

Resource Summary Report

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EMGlib - Enhanced Microbial Genomes Library

RRID:SCR_007638

Type: Tool

Proper Citation

EMGlib - Enhanced Microbial Genomes Library (RRID:SCR_007638)

Resource Information

URL: <http://pbil.univ-lyon1.fr/emglib/emglib.html>

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Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented August 22, 2016. A database devoted to the completely sequenced bacterial genomes and the yeast genome. Starting from the sequences available in the "genome" division of GenBank, we have improved and corrected their annotations and structured the flat files using the ACNUC database management system.

Synonyms: EMGlib

Resource Type: data or information resource, database

Keywords: archaea genome, bacterial genome, prokaryotic genome, yeast genome

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: EMGlib - Enhanced Microbial Genomes Library

Resource ID: SCR_007638

Alternate IDs: nif-0000-02796

Record Creation Time: 20220129T080242+0000

Record Last Update: 20260905T133142+0000

Ratings and Alerts

No rating or validation information has been found for EMGlib - Enhanced Microbial Genomes Library.

No alerts have been found for EMGlib - Enhanced Microbial Genomes Library.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 37 mentions in open access literature.

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

Shelton AN, et al. (2025) Abundant and active community members respond to diel cycles in hot spring phototrophic mats. *The ISME journal*, 19(1).

Basik AA, et al. (2024) Genomic insights into *Dactylosporangium* sp. AC04546, a rubber degrader with three latex clearing proteins. *Frontiers in microbiology*, 15, 1378082.

Bernal-Bernal D, et al. (2024) Structural basis for regulation of a CBASS-CRISPR-Cas defense island by a transmembrane anti- σ factor and its ECF σ partner. *Science advances*, 10(43), eadp1053.

Akinyemi MO, et al. (2024) Genomic characterisation of an extended-spectrum β -Lactamase-producing *Klebsiella pneumoniae* isolate assigned to a novel sequence type (6914). *Gut pathogens*, 16(1), 69.

Mayers JR, et al. (2023) Identification and targeting of microbial putrescine acetylation in bloodstream infections. *bioRxiv : the preprint server for biology*.

Brinkmann S, et al. (2022) Genomic and Chemical Decryption of the Bacteroidetes Phylum for Its Potential to Biosynthesize Natural Products. *Microbiology spectrum*, 10(3), e0247921.

Mackelprang R, et al. (2022) Adaptation to Environmental Extremes Structures Functional Traits in Biological Soil Crust and Hypolithic Microbial Communities. *mSystems*, 7(4), e0141921.

Zamkovaya T, et al. (2021) A network approach to elucidate and prioritize microbial dark matter in microbial communities. *The ISME journal*, 15(1), 228.

Rajakovich LJ, et al. (2021) Elucidation of an anaerobic pathway for metabolism of L-carnitine-derived β -butyrobetaine to trimethylamine in human gut bacteria. *Proceedings of the National Academy of Sciences of the United States of America*, 118(32).

Gonzalez JM, et al. (2020) On a Non-Discrete Concept of Prokaryotic Species. *Microorganisms*, 8(11).

Wang JH, et al. (2020) Genomic investigation of emerging zoonotic pathogen *Shewanella xiamenensis*. *Ci ji yi xue za zhi = Tzu-chi medical journal*, 32(2), 162.

Nowinski B, et al. (2019) Microbial metagenomes and metatranscriptomes during a coastal phytoplankton bloom. *Scientific data*, 6(1), 129.

Uritskiy G, et al. (2019) Applying Genome-Resolved Metagenomics to Deconvolute the Halophilic Microbiome. *Genes*, 10(3).

Cole BK, et al. (2019) Antibiotic resistance and molecular characterization of bacteremia *Escherichia coli* isolates from newborns in the United States. *PloS one*, 14(7), e0219352.

Fernandez-Garcia L, et al. (2018) Relationship Between the Quorum Network (Sensing/Quenching) and Clinical Features of Pneumonia and Bacteraemia Caused by *A. baumannii*. *Frontiers in microbiology*, 9, 3105.

Borton MA, et al. (2018) Coupled laboratory and field investigations resolve microbial interactions that underpin persistence in hydraulically fractured shales. *Proceedings of the National Academy of Sciences of the United States of America*, 115(28), E6585.

Lee JH, et al. (2018) Genomic insights into *Staphylococcus equorum* KS1039 as a potential starter culture for the fermentation of high-salt foods. *BMC genomics*, 19(1), 136.

Adamek M, et al. (2018) Comparative genomics reveals phylogenetic distribution patterns of secondary metabolites in *Amycolatopsis* species. *BMC genomics*, 19(1), 426.

Rath S, et al. (2017) Uncovering the trimethylamine-producing bacteria of the human gut microbiota. *Microbiome*, 5(1), 54.

Cole BK, et al. (2017) Route of infection alters virulence of neonatal septicemia *Escherichia coli* clinical isolates. *PloS one*, 12(12), e0189032.