RANOMICS

Accelerating discoveries using high throughput functional genomics

GET YOUR CUSTOM DNA

VARIANT LIBRARIES

Innovation and custom solutions are at the core of everything we do at Ranomics.

Visit Our Website

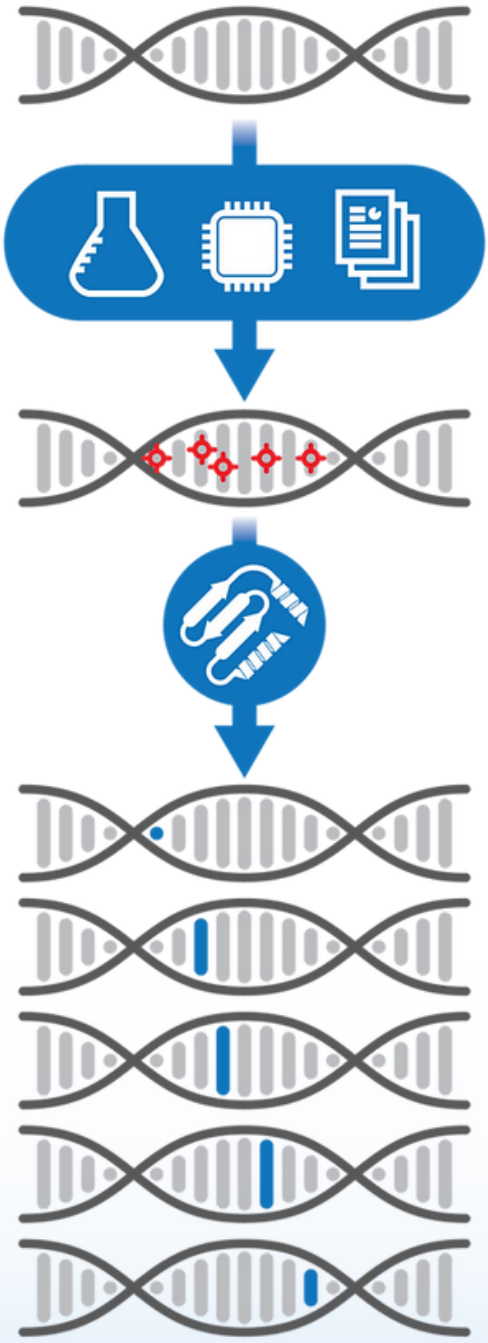
www.ranomics.com

As low as $45.00 USD for a single residue

Ranomics has developed a proprietary DNA mutagenesis library construction technology called VariantFind™, which is protected by patent. Using a series of in-house computational tools and multiplex PCR assembly reactions, Ranomics can construct precise scanning site-saturation libraries, single site-saturation libraries and combinatorial libraries.

Our stringent libraries are all sequenced verified and easily assembled into any vector for **PROTEIN ENGINEERING, STRAIN ENGINEERING OR DIRECTED EVOLUTION PURPOSES**

The VariantFind Platform



Your sequence of interest

Our custom algorithm

Precise codon targeting

Enzyme mediated assembly

Library of mutations

Customize Any Amino Acid Residue as a Standalone Mutation or in Combination with Other Residues in Your Protein

VariantFind Advantage

VariantFind DNA libraries are highly advantageous over traditional chemical synthesis variant libraries. VariantFind libraries can help you achieve:

- **Precise libraries of long gene sequences (>5kb)**
- **Mutate residues in complex (high- / low-GC) regions**
- **Control codon distribution for multiple residues**
- **Codon optimization for a particular host organism**
- **Readily mutate continuous and discontinuous residues easily**

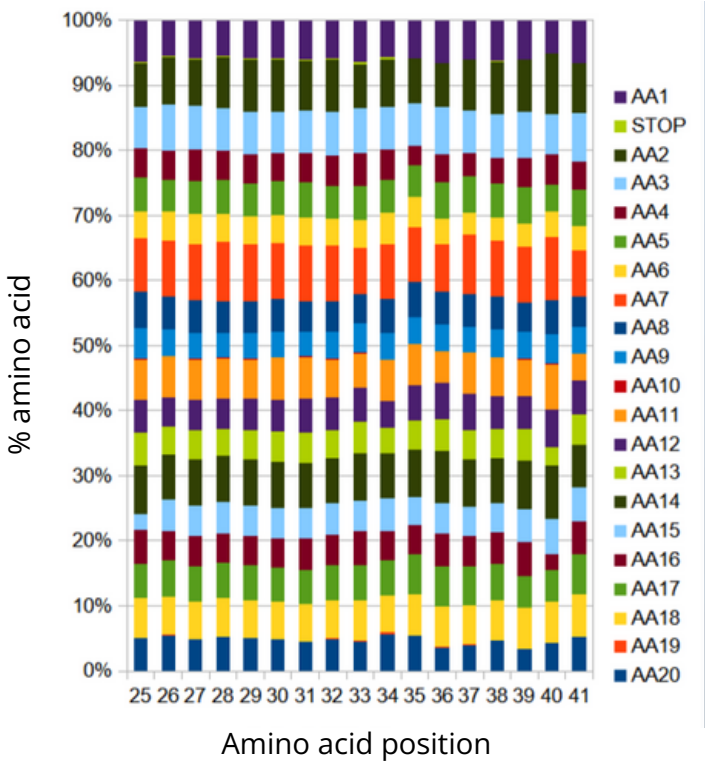
Flexible and Custom Deliverables for Your Research

	Double Stranded DNA	Cloned into custom vector
Pooled	✓	✓
Arrayed 96/384 well plate or single tube	✓	✓

Our DNA variant libraries are shipped in 4-6 weeks

Case Study

The amino acid distribution of the custom scanning saturation mutagenesis library determined by the next generation sequencing (NGS) technology.



Deep sequencing of a scanning mutagenesis library

Each multi-colored bar is an individual site, and each color represents an amino acid. The thickness of each colored and is the % of each mutant with that particular amino acid at that site.

- **Even distribution of amino acids with minimal bias**
- **Ensures precise manipulation of codons for each mutant**
- **All 64 codons are available**
- **Unattainable in libraries created through conventional methods involving error-prone PCR**

Stringent Quality Control

We guarantee 100% sequence accuracy:

- Verified by sanger sequencing or NGS
- Sequence chromatograms for each gene variant
- Construct map for the plasmid
- Quality assurance certificate

Why Choose Us

Rigorous Confidentiality
You can confidently share your DNA sequences, knowing that we maintain strict confidentiality standards to protect your data.

Comprehensive Support
Our team of highly skilled scientists is available to provide comprehensive support, from experimental design to data analysis, ensuring that you get the most out of your research.

"We are very pleased with the diversity and specific composition of the synthetic variant libraries produced by Ranomics. Our projects were executed on time or ahead of schedule and throughout the process Leo and Jonathan were always available to answer any questions we had. Working with the Ranomics team has been a pleasure."

Mara Inniss, Director
Obsidian Therapeutics

Request a quote

www.ranomics.com