Resource Summary Report

Generated by NIF on May 14, 2025

NCBI GenBank via FTP

RRID:SCR_010535
Type: Tool

Proper Citation

NCBI GenBank via FTP (RRID:SCR_010535)

Resource Information

URL: http://www.ncbi.nlm.nih.gov/genbank/GenBankFtp.html

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Description: Files of the full release and daily updates of the GenBank database are available for anonymous FTP. The full release in flat-file format is available as compressed files in the directory genbank. It is created every two months. Individual files for each day''s new or updated sequence entries processed since close of data for the latest release are located in the sub-directory daily-nc. ASN.1 formatted data is in the directory ncbi-asn1. Lists of all nucleotide and protein accession numbers, generated each Sunday evening, are available in the Live lists directory.

Synonyms: GenBank via FTP

Resource Type: data or information resource, database

Keywords: gold standard

Funding:

Resource Name: NCBI GenBank via FTP

Resource ID: SCR_010535

Alternate IDs: nlx_24157

Record Creation Time: 20220129T080259+0000

Record Last Update: 20250507T060730+0000

Ratings and Alerts

No rating or validation information has been found for NCBI GenBank via FTP.

No alerts have been found for NCBI GenBank via FTP.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 68 mentions in open access literature.

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

Dobhal S, et al. (2025) Development and validation of genome-informed and multigene-based qPCR and LAMP assays for accurate detection of Dickeya solani: a critical quarantine pathogen threatening the potato industry. Microbiology spectrum, 13(1), e0078424.

Nahor O, et al. (2024) Epiphytic microbiome associated with intertidal seaweeds in the Mediterranean Sea: comparative analysis of bacterial communities across seaweed phyla. Scientific reports, 14(1), 18631.

Dobhal S, et al. (2024) Dickeya ananae sp. nov., pectinolytic bacterium isolated from pineapple (Ananas comosus). bioRxiv : the preprint server for biology.

Heydecke A, et al. (2024) Whole-Genome Sequencing of Invasive Neonatal Escherichia coli From Uppsala County, Sweden. The Journal of infectious diseases, 230(5), e1136.

Jeon J, et al. (2024) Wing geometric morphometrics and COI barcoding of Culex pipiens subgroup in the Republic of Korea. Scientific reports, 14(1), 878.

Gay SA, et al. (2024) Phylogenetic inference of inter-population transmission rates for infectious diseases. Briefings in bioinformatics, 25(4).

Hong R, et al. (2024) Pathogen spectrum and microbiome in lower respiratory tract of patients with different pulmonary diseases based on metagenomic next-generation sequencing. Frontiers in cellular and infection microbiology, 14, 1320831.

Hernández D, et al. (2023) Fungal Pathogens Associated with Aerial Symptoms of Avocado (Persea americana Mill.) in Tenerife (Canary Islands, Spain) Focused on Species of the Family Botryosphaeriaceae. Microorganisms, 11(3).

Fu P, et al. (2023) VIGA: a one-stop tool for eukaryotic virus identification and genome assembly from next-generation-sequencing data. Briefings in bioinformatics, 25(1).

Wang Y, et al. (2023) An explainable language model for antibody specificity prediction using curated influenza hemagglutinin antibodies. bioRxiv : the preprint server for biology.

Kim TK, et al. (2023) Stable internal reference genes for quantitative RT-PCR analyses in Rhipicephalus microplus during embryogenesis. Ticks and tick-borne diseases, 14(6), 102251.

Cui L, et al. (2023) Four additional natural 7-deazaguanine derivatives in phages and how to make them. Nucleic acids research, 51(17), 9214.

Kim YB, et al. (2023) In-depth metataxonomic investigation reveals low richness, high intervariability, and diverse phylotype candidates of archaea in the human urogenital tract. Scientific reports, 13(1), 11746.

Zlatohurska M, et al. (2023) Broad-host-range lytic Erwinia phage Key with exopolysaccharide degrading activity. Virus research, 329, 199088.

Cho HJ, et al. (2022) Development of an efficient marker-free soybean transformation method using the novel bacterium Ochrobactrum haywardense H1. Plant biotechnology journal, 20(5), 977.

Phi DL, et al. (2022) Outbreak of central nervous system infections among children in Thai Binh, Viet Nam. Emerging microbes & infections, 11(1), 1683.

Tan XJ, et al. (2022) Genomic and phenotypic biology of a novel Dickeya zeae WH1 isolated from rice in China: Insights into pathogenicity and virulence factors. Frontiers in microbiology, 13, 997486.

Colson P, et al. (2022) A 21L/BA.2-21K/BA.1 "MixOmicron" SARS-CoV-2 hybrid undetected by qPCR that screen for variant in routine diagnosis. Infection, genetics and evolution : journal of molecular epidemiology and evolutionary genetics in infectious diseases, 105, 105360.

DeLude A, et al. (2022) Loop-mediated isothermal amplification (LAMP) assay for specific and rapid detection of Dickeya fangzhongdai targeting a unique genomic region. Scientific reports, 12(1), 19193.

Rodino KG, et al. (2022) Partial ORF1ab Gene Target Failure with Omicron BA.2.12.1. Journal of clinical microbiology, 60(6), e0060022.