

Resource Summary Report

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Ensembl Bacteria

RRID:SCR_008679

Type: Tool

Proper Citation

Ensembl Bacteria (RRID:SCR_008679)

Resource Information

URL: <http://bacteria.ensembl.org/index.html>

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Description: The Ensembl Genomes project produces genome databases for important species from across the taxonomic range, using the Ensembl software system. Five sites are now available, one of which is Ensembl Bacteria, which houses bacterial species. All bacterial collections in Ensembl Bacteria have been updated with the latest data from ENA and UniProtKB. New genomes have been added to Escherichia/Shigella (3 additional genomes) and Staphylococcus (3 additional genomes). The mapping of array probes has been expanded to all genomes in the Escherichia/Shigella and Staphylococcus collections. Ensembl Bacteria also now features improved interfaces for selecting regions of circular molecules a new visualisation allowing the large scale comparison of multiple genomes. In multi-synteny view, users can select multiple genomes and observe the syntenic relationships between them. Sponsors: EnsemblBacteria is a project run by EMBL - EBI to maintain annotation on selected genomes, based on the software developed in the Ensembl project developed jointly by the EBI and the Wellcome Trust Sanger Institute.

Synonyms: EnsemblBacteria

Resource Type: data or information resource, database

Keywords: escherichia, array, bacterial, bacterium, circular, database, genome, mapping, molecule, proble, shigella, software, specie, staphyococcus, taxonomic, visualization, FASEB list

Resource Name: Ensembl Bacteria

Resource ID: SCR_008679

Alternate IDs: r3d100011195, nif-0000-33711

Alternate URLs: <https://doi.org/10.17616/R3WD1C>, <https://doi.org/10.17616/R3WD1C>

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Record Last Update: 20260729T044213+0000

Ratings and Alerts

No rating or validation information has been found for Ensembl Bacteria.

No alerts have been found for Ensembl Bacteria.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 78 mentions in open access literature.

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

Werner E, et al. (2025) The role of the LysR-type transcription factor PacR in regulating nitrogen metabolism in *Anabaena* sp. PCC7120. *Physiologia plantarum*, 177(3), e70248.

Royer ALM, et al. (2025) Structural determinants of SlpA-mediated phage recognition in *Clostridioides difficile*. *PLoS pathogens*, 21(11), e1013724.

Riquelme-Barrios S, et al. (2025) Direct RNA sequencing of the *Escherichia coli* epitranscriptome uncovers alterations under heat stress. *Nucleic acids research*, 53(6).

Sawant DV, et al. (2025) *Rickettsia parkeri* hypothetical protein RPATATE_1266, a homolog of exopolyphosphatase/guanosine pentaphosphate phosphohydrolase, regulates tick cell apoptosis. *Microbiology spectrum*, 13(8), e0015125.

Ghatbale P, et al. (2025) In vitro resensitization of multidrug-resistant clinical isolates of *Enterococcus faecium* and *E. faecalis* through phage-antibiotic synergy. *Antimicrobial agents and chemotherapy*, 69(2), e0074024.

Muro EM, et al. (2025) The emergence of eukaryotes as an evolutionary algorithmic phase transition. *Proceedings of the National Academy of Sciences of the United States of America*, 122(13), e2422968122.

Brettner L, et al. (2024) Single-cell heterogeneity in ribosome content and the consequences for the growth laws. *bioRxiv : the preprint server for biology*.

Atay G, et al. (2024) Evolutionary engineering and molecular characterization of cobalt-resistant *Rhodobacter sphaeroides*. *Frontiers in microbiology*, 15, 1412294.

Cyriaque V, et al. (2024) Single-cell RNA sequencing reveals plasmid constrains bacterial population heterogeneity and identifies a non-conjugating subpopulation. *Nature communications*, 15(1), 5853.

Riesco R, et al. (2024) Update on the proposed minimal standards for the use of genome data for the taxonomy of prokaryotes. *International journal of systematic and evolutionary microbiology*, 74(3).

Dias HM, et al. (2024) TH11 Gene Evolutionary Trends: A Comprehensive Plant-Focused Assessment via Data Mining and Large-Scale Analysis. *Genome biology and evolution*, 16(10).

Pan H, et al. (2024) Hopanoid lipids promote soybean-*Bradyrhizobium* symbiosis. *mBio*, 15(4), e0247823.

Ishak S, et al. (2024) Boreal moss-microbe interactions are revealed through metagenome assembly of novel bacterial species. *Scientific reports*, 14(1), 22168.

Can H, et al. (2023) Integration of Meta-Multi-Omics Data Using Probabilistic Graphs and External Knowledge. *Cells*, 12(15).

Jacques F, et al. (2023) Roadmap to the study of gene and protein phylogeny and evolution-A practical guide. *PloS one*, 18(2), e0279597.

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.

Seebach E, et al. (2023) *Staphylococcus aureus* planktonic but not biofilm environment induces an IFN- γ macrophage immune response via the STING/IRF3 pathway. *Virulence*, 14(1), 2254599.

Yates AD, et al. (2022) Ensembl Genomes 2022: an expanding genome resource for non-vertebrates. *Nucleic acids research*, 50(D1), D996.

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.

Esercizio N, et al. (2022) Occurrence of Capnophilic Lactic Fermentation in the Hyperthermophilic Anaerobic Bacterium *Thermotoga* sp. Strain RQ7. *International journal of molecular sciences*, 23(19).