

Related Works

circIncRNAnet : it is lack of protein-coding potential, long noncoding RNAs (lncRNAs) and circular RNAs (circRNAs) have explained as key determinants in regulating gene , acting to fine-tune transcriptional and signaling output.

Protein–protein interaction network and transcriptional regulatory network : GeneMANIA is a flexible platform that can expect gene function, analyze gene lists and sequence genes with function assays, that gives three main cases: single gene queries, multiple gene queries and network search. The online tool can construct protein–protein interaction (PPI) network and protein-DNA interaction, investigate potential signal pathway, gene and protein expression and protein domains. We explored lncRNA-related proteins and transcriptional regulatory molecules with AnnoLnc, and visualized the functions and regulatory networks of these molecules using GeneMANIA.

ImmLnc :

Long noncoding RNAs (lncRNAs) are emerging as critical regulators of gene expression and paly crucial roles in immune regulation. However,high-throughput methods for the identification of lncRNAs that affect immune pathway activity are still largely unavailable. ImmLnc is a web-based resource for investigating the immune-related function of lncRNAs across cancer types. In this resource, the users can query the lncRNA-pathways, lncRNA-immune cell type's correlation, and cancer-related lncRNAs across 33 cancer types. The ImmLnc pipeline and the resulting data provided here are intended to serve as a valuable resource for understanding the lncRNA function and to further advance the identification of immunotherapy targets.