

Resource Summary Report

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NCBI Assembly Archive Viewer

RRID:SCR_012917

Type: Tool

Proper Citation

NCBI Assembly Archive Viewer (RRID:SCR_012917)

Resource Information

URL: <https://www.ncbi.nlm.nih.gov/assembly>

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Description: Database providing information on structure of assembled genomes, assembly names and other meta-data, statistical reports, and links to genomic sequence data. The Archive links the raw sequence information found in the Trace Archive with assembly information found in publicly available sequence repositories (GenBank/EMBL/DDBJ).

Abbreviations: NCBI Assembly Archive Viewer

Synonyms: Assembly Archive Viewer, NCBI Assembly, Assembly

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

Keywords: sequence alignment, sequence chromatogram, assembly, virus

Resource Name: NCBI Assembly Archive Viewer

Resource ID: SCR_012917

Alternate IDs: OMICS_00890, r3d100012688

Alternate URLs: <http://www.ncbi.nlm.nih.gov/assembly>,
<https://doi.org/10.17616/R31NJMA8>

Old URLs: <http://www.ncbi.nlm.nih.gov/Traces/assembly/assmbrowser.cgi>

Record Creation Time: 20220129T080313+0000

Record Last Update: 20260821T194004+0000

Ratings and Alerts

No rating or validation information has been found for NCBI Assembly Archive Viewer.

No alerts have been found for NCBI Assembly Archive Viewer.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 313 mentions in open access literature.

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

Valente R, et al. (2026) Parallel Erosion of a Testis-Specific Na⁺/K⁺ ATPase in Three Mammalian Lineages Sheds Light into the Evolution of Spermatozoa Energetics. *Genome biology and evolution*, 18(2).

Lee J, et al. (2026) MlrROR release 02: Expanded and refined 16S-ITS-23S rRNA operon dataset. *Scientific data*, 13(1).

Xia Z, et al. (2026) Pan-Genome Analysis and Expression Profiling of HIPP Gene Family in Cassava. *Genes*, 17(2).

Layana L, et al. (2026) Causes and consequences of sex-chromosome turnovers in Diptera. *Evolution letters*, 10(3), 253.

Wang X, et al. (2026) Colonic Engyodontium fungus triggers neutrophil antimicrobial activity to suppress *Lactobacillus johnsonii*-derived glutamic acid-maintained Tregs. *The Journal of clinical investigation*, 136(8).

Lo G, et al. (2026) Metabolism of ??-mannans by representative, understudied Bacillota species from the human colon. *FEMS microbiology ecology*, 102(7).

Hwang CY, et al. (2025) Genome-based classification of *Halonovum salinarum* gen. nov., sp. nov., and *Halonovum rutilum* sp. nov., two novel halophilic archaea isolated from a solar saltern. *BMC microbiology*, 26(1), 6.

Gerbec ZJ, et al. (2025) Identification of intratumoral bacteria that enhance breast tumor metastasis. *mBio*, 16(3), e0359524.

Gonzalez-Garcia LN, et al. (2025) Genetic diversity and comparative genomics across *Leishmania* (Viannia) species. *Communications biology*, 8(1), 925.

Yang M, et al. (2025) Genomic insights into the domestication and genetic basis of yield in papaya. *Horticulture research*, 12(5), uhaf045.

Li H, et al. (2025) Reactive oxygen species mediate bioeffects of static magnetic field via impairment of long-chain fatty acid degradation in *Escherichia coli*. *Frontiers in microbiology*, 16, 1586233.

Leon-Sampedro R, et al. (2025) Multi-layered ecological interactions determine growth of clinical antibiotic-resistant strains within human microbiomes. *Nature communications*, 16(1), 9733.

Leibler C, et al. (2025) Divergent TIR signaling domains in TLR7 and TLR9 control opposing effects on systemic autoimmunity. *The Journal of clinical investigation*, 135(21).

Wang Y, et al. (2025) A global atlas and drivers of antimicrobial resistance in *Salmonella* during 1900-2023. *Nature communications*, 16(1), 4611.

Newstead L, et al. (2025) Genomic characterization of *Pseudomonas aeruginosa* from canine otitis highlights the need for a One Health approach to this opportunistic pathogen. *Microbial genomics*, 11(5).

Guo X, et al. (2025) Pangenome-scale annotation of mycobacteriophages for dissecting phage-host interactions based on a sequence clustering and structural homology analysis strategy. *mSystems*, 10(8), e0050825.

Han C, et al. (2025) Machine learning based on pangenome-wide association studies reveals the impact of host source on the zoonotic potential of closely related bacterial pathogens. *Communications biology*, 8(1), 1253.

Antoine R, et al. (2025) Multinuclear non-haem iron-dependent oxidative enzymes: landscape of their substrates, partner proteins and biosynthetic gene clusters. *Microbial genomics*, 11(7).

Dagliesh C, et al. (2025) An ultra-conserved poison exon in the *Tra2b* gene encoding a splicing activator is essential for male fertility and meiotic cell division. *The EMBO journal*, 44(3), 877.

Ametrano CG, et al. (2025) UnFATE: A Comprehensive Probe Set and Bioinformatics Pipeline for Phylogeny Reconstruction and Multilocus Barcoding of Filamentous Ascomycetes (Ascomycota, Pezizomycotina). *Systematic biology*, 74(5), 740.