

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 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>

Proper Citation: NCBI Genome (RRID:SCR_002474)

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, storage service resource, database, 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: 20260801T042524+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 577 mentions in open access literature.

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

Fogg LG, et al. (2026) The visual system of the longest-living vertebrate, the Greenland shark. Nature communications, 17(1), 39.

Turner LA, et al. (2025) Differences in gene expression between high and low tolerance rainbow trout (*Oncorhynchus mykiss*) to acute thermal stress. PloS one, 20(1), e0312694.

Fierro Morales JC, et al. (2025) Reduced cell-substrate adhesion formation promotes cell migration in *Dictyostelium*. Molecular biology of the cell, 36(8), ar98.

Megrian D, et al. (2025) Evolutionary plasticity and functional repurposing of the essential metabolic enzyme MoeA. Communications biology, 8(1), 49.

Alvarez-Ponce D, et al. (2025) Organismal complexity strongly correlates with the number of protein families and domains. Proceedings of the National Academy of Sciences of the United States of America, 122(5), e2404332122.

Ha YJ, et al. (2025) Molecular characterization of *Pseudomyxoma peritonei* with single-cell and bulk RNA sequencing. Scientific data, 12(1), 213.

Pradal I, et al. (2025) The production of esters by specific sourdough lactic acid bacteria species is limited by the precursor concentrations. Applied and environmental microbiology, 91(3), e0221624.

Kidd SE, et al. (2025) *Sporothrix davidellisii* : A new pathogenic species belonging to the *Sporothrix pallida* complex. Medical mycology, 63(4).

Wang R, et al. (2025) Combining whole genome and transcriptome sequencing to analyze the pathogenic mechanism of *Diplodia sapinea* blight in *Pinus sylvestris* var. *mongolica* Litv. Virulence, 16(1), 2490216.

Bartas M, et al. (2025) CpX Hunter web tool allows high-throughput identification of CpG, CpA, CpT, and CpC islands: A case study in *Drosophila* genome. *The Journal of biological chemistry*, 301(6), 108537.

Sui Y, et al. (2025) Viral hijacking of host DDX60 promotes Crimean-Congo haemorrhagic fever virus replication via G-quadruplex unwinding. *PLoS pathogens*, 21(6), e1013278.

Chen YC, et al. (2025) Optimization of Metagenomic Next-Generation Sequencing Workflow with a Novel Host Depletion Method for Enhanced Pathogen Detection. *Molecular diagnosis & therapy*, 29(5), 689.

Gong X, et al. (2025) Chromosome-level genome assembly of *Iodes seguinii* and its metabonomic implications for rheumatoid arthritis treatment. *The plant genome*, 18(1), e20534.

Tosiano MA, et al. (2025) Roles of P-body factors in *Candida albicans* filamentation and stress response. *bioRxiv : the preprint server for biology*.

Khalaf A, et al. (2025) Forty new genomes shed light on sexual reproduction and the origin of tetraploidy in *Microsporidia*. *PLoS biology*, 23(10), e3003446.

Du LF, et al. (2025) Genome-resolved metagenomics reveals microbiome diversity across 48 tick species. *Nature microbiology*, 10(10), 2631.

Ao P, et al. (2025) Transcriptomic and Metabolic Profiles of Apple Peels of Different Colors. *Plants (Basel, Switzerland)*, 14(21).

Luque-Jimenez E, et al. (2025) Discovery of a bacteriophage sequence in a mite genome assembly reveals bacterial contamination and opens new possibilities for exploring arthropod symbionts. *Microbial genomics*, 11(10).

Shirsath A, et al. (2025) Hidden Markov Model-Based Prokaryotic Genome Space Mining Reveals the Widespread Pervasiveness of Complex I and Its Potential Evolutionary Scheme. *Genome biology and evolution*, 17(8).

Han C, et al. (2025) Omic AI reveals new autophagy regulators from the Atg1 interactome in *Saccharomyces cerevisiae*. *Frontiers in cell and developmental biology*, 13, 1554958.