

## The Epitranscriptome: Challenges in Measuring Dynamic RNA Modifications



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The post-transcriptional modification of RNA by the addition of one or more chemical groups has been known for over 50 years. These chemical modifications, once thought to be static, are now being discovered to play key regulatory roles in gene expression. The advent of massive parallel sequencing of RNA (RNA-seq) now allows us to probe the complexity of cellular RNA and how chemically altering RNA structure expands the RNA vocabulary. This presentation will overview the various strategies and technologies that are available to profile RNA chemical modifications at the cellular level, with a focus on the utility of mass spectrometry-based approaches for characterizing heavily modified small RNAs.