

Resource Summary Report

Generated by [kravitz2](#) on Sep 5, 2026

NCBI Taxonomy

RRID:SCR_003256

Type: Tool

Proper Citation

NCBI Taxonomy (RRID:SCR_003256)

Resource Information

URL: <http://www.ncbi.nlm.nih.gov/taxonomy/>

Proper Citation: NCBI Taxonomy (RRID:SCR_003256)

Description: Database for a curated classification and nomenclature that contains the names of all organisms that are represented in the public sequence databases with at least one nucleotide or protein sequence. Data provided encompasses archaea, bacteria, eukaryota, viroids and viruses. The NCBI taxonomy database is not a primary source for taxonomic or phylogenetic information. Furthermore, the database does not follow a single taxonomic treatise but rather attempts to incorporate phylogenetic and taxonomic knowledge from a variety of sources, including the published literature, web-based databases, and the advice of sequence submitters and outside taxonomy experts. Consequently, the NCBI taxonomy database is not a phylogenetic or taxonomic authority and should not be cited as such.

Abbreviations: NCBI Taxonomy

Synonyms: NCBI Taxonomy Browser, Taxonomy Browser, Entrez Taxonomy Browser, NCBI Taxonomy Database

Resource Type: data or information resource, database

Defining Citation: [PMID:18940862](#), [PMID:18940867](#)

Keywords: viroid, virus, nucleotide, protein, sequence, phylogeny, taxonomic, taxonomy, nomenclature, cladistics, classification, animal, genetic code, gold standard

Availability: Free, Freely available

Resource Name: NCBI Taxonomy

Resource ID: SCR_003256

Alternate IDs: nif-0000-03179, r3d100010776

Alternate URLs: <http://www.ncbi.nlm.nih.gov/Taxonomy/taxonomyhome.html>,
<https://doi.org/10.17616/R3X039>

Record Creation Time: 20220129T080218+0000

Record Last Update: 20260904T000130+0000

Ratings and Alerts

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

No alerts have been found for NCBI Taxonomy.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 296 mentions in open access literature.

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

Zhang Y, et al. (2026) Evidence of human exposure to tick-borne viruses based on viromes of ticks and presence of specific antibodies among patients in Hainan Island, southern China. *Virologica Sinica*, 41(1), 70.

Mohamed ET, et al. (2026) Antifungal efficacy of linoleic-acid-rich *Cucurbita pepo* L. seed oil revealed by GC-MS profiling of lipids and bioactive markers, ergosterol depletion, and network pharmacology. *BMC microbiology*, 26(1).

Shen X, et al. (2026) A foundation model for nucleotide sequences. *Nucleic acids research*, 54(6).

Nishiduka E, et al. (2026) Chromosome-scale genome assembly and developmental transcriptome of *Aedes triseriatus*, vector of La Crosse virus. *BMC genomics*, 27(1).

Humphrey S, et al. (2026) Nudibranch color diversity shares a common physical basis in guanine photonic structure 'pixels'. *Proceedings of the National Academy of Sciences of the United States of America*, 123(12), e2525419123.

Zhang H, et al. (2026) Experimental hepatitis E virus genotype 1 infection in three types of wild rodents. *PLoS pathogens*, 22(3), e1014050.

Orsholm J, et al. (2026) A multi-modal dataset for insect biodiversity with imagery and DNA at the trap and individual level. *Scientific data*, 13(1).

Karki BR, et al. (2026) Divergent evolution of the PRPS enzymes across the tree of life. *bioRxiv* : the preprint server for biology.

Osterhof C, et al. (2026) Ancient conservation of androglobin expression reveals its evolutionary link to ciliary processes. *Molecular biology and evolution*, 43(7).

Qian X, et al. (2026) 4-hydroxy-5-methyl-3(2H)-furanone mediates widespread interkingdom communications between fungi and prokaryotes. *Genome biology*, 27(1).

Zhang Z, et al. (2026) PRIME: a database for 16S rRNA microbiome data with phenotypic reference and comprehensive metadata. *Nucleic acids research*, 54(D1), D255.

Zhu T, et al. (2026) MitoNGS: an online platform to analyze fish metabarcoding data in high resolution. *Molecular biology and evolution*, 43(3).

Zhao D, et al. (2026) A Unified Framework to Prioritize RNA Virus Cross-Species Transmission Risk Across an Expansive Host Landscape. *Viruses*, 18(2).

Sullivan AE, et al. (2025) The Panoptes system uses decoy cyclic nucleotides to defend against phage. *Nature*, 647(8091), 988.

Imam FT, et al. (2025) Developing a multiscale neural connectivity knowledgebase of the autonomic nervous system. *Frontiers in neuroinformatics*, 19, 1541184.

Sianga-Mete R, et al. (2025) Viral genome sequence datasets display pervasive evidence of strand-specific substitution biases that are best described using non-reversible nucleotide substitution models. *Research square*.

Vaglietti S, et al. (2025) Divergent evolution of low-complexity regions in the vertebrate CPEB protein family. *Frontiers in bioinformatics*, 5, 1491735.

Zhang Z, et al. (2025) Origin, evolution and diversification of plant caleosins. *BMC plant biology*, 25(1), 433.

Jamilano-Llames LC, et al. (2025) Comparative Antagonistic Activities of Endolichenic Fungi Isolated from the Fruticose Lichens *Ramalina* and *Usnea*. *Journal of fungi (Basel, Switzerland)*, 11(4).

Wang Q, et al. (2025) Discovery of novel mycoviruses from fungi associated with mango leaf spots. *Frontiers in microbiology*, 16, 1545534.