LENSᵃⁱ™ BioIntelligence Suite
Epitope Binning

Effortless *in silico* mAb Epitope Binning with proven wet lab validation

Next-level in silico epitope binning, powered by LENSᵃⁱ technology, offers a pivotal advancement with its ability to analyze over 5,000 sequences, delivering rapid insights for early triaging. This advanced method allows you, within large pools of antibodies, to detect clusters of clones that share similar target binding regions ensuring a thorough and inclusive selection process. LENSᵃⁱ epitope binning smart algorithms enhance biological research, offering accurate, high-throughput candidate selection while reducing time and costs.

Speed and High-throughput
Results within hours for small subsets to 2 weeks for >5k antibodies.

Early epitope landscape profiling:
More-informed early triaging of lead candidate panel.

Proven:
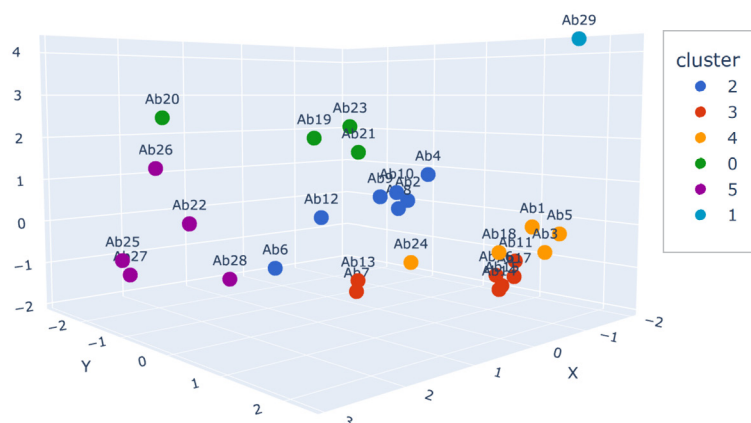Matches wet lab binning methods with high accuracy.

Effortless:
Only requires protein sequences — no need to produce physical materials.

Innovate earlier. Scale smarter.

Significant high-throughput analysis for early triaging

Advance all mAb program types including challenging and hard to produce target proteins

Designed to reduce time and costs

Easily profile the epitope landscape

A critical step in antibody selection.

Epitope binning is crucial in the early stages of antibody discovery, as it facilitates the categorization of antibodies with similar binding regions on the target. In general, insights in the epitope landscape of antibody panels significantly advance development of multi-targeting approaches. Additionally, understanding which protein regions are targeted by your antibody panel can significantly enhance intellectual property security.

Maximize early triaging with high efficiency

High precision with multi-dimensional clustering

LENS^ai proprietary Epitope Binning algorithm includes:

- Antibody sequential and structural profiling
- Docking information, accounting for steric hindrance and glycosylation sites
- Atomic interactions of Ab-Ag complexes

Multiple output formats providing actionable insights
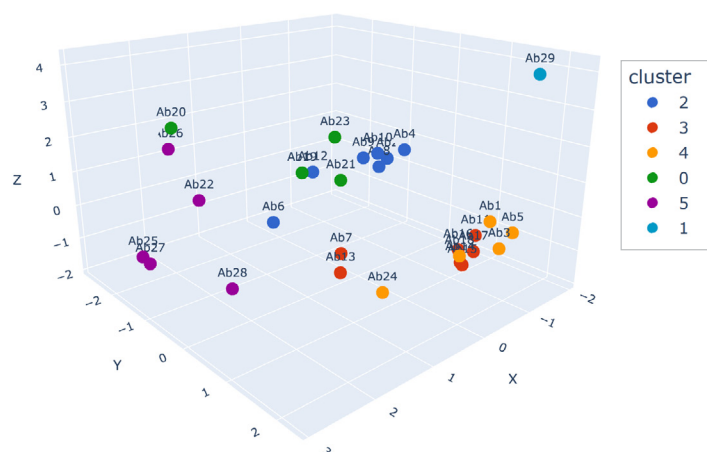
3D grid view:
Clusters group antibodies that share a similar target binding region. Quick view on cluster proximity.
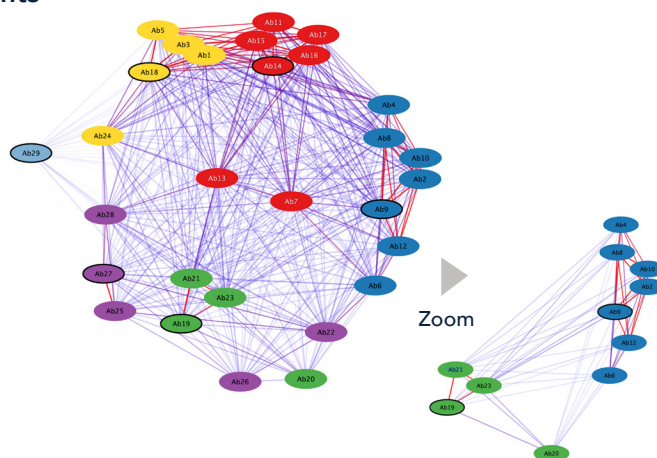
Graph view:
Lines show similarity between Abs within and between clusters (red=high, blue = low). Select and zoom in (panel on the right). Ab closest to all other members of its cluster are denoted with black border.

Proven technology

Blinded wet lab validation of *in silico* prediction of epitope bins:

- Example set of 29 antibodies
- LENS^ai *in silico* epitope prediction versus classical *in vitro* competition assay for binning
- Inter-annotator agreement analysis (Cohen's Kappa test) using a majority consensus label mapping

Result:
Excellent agreement between LENS^ai binning and *in vitro* binning

Cohen's Kappa test

Label mapping	κ
LENS^ai cluster > Wet lab bin	0.925
Wet lab bin > LENS^ai cluster	0.842

Coefficient value key:
> 0.8: Near perfect agreement

Biostrand.ai

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