

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 regulatory 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, phosphorylation 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 proteomics 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., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: PRODORIC

Synonyms: Prokaryotic Database of Gene Regulation

Resource Type: data or information resource, database

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: THIS RESOURCE IS NO LONGER IN SERVICE

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: 20260821T193818+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 57 mentions in open access literature.

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

Rasheed N, et al. (2025) The function of Anr in the differential effects of oxygen levels on biofilm development and nitrogenase performance in *Pseudomonas stutzeri* A1501. *PLoS one*, 20(9), e0333183.

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.

Shem-Tov R, et al. (2025) HilE mediates motility thermoregulation in typhoidal *Salmonella* serovars at elevated physiological temperatures. *PLoS pathogens*, 21(10), e1013133.

Peng Y, et al. (2025) ArgR-dependent bacterial resistance to host lipid droplets in *Edwardsiella piscicida*. *Communications biology*, 8(1), 333.

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

Mejia-Ventura S, et al. (2025) The Nucleoid-Associated Protein Fis Represses Type 3 Fimbriae to Modulate Biofilm and Adherence Formation in *Klebsiella pneumoniae*. *Microorganisms*, 13(11).

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.

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.

Pucelik S, et al. (2024) The blue light-dependent LOV-protein LdaP of *Dinoroseobacter shibae* acts as antirepressor of the PpsR repressor, regulating photosynthetic gene cluster expression. *Frontiers in microbiology*, 15, 1351297.

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

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

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

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

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

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).

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.

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

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