

Spread-Out Low Diversity (SOLD) Libraries

Enzyme evolution and protein engineering have become widely used strategies for the development of enzymes with improved specificity, thermostability, processivity and performance. These optimized enzymes are indispensable tools for improving product yield in metabolic engineering and industrial biocatalysis.

Twist Bioscience's Spread-Out Low Diversity (SOLD) Libraries are a time- and money-saving tool for researchers who want to efficiently investigate combinatorial possibilities. A library of precise combinatorial variants with uniform amino acid distribution, balanced codon usage and the ability to avoid unwanted restriction sites, provides the ultimate tool to explore the variant space. All SOLD Libraries are NGS-verified, cloning-ready, and created using Twist's patented silicon-based synthesis platform, ensuring low error rates.

SPECIFICATIONS

- **Product Format:** Linear double-stranded DNA, optional cloning
- **Delivery and Yield:** All variants pooled in a single tube, deliver up to 1 µg/tube
- **Price:** Competitive pricing
- **Rapid Turnaround Time:** 4 weeks, project dependent

KEY BENEFITS

High fidelity and cost effective

- Precise alternative to NNK, TRIM, error-prone PCR, random mutagenesis, and DNA shuffling
- Created using Twist's patented silicon-based synthesis platform that requires no template
- Balanced codon usage, no restriction sites or unnecessary mutations

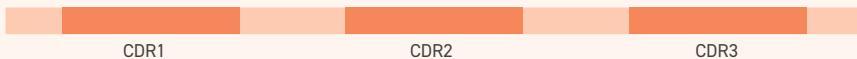
Verified Quality and Flexibility

- <1,500 bp gene variant library with diversity scattered across wild-type sequence
- Not restricted to domains
- Multiple mutations can be explored simultaneously
- NGS-verified and cloning-ready

Explore sequence space with a diverse library of proteins

STANDARD CVL

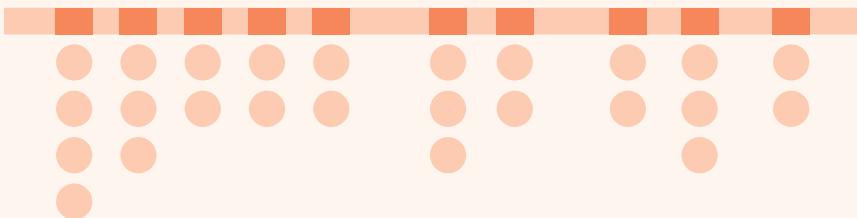
Diversity is confined to domains along the WT sequence



VERSUS

SOLD LIBRARY

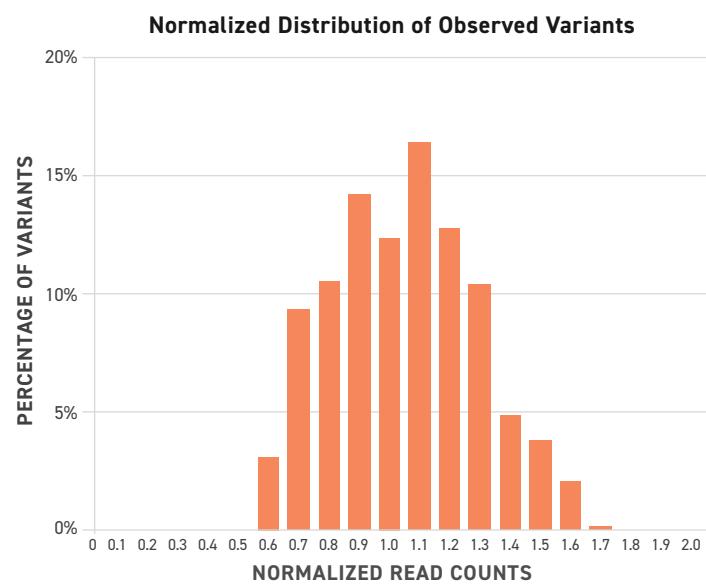
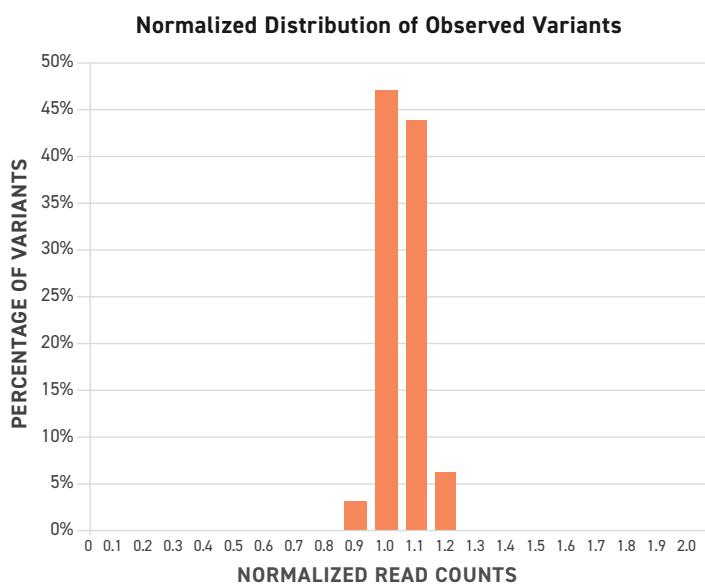
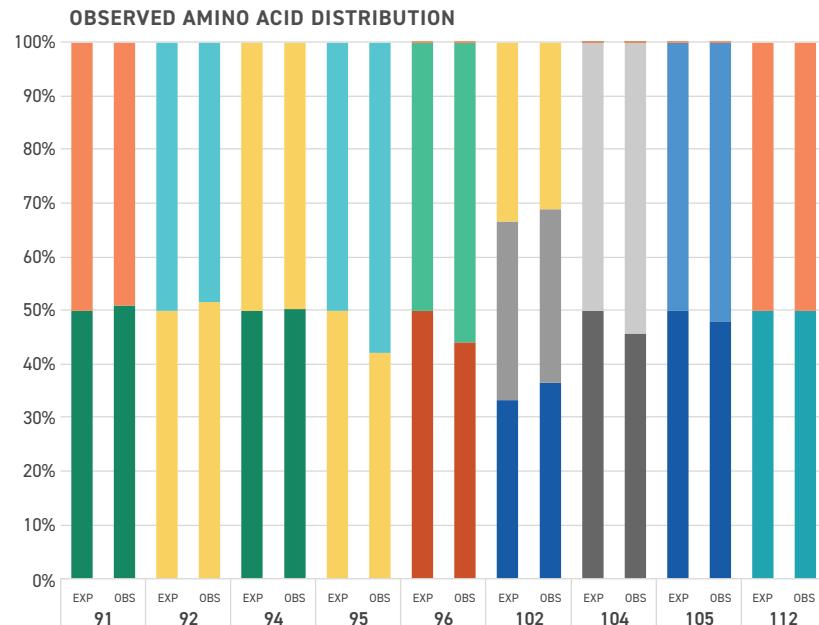
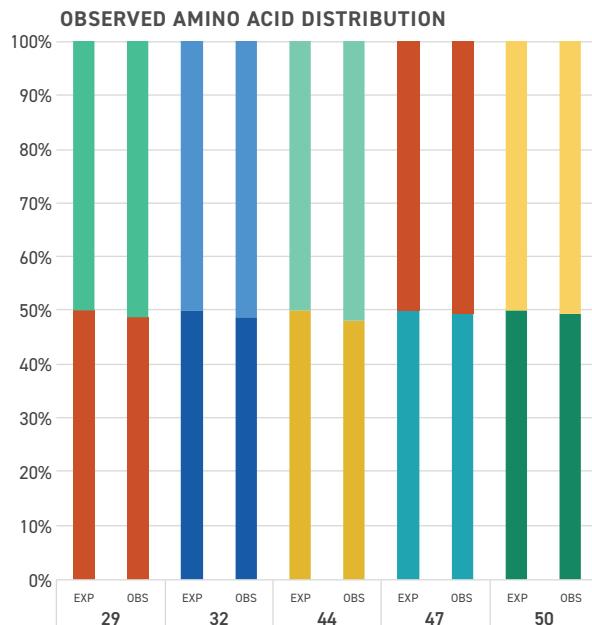
Diversity is scattered along the WT sequence



Unlike combinatorial variant libraries (CVLs), Twist's SOLD Libraries have the benefit of precisely incorporating diversity across a wild-type sequence without restricting that diversity to small variant domains. This ability to simultaneously investigate multiple amino acid positions across a sequence allows researchers to investigate, and optimize, the activity of a protein both rapidly and effectively.

A high-fidelity synthetic construct

Through extensive research and development, Twist's SOLD Libraries have shown their ability to consistently deliver amino acid distributions that closely match the requested amino acid frequencies, with a uniform distribution of variants and no dropouts.



YOU DESIGN IT, WE BUILD IT. Get in touch at library@twistbioscience.com or learn more at twistbioscience.com

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