Synthetic 5'-untranslated regions for fine-tunable and predictable gene expression in *Escherichia coli*

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"Metabolic Engineering" aims the purposeful redesign of the biological systems and requires the accurate information of the cellular metabolic networks and proper tools for the reconstruction of the biological. Numerous regulatory elements such as promoter libraries and RBS calculator can be applied for the modulation of gene expression. However, without carefully considering the structural information of 5'-unstranslated region (5'-UTR) sequence, it is insufficient to precisely design and modulate the gene expression level. To address this issue, in this study, we randomized 5'-UTRs maintaining ribosome binding affinity using superfolder GFP as a reporting system in *Escherichia coli*. A mathematical model was constructed by mapping between the secondary structures of 5'-UTRs and the expression level of superfolder GFP. Examples using the other genetic contexts will show the potentials of this model to predict the precise expression level based on the structural information and consequently will provide a valuable tool for "Metabolic Engineering".