Resource Summary Report

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DBTBS

RRID:SCR_002345
Type: Tool

Proper Citation

DBTBS (RRID:SCR_002345)

Resource Information

URL: http://dbtbs.hgc.jp/

Proper Citation: DBTBS (RRID:SCR_002345)

Description: Database of experimentally validated gene regulatory relations and the corresponding transcription factor binding sites upstream of Bacillus subtilis genes. The database allows the comparison of systematic experiments with individual experimental results in order to facilitate the elucidation of the complete B. subtilis gene regulatory network. The current version is constructed by surveying 947 references and contains the information of 120 binding factors and 1475 gene regulatory relations. For each promoter, all of its known cis-elements are listed according to their positions, while these cis-elements are aligned to illustrate the consensus sequence for each transcription factor. All probable transcription factors coded in the genome were classified using Pfam motifs. The DBTBS database was reorganized to show operons instead of individual genes as the building blocks of gene regulatory networks. It now contains 463 experimentally known operons, as well as their terminator sequences if identifiable. In addition, 517 transcriptional terminators were identified computationally. (De Hoon, M.J.L. et al., PLoS Comput. Biol. 1, e25 (2005)). A new section was added under "Motif conservation", which presents hexameric motifs found to be conserved to different extents between upstream intergenic regions of genus-specific subgroups of homologous proteins.

Abbreviations: DBTBS

Synonyms: DBTBS: a database of Bacillus subtilis promoters and transcription factors., DBTBS: a database of Bacillus subtilis promoters and transcription factors

Resource Type: data or information resource, database

Defining Citation: PMID:17962296, PMID:14681362, PMID:11125112

Keywords: gene, gene regulatory network, transcription factor binding site, transcription factor, regulated operon, motif, promoter, motif conservation

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Availability: Acknowledgement requested

Resource Name: DBTBS

Resource ID: SCR_002345

Alternate IDs: nif-0000-02736, OMICS_01859

Record Creation Time: 20220129T080212+0000

Record Last Update: 20260801T190914+0000

Ratings and Alerts

No rating or validation information has been found for DBTBS.

No alerts have been found for DBTBS.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 30 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

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

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

Zhang L, et al. (2024) Transcriptional regulation of cellobiose utilization by PRD-domain containing Sigma54-dependent transcriptional activator (CelR) and catabolite control protein A (CcpA) in Bacillus thuringiensis. Frontiers in microbiology, 15, 1160472.

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

Qin J, et al. (2022) NupR Responding to Multiple Signals Is a Nucleoside Permease Regulator in Bacillus thuringiensis BMB171. Microbiology spectrum, 10(4), e0154322.

Liu X, et al. (2021) Identification and Functional Characterization of Two Homologous SpoVS Proteins Involved in Sporulation of Bacillus thuringiensis. Microbiology spectrum, 9(2), e0088121.

Zhou C, et al. (2021) Transcriptome based functional identification and application of regulator AbrB on alkaline protease synthesis in Bacillus licheniformis 2709. International journal of biological macromolecules, 166, 1491.

Shen P, et al. (2021) Exploitation of ammonia-inducible promoters for enzyme overexpression in Bacillus licheniformis. Journal of industrial microbiology & biotechnology, 48(5-6).

Maan H, et al. (2021) Bacillus subtilis Colonization of Arabidopsis thaliana Roots Induces Multiple Biosynthetic Clusters for Antibiotic Production. Frontiers in cellular and infection microbiology, 11, 722778.

Han L, et al. (2020) Realization of Robust and Precise Regulation of Gene Expression by Multiple Sigma Recognizable Artificial Promoters. Frontiers in bioengineering and biotechnology, 8, 92.

Yuan F, et al. (2020) Identification of two novel highly inducible promoters from Bacillus licheniformis by screening transcriptomic data. Genomics, 112(2), 1866.

Hashim FA, et al. (2019) Review of Different Sequence Motif Finding Algorithms. Avicenna journal of medical biotechnology, 11(2), 130.

Vahed M, et al. (2019) DIpartite: A tool for detecting bipartite motifs by considering base interdependencies. PloS one, 14(8), e0220207.

Han L, et al. (2019) Development of a novel strategy for robust synthetic bacterial promoters based on a stepwise evolution targeting the spacer region of the core promoter in Bacillus subtilis. Microbial cell factories, 18(1), 96.

Lai HY, et al. (2019) iProEP: A Computational Predictor for Predicting Promoter. Molecular therapy. Nucleic acids, 17, 337.

Coelho RV, et al. (2018) Bacillus subtilis promoter sequences data set for promoter prediction in Gram-positive bacteria. Data in brief, 19, 264.

Perez-Rueda E, et al. (2018) Abundance, diversity and domain architecture variability in prokaryotic DNA-binding transcription factors. PloS one, 13(4), e0195332.

Choi J, et al. (2017) The LacI family protein GlyR3 co-regulates the celC operon and manB in Clostridium thermocellum. Biotechnology for biofuels, 10, 163.

Ramaniuk O, et al. (2017) Kinetic modelling and meta-analysis of the B. subtilis SigA regulatory network during spore germination and outgrowth. Biochimica et biophysica acta. Gene regulatory mechanisms, 1860(8), 894.

Ploss TN, et al. (2016) Homogeneity and heterogeneity in amylase production by Bacillus subtilis under different growth conditions. Microbial cell factories, 15, 57.