A resource for studying the role of RNA-binding proteins in human disease

Advances in science and technology have not only made accessing and analyzing the personal genomic information a reality but also rapid and cost effective. Every living organism is made of cells and every cell is made of many sub cellular components and interactions among them, which lead to life related activities such as metabolism, growth and aging. Disruption in cellular activities can lead to complex diseases such as alzheimers, diabetes and various forms of cancer. Therefore, uncovering the blueprint of the cell and the intricate interconnections between various molecular components will help elucidate the cellular activities, thereby helping scientists to come up with an effective cure for such diseases and a better quality of life.

High-throughput sequencing technologies enable extracting the genomic information and empowering researchers to have an enhanced insight of the cellular components, processes and their alterations in disease states.   Genes are functional cellular components that play a fundamental role in regulating the cellular activities. Functional impact of a gene is typically measured by estimating its abundance in a tissue or cell type known as gene expression. Genes perform their specific functions by giving rise to proteins.

A major class of proteins, which control the metabolism of RNA, a fundamental cellular component in the cell, is RNA-binding proteins (RBPs). Though it is known from several studies that control of cellular RNAs by specific RBPs is responsible for controlling diverse range of functions and cellular processes, it is unclear what these cellular interactions are and their design principles, governed by hundreds of experimentally confirmed RBPs across species and how cross-talk and communication among them contribute to the phenotypes due to changes in the activity of these molecules. RBPs bind to their target RNAs by recognizing a specific sequence pattern known as motif. However, for most RNA-binding proteins (RBPs), their interacting target components are likely unknown or uncharacterized in humans as well as other model organisms.

To centralize and facilitate the access to various levels of knowledge and information associated with these important regulatory molecules in the cell, we developed RNA Binding Protein (RBP) Expression And Disease dynamics database (READ DB), a non-redundant, curated database of human RBPs. RBPs curated from different experimental studies are reported with their annotation, tissue-wide gene and protein expression levels, evolutionary conservation, disease associations, their cross talk information with other proteins, their known target recognition patterns as well as predicted binding targets and associated functional themes, providing a one stop portal for understanding the expression, evolutionary trajectories and disease dynamics of RBPs in the context of human tissues.

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Publications

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