Advancing life science with Synbio innovation

Customized Mutant Library Service

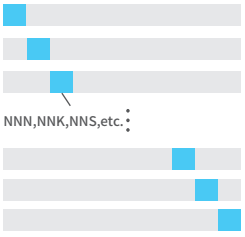
Mutant libraries are essential tools in research fields such as antibody engineering, enzyme-directed evolution, drug target screening, and gene therapy. Faced with the complex requirements of long sequences, multiple sites, and high-diversity combinations, traditional construction methods often face dual bottlenecks of scale and quality. Through technological innovation, GCATbio has successfully overcome these challenges and provided customized solutions to empower researchers to push the boundaries of functional discovery.

All-type Customized Library Solutions

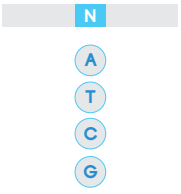
GCATbio offers a variety of customized mutant library services tailored to meet diverse research needs.

Site-Directed Mutant Library

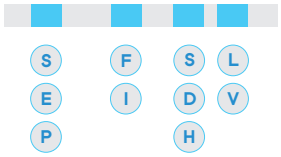
Deep Mutational Scanning Library



Degenerated Mutant Library



Combinatorial Mutant Library



Trimer Mutant Library

Codon tables optimized for E. coli and yeast expression systems.

K	N	T	I	M
AAA	AAC	ACT	ATC	ATG
Q	H	P	R	L
CAG	CAT	CCG	CGT	CTG
E	D	A	G	V
GAA	GAC	GCT	GGT	GTT
Y	S	W	F	C
TAC	TCT	TGG	TTC	TGC

Service Process

Mutation region analysis
Identify target mutation sites and evaluate the required diversity

»

Project design
Design the optimal construction strategy based on requirements

»

Library construction
Efficient and precise synthesis of mutant libraries

»

High-throughput sequencing validation
Rigorous validation of library coverage and accuracy

»

Delivery
Offer fragment libraries or cloned libraries, with delivery options including lyophilized DNA, plasmids,and glycerol stocks

Core Advantages

High library quality
- High coverage(>99%)
- Excellent uniformity (≤10)

Flexible customization
- Customizable codon distribution
- Customizable amino acid ratio

High accuracy
- High sequence accuracy
- Error rate as low as 1: 2000

Delivery Form

Synthesized Fragments	Lyophilized synthetic DNA fragments
Clonal Library	Lyophilized plasmid DNA or *E.coli* lycerol stocks harboring the plasmid
Standard delivery amount	>10 μg

For other custom requirements, please contact technical support or your account representative.

Customized Mutant Library Service

GCATbio Co., Limited

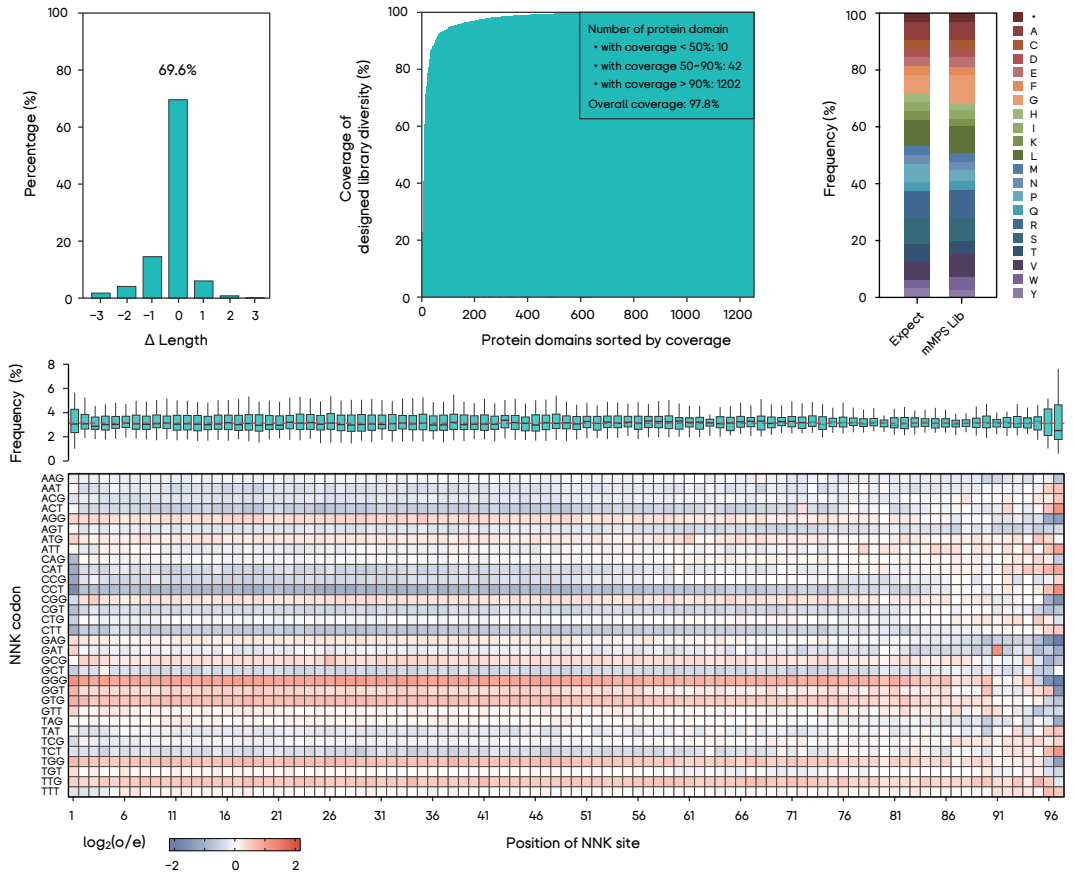
Case Study

01 Large-scale mutational study of human protein domains

Relying on our independently developed mMPS high-throughput parallel synthesis platform, we have successfully collaborated with CRG to construct a precision saturation mutant library comprising over 1.2 million mutants, covering 522 human protein domains. The library quality is outstanding:

- The codon distribution is highly uniform, closely matching theoretical expectations
- The proportion of full-length clones in the library reaches 70%
- The mutation coverage is as high as 98%

This library supported the construction of the world's first " Human Domainome 1" dataset, published in Nature on January 8, 2025. The study revealed that 60% of pathogenic missense mutations cause disease by disrupting protein stability, providing profound insights into the relationship between protein structure and mutant function.



By precisely controlling the distribution of each NNK codon, we achieved high uniformity and high diversity in the library:

Mutation sites are evenly distributed:

The 32 NNK codons at each site exhibit nearly uniform frequencies, ensuring a rich and diverse set of mutation combinations.

Frequencies closely match theoretical distribution:

Maximize functional screening efficiency.

log2(o/e) standardized evaluation:

Real-time monitoring and optimization of codon bias to ensure comprehensive library quality assurance.

The figure illustrates the NNK codon frequency distribution at each site, validating our precise control and high-quality output throughout the library construction process.

Reference

1.Beltran A, Jiang X, Shen Y, Lehner B. Site-saturation mutagenesis of 500 human protein domains. Nature. 2025: 1-10.

2.Zhang X*, Jiang X*. et al. Revolutionizing large-scale DNA synthesis with microchip-based massive in parallel synthesis system. https://www.biorxiv.org/content/10.1101/2024.10.30.619547v1.

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