

Resource Summary Report

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doRiNA

RRID:SCR_013222

Type: Tool

Proper Citation

doRiNA (RRID:SCR_013222)

Resource Information

URL: http://dorina.mdc-berlin.de/rbp_browser/dorina.html

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Description: In animals, RNA binding proteins (RBPs) and microRNAs (miRNAs) post-transcriptionally regulate the expression of virtually all genes by binding to RNA. Recent advances in experimental and computational methods facilitate transcriptome-wide mapping of these interactions. It is thought that the combinatorial action of RBPs and miRNAs on target mRNAs form a post-transcriptional regulatory code. We provide a database that supports the quest for deciphering this regulatory code. Within doRiNA, we are systematically curating, storing and integrating binding site data for RBPs and miRNAs. Users are free to take a target (mRNA) or regulator (RBP and/or miRNA) centric view on the data. We have implemented a database framework with short query response times for complex searches (e.g. asking for all targets of a particular combination of regulators). All search results can be browsed, inspected and analyzed in conjunction with a huge selection of other genome-wide data, because our database is directly linked to a local copy of the UCSC genome browser. At the time of writing, doRiNA encompasses RBP data for the human, mouse and worm genomes. For computational miRNA target site predictions, we provide an update of PicTar predictions.

Abbreviations: doRiNA

Resource Type: data or information resource, database

Defining Citation: [PMID:22086949](#)

Keywords: binding site, rna binding protein, microRNA, post-transcription, rna, gene, genome, mammal, population variation, gene expression, transcript, regulator, protein, binding

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Resource Name: doRiNA

Resource ID: SCR_013222

Alternate IDs: nlx_151321

Record Creation Time: 20220129T080314+0000

Record Last Update: 20250507T060907+0000

Ratings and Alerts

No rating or validation information has been found for doRiNA.

No alerts have been found for doRiNA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 14 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Schwarzl T, et al. (2024) Improved discovery of RNA-binding protein binding sites in eCLIP data using DEWSeq. Nucleic acids research, 52(1), e1.

Sekar V, et al. (2024) Detection of transcriptome-wide microRNA-target interactions in single cells with agoTRIBES. Nature biotechnology, 42(8), 1296.

Horlacher M, et al. (2023) A systematic benchmark of machine learning methods for protein-RNA interaction prediction. Briefings in bioinformatics, 24(5).

Dal Molin A, et al. (2022) CRAFT: a bioinformatics software for custom prediction of circular RNA functions. *Briefings in bioinformatics*, 23(2).

Wang S, et al. (2021) Quaking 5 suppresses TGF- β -induced EMT and cell invasion in lung adenocarcinoma. *EMBO reports*, 22(6), e52079.

Elhasnaoui J, et al. (2020) DSCAM-AS1-Driven Proliferation of Breast Cancer Cells Involves Regulation of Alternative Exon Splicing and 3'-End Usage. *Cancers*, 12(6).

Shatoff E, et al. (2020) Single nucleotide polymorphisms affect RNA-protein interactions at a distance through modulation of RNA secondary structures. *PLoS computational biology*, 16(5), e1007852.

Carazo F, et al. (2019) Integration of CLIP experiments of RNA-binding proteins: a novel approach to predict context-dependent splicing factors from transcriptomic data. *BMC genomics*, 20(1), 521.

Adinolfi M, et al. (2019) Discovering sequence and structure landscapes in RNA interaction motifs. *Nucleic acids research*, 47(10), 4958.

Pan X, et al. (2018) Prediction of RNA-protein sequence and structure binding preferences using deep convolutional and recurrent neural networks. *BMC genomics*, 19(1), 511.

Jalali S, et al. (2018) Distinct and Modular Organization of Protein Interacting Sites in Long Non-coding RNAs. *Frontiers in molecular biosciences*, 5, 27.

Bhandare S, et al. (2017) Discriminating between HuR and TTP binding sites using the k-spectrum kernel method. *PloS one*, 12(3), e0174052.

HafezQorani S, et al. (2016) Modeling the combined effect of RNA-binding proteins and microRNAs in post-transcriptional regulation. *Nucleic acids research*, 44(9), e83.

Wang Y, et al. (2013) Integrative analysis revealed the molecular mechanism underlying RBM10-mediated splicing regulation. *EMBO molecular medicine*, 5(9), 1431.