

Resource Summary Report

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MBGD - Microbial Genome Database

RRID:SCR_012824

Type: Tool

Proper Citation

MBGD - Microbial Genome Database (RRID:SCR_012824)

Resource Information

URL: <http://mbgd.genome.ad.jp/>

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Description: MBGD is a database for comparative analysis of completely sequenced microbial genomes, the number of which is now growing rapidly. The aim of MBGD is to facilitate comparative genomics from various points of view such as ortholog identification, paralog clustering, motif analysis and gene order comparison. The heart of MBGD function is to create orthologous or homologous gene cluster table. For this purpose, similarities between all genes are precomputed and stored into the database, in addition to the annotations of genes such as function categories that were assigned by the original authors and motifs that were found in the translated sequence. Using these homology data, MBGD dynamically creates orthologous gene cluster table. Users can change a set of organisms or cutoff parameters to create their own orthologous grouping. Based on this cluster table, users can further analyze multiple genomes from various points of view with the functions such as global map comparison, local map comparison, multiple sequence alignment and phylogenetic tree construction.

Synonyms: MBGD

Resource Type: data or information resource, database

Keywords: bio.tools, FASEB list

Resource Name: MBGD - Microbial Genome Database

Resource ID: SCR_012824

Alternate IDs: nif-0000-03105, biotools:mbgd

Alternate URLs: <https://bio.tools/mbgd>

Record Creation Time: 20220129T080312+0000

Ratings and Alerts

No rating or validation information has been found for MBGD - Microbial Genome Database.

No alerts have been found for MBGD - Microbial Genome Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 62 mentions in open access literature.

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

Jeong H, et al. (2026) Data-driven classification of Escherichia coli using protein language model ascertains O-serotype determining genes. Scientific reports, 16(1).

Yoshida S, et al. (2025) Towards molecular evolutionary epigenomics with an expanded nucleotide code involving methylated bases. DNA research : an international journal for rapid publication of reports on genes and genomes, 32(6).

Sarton-Loh??ac G, et al. (2025) Reconstructing Evolutionary Histories with Hierarchical Orthologous Groups. Journal of molecular evolution, 93(6), 740.

Tao T, et al. (2024) Conservation genomic investigation of an endangered conifer, Thuja sutchuenensis, reveals low genetic diversity but also low genetic load. Plant diversity, 46(1), 78.

Pasternak Z, et al. (2022) Identifying protein function and functional links based on large-scale co-occurrence patterns. PloS one, 17(3), e0264765.

Yang H, et al. (2022) Genomic insights into the genotype-environment mismatch and conservation units of a Qinghai-Tibet Plateau endemic cypress under climate change. Evolutionary applications, 15(6), 919.

Laursen MF, et al. (2021) Bifidobacterium species associated with breastfeeding produce aromatic lactic acids in the infant gut. Nature microbiology, 6(11), 1367.

Cassier-Chauvat C, et al. (2021) Genetic, Genomics, and Responses to Stresses in Cyanobacteria: Biotechnological Implications. Genes, 12(4).

Wu Z, et al. (2021) Microbial production of small peptide: pathway engineering and synthetic biology. Microbial biotechnology, 14(6), 2257.

Elzeki OM, et al. (2021) COVID-19: a new deep learning computer-aided model for classification. PeerJ. Computer science, 7, e358.

Okubo T, et al. (2021) The physiological potential of anammox bacteria as revealed by their core genome structure. DNA research : an international journal for rapid publication of reports on genes and genomes, 28(1).

Ramchandrar N, et al. (2020) Diagnosis of cytomegalovirus infection from clinical whole genome sequencing. Scientific reports, 10(1), 11020.

Li H, et al. (2020) Analysis of the pattern recognition algorithm of broadband satellite modulation signal under deformable convolutional neural networks. PloS one, 15(7), e0234068.

Sirand-Pugnet P, et al. (2020) Reductive Evolution and Diversification of C5-Uracil Methylation in the Nucleic Acids of Mollicutes. Biomolecules, 10(4).

Tian L, et al. (2020) Deciphering functional redundancy in the human microbiome. Nature communications, 11(1), 6217.

Lu Z, et al. (2020) A New In-Flight Alignment Method with an Application to the Low-Cost SINS/GPS Integrated Navigation System. Sensors (Basel, Switzerland), 20(2).

Li J, et al. (2020) Contents, Construction Methods, Data Resources, and Functions Comparative Analysis of Bacteria Databases. International journal of biological sciences, 16(5), 838.

Montero-Blay A, et al. (2020) Inferring Active Metabolic Pathways from Proteomics and Essentiality Data. Cell reports, 31(9), 107722.

Jackson LK, et al. (2020) Helicobacter pylori diversification during chronic infection within a single host generates sub-populations with distinct phenotypes. PLoS pathogens, 16(12), e1008686.

Liu B, et al. (2020) Identification of Genome Sequences of Polyphosphate-Accumulating Organisms by Machine Learning. Frontiers in cell and developmental biology, 8, 626221.