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GenScript initiates precision mutant library services

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Services expedite downstream screening time with precision control and complete variant coverage

GenScript, the world's leading gene synthesis provider has announced the launch of its Precision Mutant Library Services for the drug development, industrial chemical and synthetic biology markets. The service overcomes the challenges of traditional library construction methods, saving researchers valuable screening time, expediting drug discovery and reducing costs.

Mutant libraries are powerful, high-throughput tools for optimizing protein structure and function. However, traditional methods for library construction, including error-prone PCR or degenerate methods, suffer from limited control over codon usage and poor variant representation. These limitations require researchers to perform multiple rounds of screening to capture the entire variation of the library. The new Precision Mutant Library Services utilizes GenScript's proprietary semiconductor oligo synthesis technology to deliver precise control over each synthesized variant. The result is a more diverse and fully covered mutant library with unbiased distribution.

"GenScript was able to create a mutant library that had 100 percent coverage of all expected variants before and after viral packaging, and excluded variants that contained amino acids that I did not want present at these sites," said Susan Butler, a PhD student in Junghae Suh's Synthetic Virology Lab at Rice University who was working to create a library of mutant caspids for adeno-associated vectors. "Having a library with only the variants that I wanted to test was able to reduce my screening efforts and maximize my time in finding my optimal viral vector sequence."

GenScript's patented semiconductor technology-based platform uses CMOS technology to construct integrated circuit chips, providing electronic control over oligonucleotide synthesis and allowing precise control of the composition and proportions of amino acids at one or multiple variant sites in a single protein. Although degenerate NNK and NNS libraries have proved economical, scientists waste valuable screening time due to the poor representation of variants and desired amino acids at certain positions.

"GenScript's Precision Mutant Library Services is a significant advancement over existing technologies and is as reliable as your iPhone," said Dr. Cedric Wu, senior director of research and development. "Researchers now have a new tool for developing better, safer drugs faster, and for many applications in the industrial chemical and synthetic biology markets."

GenScript's Precision Mutant Library Services include site-saturation mutagenesis, saturation scanning mutagenesis, or combinatorial mutagenesis libraries. Saturation mutagenesis libraries provide the ability to screen mutations located at several sites within a protein sequence or across the total sequence space. Each position is mutated to all 19 non-wild-type amino acids. Combinatorial mutagenesis libraries involve mutating multiple positions simultaneously across specific target regions of a protein and exploring all possible combinations of mutations.