

Resource Summary Report

Generated by [kravitz2](#) on Sep 5, 2026

iRegulon

RRID:SCR_028223

Type: Tool

Proper Citation

iRegulon (RRID:SCR_028223)

Resource Information

URL: <http://iregulon.aertslab.org/>

Proper Citation: iRegulon (RRID:SCR_028223)

Description: Software tool to reverse-engineer transcriptional regulatory networks from co-expressed gene sets by identifying master transcription factors (TFs) and their direct target genes. It operates by scanning for enriched TF binding motifs in promoter regions, utilizing over 10,000 position weight matrices (PWMs) for human, mouse, and Drosophila. Used to enable gene regulatory network mapping directly based on motif enrichment in co-expressed gene set.

Resource Type: software application, software resource, source code

Defining Citation: [PMID:25058159](#)

Keywords: reverse-engineer transcriptional regulatory networks, co-expressed gene sets, identifying master transcription factors and their direct target genes,

Availability: Free, Available for download, Freely available

Resource Name: iRegulon

Resource ID: SCR_028223

Alternate URLs: <https://github.com/aertslab/iRegulon>

Record Creation Time: 20260402T060015+0000

Record Last Update: 20260904T001152+0000

Ratings and Alerts

No rating or validation information has been found for iRegulon.

No alerts have been found for iRegulon.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 9 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Piroozmand S, et al. (2026) Suboptimal Responses to Anti-VEGF in Retinal Neurovascular Diseases: Linking Aging and Alternative Angioinflammatory Pathways. Investigative ophthalmology & visual science, 67(5), 4.

Abril-Parreño L, et al. (2025) Deciphering differences in DNA methylation and transcriptome profiles of oocytes from pigs with high and low developmental competence. Environmental epigenetics, 11(1), dvaf018.

Corti S, et al. (2025) Recreating pathophysiology of CLN2 disease and demonstrating reversion by TPP1 gene therapy in hiPSC-derived retinal organoids and retina-on-chip. Cell reports. Medicine, 6(8), 102244.

Duong HA, et al. (2024) Environmental circadian disruption re-writes liver circadian proteomes. Nature communications, 15(1), 5537.

Jin Y, et al. (2024) Advanced glycation end products regulate macrophage apoptosis and influence the healing of diabetic foot wound through miR-361-3p/CSF1R and PI3K/AKT pathway. Heliyon, 10(2), e24598.

Tang H, et al. (2022) Screening of Important Markers in Peripheral Blood Mononuclear Cells to Predict Female Osteoporosis Risk Using LASSO Regression Algorithm and SVM Method. Evolutionary bioinformatics online, 18, 11769343221075014.

Miglietta G, et al. (2021) G-quadruplex binders as cytostatic modulators of innate immune genes in cancer cells. Nucleic acids research, 49(12), 6673.

Ji S, et al. (2020) Screening of potential genes and transcription factors involved in post-radiation cognitive dysfunction in mice via bioinformatics. Translational cancer research, 9(10), 6383.

Örd T, et al. (2015) TRIB3 enhances cell viability during glucose deprivation in HEK293-derived cells by upregulating IGFBP2, a novel nutrient deficiency survival factor. Biochimica et biophysica acta, 1853(10 Pt A), 2492.