

Resource Summary Report

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Plasmid Genome Database

RRID:SCR_008228

Type: Tool

Proper Citation

Plasmid Genome Database (RRID:SCR_008228)

Resource Information

URL: <http://www.ebi.ac.uk/genomes/plasmid.html>

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Description: The Plasmid Genome Database aims to collate biological and genomic data for all bacterial plasmids in the hopes of enabling rapid, interrogation of both meta- and genomic data. Data maintained includes access to all plasmid genomes and information on core genomic features obtained from parsing the original EMBL/DDBJ/NCBI submission. In addition a suite of third party analyses has been performed for each genome to supplement the original annotation. This site also links to Genome Atlases provided by the Centre for Biological Sequence Analysis (CBS). The motivation behind the construction of this site derived from observations from genome sequencing projects: the abundance and inferred importance of the horizontal gene pool (HGP) in bacterial adaptation and evolution. In so far as plasmids are autonomously replicating, extrachromosomal elements they are a readily identifiable and accessible component of the HGP. Also plasmids have been identified in almost all bacterial divisions, ranging in size from less than 2 kbp to > 1.5 Mbp and as such represent a defined, yet diverse and complex sample of genes in the HGP.

Synonyms: PGD

Resource Type: data or information resource, database

Keywords: element, evolution, extrachromosomal, gene, adaptation, atlas, autonomous, bacterial, biological, division, genome, genomic, hgp, plasmid, pool, prokaryote databases, replicate

Resource Name: Plasmid Genome Database

Resource ID: SCR_008228

Alternate IDs: nif-0000-21323

Old URLs: <http://www.genomics.ceh.ac.uk/plasmidddb/>

Record Creation Time: 20220129T080246+0000

Record Last Update: 20260729T044205+0000

Ratings and Alerts

No rating or validation information has been found for Plasmid Genome Database.

No alerts have been found for Plasmid Genome Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 21 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Qin S, et al. (2025) Complete genome sequence of *Bacillus subtilis* GL-4. Microbiology resource announcements, 14(2), e0055024.

Wackett LP, et al. (2023) Plasmids in environmental microbes: An annotated selection of World Wide Web sites relevant to the topics in environmental microbiology. Environmental microbiology reports, 15(6), 820.

Sun X, et al. (2023) Metabolic interactions affect the biomass of synthetic bacterial biofilm communities. mSystems, 8(6), e0104523.

Liu JY, et al. (2023) Proposal to classify *Ralstonia solanacearum* phylotype I strains as *Ralstonia nicotianae* sp. nov., and a genomic comparison between members of the genus *Ralstonia*. Frontiers in microbiology, 14, 1135872.

Sun X, et al. (2022) *Bacillus velezensis* stimulates resident rhizosphere *Pseudomonas stutzeri* for plant health through metabolic interactions. The ISME journal, 16(3), 774.

Andreopoulos WB, et al. (2022) Deeplasmid: deep learning accurately separates plasmids from bacterial chromosomes. Nucleic acids research, 50(3), e17.

Li J, et al. (2022) Cultured Bacteria Provide Insight into the Functional Potential of the Coral-Associated Microbiome. mSystems, 7(4), e0032722.

Xu P, et al. (2021) Analysis of the Taxonomy and Pathogenic Factors of *Pectobacterium aroidearum* L6 Using Whole-Genome Sequencing and Comparative Genomics. Frontiers in microbiology, 12, 679102.

Ye Y, et al. (2020) Discovery of Three 22-Membered Macrolides by Deciphering the Streamlined Genome of Mangrove-Derived *Streptomyces* sp. HM190. *Frontiers in microbiology*, 11, 1464.

Zou J, et al. (2020) Genome Sequence of *Klebsiella pneumoniae* YBQ, a Clinical Strain Isolated from the Sputum of a Patient with Severe Pneumonia. *Microbiology resource announcements*, 9(47).

Pu N, et al. (2020) Complete genome sequence of *Neptunomonas concharum* JCM17730T: An acetate assimilating bacterium isolated from a dead ark clam. *Marine genomics*, 53, 100754.

Bradley P, et al. (2019) Ultrafast search of all deposited bacterial and viral genomic data. *Nature biotechnology*, 37(2), 152.

Liang CY, et al. (2019) Genomic Features, Comparative Genomic Analysis, and Antimicrobial Susceptibility Patterns of *Chryseobacterium arthrosphaerae* Strain ED882-96 Isolated in Taiwan. *Genes*, 10(4).

Wu Y, et al. (2019) Microevolution within ST11 group *Clostridioides difficile* isolates through mobile genetic elements based on complete genome sequencing. *BMC genomics*, 20(1), 796.

Ai L, et al. (2019) Complete Genome Sequence of the Ebosin-Producing Strain *Streptomyces* sp. 139. *Microbiology resource announcements*, 8(49).

Liao W, et al. (2019) Complete Genome of the Chitin-Degrading Bacterium, *Paenibacillus xylanilyticus* W4. *Genome biology and evolution*, 11(11), 3252.

Sharma G, et al. (2016) Complete Genome of the Starch-Degrading Myxobacteria *Sandaracinus amylolyticus* DSM 53668T. *Genome biology and evolution*, 8(8), 2520.

Zolfaghari Emameh R, et al. (2016) Horizontal transfer of α -carbonic anhydrase genes from prokaryotes to protozoans, insects, and nematodes. *Parasites & vectors*, 9, 152.

Garrett RA, et al. (2015) CRISPR-Cas Adaptive Immune Systems of the Sulfolobales: Unravelling Their Complexity and Diversity. *Life (Basel, Switzerland)*, 5(1), 783.

Hamidian M, et al. (2014) A GC1 *Acinetobacter baumannii* isolate carrying AbaR3 and the aminoglycoside resistance transposon TnaphA6 in a conjugative plasmid. *The Journal of antimicrobial chemotherapy*, 69(4), 955.