

Resource Summary Report

Generated by [RRID](#) on Aug 10, 2026

RegTransBase

RRID:SCR_013047

Type: Tool

Proper Citation

RegTransBase (RRID:SCR_013047)

Resource Information

URL: <http://regtransbase.lbl.gov>

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Description: It consists of two modules - a database of regulatory interactions based on literature and an expertly curated database of transcription factor binding sites. The literature based information in RegTransBase is a manually curated database of regulatory interactions in prokaryotes, captures the knowledge in published scientific literature using a controlled vocabulary. RegTransBase describes a large number of regulatory interactions reported in many organisms and contains various types of experimental data, in particular: * the activation or repression of transcription by an identified direct regulator * determining the transcriptional regulatory function of a protein (or RNA) directly binding to DNA or RNA * mapping or prediction of binding sites for a regulatory protein * characterization of regulatory mutations The analysis section of RegtransBase is based on a set of manually curated alignments of transcription factor binding sites and allows you to search for new binding sites and verify conservation of bindings sites across multiple species through the use of web based analysis tools.

Synonyms: RegTransBase

Resource Type: database, data or information resource

Resource Name: RegTransBase

Resource ID: SCR_013047

Alternate IDs: nif-0000-03398

Record Creation Time: 20220129T080314+0000

Record Last Update: 20260808T190424+0000

Ratings and Alerts

No rating or validation information has been found for RegTransBase.

No alerts have been found for RegTransBase.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Mao Y, et al. (2023) Genetically Encoded Biosensor Engineering for Application in Directed Evolution. *Journal of microbiology and biotechnology*, 33(10), 1257.

Taboada-Castro H, et al. (2020) RhizoBindingSites, a Database of DNA-Binding Motifs in Nitrogen-Fixing Bacteria Inferred Using a Footprint Discovery Approach. *Frontiers in microbiology*, 11, 567471.

Andreevskaya M, et al. (2016) *Lactobacillus oligofermentans* glucose, ribose and xylose transcriptomes show higher similarity between glucose and xylose catabolism-induced responses in the early exponential growth phase. *BMC genomics*, 17, 539.

Del??pine B, et al. (2016) SensiPath: computer-aided design of sensing-enabling metabolic pathways. *Nucleic acids research*, 44(W1), W226.

Blow MJ, et al. (2016) The Epigenomic Landscape of Prokaryotes. *PLoS genetics*, 12(2), e1005854.

Robinson M, et al. (2014) Transcription factor MrpC binds to promoter regions of hundreds of developmentally-regulated genes in *Myxococcus xanthus*. *BMC genomics*, 15, 1123.