

Resource Summary Report

Generated by [NIF](#) on Aug 4, 2026

[iRegulon](#)

RRID:SCR_028223

Type: Tool

Proper Citation

iRegulon (RRID:SCR_028223)

Resource Information

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

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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: 20260805T044626+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 have not found any literature mentions for this resource.