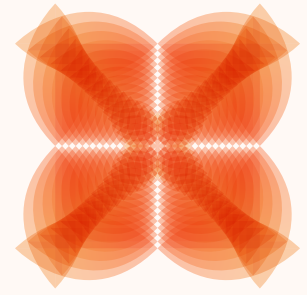
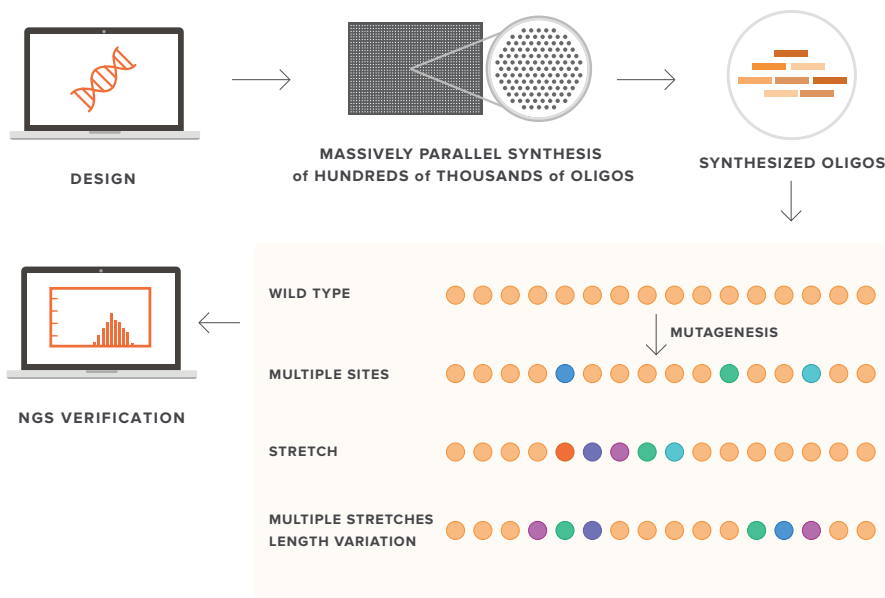


# Combinatorial Variant Libraries

Twist Bioscience's unique capability to synthesize very large numbers of high quality oligos with our massively parallel silicon-based DNA synthesis platform, combined with our well established molecular biology expertise, allow the controlled fabrication of highly diverse gene mutant libraries with highly specific, user-defined, composition.



## Precision Library Generation Fueled By Silicon-Based DNA Synthesis Platform



Massively parallel oligonucleotide synthesis combined with molecular biology expertise and high-throughput automation approaches generates extremely precise combinatorial libraries for use in antibody and protein engineering screens.

### COMPARISON OF COMBINATORIAL VARIANT LIBRARY GENERATION METHODS

	Degenerate (NNK/NNS)	TRIM/Trimer Controlled	Twist Combinatorial Variant Libraries
Eliminates Sequence Bias	No	No	<b>YES</b>
Number of Codons Available	32	20	<b>All 64</b>
Prevents Undesirable Motifs	No	No	<b>YES</b>
Allows Codon Optimization	No	No	<b>YES</b>
Avoids Stop Codons	No	Yes	<b>YES</b>

### PRODUCT SPECS

- Product Format: Linear double-stranded DNA, NGS-verified
- Delivery and Yield: All variants pooled in a single tube, up to 1 µg (depending on length of fragment)
- Price: Project dependent
- Turnaround Time: Project dependent

### KEY BENEFITS

#### High Diversity Precision

- Multi-variant domains in single or multiple scaffolds (up to  $>10^{10}$  variants)
- Precise control over codon usage (all 64 codons), amino acid distribution, and length variation

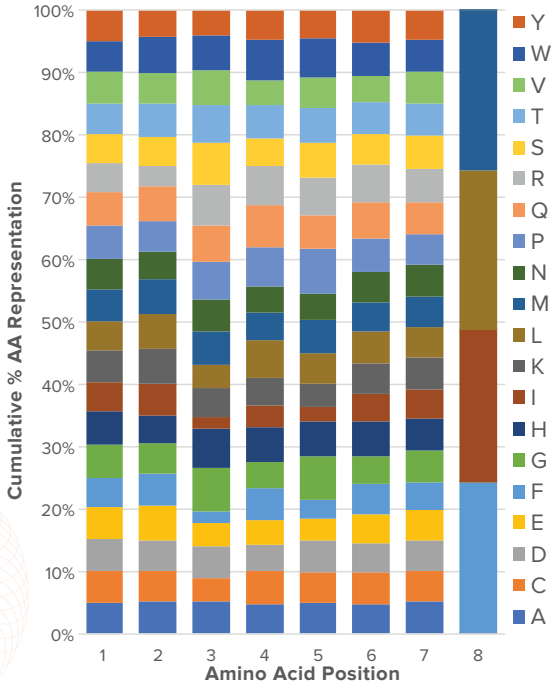
#### Verified Quality

- Rigorous quality control, including NGS-verification of modified regions
- Sequence variant ratios documented

#### Flexibility

- Design all sequences, single or multiple domains and combinations - single, pairwise, or triple variants
- Modular synthesis system enables iteration and of future libraries

# Twist's Rationally Sculpted Libraries Are Unparalleled in Quality and Composition



Generation of a high diversity combinatorial variant library. Variants in 8 sequential amino acid positions were generated, with all 20 AA residues in the first seven sites (5% representation expected for each) and 4 AAs in the eighth (25% each), in all combinations, for a total diversity of  $5 \times 10^9$ . All expected variants at all positions were present and nearly all were at the desired ratio.

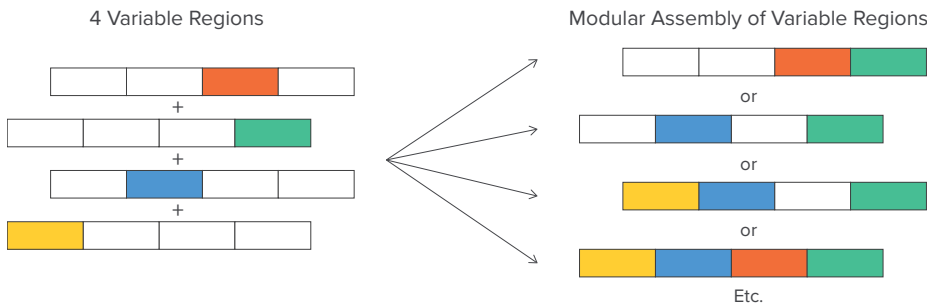
## WE DELIVER PRECISELY WHAT YOU DESIGN

- Precisely controlled single, pairwise, and triple combinatorial variation
- Multi-variant domains in single or multiple scaffolds
- Accurate ratio control of amino acid distribution and length variation within domains
- All possible binary substitutions within domains for effective humanization
- Avoid or minimize unwanted sequence motifs and restriction sites
- All library sequences are NGS-verified so you know what you're screening

## Modular, Multi-Use Libraries

Another area where the Twist library fabrication technology excels is in the construction and archiving of cassettes or modules of diversity and constant regions. This confers the ability to deliver sophisticated diversity faster and for lower cost, as if "off-the-shelf." A selection of complex libraries is fabricated by assembling several specific of cassettes with different design and diversity. Much like Lego blocks, Twist can provide its library users with a variety of interchangeable building blocks that can be assembled in different ways to create similar, but different, structures. This benefits antibody developers and protein engineers by providing the ability to iteratively alter and evolve library designs on an ongoing, as needed basis.

## Build New Diversity Into Your Libraries for More Comprehensive Analyses



Twist's modular fabrication strategy and ability to create libraries with defined composition delivers a practical, multi-use approach to library fabrication. This approach is both rapid and cost effective.