Enabling Transformative Discoveries using Genomics

Yeast Display Affinity Maturation Platform

Ranomics’ affinity maturation analysis platform is well-suited for discovering better performing antibodies in a high-throughput and quantitative manner. Starting with the parental antibody’s native sequence, Ranomics’ VariantFind library building technology produces diverse antibody libraries with high specificity and control. Antibody libraries are transformed into and displayed on the surface of yeast cells, followed by cycles of panning for antigen protein. By conjugating soluble antigen proteins to fluorescence markers, Ranomics can rapidly isolate and identify high-affinity antibody-antigen interactions using fluorescence-activated cell sorting and next-generation sequencing, respectively.

**Pipeline overview**

1. Generate a custom antibody variant library (scanning or mild-combinatorial) across CDRs. Highly diverse antibody libraries (10^4 to 10^6) are transformed into yeast cells for cell surface display. Cell surface display is established by expressing antibody scFv in a single polypeptide with the Aga2 protein.

2. Antibody displaying yeast cells are exposed to fluorescence-labelled antigen protein. Cells bound to differing levels of antigen are sorted and isolated using FACS. Multiple cycles of panning can be conducted to enrich for high-affinity binders.

3. DNA is isolated from high-affinity yeast cells and analyzed by deep sequencing. Amino acid distributions at CDR residues and linkage analysis within deep sequencing amplicons reveals critical elements in high-binding antibodies.

**Advantages of our platform**

**Selection for functional antibodies**

Yeast display provides a eukaryotic folding, maturation and post-translational modification system to support the expression of functional antibodies. Unlike phage display, yeast display selects for antibodies with favourable stability and manufacturability.

**High quality DNA libraries**

VariantFind technology synthesizes high quality DNA variant libraries with high specificity and control. Our technology can fine-tune mutational loads across CDR segments and utilize custom amino acid mixtures.

**Deep sequencing technology**

Cell sorting combined with deep sequencing technology provides the most quantitative and comprehensive insights in any affinity maturation experiment. Generate meaningful insights into critical CDR residues and residue combinations that can lead to improved affinity.

**Save Time and Money**

Library construction and screening can be done in 2 to 3 months. Avoid the cost of setting up in-house pipelines by using our turnkey solution.