

**NYU**

Codon Library for High-Throughput Functional Assessment of mRNA Translation Efficiencies

An advanced tool that can precisely measure how genetic and environmental factors affect mRNA translation on all 61 amino acid codons in a high-throughput manner.

Technology

This innovative platform enables multiplexed, high-throughput evaluation of mRNA translation efficiencies (mTE) for all 61 amino acid (AA) codons in living cells. It employs a barcoded lentiviral library combined with a dual reporter system (GFPd2 + mCherry), enabling comparison of codon-specific translational changes under different environmental or genetic conditions (e.g., amino acid deprivation, drug treatment, UV exposure). The lentiviral codon library has been constructed, validated, and tested under tyrosine deprivation conditions in mammalian cells, demonstrating the technology's ability to detect codon-specific translation differences across various amino acid conditions. This system captures subtle shifts in translation efficiency that other methods, such as ribosome profiling, may miss. This technology can help discover novel translational control mechanisms and therapeutic targets, especially in cancer and other complex diseases.

Background

Codon usage affects translation efficiency, protein expression, and cellular function. Environmental conditions such as nutrient availability or stress, and genetic changes, can disrupt codon-specific translation. However, existing tools like Ribo-seq only detect major ribosome pausing and cannot resolve fine-grained codon responses across the genome. This can be overcome by employing a dual-reporter lentiviral library designed to systematically track the behavior of all 61 codons in real time within cells.

Development Stage

The team is currently expanding the platform's use to other environmental stimuli and plans to investigate codon usage changes across disease-relevant states and cell types in the next phase of research.

Applications

Technology ID

BAN03-01

Category

Life Sciences/Platform
Technology

Life Sciences/Genetic
Engineering
Life Sciences/Research
tools/Sequencing
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- **Target discovery:** Identifies codons whose translation is selectively impaired in a range of diseases under nutrient stress.
- **Drug screening:** Evaluates how small molecules modulate translation at the codon level to optimize therapeutic windows.
- **Synthetic biology:** Optimizes cDNA sequences for protein expression in specific cell types or conditions.

Advantages

- **High-throughput:** Simultaneously measures translation efficiency across all 61 codons in a single assay.
- **Sensitive and quantitative:** Detects subtle shifts in codon usage that ribosome profiling cannot capture.
- **Internal normalization:** Dual-reporter design (GFPd2 + mCherry) improves accuracy by correcting for technical variability.
- **Customizable stimuli:** Compatible with various environmental or genetic perturbations (e.g., amino acids, drugs, UV).
- **Scalable and multiplexed:** Designed for NGS-based readout and compatible with high-throughput experiments.
- **Compatible and versatile platform:** Can be adapted to different cell types and experimental conditions.

Development Stage

The team is currently expanding the platform's use to other environmental stimuli and plans to investigate codon usage changes across disease-relevant states and cell types in the next phase of research.

Intellectual property

NYU has filed a U.S. provisional patent application covering the composition of a codon-optimized, barcoded reporter library and its method of use.