Resource Summary Report

Generated by NIF on May 7, 2025

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

Proper Citation: NCBI Assembly Archive Viewer (RRID:SCR_012917)

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 set, data or information resource, service resource, data repository, storage service resource

Keywords: sequence alignment, sequence chromatogram, assembly, virus

Funding:

Resource Name: NCBI Assembly Archive Viewer

Resource ID: SCR_012917

Alternate IDs: OMICS_00890

Alternate URLs: http://www.ncbi.nlm.nih.gov/assembly

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

Record Creation Time: 20220129T080313+0000

Record Last Update: 20250507T060856+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 258 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Farrell AA, et al. (2025) Bacterial Growth Temperature as a Horizontally Acquired Polygenic Trait. Genome biology and evolution, 17(1).

Maul JE, et al. (2025) Genomic and mutational analysis of Pseudomonas syringae pv. tagetis EB037 pathogenicity on sunflower. BMC microbiology, 25(1), 43.

Zheng X, et al. (2024) Diverse non-canonical electron bifurcating [FeFe]-hydrogenases of separate evolutionary origins in Hydrogenedentota. mSystems, 9(9), e0099924.

Burcham ZM, et al. (2024) Comparative genomic analysis of an emerging Pseudomonadaceae member, Thiopseudomonas alkaliphila. Microbiology spectrum, 12(8), e0415723.

Rojas-Vargas J, et al. (2024) A comparative genomic study of a hydrocarbon-degrading marine bacterial consortium. PloS one, 19(8), e0303363.

Liu W, et al. (2024) Isolation and identification of uric acid-dependent Aciduricibacillus chroicocephali gen. nov., sp. nov. from seagull feces and implications for hyperuricemia treatment. mSphere, 9(6), e0002524.

Sidorczuk K, et al. (2024) adhesiomeR: a tool for Escherichia coli adhesin classification and analysis. BMC genomics, 25(1), 609.

Wang H, et al. (2024) Pangenome analysis of Shewanella xiamenensis revealed important genetic traits concerning genetic diversity, pathogenicity and antibiotic resistance. BMC genomics, 25(1), 216.

Butt M, et al. (2024) Shewanella phaeophyticola sp. nov. and Vibrio algarum sp. nov., isolated from marine brown algae. International journal of systematic and evolutionary microbiology, 74(5).

Tomasch J, et al. (2024) On the evolution of chromosomal regions with high gene strand bias in bacteria. mBio, 15(6), e0060224.

Niimura Y, et al. (2024) Synchronized Expansion and Contraction of Olfactory, Vomeronasal, and Taste Receptor Gene Families in Hystricomorph Rodents. Molecular biology and evolution, 41(4).

Rimal B, et al. (2024) Bile salt hydrolase catalyses formation of amine-conjugated bile acids. Nature, 626(8000), 859.

Yang Z, et al. (2024) Genome-wide association study reveals serovar-associated genetic loci in Riemerella anatipestifer. BMC genomics, 25(1), 57.

Xu YH, et al. (2024) Evolutionary Modes of wtf Meiotic Driver Genes in Schizosaccharomyces pombe. Genome biology and evolution, 16(10).

Bian P, et al. (2024) A Graph-based Goat Pangenome Reveals Structural Variations Involved in Domestication and Adaptation. Molecular biology and evolution, 41(12).

Barroso RA, et al. (2024) Evolutionary Analysis of Cnidaria Small Cysteine-Rich Proteins (SCRiPs), an Enigmatic Neurotoxin Family from Stony Corals and Sea Anemones (Anthozoa: Hexacorallia). Toxins, 16(2).

Guerrero-Egido G, et al. (2024) bacLIFE: a user-friendly computational workflow for genome analysis and prediction of lifestyle-associated genes in bacteria. Nature communications, 15(1), 2072.

Gao X, et al. (2024) The P10K database: a data portal for the protist 10 000 genomes project. Nucleic acids research, 52(D1), D747.

Kogay R, et al. (2024) Co-evolution of gene transfer agents and their alphaproteobacterial hosts. Journal of bacteriology, 206(2), e0039823.

Kajdanek A, et al. (2024) A Rapid and Inexpensive PCR Test for Mastitis Diagnosis Based on NGS Data. Pathogens (Basel, Switzerland), 13(5).