Resource Summary Report

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PRODORIC

RRID:SCR_007074
Type: Tool

Proper Citation

PRODORIC (RRID:SCR_007074)

Resource Information

URL: http://prodoric.tu-bs.de/

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Description: Database about gene regulation and gene expression in prokaryotes. It includes a manually curated and unique collection of transcription factor binding sites. A variety of bioinformatics tools for the prediction, analysis and visualization of regulons and gene reglulatory networks is included. The integrated approach provides information about molecular networks in prokaryotes with focus on pathogenic organisms. In detail this concerns: * transcriptional regulation (transcription factors and their DNA binding sites * signal transduction (two-component systems, phosphylation cascades) * protein interactions (complex formation, oligomerization) * biochemical pathways (chemical reactions) * other regulation events (e.g. codon usage, etc. ...) It aims to be a resource to model protein-host interactions and to be a suitable platform to analyze high-throughput data from proteomis and transcriptomics experiments (systems biology). Currently it mainly contains detailed information about operon and promoter structures including huge collections of transcription factor binding sites. If an appropriate number of regulatory binding sites is available, a position weight matrix (PWM) and a sequence logo is provided, which can be used to predict new binding sites. This data is collected manually by screening the original scientific literature. PRODORIC also handles protein-protein interactions and signal-transduction cascades that commonly occur in form of two-component systems in prokaryotes. Furthermore it contains metabolic network data imported from the KEGG database.

Abbreviations: PRODORIC

Synonyms: Prokaryotic Database of Gene Regulation

Resource Type: database, data or information resource

Defining Citation: PMID:18974177

Keywords: gene regulation, transcription factor binding site, promoter structure, gene expression, genome, regulon, network, visualization, gene regulatory network, pathogen, transcriptional regulation, transcription factor, dna binding site, signal transduction, protein interaction, pathway, regulation, protein-protein interaction, signal-transduction cascade, operon, promoter, structure, position weight matrix, FASEB list

Funding: BMBF

Availability: Acknowledgement requested, Free for academic use, Non-commercial

Resource Name: PRODORIC

Resource ID: SCR_007074

Alternate IDs: nif-0000-03343, OMICS_01872

Alternate URLs: http://www.prodoric.de

Record Creation Time: 20220129T080239+0000

Record Last Update: 20250412T055146+0000

Ratings and Alerts

No rating or validation information has been found for PRODORIC.

No alerts have been found for PRODORIC.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 50 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Achterberg T, et al. (2025) ProPr54 web server: predicting ?54 promoters and regulon with a hybrid convolutional and recurrent deep neural network. NAR genomics and bioinformatics, 7(1), lqae188.

De la Cruz MA, et al. (2025) The transcriptional regulator Lrp activates the expression of genes involved in the biosynthesis of tilimycin and tilivalline enterotoxins in Klebsiella

oxytoca. mSphere, 10(1), e0078024.

Tomasch J, et al. (2024) A photoheterotrophic bacterium from Iceland has adapted its photosynthetic machinery to the long days of polar summer. mSystems, 9(3), e0131123.

Coves X, et al. (2024) The Mla system and its role in maintaining outer membrane barrier function in Stenotrophomonas maltophilia. Frontiers in cellular and infection microbiology, 14, 1346565.

David C, et al. (2024) Intestinal carbapenem-resistant Klebsiella pneumoniae undergoes complex transcriptional reprogramming following immune activation. Gut microbes, 16(1), 2340486.

Molina-Henares MA, et al. (2024) Gene expression reprogramming of Pseudomonas alloputida in response to arginine through the transcriptional regulator ArgR. Microbiology (Reading, England), 170(3).

Kopejtka K, et al. (2024) Minimal transcriptional regulation of horizontally transferred photosynthesis genes in phototrophic bacterium Gemmatimonas phototrophica. mSystems, 9(9), e0070624.

Elsen S, et al. (2024) Cross-regulation and cross-talk of conserved and accessory two-component regulatory systems orchestrate Pseudomonas copper resistance. PLoS genetics, 20(6), e1011325.

Lestin L, et al. (2024) The bacterial strains JAM1T and GP59 of the species Methylophaga nitratireducenticrescens differ in their expression profiles of denitrification genes in oxic and anoxic cultures. PeerJ, 12, e18361.

Bientz V, et al. (2024) OxyR is required for oxidative stress resistance of the entomopathogenic bacterium Xenorhabdus nematophila and has a minor role during the bacterial interaction with its hosts. Microbiology (Reading, England), 170(7).

Troitzsch D, et al. (2024) Characterizing the flavodoxin landscape in Clostridioides difficile. Microbiology spectrum, 12(3), e0189523.

Wang L, et al. (2024) A novel esterase regulates Klebsiella pneumoniae hypermucoviscosity and virulence. PLoS pathogens, 20(10), e1012675.

Price MN, et al. (2024) Interactive tools for functional annotation of bacterial genomes. Database : the journal of biological databases and curation, 2024.

Li Q, et al. (2024) Physiological Functions of the Cello-Oligosaccharides Binding CebE in the Pathogenic Streptomyces sp. AMCC400023. Microorganisms, 12(3).

Truchon AN, et al. (2023) Plant-Pathogenic Ralstonia Phylotypes Evolved Divergent Respiratory Strategies and Behaviors To Thrive in Xylem. mBio, 14(1), e0318822.

Cho C, et al. (2023) Characterization of radiation-resistance mechanism in Spirosoma montaniterrae DY10T in terms of transcriptional regulatory system. Scientific reports, 13(1), 4739.

Yoon CK, et al. (2021) Vibrio cholerae FruR facilitates binding of RNA polymerase to the fru promoter in the presence of fructose 1-phosphate. Nucleic acids research, 49(3), 1397.

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

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.

Meng X, et al. (2020) Molecular Mechanisms of Phosphate Stress Activation of Pseudomonas aeruginosa Quorum Sensing Systems. mSphere, 5(2).