

# Resource Summary Report

Generated by [kravitz2](#) on Jul 29, 2026

## MicrobesOnline

RRID:SCR\_005507

Type: Tool

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### Proper Citation

MicrobesOnline (RRID:SCR\_005507)

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### Resource Information

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

**Proper Citation:** MicrobesOnline (RRID:SCR\_005507)

**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:** service resource, data or information resource, data analysis service, database, software resource, source code, production service resource, analysis service 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:** 20260729T044124+0000

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## Ratings and Alerts

No rating or validation information has been found for MicrobesOnline.

No alerts have been found for MicrobesOnline.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 156 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [kravitz2](#) .

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.

Giulieri SG, et al. (2025) A multi-hospital, clinician-initiated bacterial genomics programme to investigate treatment failure in severe *Staphylococcus aureus* infections. *Nature communications*, 16(1), 4869.

Ghosh A, et al. (2025) The *Agrobacterium fabrum* efflux pump PecM is produced in response to the plant exudate 4-hydroxybenzaldehyde to avoid disruption of central metabolism. *Journal of bacteriology*, 207(7), e0015025.

Guío J, et al. (2025) Regulatory networks of FUR and NtcA are intertwined by transcriptional regulators, two-component systems, serine/threonine kinases, and sigma factors in *Anabaena* sp. PCC 7120. *mSystems*, 10(7), e0037325.

Abulude IJ, et al. (2025) Using AlphaFold-Multimer to study novel protein-protein interactions of predation essential hypothetical proteins in *Bdellovibrio*. *Frontiers in bioinformatics*, 5, 1566486.

Guío J, et al. (2025) NsrM (AlI0345) and NsrX (Alr1976), two FurC (PerR)-targeted transcriptional regulators, modulate nitrogen metabolism and heterocyst differentiation genes in the cyanobacterium *Anabaena* sp. strain PCC 7120. *Microbiology spectrum*, 13(11), e0231125.

Robin B, et al. (2025) Exploring temperature-dependent transcriptomic adaptations in *Yersinia pestis* using direct cDNA sequencing by Oxford Nanopore Technologies. *Scientific reports*, 15(1), 20564.

Olivan-Muro I, et al. (2025) Towards the control of biofilm formation in *Anabaena* (Nostoc) sp. PCC7120: novel insights into the genes involved and their regulation. *The New phytologist*, 247(4), 1805.

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.

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.

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- $\beta$ -glucan synthases. *PloS one*, 18(6), e0286540.

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

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.

Drousotis 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).

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).

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).