

## New Challenges in Prokaryotic Transcriptomics

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The past decade has seen an exponential growth in genome-wide data measuring diverse cellular parameters, such as transcription factor binding, gene expression, translation, protein abundance, protein-protein interactions, and genetic-phenotypic interaction. In particular, prokaryotic transcriptomics have undergone an especially massive revolution. With increased sequencing capacity and novel protocols, it has recently become possible to explore the prokaryotic transcriptome with an unprecedented depth. Recent advances uncovered a more complex and plastic view than expected, with frequent alternative transcripts inside operons and the presence of abundant antisense and non-overlapping non-coding RNAs. These data have triggered an important change of paradigm for prokaryotic transcription, which abandons the classic operon definition for a more flexible view akin in some respect to the alternative exon combinations in eukaryotes. Here, we introduce recent progresses in describing prokaryotic transcriptomes using emerging technologies. By integrating with other layers of information including proteomics and fluxomics, these efforts will provide a new foundation to develop novel engineered strains for industrial uses.