

## Global analyses of post-transcriptional gene regulatory networks in tissue development

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Gene expression is highly regulated to ensure that each cell contains the correct complement of proteins necessary for proper cellular functions. During cell development, extensive 'switch-like' changes in gene expression occur through post-transcriptional regulation of mRNA. This includes changes in alternative mRNA splicing and polyadenylation, as well as regulation of mRNA stability and translation. Mutations which perturb cell-specific mRNA regulatory programs are associated with growing lists of human diseases, thus a greater understanding of how post-transcriptional mRNA regulatory networks are controlled in different cell types and stages of development is needed. The presentation will discuss the roles of RNA binding proteins in the regulation of gene expression in mammalian tissue development. In addition, the talk will describe how new biochemical-enrichment strategies combined with deep sequencing are providing new transcriptome-wide insights into mechanisms of post-transcriptional gene regulation in mammalian tissue development.

### Biography

Donny D. Licatalosi is an Assistant Professor in the Center for RNA Molecular Biology at Case Western Reserve University. His lab combines genetic tools, biochemical-enrichment methods, deep sequencing, and bioinformatics to investigate how post-transcriptional gene regulatory networks are controlled during tissue development.

He received his Ph.D. from the Department of Biochemistry and Molecular Genetics at the University of Colorado Health Sciences Center. As a postdoctoral associate with Dr. Robert Darnell at Rockefeller University, he pioneered the use of HITS-CLIP as a powerful new approach to study RNA binding proteins in an unbiased and transcriptome-wide manner *in vivo*.

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