

Resource Summary Report

Generated by [dkNET](#) on Aug 12, 2026

NCBI Datasets

RRID:SCR_022569

Type: Tool

Proper Citation

NCBI Datasets (RRID:SCR_022569)

Resource Information

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

Proper Citation: NCBI Datasets (RRID:SCR_022569)

Description: Platform to let you gather data from across NCBI databases. Allows to find and download gene, transcript, protein and genome sequences, annotation and metadata.

Resource Type: data or information resource, portal, organization portal

Keywords: NCBI databases data, find and download gene, transcript, protein and genome sequences, annotation and metadata

Availability: Free, Freely available

Resource Name: NCBI Datasets

Resource ID: SCR_022569

Record Creation Time: 20220720T050146+0000

Record Last Update: 20260812T044425+0000

Ratings and Alerts

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

No alerts have been found for NCBI Datasets.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 72 mentions in open access literature.

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

Schäuble S, et al. (2026) FungiNetDB: a uniform (pre-)processing platform for fungal expression data. *microLife*, 7, uqag012.

Kürekci C, et al. (2026) Whole-Genome Insights Into Tigecycline-Resistant *Klebsiella* Spp. Harboring Colistin Resistance Gene From Food Animals in Türkiye. *Transboundary and emerging diseases*, 2026, 9122655.

Wiradiputra MRD, et al. (2026) Genomic signatures of dominant clones and evolutionary divergence of *Acinetobacter baumannii* in Thailand. *Microbial genomics*, 12(5).

Zeng J, et al. (2026) Histone demethylase CsJMJ12 enhances resistance of Navel orange to *Penicillium digitatum* via H3K27me3 demethylation. *Journal of advanced research*, 85, 91.

Sapino R, et al. (2026) Development of Metagenomic Methods for Health Monitoring of Endangered Species Using Fecal Samples. *Evolutionary applications*, 19(2), e70199.

Saghaei S, et al. (2026) VirJenDB: a FAIR (meta)data and bioinformatics platform for all viruses. *Nucleic acids research*, 54(D1), D912.

Peaslee C, et al. (2026) Mapping whole-organism genetic comorbidities across model Species using unified ontologies. *Genetics*, 232(4).

Greco JPG, et al. (2026) A pangenome-based strategy for designing a multi-epitope vaccine against non-toxin antigens of necrotic enteritis-associated *Clostridium perfringens*. *Brazilian journal of microbiology* : [publication of the Brazilian Society for Microbiology], 57(1).

Moses AM, et al. (2026) Inferring fungal cis-regulatory networks from genome sequences via unsupervised and interpretable representation learning. *Genetics*, 232(1).

Yano H, et al. (2026) Giant linear plasmids in *Mycobacterium avium* harbour a tRNA array unit. *DNA research* : an international journal for rapid publication of reports on genes and genomes, 33(1).

Rose AE, et al. (2026) Rational engineering of facultative anaerobiosis enables commensal survival in the oxygenated gut. *bioRxiv* : the preprint server for biology.

Acho-Vasquez HJ, et al. (2026) Integrative phylogenomic and pangenome landscape of *Bacillus*: insights from 10,000 genomes into taxonomy, functional potential, and biotechnological applications. *World journal of microbiology & biotechnology*, 42(4).

Alswat A, et al. (2026) Genomic diversity of culturable *Paraburkholderia* and *Burkholderia* species isolated from Bornean rainforest rhizosphere. *Microbial genomics*, 12(5).

Tsangaras K, et al. (2025) Crossing Wallace's line: an evolutionarily young gibbon ape leukemia virus like endogenous retrovirus identified from the Philippine flying lemur (*Cynocephalus volans*). *Scientific reports*, 15(1), 9790.

Martins-Gonçalves T, et al. (2025) Phylogenomic analysis of aquatic and clinical OXA-23-positive *Acinetobacter baumannii* belonging to the international clone 5 (ST79) from Southeast Brazil. *One health (Amsterdam, Netherlands)*, 21, 101140.

Lim RM, et al. (2025) How useful is Nanopore adaptive sampling for sequencing *Schistosoma mansoni* miracidia? *Wellcome open research*, 10, 239.

Zhang MY, et al. (2025) ?Molecular and morphological characterization of four new *Phyllosticta* species (Botryosphaerales, Phyllostictaceae): Genomic insights into evolutionary dynamics and metabolic adaptation. *IMA fungus*, 16, e168055.

Lukhtanov VA, et al. (2025) Cytogenetics of insects in the era of chromosome-level genome assemblies. *Vavilovskii zhurnal genetiki i selektsii*, 29(2), 230.

Byers AK, et al. (2025) Whole genome sequencing of *Penicillium* and *Burkholderia* strains antagonistic to the causal agent of kauri dieback disease (*Phytophthora agathidicida*) reveals biosynthetic gene clusters related to antimicrobial secondary metabolites. *Molecular ecology resources*, 25(2), e13810.

Rigden DJ, et al. (2025) The 2025 Nucleic Acids Research database issue and the online molecular biology database collection. *Nucleic acids research*, 53(D1), D1.