

Resource Summary Report

Generated by SPARC SAWG on Aug 30, 2026

NCBI Genome

RRID:SCR_002474

Type: Tool

Proper Citation

NCBI Genome (RRID:SCR_002474)

Resource Information

URL: <http://www.ncbi.nlm.nih.gov/genome>

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Description: Database that organizes information on genomes including sequences, maps, chromosomes, assemblies, and annotations in six major organism groups: Archaea, Bacteria, Eukaryotes, Viruses, Viroids, and Plasmids. Genomes of over 1,200 organisms can be found in this database, representing both completely sequenced organisms and those for which sequencing is in progress. Users can browse by organism, and view genome maps and protein clusters. Links to other prokaryotic and archaeal genome projects, as well as BLAST tools and access to the rest of the NCBI online resources are available.

Abbreviations: Genome

Synonyms: Entrez Genomes, Entrez Genome, NCBI, Genome, Genome Database, Genome: Information by genome sequence

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

Keywords: chromosome, organelle, plasmid, viroid, virus, genome, sequence, map, assembly, annotation, gene mapping, dna, blast, protein cluster, gold standard

Availability: Free, Freely available

Resource Name: NCBI Genome

Resource ID: SCR_002474

Alternate IDs: nif-0000-02802, r3d100010785

Alternate URLs: <http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=Genome>, <https://doi.org/10.17616/R3R89S>

Record Creation Time: 20220129T080213+0000

Record Last Update: 20260829T182121+0000

Ratings and Alerts

No rating or validation information has been found for NCBI Genome.

No alerts have been found for NCBI Genome.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 618 mentions in open access literature.

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

Black JJ, et al. (2026) The Legionella pneumophila effector SidL is an adenylyltransferase that modifies the glycolytic intermediate 3-phosphoglycerate. Molecular cell.

Jothi R, et al. (2026) New genotyping method for Escherichia coli using RSXC repeat polymorphism and gene-neighborhood architecture. BMC genomics, 27(1).

Sun Y, et al. (2026) Diversity Patterns of Domestic Herbivore Viruses in China Reveal Transmission Dynamics with Disease Management Implications. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(32), e17444.

Cheng X, et al. (2026) Comparative Genomics Analysis Reveals the Genomic Basis of S8 Proteases, CAZymes, and Secondary Metabolism Associated with Nematode Biocontrol in Purpureocillium lilacinum. International journal of molecular sciences, 27(11).

Ji R, et al. (2026) GdbMTB: a manually curated genomic database of magnetotactic bacteria. Database : the journal of biological databases and curation, 2026.

Khanal Pokharel S, et al. (2026) Establishing conserved biosynthetic gene clusters of the phylum Myxococcota. Applied and environmental microbiology, 92(1), e0215125.

Strunecký O, et al. (2026) To multicellularity and back again: Description of two new coccoid genera (Portococcus gen. nov. and Pseudanabaenococcus gen. nov.) in the basal "filamentous" order Pseudanabaenales, Cyanobacteria. Journal of phycology, 62(1), 234.

Goto T, et al. (2026) Cyclophilin A-mediated cis/trans isomerization modulates RIN4 to control intracellular rhizobial infection in legumes. The New phytologist, 250(6), 3932.

Liu R, et al. (2026) Functional Characterization of Fad Genes from Two Chemosymbiotic Bivalves Inhabiting the Haima Cold Seep. Genes, 17(6).

Huang YT, et al. (2026) Genome diversification of symbiotic fungi in beetle-fungus mutualistic symbioses. *The ISME journal*, 20(1).

Qabar CM, et al. (2026) Leveraging a synthetic biology approach to enhance BCG-mediated expansion of V α 9V β 2 T cells. *PloS one*, 21(4), e0343925.

Awad MM, et al. (2026) Comparative genomic analysis of RNA-binding proteins across some drug resistant and sensitive *Staphylococcus aureus*. *Applied microbiology and biotechnology*, 110(1).

Wu M, et al. (2026) Epitranscriptomic RNA editing resolves Mus81 DNA repair tradeoffs in heat tolerance and meiosis. *Nature communications*, 17(1).

Weremczuk A, et al. (2026) Functional and biosynthetic investigation of polyisoprenoids in roses leaves. *Planta*, 263(2), 54.

Kim J, et al. (2026) Complete genome and functional insights into *Microbacterium* sp. strain FBCC-B4120, a novel freshwater isolate with diverse biotechnological traits. *PloS one*, 21(5), e0347549.

Khan MAS, et al. (2026) Clonal spread of multidrug-resistant *Salmonella* Kentucky ST198 in poultry market environments in Dhaka city, Bangladesh. *PloS one*, 21(4), e0342231.

Köffer J, et al. (2026) Comparative evaluation of two MALDI-TOF MS systems for microbial identification: accuracy and workflow efficiency in a clinical microbiology laboratory. *Microbiology spectrum*, 14(3), e0298125.

Liu H, et al. (2026) Functional Characterisation of HAIRPLUS (NtHAP) Genes Involved in Trichome Development and Specialised Metabolism of Tobacco. *Plant biotechnology journal*, 24(7), 4640.

Stephenson MJ, et al. (2026) Large-scale mining of plant genomes unlocks the diversity of oxidosqualene cyclases. *Nature chemical biology*, 22(2), 249.

Fonton P, et al. (2026) Epidemiological and Molecular Surveillance of Multiresistant *Citrobacter freundii* Complex in a Tertiary Care Hospital: A Retrospective Cohort Study. *The Journal of infectious diseases*, 233(5), e1181.