

Quantitative correlation between mRNA secondary structure around the region downstream of the initiation codon and translational efficiency in *Escherichia coli*

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Several quantitative studies have reported that translational efficiency is attributable to effects on ribosome accessibility predominantly caused by the secondary structure surrounding the ribosome-binding site. However, the influence of mRNA secondary structure around regions downstream of the initiation codon on translational efficiency after ribosome-binding step has not been quantitatively studied. Here, we quantitatively analyzed the relationship between secondary structure of mRNA surrounding the region downstream of the initiation codon (DR) and protein expression levels. Modified hairpin structures containing the initiation codon were constructed by site-directed mutagenesis, and their effects on expression were analyzed in vivo. The minimal folding free energy (dG) of a local hairpin structure was found to be linearly correlated with the relative expression level over a range of 0.3- to 1.2-fold that of the wild-type structure. These results demonstrate that expression can be quantitatively controlled by changing the stability of the secondary structure surrounding the DR.