

Resource Summary Report

Generated by [FDI Lab - SciCrunch.org](http://FDILab.SciCrunch.org) on May 12, 2025

MicrobesOnline

RRID:SCR_005507

Type: Tool

Proper Citation

MicrobesOnline (RRID:SCR_005507)

Resource Information

URL: <http://microbesonline.org/>

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Description: MicrobesOnline is designed specifically to facilitate comparative studies on prokaryotic genomes. It is an entry point for operon, regulons, cis-regulatory and network predictions based on comparative analysis of genomes. The portal includes over 1000 complete genomes of bacteria, archaea and fungi and thousands of expression microarrays from diverse organisms ranging from model organisms such as *Escherichia coli* and *Saccharomyces cerevisiae* to environmental microbes such as *Desulfovibrio vulgaris* and *Shewanella oneidensis*. To assist in annotating genes and in reconstructing their evolutionary history, MicrobesOnline includes a comparative genome browser based on phylogenetic trees for every gene family as well as a species tree. To identify co-regulated genes, MicrobesOnline can search for genes based on their expression profile, and provides tools for identifying regulatory motifs and seeing if they are conserved. MicrobesOnline also includes fast phylogenetic profile searches, comparative views of metabolic pathways, operon predictions, a workbench for sequence analysis and integration with RegTransBase and other microbial genome resources. The next update of MicrobesOnline will contain significant new functionality, including comparative analysis of metagenomic sequence data. Programmatic access to the database, along with source code and documentation, is available at <http://microbesonline.org/programmers.html>.

Abbreviations: MicrobesOnline

Synonyms: Microbial Genomics Database, Microbes Online

Resource Type: source code, data or information resource, analysis service resource, service resource, database, production service resource, data analysis service, software resource

Defining Citation: [PMID:19906701](#)

Keywords: microbe, genome, bacteria, archaea, fungi, prokaryote, bio.tools, FASEB list

Funding: DOE DE-AC02-05CH11231

Resource Name: MicrobesOnline

Resource ID: SCR_005507

Alternate IDs: nlx_144607, biotools:microbesonline

Alternate URLs: <https://bio.tools/microbesonline>

Record Creation Time: 20220129T080230+0000

Record Last Update: 20250509T055726+0000

Ratings and Alerts

No rating or validation information has been found for MicrobesOnline.

No alerts have been found for MicrobesOnline.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 149 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Pickens CP, et al. (2025) Absence of biofilm adhesin proteins changes surface attachment and cell strategy for *Desulfovibrio vulgaris* Hildenborough. *Journal of bacteriology*, 207(1), e0037924.

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.

Remy O, et al. (2024) Distinct dynamics and proximity networks of hub proteins at the prey-invading cell pole in a predatory bacterium. *Journal of bacteriology*, 206(4), e0001424.

Zhong X, et al. (2024) The two-component system TtrRS boosts *Vibrio parahaemolyticus* colonization by exploiting sulfur compounds in host gut. *PLoS pathogens*, 20(7), e1012410.

Farci D, et al. (2024) Structural characterization and functional insights into the type II secretion system of the poly-extremophile *Deinococcus radiodurans*. *The Journal of biological chemistry*, 300(2), 105537.

Fukudome M, et al. (2023) Reactive Sulfur Species Produced by Cystathionine γ -lyase Function in the Establishment of *Mesorhizobium loti*-*Lotus japonicus* Symbiosis. *Microbes and environments*, 38(3).

Chávez-Jacobo VM, et al. (2023) The *Sinorhizobium meliloti* NspS-MbaA system affects biofilm formation, exopolysaccharide production and motility in response to specific polyamines. *Microbiology (Reading, England)*, 169(1).

Spiers AJ, et al. (2023) Bioinformatics characterization of BcsA-like orphan proteins suggest they form a novel family of pseudomonad cyclic- β -glucan synthases. *PloS one*, 18(6), e0286540.

Larson CL, et al. (2023) Identification of Type 4B Secretion System Substrates That Are Conserved among *Coxiella burnetii* Genomes and Promote Intracellular Growth. *Microbiology spectrum*, 11(3), e0069623.

Dong H, et al. (2023) Suppressor mutants demonstrate the metabolic plasticity of unsaturated fatty acid synthesis in *Pseudomonas aeruginosa* PAO1. *Microbiology (Reading, England)*, 169(10).

Drousiotis K, et al. (2023) Characterization of the l-arabinofuranose-specific GafABCD ABC transporter essential for l-arabinose-dependent growth of the lignocellulose-degrading bacterium *Shewanella* sp. ANA-3. *Microbiology (Reading, England)*, 169(3).

Krishnakumar R, et al. (2022) OperonSEQer: A set of machine-learning algorithms with threshold voting for detection of operon pairs using short-read RNA-sequencing data. *PLoS computational biology*, 18(1), e1009731.

Krieger MC, et al. (2022) A Peroxide-Responding sRNA Evolved from a Peroxidase mRNA. *Molecular biology and evolution*, 39(2).

Chang SJ, et al. (2022) Typhoid toxin sorting and exocytic transport from *Salmonella* Typhi-infected cells. *eLife*, 11.

Suvorova IA, et al. (2021) Comparative Analysis of the IclR-Family of Bacterial Transcription Factors and Their DNA-Binding Motifs: Structure, Positioning, Co-Evolution, Regulon Content. *Frontiers in microbiology*, 12, 675815.

Kołodziej M, et al. (2021) Lsr2 and Its Novel Parologue Mediate the Adjustment of *Mycobacterium smegmatis* to Unfavorable Environmental Conditions. *mSphere*, 6(3).

Azer K, et al. (2021) History and Future Perspectives on the Discipline of Quantitative Systems Pharmacology Modeling and Its Applications. *Frontiers in physiology*, 12, 637999.

Zangelmi E, et al. (2021) Discovery of a New, Recurrent Enzyme in Bacterial Phosphonate Degradation: (R)-1-Hydroxy-2-aminoethylphosphonate Ammonia-lyase. *Biochemistry*, 60(15), 1214.

Cheon W, et al. (2021) Distinct Transcriptional Programs Underlie Differences in Virulence of Isolates on Host Plants in a Fungal Pathogen, *Colletotrichum gloeosporioides*. *Frontiers in microbiology*, 12, 743776.

Wadie B, et al. (2021) In Silico Characterization of Toxin-Antitoxin Systems in *Campylobacter* Isolates Recovered from Food Sources and Sporadic Human Illness. *Genes*, 12(1).