Resource Summary Report

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RegPrecise

RRID:SCR_002149
Type: Tool

Proper Citation

RegPrecise (RRID:SCR_002149)

Resource Information

URL: https://enigma.lbl.gov/regprecise/

Proper Citation: RegPrecise (RRID:SCR_002149)

Description: Collection of manually curated inferences of regulons in prokaryotic genomes. Database for capturing, visualization and analysis of transcription factor regulons that were reconstructed by comparative genomic approach in wide variety of prokaryotic genomes.

Abbreviations: RegPrecise

Resource Type: database, data or information resource

Defining Citation: PMID:24175918

Keywords: regulon, genome, transcription factor, gene, operon, transcription factor binding site, taxonomy, rna, effector, pathway, ortholog, function, FASEB list

Funding: Department of Energy ;
NSF DBI-0850546

Availability: Free, Freely available

Resource Name: RegPrecise

Resource ID: SCR_002149

Alternate IDs: OMICS_01869

Record Creation Time: 20220129T080211+0000

Record Last Update: 20250412T054652+0000

Ratings and Alerts

No rating or validation information has been found for RegPrecise.

No alerts have been found for RegPrecise.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 76 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Putumbaka S, et al. (2025) Tungsten is utilized for lactate consumption and SCFA production by a dominant human gut microbe Eubacterium limosum. Proceedings of the National Academy of Sciences of the United States of America, 122(1), e2411809121.

Chen F, et al. (2024) Citrate serves as a signal molecule to modulate carbon metabolism and iron homeostasis in Staphylococcus aureus. PLoS pathogens, 20(7), e1012425.

Josephs-Spaulding J, et al. (2024) Reconstructing the transcriptional regulatory network of probiotic L. reuteri is enabled by transcriptomics and machine learning. mSystems, 9(3), e0125723.

Ryan D, et al. (2024) An expanded transcriptome atlas for Bacteroides thetaiotaomicron reveals a small RNA that modulates tetracycline sensitivity. Nature microbiology, 9(4), 1130.

Yu J, et al. (2023) Identification of Staphylococcus aureus virulence-modulating RNA from transcriptomics data with machine learning. Virulence, 14(1), 2228657.

Marshall A, et al. (2023) One size does not fit all - Trehalose metabolism by Clostridioides difficile is variable across the five phylogenetic lineages. Microbial genomics, 9(9).

Duboux S, et al. (2023) The Pleiotropic Effects of Carbohydrate-Mediated Growth Rate Modifications in Bifidobacterium longum NCC 2705. Microorganisms, 11(3).

Zheng C, et al. (2023) ZrgA contributes to zinc acquisition in Vibrio parahaemolyticus. Virulence, 14(1), 2156196.

Doing G, et al. (2023) Computationally Efficient Assembly of Pseudomonas aeruginosa Gene Expression Compendia. mSystems, 8(1), e0034122.

Arzamasov AA, et al. (2022) Human Milk Oligosaccharide Utilization in Intestinal Bifidobacteria Is Governed by Global Transcriptional Regulator NagR. mSystems, 7(5), e0034322.

Roux AE, et al. (2022) The Role of Regulator Catabolite Control Protein A (CcpA) in Streptococcus agalactiae Physiology and Stress Response. Microbiology spectrum, 10(6), e0208022.

Mikhaylina A, et al. (2022) A single sensor controls large variations in zinc quotas in a marine cyanobacterium. Nature chemical biology, 18(8), 869.

Duboux S, et al. (2021) Carbohydrate-controlled serine protease inhibitor (serpin) production in Bifidobacterium longum subsp. longum. Scientific reports, 11(1), 7236.

Iablokov SN, et al. (2021) Binary Metabolic Phenotypes and Phenotype Diversity Metrics for the Functional Characterization of Microbial Communities. Frontiers in microbiology, 12, 653314.

Eddie BJ, et al. (2021) Marinobacter atlanticus electrode biofilms differentially regulate gene expression depending on electrode potential and lifestyle. Biofilm, 3, 100051.

Rodionov DA, et al. (2021) Transcriptional Regulation of Plant Biomass Degradation and Carbohydrate Utilization Genes in the Extreme Thermophile Caldicellulosiruptor bescii. mSystems, 6(3), e0134520.

Duru IC, et al. (2021) Transcriptomic time-series analysis of cold- and heat-shock response in psychrotrophic lactic acid bacteria. BMC genomics, 22(1), 28.

Nikparvar B, et al. (2021) Analysis of temporal gene regulation of Listeria monocytogenes revealed distinct regulatory response modes after exposure to high pressure processing. BMC genomics, 22(1), 266.

Duru IC, et al. (2021) High-pressure processing-induced transcriptome response during recovery of Listeria monocytogenes. BMC genomics, 22(1), 117.

Chen C, et al. (2020) The local transcriptional regulators SacR1 and SacR2 act as repressors of fructooligosaccharides metabolism in Lactobacillus plantarum. Microbial cell factories, 19(1), 161.