Site Saturation Variant Libraries

Protein engineering screens using single site variant libraries allow researchers to explore a protein's sequence space and investigate the relationship between sequence and protein structure and function. Many methods exist to generate variant libraries, but they generally have significant drawbacks and limitations, including lack of codon control, sequence biases, and incomplete generation of desired variants.

Twist Bioscience Site Saturation Variant Libraries leverage massively parallel oligonucleotide synthesis using a silicon-based DNA synthesis platform and extensive molecular biology expertise to systematically and precisely construct variant libraries. Twist libraries are NGS-verified to confirm that all desired variants are present in the correct ratios.

SPECIFICATIONS

- Price: $50 per position
- Product Format: Linear double-stranded DNA
- Delivery Formats and Yield:
  - >1 µg (project dependent) additional fee applies
  - 96-well plate, 1 position per well, 50–100 ng each
- Turnaround Time: 4 weeks or less; dependent on project

KEY BENEFITS

Precisely Crafted Variant Libraries

- Complete control over codon usage (all 64 codons available)
- High uniformity of variant representation at every site
- No unwanted codons or premature stop codons

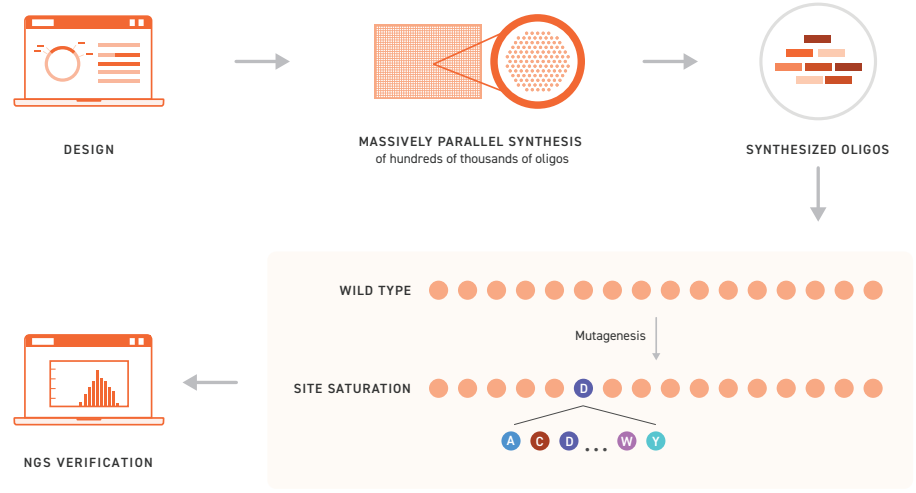
Verified Quality

- Rigorous quality control
- Verified uniformity of variant representation by NGS analysis of mutagenic region
- Representation of each site normalized by mass

Flexibility

- Pooled library or pooled per position delivery options
- Screen one or up to all 20 different amino acid combinations at each position
- Investigate sequence variants and/or indels

Improved Library Generation Fueled by a Silicon-Based DNA Synthesis Platform



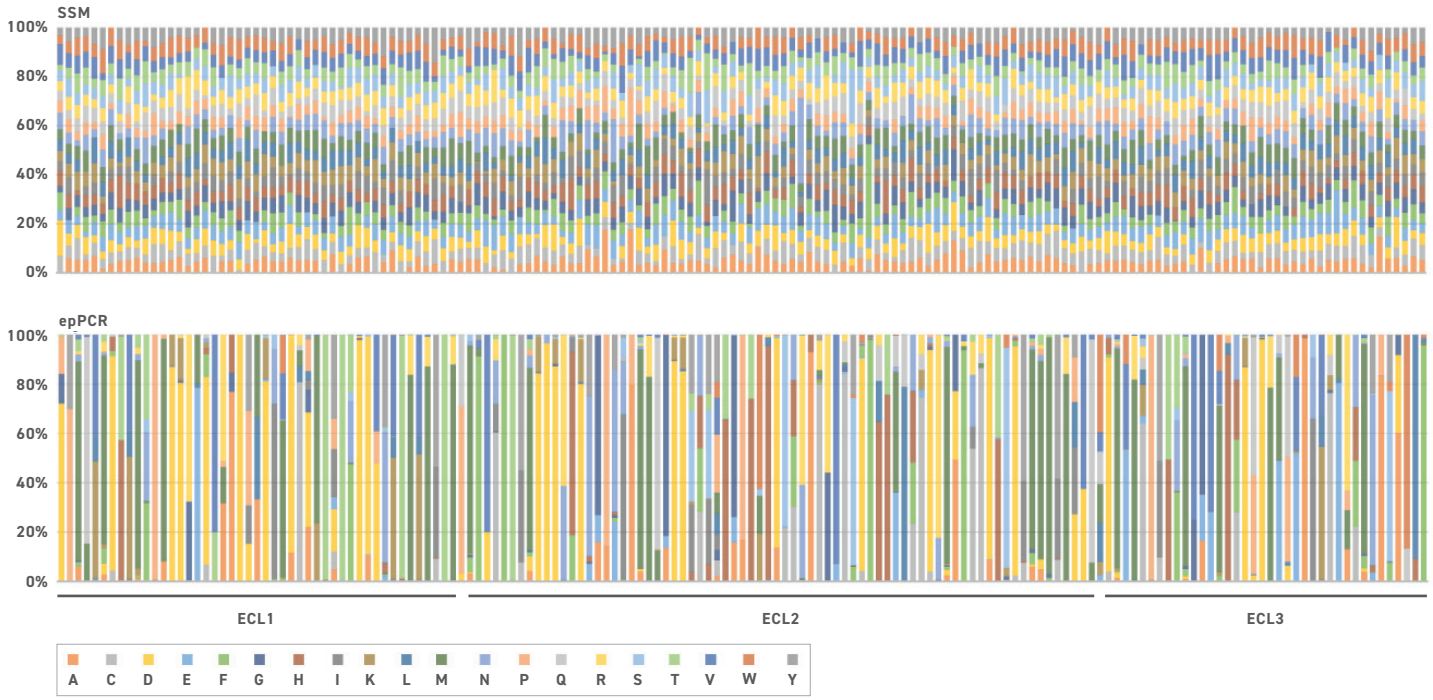
The Twist Bioscience Site Saturation Variant Library synthesis workflow. Massively parallel oligonucleotide synthesis, advanced molecular biology experience, and high-throughput automation approaches result in precisely crafted libraries with all expected variants represented at the desired ratios.

	ERROR PRONE PCR	DEGENERATE (NNK/NNS)	TWIST SITE SATURATION VARIANT LIBRARIES
Eliminates sequence bias	No	No	Yes
Number of codons available	Unknown	32	All 64
Prevents undesirable motifs	No	No	Yes
Allows codon optimization	No	No	Yes
Avoids stop codons	No	Yes	Yes

Comparison of Site Saturation Variant Library Generation Methods.

Unleash the Full Power of a Well-Designed Library

With Twist Bioscience Site Saturation Variant Libraries, high quality rationally designed libraries are finally within reach. You are assured that the library you design contains the desired modifications, exactly where you want them, and encoded by the selected codon. Avoid unwanted bias which results in increased screening efforts. Be confident that the library you design contains the desired variants



Precision crafted libraries enable efficient sampling of a protein's sequence space in screening assays. Each bar represents an amino acid position, and each color indicates the observed variant frequency. These data are from a SIte Saturation Variant Library with variants at 65 positions, with 19 variants at each. All variants are present in the expected ratios. On average, Twist libraries contain 99% of desired variants.

Your Discoveries, Precisely Controlled

Precise control over variants, including codon usage: The variants generated match the experimental design at desired ratios, without limitations or bias

Variant representation confirmed by NGS: You can be confident on the variants present in the library

Flexibility to avoid unwanted sequence motifs: Eliminate introduction of unwanted genetic elements, such as premature stop codons, restriction enzyme sites, TF binding sites, etc.