody affinity



Goal: Dial-in antibody affinity

Goal

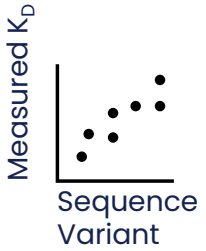


WT mAb

mAb with desired affinity

Overview of workflow

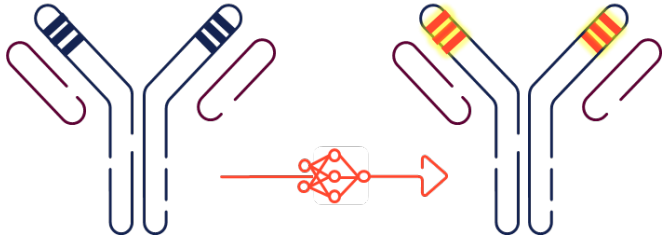
Lab assays



AI models

Goal: Dial-in antibody affinity

Goal



WT mAb

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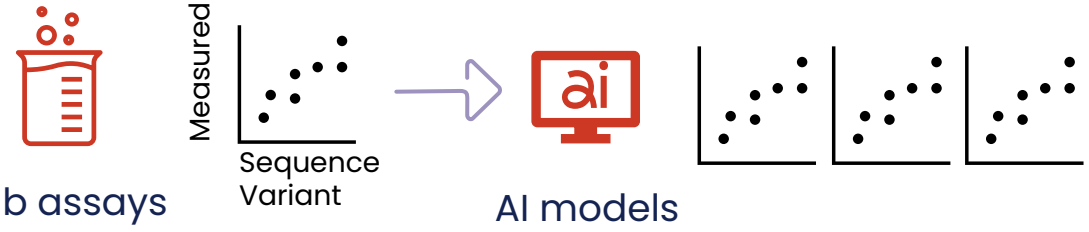


Lab assays

AI models

Absci's quantitative binding predictions are beyond the state-of-the-art

Absci has developed assays and AI models providing

quantitative

binding predictions, thereby enabling genuine *in silico* design of desired affinity

AI model robustly simulates wet lab results *in silico*

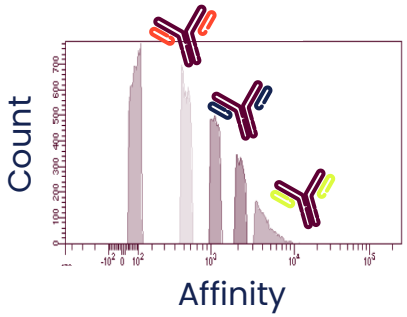
SoluPro® strain

+

Library of trastuzumab CDR(H3) variants

Proprietary primary screening
Rank variants by affinity

ACE Assay™ technology with SoluPro® strain



Rescreening
Increase accuracy in K_D range of interest

Training AI model
Screen unseen variants *in silico*

trastuzumab variants with desired affinity

AI model robustly simulates wet lab results *in silico*

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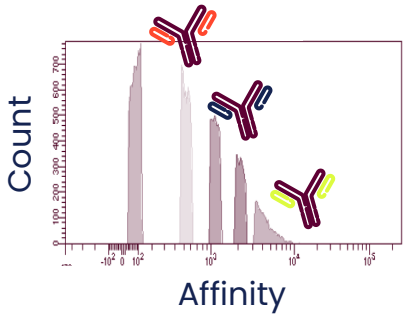
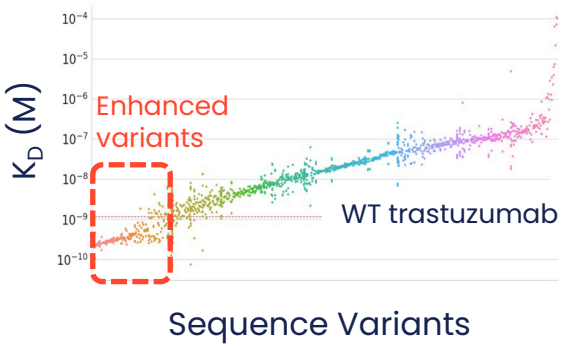


Rescreening

Increase accuracy in K_D range of interest

Optimized mid-throughput SPR methods



Training AI model

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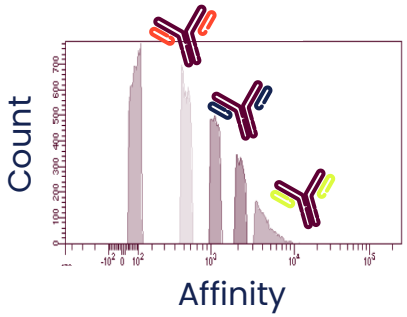

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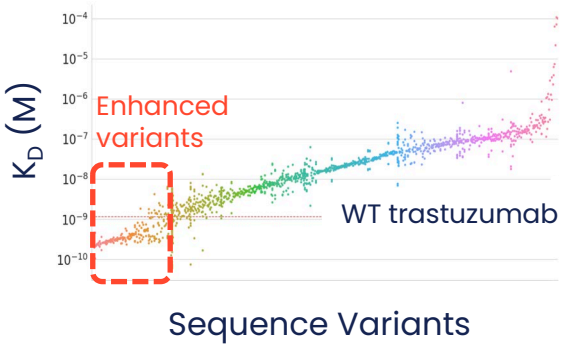


Training AI model

Screen unseen variants *in silico*

Denovium Engine™ technology

trastuzumab variants with desired affinity

- Absci's AI model is pretrained on human Ab sequences and can score "naturalness" of variants, followed by further training with affinity data

AI model robustly simulates wet lab results *in silico*

SoluPro® strain

+

Library of trastuzumab CDR(H3) variants

Proprietary primary screening
Rank variants by affinity

ACE Assay™ technology with SoluPro® strain

Rescreening
Increase accuracy in K_D range of interest

Optimized mid-throughput SPR methods

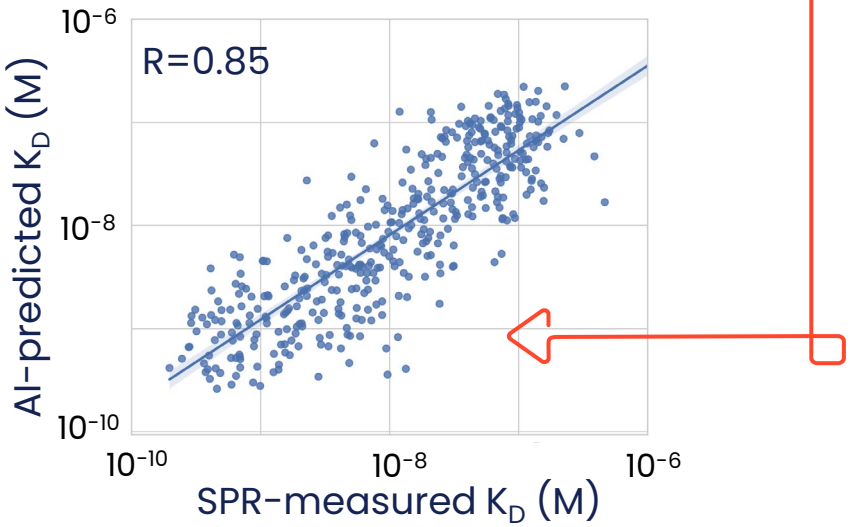
Training AI model
Screen unseen variants *in silico*

Denovium Engine™ technology

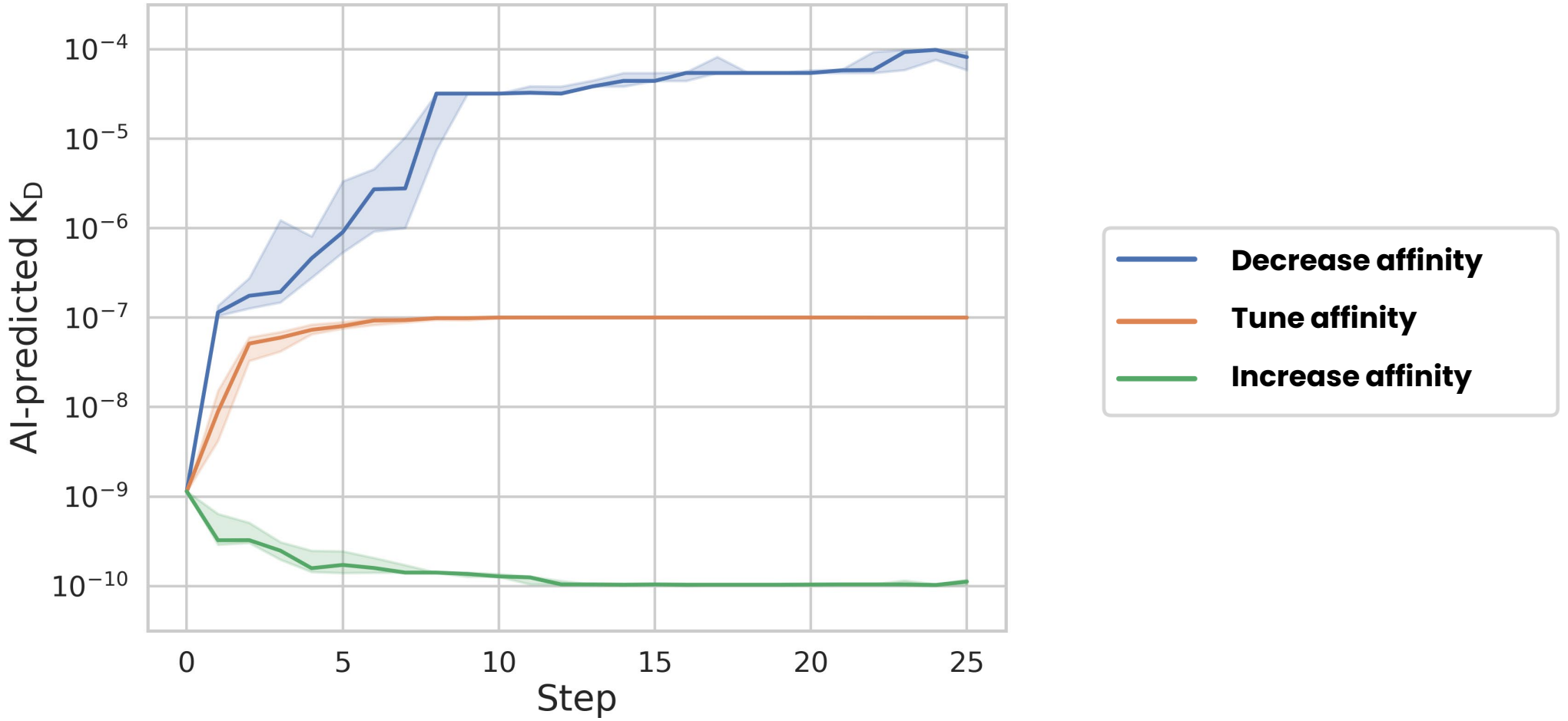
trastuzumab variants with desired affinity

Absci designed desired target affinity *in silico* with high confidence (R = 0.85)

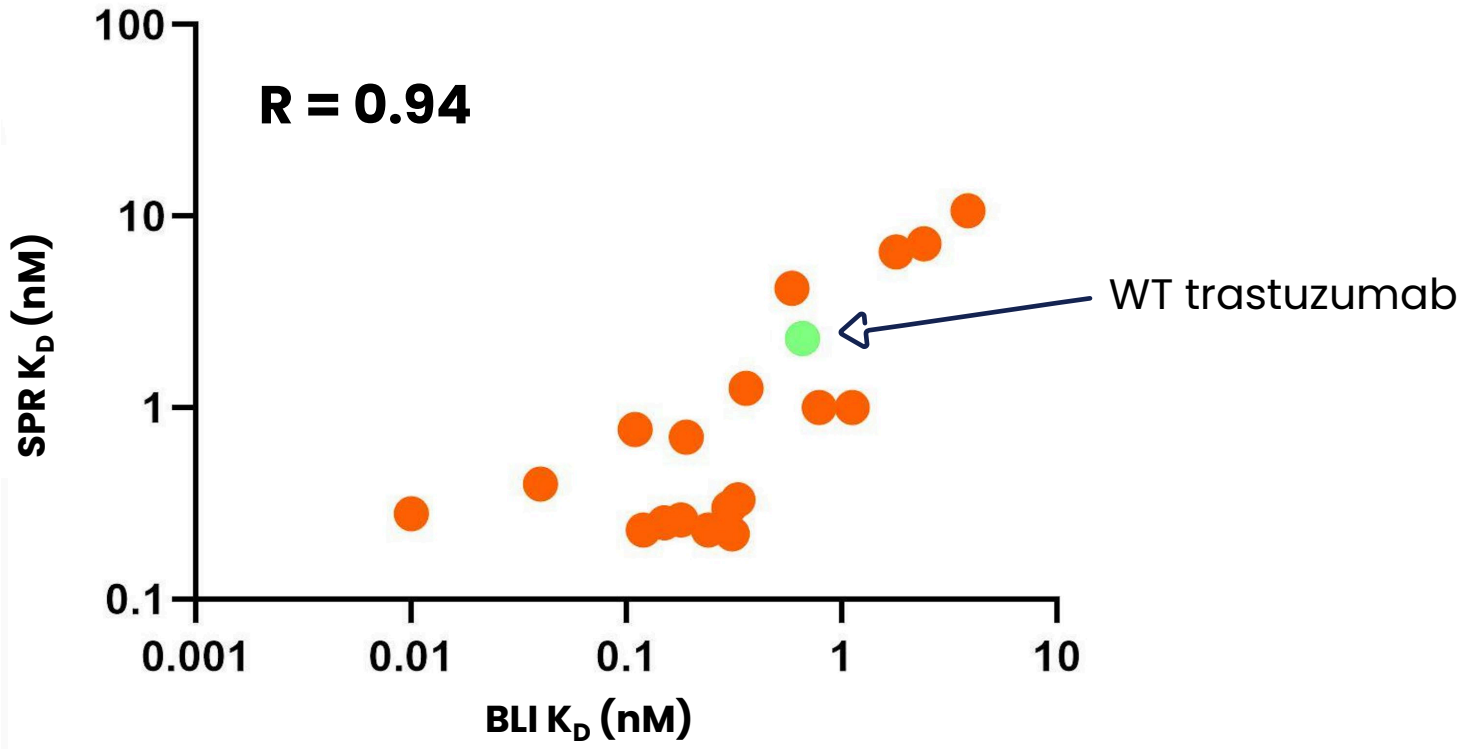
Binding affinity
AI-predicted vs SPR-measured



Designing optimized antibody variants *in silico*



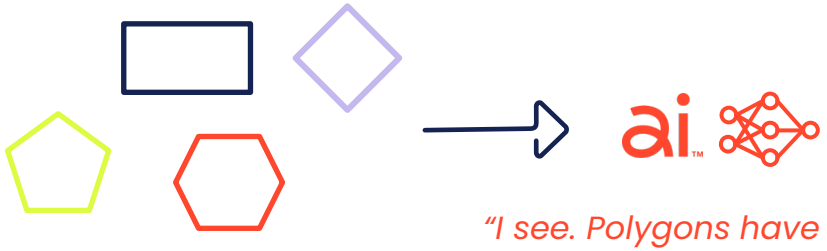
AI-generated trastuzumab variant with two orders of magnitude higher affinity



A model's understanding of nature

Training

"These are examples of how natural polygons look"



"I see. Polygons have straight lines and they are closed, but color does not matter"

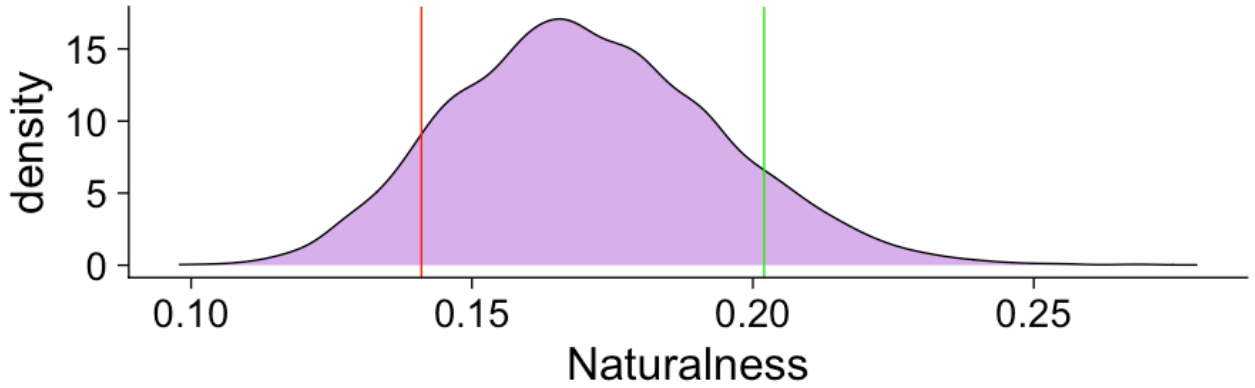
Prediction

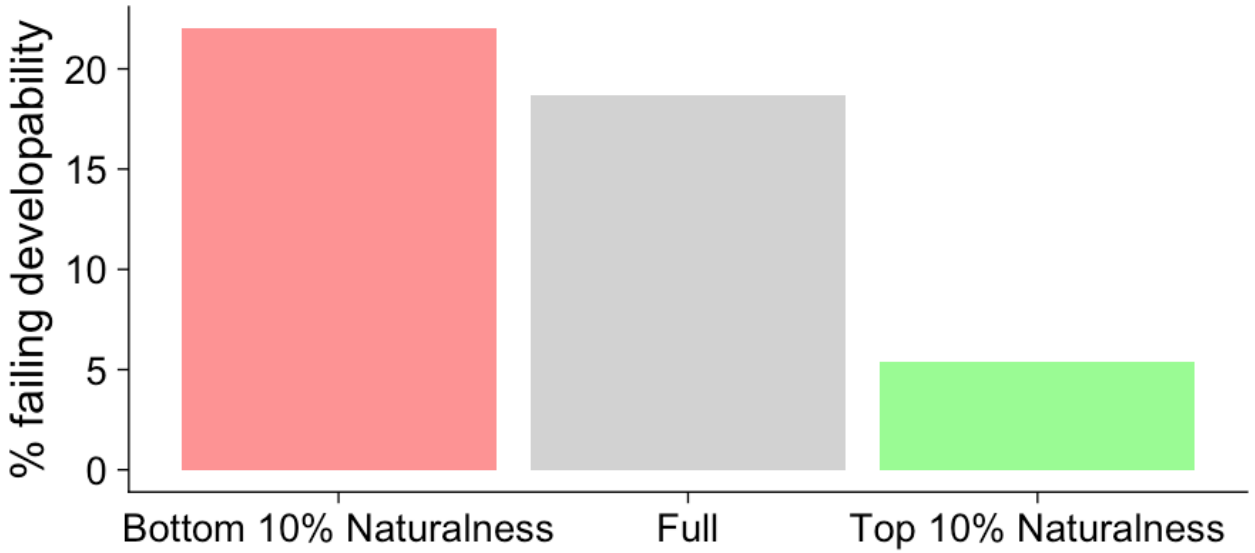
"Are these natural polygons?"

We *teach* naturalness using hundreds of millions of antibody sequences from multiple species

We *predict* naturalness of antibodies of interest, such as sequence variants

Modeling antibody “naturalness” with AI

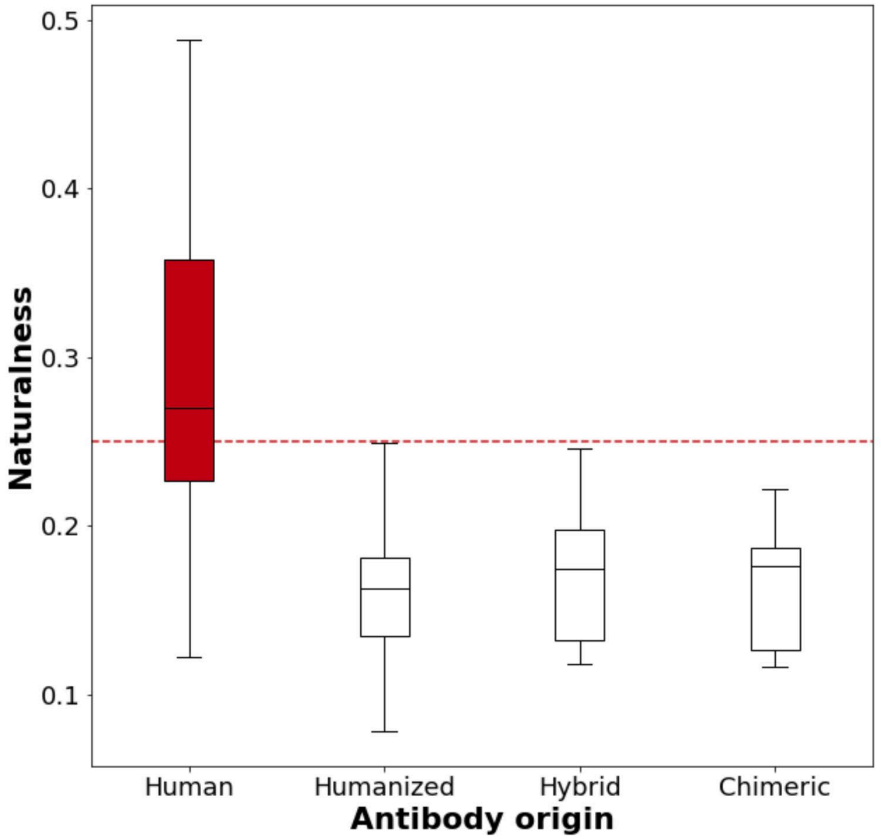


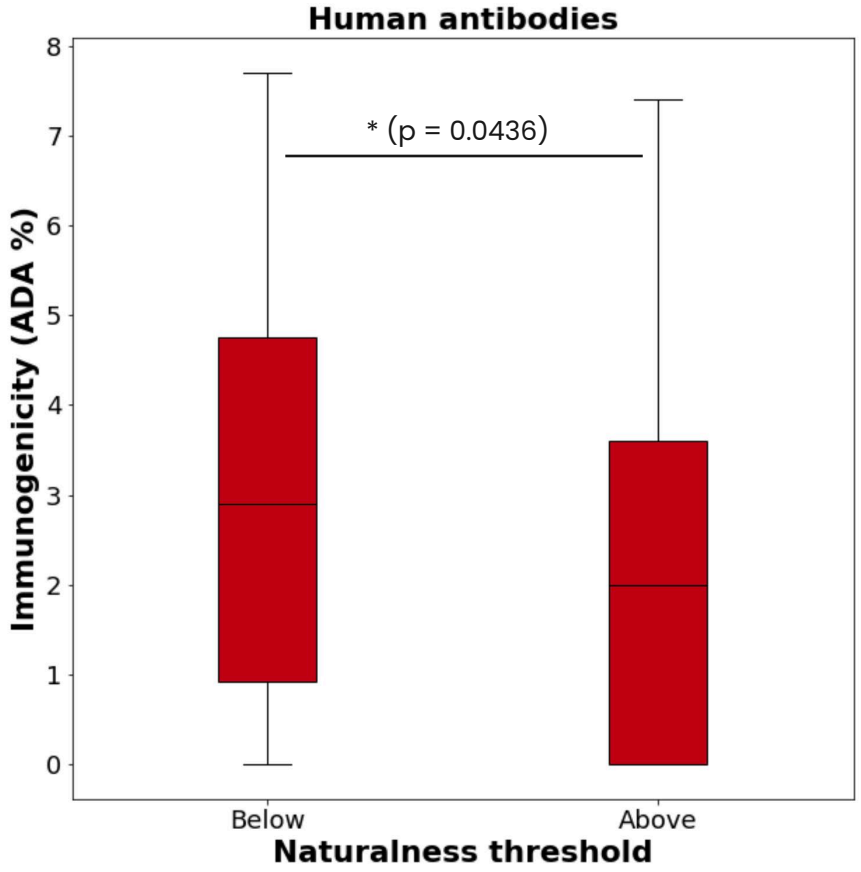


Developability assessed using OPIG’s Therapeutic Antibody Profiler on 5000 top hits after 3 rounds of phage display.

1. Liu et al, Bioinformatics 36:2126 (2020).
2. Raybould et al, PNAS 116:4025 (2019)

Naturalness is (inversely) associated with immunogenicity

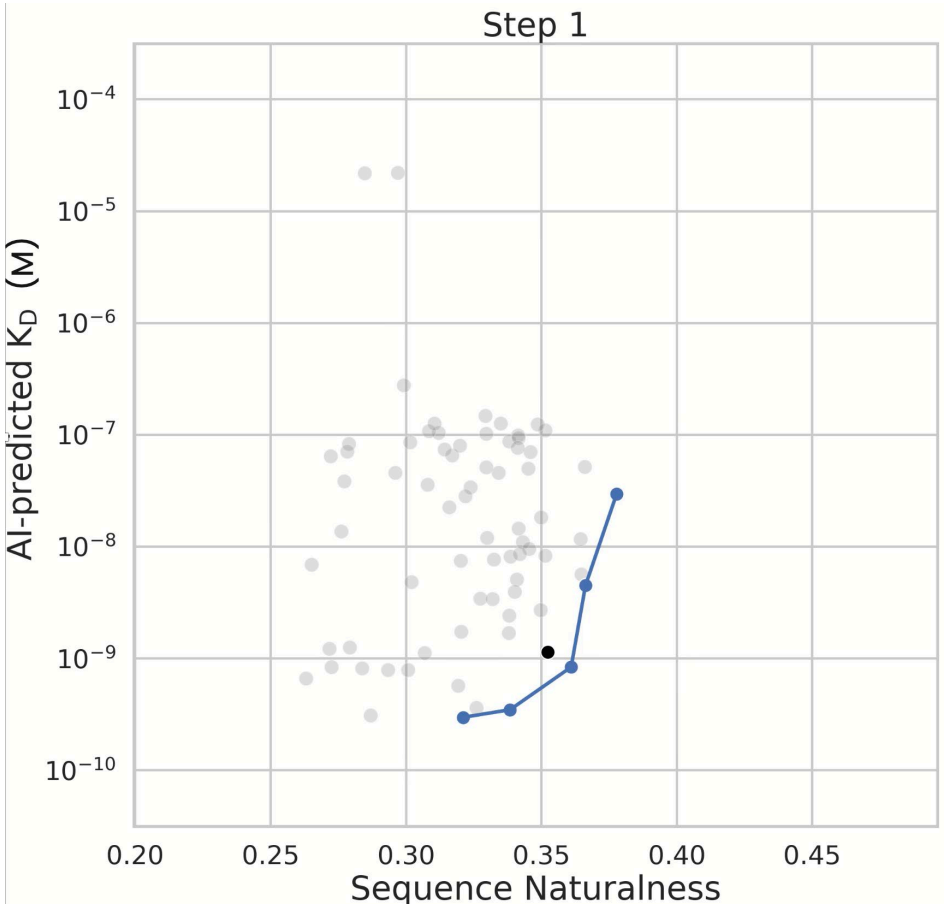




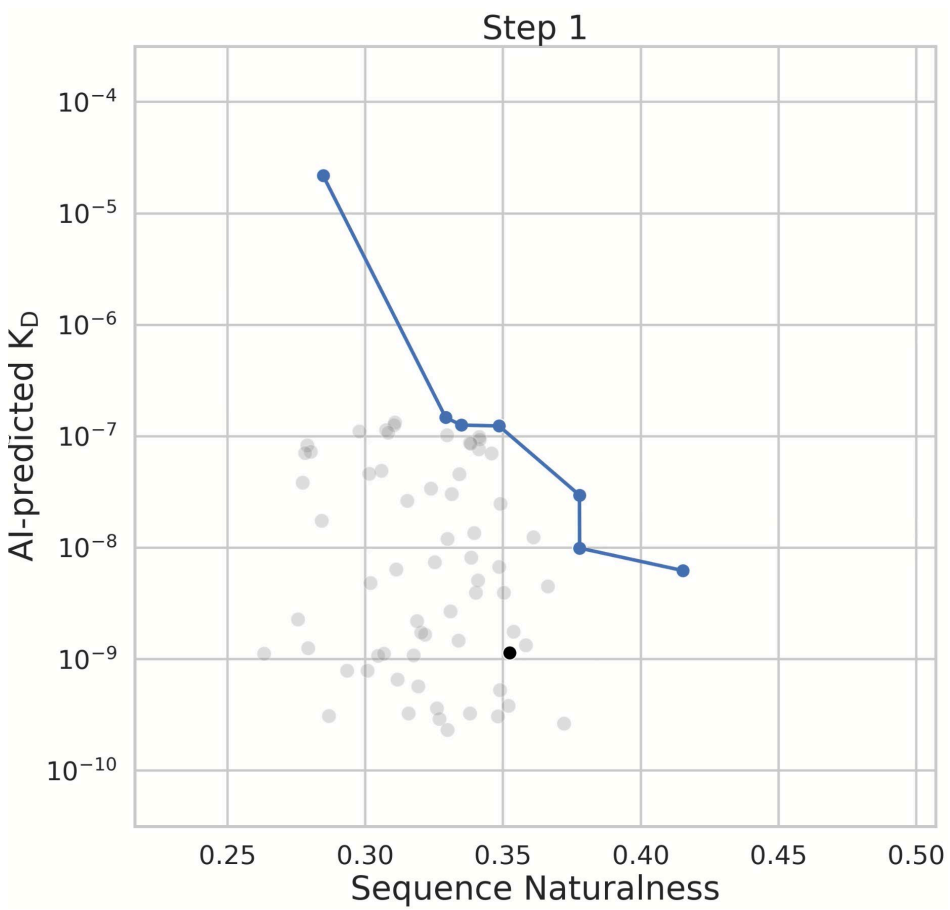
Therapeutic antibodies and ADA responses from Marks et al, Bioinformatics 37:4041 (2021)

Simultaneously optimizing for affinity and naturalness

Maximize Affinity, Maximize Naturalness



Minimize Affinity, Minimize Naturalness



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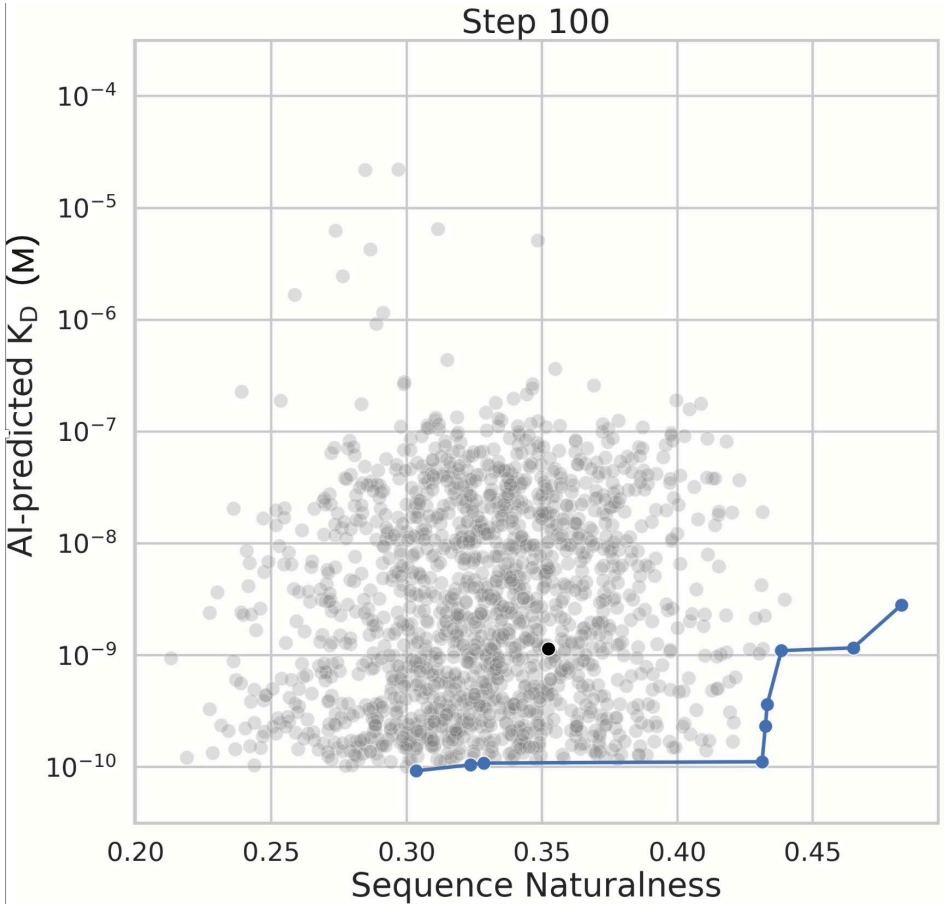
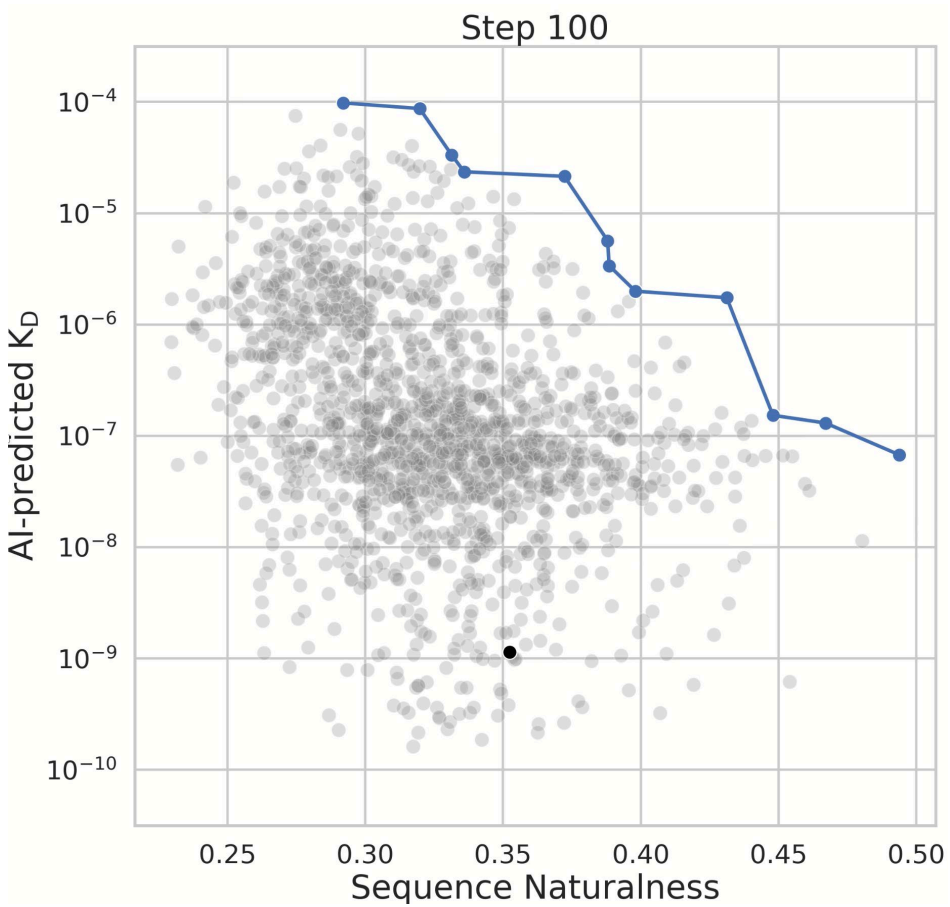


Minimize Affinity, Minimize Naturalness



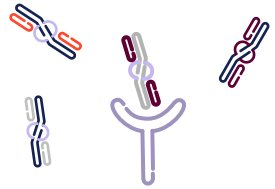
The new paradigm for protein-based drug discovery: Going fully *in silico*

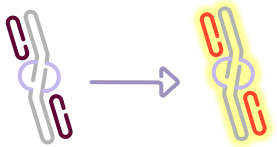
De Novo Discovery *In Silico*

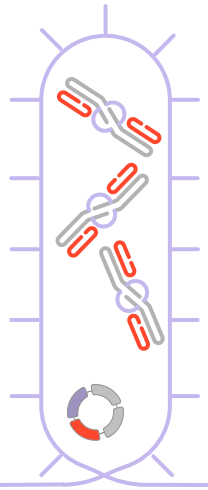
target -> antibody lead

Lead Optimization *In Silico*

antibody lead -> antibody drug

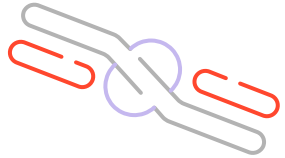






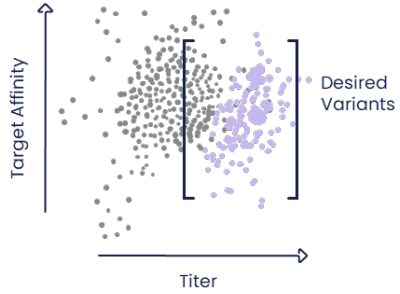
Disease

Drug



Screening 10^{10} drug candidates per week with Absci's proprietary synthetic biology engine

Absci ACE Assay™



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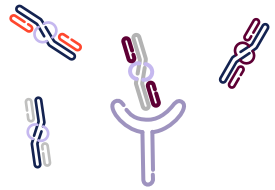

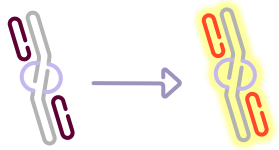

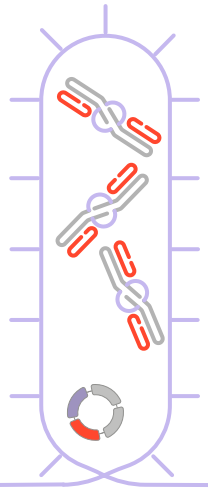

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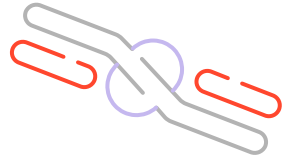

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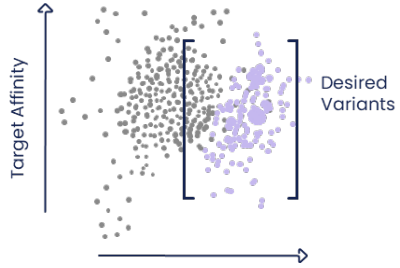

NVIDIA technologies are enabling absci to scale its fully *in silico capabilities*

- Accelerators
- GNN SE(3) Transformer
- DGX Foundry
- 80GB A100 supercomputer

absci NVIDIA