OVERVIEW Ultra-high throughput methods for binder screening

EncapS Encapsulation & Screening

Host Organism	Yeast or Mammalian (including primary cells)
Library Size	10,000 - 100,000
Expression	Secreted and Cell Surface
Assay	Binding or Cytokine Secretion
Precision (K _D)	Semi-Quantitative (Low/Med/High Affinity)
Timeline	Standard Offering: 5-6 months

BindSeq Affinity measurements from sequence data

Yeast

1,000 - 10,000

Cell Surface

Binding

Quantitative Measurement of Binding Affinity (K_D)

Standard Offering: 2-3 Months



binder discovery in ultra-high throughput S Biologic



Encaps Encapsulation & Screening in nanoliter-scale reactors (NLRs)



Phenotypic assay

Ultra-high throughput, nanoliter scale

The EncapS technique packages single cells into microscopic hydrogel beads called Nanoliter-Scale Reactors (NLRs).

Up to 100,000 clones per run

By combining multiple runs, single screening campaigns can reach a million clones or more.

Versatile fluorescence measurements

NLRs are sorted with lasers similar to FACS and the platform supports a range of fluorescence-based assays.

Growing cells and secreted products

NLRs support cell growth and proliferation while capturing secreted products, unlocking more complex assays.

Increased sensitivity, reduced noise

Cells in NLRs can proliferate into microcolonies, allowing robust measurements with less cell-cell variation.

Diverse cell types and culture conditions

The platform has been tested with many different media and cell types: bacteria, yeast and mammalian cell lines.







BindSeq Precise affinity measurements from sequencing data

Binders barcoded for NGS

BindSeq assembles nanobodies, scFv or other binder libraries for yeast display with barcodes identifiable by next-gen sequencing (NGS).

Up to 10,000 candidates in parallel

Binder libraries are mixed with fluorescencelabeled targets at a range of concentrations and sorted with FACS according to binding signal.



Rich datasets at high resolution

By measuring the abundance of barcodes at a different target concentrations, we can estimate the affinity (K_D) for each binder in the library.







