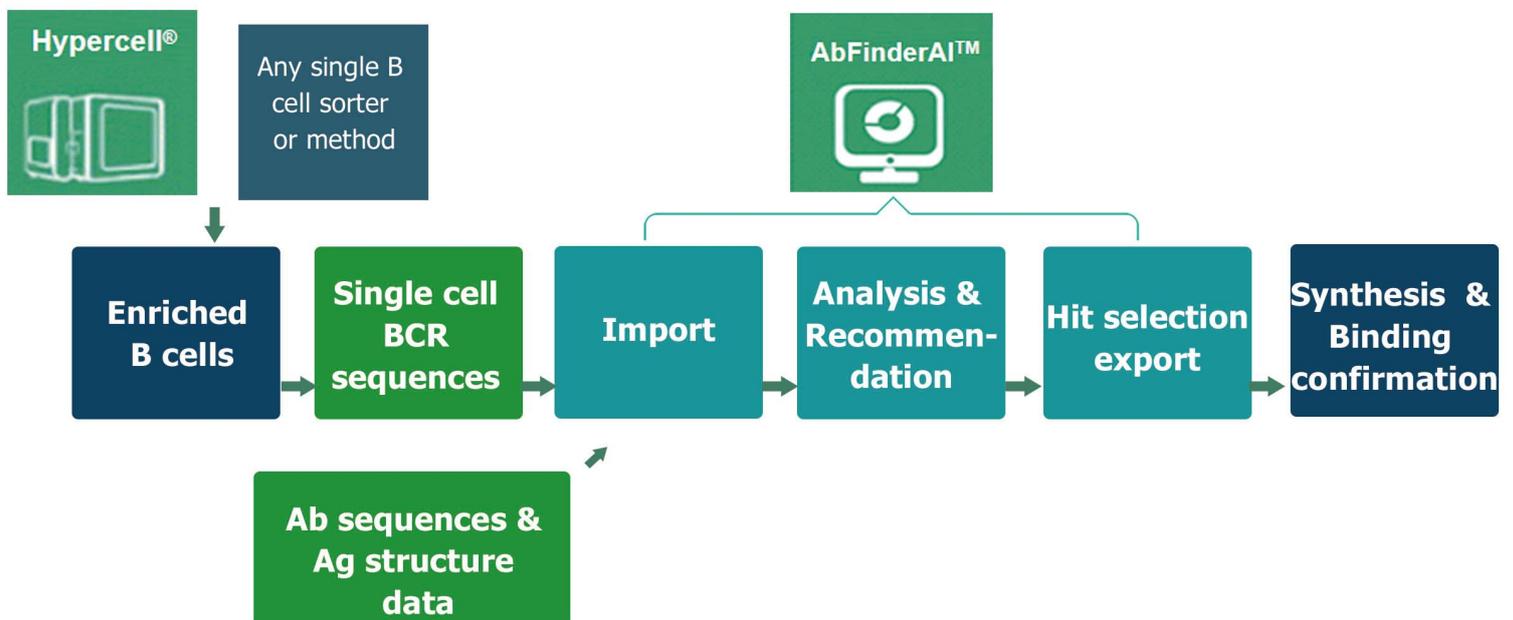


ABOUT ABFINDERAI™

AbFinderAI™ is a user-friendly analysis tool specifically designed for single-cell BCR sequencing data. It simplifies the process of interpreting and understanding the complex data generated from single-cell BCR sequencing experiments, helping lab scientists accelerate their research and make informed decisions.

- ☑ Accelerating Antibody Candidate Identification
- ☑ Tailored for Lab Scientists
- ☑ AI-Powered Insights
- ☑ From Repertoire to Hit List
- ☑ Faster Data Processing



As the perfect partner for high-throughput single-cell sorters, AbFinderAI™ leverages next-generation sequencing (NGS) and AI-driven models to optimize antibody discovery.

Comprehensive BCR Analysis

Identify clonal expansion and somatic hypermutation.
Quantify repertoire diversity.

Annotation

Automatically annotate CDRs, V-genes, and J-genes of VH and VL.
Detect liabilities in CDR regions.
Supports diverse germline databases including human, mouse, and rabbit.

Automated Workflow & Usability

Automates repetitive tasks with a user-friendly interface.
AI-powered hit selection ensures optimal candidate identification.

Security & Accessibility

Protect sensitive data with enterprise-grade encryption.
Available on the Cloud (SaaS) and On-Premises.

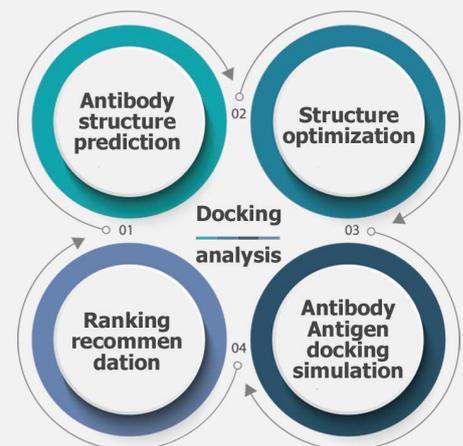
Visualization & Comparison

Explore and compare BCR datasets.
Graphically analyze V-gene usage, CDR length distribution, and clonotype diversity.
Leverage phylogenetic analysis to group similar antibodies.

SEQUENCE ANALYSIS



DOCKING ANALYSIS



APPLICATIONS IN AI-POWERED ANTIBODY DISCOVERY

Hit Selection with AI

Key features, liabilities, and phylogenetic relationships are presented to assist researchers in efficiently selecting the optimal and most diverse panel of hits for downstream expression and characterization.

AI-enhanced Insight

AbFinderAI™ provides scientists with AI-enhanced insights through structural modeling to refine candidate selection and expansion while predicting developability.

Hit Expansion with AI

Sequence or structural similarity analysis can be applied to mine antibody repertoires and expand potential hit sequences from known antibody sequences.

