

Resource Summary Report

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Genomes Online Database

RRID:SCR_002817

Type: Tool

Proper Citation

Genomes Online Database (RRID:SCR_002817)

Resource Information

URL: <http://www.genomesonline.org/>

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Description: Database of information regarding genome and metagenome sequencing projects, and their associated metadata, around the world. It also provides information related to organism properties such as phenotype, ecotype and disease. Both complete and ongoing projects, along with their associated metadata, can be accessed. Users can also register, annotate and publish genome and metagenome data.

Abbreviations: GOLD

Synonyms: Genomes On Line Database (GOLD), GOLD:Genomes Online Database

Resource Type: data or information resource, data repository, database, service resource, storage service resource

Defining Citation: [PMID:22135293](#), [PMID:19914934](#), [PMID:17981842](#), [PMID:16381880](#), [PMID:11125068](#), [PMID:10498782](#)

Keywords: genome, genetics, metagenome, biosample, phenotype, ecotype, disease, sequencing, FASEB list

Availability: Free, Freely available, Available for download

Resource Name: Genomes Online Database

Resource ID: SCR_002817

Alternate IDs: r3d100010808, nif-0000-02918

Alternate URLs: <https://doi.org/10.17616/R39310>

Record Creation Time: 20220129T080215+0000

Ratings and Alerts

No rating or validation information has been found for Genomes Online Database.

No alerts have been found for Genomes Online Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 161 mentions in open access literature.

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

Antequera-Zambrano L, et al. (2025) Distribution of Genetic Determinants Associated with CRISPR-Cas Systems and Resistance to Antibiotics in the Genomes of Archaea and Bacteria. *Microorganisms*, 13(6).

Gao J, et al. (2023) Establishment, optimization, and application of genetic technology in *Aspergillus* spp. *Frontiers in microbiology*, 14, 1141869.

Parra-Sánchez Á, et al. (2023) Comparative Analysis of CRISPR-Cas Systems in *Pseudomonas* Genomes. *Genes*, 14(7).

Ebner JN, et al. (2021) Trends in the Application of "Omics" to Ecotoxicology and Stress Ecology. *Genes*, 12(10).

Crump BC, et al. (2018) Metatranscriptomics and Amplicon Sequencing Reveal Mutualisms in Seagrass Microbiomes. *Frontiers in microbiology*, 9, 388.

Choby JE, et al. (2018) *Staphylococcus aureus* HemX Modulates Glutamyl-tRNA Reductase Abundance To Regulate Heme Biosynthesis. *mBio*, 9(1).

Li P, et al. (2018) Activation of three natural product biosynthetic gene clusters from *Streptomyces lavendulae* CGMCC 4.1386 by a reporter-guided strategy. *Synthetic and systems biotechnology*, 3(4), 254.

Zhu C, et al. (2017) Genomic and transcriptomic analyses reveal distinct biological functions for cold shock proteins (VpaCspA and VpaCspD) in *Vibrio parahaemolyticus* CHN25 during low-temperature survival. *BMC genomics*, 18(1), 436.

Ward CP, et al. (2017) Photochemical alteration of organic carbon draining permafrost soils shifts microbial metabolic pathways and stimulates respiration. *Nature communications*, 8(1), 772.

Solís-Guzmán MG, et al. (2017) Expression analysis of the *Arabidopsis thaliana* AtSpen2 gene, and its relationship with other plant genes encoding Spen proteins. *Genetics and molecular biology*, 40(3), 643.

Poehlein A, et al. (2017) The Draft Genome of the Non-Host-Associated *Methanobrevibacter arboriphilus* Strain DH1 Encodes a Large Repertoire of Adhesin-Like Proteins. *Archaea (Vancouver, B.C.)*, 2017, 4097425.

Sipler RE, et al. (2017) Microbial Community Response to Terrestrially Derived Dissolved Organic Matter in the Coastal Arctic. *Frontiers in microbiology*, 8, 1018.

Parages ML, et al. (2016) Integrated (Meta) Genomic and Synthetic Biology Approaches to Develop New Biocatalysts. *Marine drugs*, 14(3).

Dobrijevic D, et al. (2016) Functional Comparison of Bacteria from the Human Gut and Closely Related Non-Gut Bacteria Reveals the Importance of Conjugation and a Paucity of Motility and Chemotaxis Functions in the Gut Environment. *PloS one*, 11(7), e0159030.

Cao Y, et al. (2016) RevEcoR: an R package for the reverse ecology analysis of microbiomes. *BMC bioinformatics*, 17(1), 294.

Behzadi P, et al. (2016) Microarray long oligo probe designing for *Escherichia coli*: an in-silico DNA marker extraction. *Central European journal of urology*, 69(1), 105.

Verneau J, et al. (2016) MG-Digger: An Automated Pipeline to Search for Giant Virus-Related Sequences in Metagenomes. *Frontiers in microbiology*, 7, 428.

Esser D, et al. (2016) Protein phosphorylation and its role in archaeal signal transduction. *FEMS microbiology reviews*, 40(5), 625.

Eloe-Fadrosh EA, et al. (2016) Global metagenomic survey reveals a new bacterial candidate phylum in geothermal springs. *Nature communications*, 7, 10476.

Perez-Garcia O, et al. (2016) Metabolic Network Modeling of Microbial Interactions in Natural and Engineered Environmental Systems. *Frontiers in microbiology*, 7, 673.