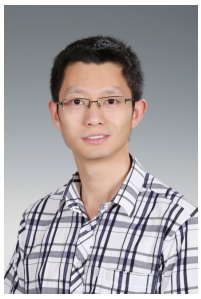
Chengqi Yi, Professor

School of Life Sciences,
Peking University, Beijing, 100871, China.
Tel: +82-10-62752895
Email: chengqi.yi @pku.edu.cn



01/2019 – present, Boya Professor, Peking University
01/2012 – 12/2018, Assistant Professor, Associate Professor with Tenure, Peking University
01/2012 – present, Investigator and Senior Investigator, Peking-Tsinghua Center for Life Sciences
08/2010 – 12/2011, Postdoctoral Fellow, University of Chicago
2010 PhD, University of Chicago
2005 BS, University of Science and Technology of China

Research Interests:
Epitranscriptomics, Genome editing, Single cell sequencing

Selected Publications:

1. Luo N, Huang Q, Dong L, Liu W, Song J, Sun H, Wu H, Gao Y, **Yi C***, Near-cognate tRNAs increase the efficiency and precision of pseudouridine-mediated readthrough of premature termination codons, ***Nat Biotechnol* 2024**, doi:10.1038/s41587-024-02165-8
2. Bai D, Zhang X, Xiang H, Guo Z, Zhu C*, **Yi C***, Simultaneous single-cell analysis of 5mC and 5hmC with SIMPLE-seq, ***Nat Biotechnol* 2024**, doi:10.1038/s41587-024-02148-9
3. Liu C, Sun H, Yi Y, Shen W, Li K, Xiao Y, Li F, Li Y, Hou Y, Lu B, Liu W, Meng H, Peng J, **Yi C***, Wang J*, Absolute quantification of single-base m6A methylation in the mammalian transcriptome using GLORI, ***Nat Biotechnol 2023,*** 41(3), 355-366
4. Sun H, Li K, Liu C, **Yi C***, Regulation and functions of non-m6A mRNA modifications, ***Nat Rev Mol Cell Biol* 2023**, 24(10), 714-731
5. Lei Z, Meng H, Liu L, Zhao H, Rao X, Yan Y, Wu H, Liu M, He A, **Yi C***, Mitochondrial base editor induces substantial nuclear off-target mutations, ***Nature*, 2022,** 606(7915), 804-811

A New RNA Base Editor Repairs Nonsense Mutations

Chengqi Yi
State Key Laboratory of Protein and Plant Gene Research, School of Life Sciences,
Peking University, Beijing 100871, China
chengqi.yi@pku.edu.cn

Abstract

Nonsense mutations, which lead to premature termination codons (PTCs) in mRNA coding region, account for ~20% of mutations associated with human diseases. Current treatments for diseases related to nonsense mutations often lack specificity or may cause severe off-target effects and immunogenicity. Therefore, we developed a CRISPR-independent, programmable targeted pseudouridylation method RESTART, which can efficiently and specifically edit PTC sites on mammalian cell mRNA, thereby achieving effective readthrough and functional rescue in disease cell models related to nonsense mutations. Moreover, the restricted off-target edits induced by RESTART are generally “benign” as they do not change the coding information or the global gene expression. Collectively, RESTART is a promising RNA-editing tool for research and therapeutics.

1. Luo N, Huang Q, Dong L, Liu W, Song J, Sun H, Wu H, Gao Y, **Yi C***, Near-cognate tRNAs increase the efficiency and precision of pseudouridine-mediated readthrough of premature termination codons, ***Nat Biotechnol* 2024**, doi:10.1038/s41587-024-02165-8