Resource Summary Report

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CollecTF

RRID:SCR_014405
Type: Tool

Proper Citation

CollecTF (RRID:SCR_014405)

Resource Information

URL: http://www.collectf.org/browse/home/

Proper Citation: CollecTF (RRID:SCR_014405)

Description: A database of experimentally-validate transcription factor binding sites (TFBS) in the Bacteria domain. CollecTF places special emphasis on providing a curation process that captures the experimental support for sites as reported by authors in peer-reviewed publications. Reported binding sites are mapped to NCBI RefSeq complete genome records. The database can be browsed by transcription factor families, NCBI taxonomy or experimental support, or through customized searches integrating these three elements.

Resource Type: database, data or information resource

Defining Citation: PMID:24234444

Keywords: database, transcription factor binding site, bacteria

Funding: NSF MCB-1158056

Availability: The community can contribute to this resource

Resource Name: CollecTF

Resource ID: SCR_014405

Record Creation Time: 20220129T080320+0000

Record Last Update: 20250412T055801+0000

Ratings and Alerts

No rating or validation information has been found for CollecTF.

No alerts have been found for CollecTF.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 28 mentions in open access literature.

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

Chobert SC, et al. (2025) Dynamic quinone repertoire accompanied the diversification of energy metabolism in Pseudomonadota. The ISME journal, 19(1).

Maciel-Guerra A, et al. (2024) Core and accessory genomic traits of Vibrio cholerae O1 drive lineage transmission and disease severity. Nature communications, 15(1), 8231.

Borges Farias A, et al. (2024) Predicting bacterial transcription factor binding sites through machine learning and structural characterization based on DNA duplex stability. Briefings in bioinformatics, 25(6).

Li F, et al. (2023) AIDmut-Seq: a Three-Step Method for Detecting Protein-DNA Binding Specificity. Microbiology spectrum, 11(1), e0378322.

Olbei M, et al. (2022) Multilayered Networks of SalmoNet2 Enable Strain Comparisons of the Salmonella Genus on a Molecular Level. mSystems, 7(4), e0149321.

Mascolo E, et al. (2022) The transcriptional regulator CtrA controls gene expression in Alphaproteobacteria phages: Evidence for a lytic deferment pathway. Frontiers in microbiology, 13, 918015.

Kang Y, et al. (2021) Strain heterogeneity, cooccurrence network, taxonomic composition and functional profile of the healthy ocular surface microbiome. Eye and vision (London, England), 8(1), 6.

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

Koksharova OA, et al. (2021) ?-N-Methylamino-L-Alanine (BMAA) Causes Severe Stress in Nostoc sp. PCC 7120 Cells under Diazotrophic Conditions: A Proteomic Study. Toxins, 13(5).

Hobbs ET, et al. (2021) ECO-CollecTF: A Corpus of Annotated Evidence-Based Assertions in Biomedical Manuscripts. Frontiers in research metrics and analytics, 6, 674205.

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.

Li JW, et al. (2020) Transcription Factor Engineering for High-Throughput Strain Evolution and Organic Acid Bioproduction: A Review. Frontiers in bioengineering and biotechnology, 8, 98.

Poudel S, et al. (2020) Revealing 29 sets of independently modulated genes in Staphylococcus aureus, their regulators, and role in key physiological response. Proceedings of the National Academy of Sciences of the United States of America, 117(29), 17228.

Koksharova OA, et al. (2020) The First Proteomics Study of Nostoc sp. PCC 7120 Exposed to Cyanotoxin BMAA under Nitrogen Starvation. Toxins, 12(5).

Koksharova OA, et al. (2020) Proteomic Insights into Starvation of Nitrogen-Replete Cells of Nostoc sp. PCC 7120 under ?-N-Methylamino-L-Alanine (BMAA) Treatment. Toxins, 12(6).

K?l?ç S, et al. (2020) Flexible comparative genomics of prokaryotic transcriptional regulatory networks. BMC genomics, 21(Suppl 5), 466.

Pletzer D, et al. (2020) The Stringent Stress Response Controls Proteases and Global Regulators under Optimal Growth Conditions in Pseudomonas aeruginosa. mSystems, 5(4).

Caruso SM, et al. (2019) A Novel Genus of Actinobacterial Tectiviridae. Viruses, 11(12).

Khademi SMH, et al. (2019) Within-Host Adaptation Mediated by Intergenic Evolution in Pseudomonas aeruginosa. Genome biology and evolution, 11(5), 1385.

Qi W, et al. (2019) New insights on Pseudoalteromonas haloplanktis TAC125 genome organization and benchmarks of genome assembly applications using next and third generation sequencing technologies. Scientific reports, 9(1), 16444.