

## **Identifying Coordinate Regulation of Cellular Pathways within Post-Transcriptional Networks**

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Post-transcriptional regulatory networks impose critical and cumulative effects on gene expression. In humans, more than 1500 RNA binding proteins engage specific groups or clusters of mRNAs and choreograph their processing, splicing, transport, localization, stabilization and translation. The specific constellation of RNA binding proteins that engage an mRNA defines the post-transcriptional network that it follows and understanding how these routes are perturbed among various tissues and disease states will significantly enhance our ability to translate genomic information into new medicines.

We have developed an expansive catalog of mRNA and protein expression data for the catalog of human RNA binding proteins. A surprisingly high percentage, > 10%, of those RNA binding proteins examined to date exhibit tissue specific expression or significant correlation with specific disease states. The clusters of mRNAs regulated by several tissue-specific and disease-related RNA binding proteins have also been isolated by co-immunoprecipitation and characterized by high-density microarray analysis. The results indicate that RNA binding proteins coordinately regulate gene expression within single cellular pathways as well as across distinct pathways. Details of this novel approach to gene expression analysis and progress in its application to the study insulin action, obesity, and CNS disorders will be presented.