

Ribosome drop-off rate in *E. coli* depends on mRNA properties

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Precise and accurate protein biosynthesis is crucial for cell viability. It is known to be one of the most energy-consuming process in the cell. Nevertheless, multiple events of premature termination of translation (ribosome drop-off) were reported in *E. coli* cells [1]. Some of them are thought to occur as a result of errors of various types while others may have regulatory functions. Recently, a computational approach sensitive enough to detect this - process in genome-scale ribosome profiling data has been introduced [2]. Here we use this method to compare how genome-wide ribosome drop-off rates depend on a variety of mRNA sequence properties. Our results show that the main determinant of the ribosome drop-off rate is stability of mRNA secondary structure. We also provide a condition-dependent analysis of drop-off rates using data on ethanol-treated and amino acid-deficient bacteria.

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