Introduction

Recently, RNA therapeutics has became the new tendency for treatment. In this case, circRNAs has been attracted great attention due to their unique covalently closed-loop structures, which can enhanced stability, and prolonged protein expression compared to conventional linear mRNAs. ( Cao, X., Cai, Z., Zhang, J., & Zhao, F. (2024). Engineering circular RNA medicines.). However , we still need to find a way out to achieve three critical objectives: preservation of highly efficient circularization, structural compactness of circRNA and full exploitation of IRES-mediated initiation capacity. Here, we are going to talk about a new technology whose name is circdesign which can solve the problem of the rational design of a circRNA sequence to jointly improve its stability and protein coding potential. In this approach, a specific IRES sequence is given for ensuring effective translation and catalytic region for circularization. The entire design space, integrating minimum free energy (MFE), codon adaptation index (CAI), and IRES structural deviation are all taken into account in the design of the CDS region which can contribute to design circRNA with improved circularization efficiency, stability, and translatability. It was developed by Liang Zhang’s team at the Hangzhou Institute of Medicine, Chinese Academy of Sciences, and further experimentally validated by Congcong Xu’s group from Soochow University. (Xu et al., 2025) Our assay is aimed at discussing the potential of circdesign in the future application of drug design. We will talk about it from the following perspectives like its advantages and disadvantages.