Resource Summary Report

Generated by NIF on May 16, 2025

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: EnsembBacteria 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

Funding:

Resource Name: Ensembl Bacteria

Resource ID: SCR_008679

Alternate IDs: nif-0000-33711

Record Creation Time: 20220129T080248+0000

Record Last Update: 20250507T060632+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 54 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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

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

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) THI1 Gene Evolutionary Trends: A Comprehensive Plant-Focused Assessment via Data Mining and Large-Scale Analysis. Genome biology and evolution, 16(10).

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

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

e0286540.

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.

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

Worthan SB, et al. (2022) The Identity of the Constriction Region of the Ribosomal Exit Tunnel Is Important to Maintain Gene Expression in Escherichia coli. Microbiology spectrum, 10(2), e0226121.

Zhang J, et al. (2022) Response of Fusarium pseudograminearum to Biocontrol Agent Bacillus velezensis YB-185 by Phenotypic and Transcriptome Analysis. Journal of fungi (Basel, Switzerland), 8(8).

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).

Zolfaghari Emameh R, et al. (2021) Application of beta and gamma carbonic anhydrase sequences as tools for identification of bacterial contamination in the whole genome sequence of inbred Wuzhishan minipig (Sus scrofa) annotated in databases. Database : the journal of biological databases and curation, 2021.

Li IC, et al. (2021) Comparison of Conventional Molecular and Whole-Genome Sequencing Methods for Differentiating Salmonella enterica Serovar Schwarzengrund Isolates Obtained from Food and Animal Sources. Microorganisms, 9(10).

McCoubrey LE, et al. (2021) Harnessing machine learning for development of microbiome therapeutics. Gut microbes, 13(1), 1.

Jacob C, et al. (2021) Dual transcriptomic analysis reveals metabolic changes associated with differential persistence of human pathogenic bacteria in leaves of Arabidopsis and lettuce. G3 (Bethesda, Md.), 11(12).

Mahata T, et al. (2021) A phage mechanism for selective nicking of dUMP-containing DNA. Proceedings of the National Academy of Sciences of the United States of America, 118(23).

Song ZM, et al. (2021) Anthraquinones as Potential Antibiofilm Agents Against Methicillin-Resistant Staphylococcus aureus. Frontiers in microbiology, 12, 709826.

Li IC, et al. (2021) Prevalence of IncFIB Plasmids Found among Salmonella enterica Serovar Schwarzengrund Isolates from Animal Sources in Taiwan Using Whole-Genome Sequencing. Pathogens (Basel, Switzerland), 10(8).

Aiewsakun P, et al. (2021) Transcriptional response to the host cell environment of a multidrug-resistant Mycobacterium tuberculosis clonal outbreak Beijing strain reveals its pathogenic features. Scientific reports, 11(1), 3199.

Yuan L, et al. (2021) Evolution and Functional Divergence of SUN Genes in Plants. Frontiers in plant science, 12, 646622.