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Chemo-Transcriptomic Methods to Measure RNA Structure Inside Living Cells

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ABSTRACT

The advent of deep sequencing technology has unexpectedly advanced our structural understanding of molecules composed of nucleic acids. A significant amount of progress has been made recently extrapolating the chemical methods to probe RNA structure into sequencing methods. Herein we review some of the canonical methods to analyze RNA structure, and then we outline how these have been used to probe the structure of many RNAs in parallel. The key is the transformation of structural biology problems into sequencing problems, whereby sequencing power can be interpreted to understand nucleic acid proximity, nucleic acid conformation, or nucleic acid-protein interactions. Utilizing such technologies in this way has the promise to provide novel structural insights into the mechanisms that control normal cellular physiology and provide insight into how structure could be perturbed in disease.

BIO:

Rob Spitale attended SUNY Fredonia where he graduated with a BS in both Biology and Chemistry. He obtained his Ph.D. in Chemistry from the University of Rochester, where he worked on the structure and mechanisms of non-coding RNAs (ribozymes and riboswitches). He then moved to Stanford University to develop methods for transcriptome-wide analyses of RNA structure inside living cells. He began his independent career in July of 2014 at the University of California, Irvine.