

Resource Summary Report

Generated by [RRID](#) on Sep 10, 2026

MicrobesOnline

RRID:SCR_005507

Type: Tool

Proper Citation

MicrobesOnline (RRID:SCR_005507)

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

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: 20260905T132537+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 166 mentions in open access literature.

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

Revilla-Guarinos A, et al. (2026) Streptococcus dentisani 7746 encodes a cocktail of 14 bacteriocins associated with Com and Blp-like quorum sensing regulatory systems. Journal of oral microbiology, 18(1), 2633915.

Mehlan H, et al. (2026) PneumoWiki: a pan-genome-based database for the pathogen Streptococcus pneumoniae. Microbiology spectrum, 14(4), e0295725.

Dezzani S, et al. (2026) Clostridium beijerinckii displays a soluble [FeFe]-hydrogenase/formate dehydrogenase enzyme complex that links H₂ and CO₂ metabolism. The Biochemical journal, 483(2), 177.

Becerra-Rivera VA, et al. (2026) Divergent and overlapping roles of homospermidine and spermidine in Sinorhizobium meliloti physiology and symbiotic performance. Microbiology (Reading, England), 172(2).

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.

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.

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.

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.

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.

Ong A, et al. (2024) The *Bradyrhizobium japonicum* exporter ExsFGH is involved in efflux of ferric xenosiderophores from the periplasm. *PLoS one*, 19(1), e0296306.

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.

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.

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.

Xi H, et al. (2023) A bacterial spermidine biosynthetic pathway via carboxyaminopropylagmatine. *Science advances*, 9(43), eadj9075.

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.