

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 17, 2026

RegulonDB

RRID:SCR_003499

Type: Tool

Proper Citation

RegulonDB (RRID:SCR_003499)

Resource Information

URL: <http://regulondb.ccg.unam.mx/>

Proper Citation: RegulonDB (RRID:SCR_003499)

Description: Database on transcriptional regulation in Escherichia coli K-12 containing knowledge manually curated from original scientific publications, complemented with high throughput datasets and comprehensive computational predictions. Graphic and text-integrated environment with friendly navigation where regulatory information is always at hand. They provide integrated views to understand as well as organized knowledge in computable form. Users may submit data to make it publicly available.

Abbreviations: RegulonDB

Resource Type: data or information resource, database

Defining Citation: [PMID:23203884](#)

Keywords: transcription, gene regulation, operon, bacteria, evolutionary conservation, regulatory phrase, transcriptional regulation, transcriptional regulatory network, bio.tools, FASEB list

Funding: NIGMS GM071962;

NIGMS GM077678;

Consejo Nacional de Ciencia y Tecnologia 103686;

Consejo Nacional de Ciencia y Tecnologia 179997;

Programa de Apoyo a Proyectos de Investigacion e Innovacion Tecnologica IN210810;

Programa de Apoyo a Proyectos de Investigacion e Innovacion Tecnologica IN209312

Resource Name: RegulonDB

Resource ID: SCR_003499

Alternate IDs: OMICS_01868, nif-0000-03399, biotools:regulondb

Alternate URLs: <https://bio.tools/regulondb>

Record Creation Time: 20220129T080219+0000

Record Last Update: 20260912T200009+0000

Ratings and Alerts

No rating or validation information has been found for RegulonDB.

No alerts have been found for RegulonDB.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 153 mentions in open access literature.

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

Li J, et al. (2026) Repeatability of gene expression evolution in experimental environmental adaptation. *Nature communications*, 17(1).

Ishikawa K, et al. (2026) Knockout of *tusA* confers cationic antimicrobial resistance via *fur* and *omp* genes in *Escherichia coli*. *Journal of bacteriology*, 208(5), e0010326.

Panaccione FP, et al. (2025) BioGAN: Enhancing Transcriptomic Data Generation with Biological Knowledge. *Bioengineering (Basel, Switzerland)*, 12(6).

Geng J, et al. (2025) Unveiling the landscape of prokaryotic global regulators through deep protein language models. *mSystems*, 10(12), e0095025.

Tsuru S, et al. (2025) Congruence between noise and plasticity in protein expression. *Scientific reports*, 15(1), 24529.

Hernandez-Benitez EM, et al. (2025) Computational inference of *Rhizobium phaseoli* transcriptional regulatory network predicts Transcription Factors involved in nodulation. *Briefings in functional genomics*, 24.

Boada Y, et al. (2025) Synthetic biology design principles enable efficient bioproduction of Heparosan with low molecular weight and low polydispersion index for the biomedical industry. *Synthetic biology (Oxford, England)*, 10(1), ysaf006.

Sepúlveda-Rebolledo P, et al. (2025) Comparative Genomics of Sigma Factors in *Acidithiobacillus* Sheds Light into the Transcriptional Regulatory Networks Involved in Biogeochemical Dynamics in Extreme Acidic Environments. *Microorganisms*, 13(6).

Trouillon J, et al. (2025) Predicting input signals of transcription factors in *Escherichia coli*. *Molecular systems biology*, 21(10), 1371.

Tsuru S, et al. (2025) Genetic properties underlying transcriptional variability across different perturbations. *Nature communications*, 16(1), 2421.

Lally P, et al. (2025) Predictive biophysical neural network modeling of a compendium of in vivo transcription factor DNA binding profiles for *Escherichia coli*. *Nature communications*, 16(1), 4255.

Schalck T, et al. (2025) Reprogramming the EnvZ-OmpR two-component system confers ethanol tolerance in *Escherichia coli* by stabilizing the outer membrane and altering ferric homeostasis. *PLoS genetics*, 21(12), e1011707.

Wei PJ, et al. (2024) Inference of gene regulatory networks based on directed graph convolutional networks. *Briefings in bioinformatics*, 25(4).

Borges Farias A, et al. (2024) Predicting bacterial transcription factor binding sites through machine learning and structural characterization based on DNA duplex stability. *Briefings in bioinformatics*, 25(6).

Kernfeld E, et al. (2024) Transcriptome data are insufficient to control false discoveries in regulatory network inference. *Cell systems*, 15(8), 709.

Salgado H, et al. (2024) RegulonDB v12.0: a comprehensive resource of transcriptional regulation in *E. coli* K-12. *Nucleic acids research*, 52(D1), D255.

Tsukimi T, et al. (2024) Genetic mutation in *Escherichia coli* genome during adaptation to the murine intestine is optimized for the host diet. *mSystems*, 9(2), e0112323.

Lamoureux CR, et al. (2024) *Escherichia coli* non-coding regulatory regions are highly conserved. *NAR genomics and bioinformatics*, 6(2), lqae041.

Lara P, et al. (2024) Flexible gold standards for transcription factor regulatory interactions in *Escherichia coli* K-12: architecture of evidence types. *Frontiers in genetics*, 15, 1353553.

Qiu S, et al. (2024) Inferred regulons are consistent with regulator binding sequences in *E. coli*. *PLoS computational biology*, 20(1), e1011824.