

Resource Summary Report

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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: 20260804T043202+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 273 mentions in open access literature.

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

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

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).

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. *eLife*, 12.

Barrera-Redondo J, et al. (2025) Origin and evolutionary trajectories of brown algal sex chromosomes. *Nature ecology & evolution*, 9(11), 2127.

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

Lima-Cordón R, et al. (2025) A Short-Read Amplicon Sequencing Protocol and Bioinformatic Pipeline for Ecological Surveillance of Dipteran Disease Vectors. *Molecular ecology resources*, 25(6), e14088.

Ar?n?k N, et al. (2025) Linked avian influenza epidemiological and genomic data in EMPRES-i for epidemic intelligence (2012-2021). Data in brief, 59, 111410.

Huang YX, et al. (2025) The pan-genome of *Spodoptera frugiperda* provides new insights into genome evolution and horizontal gene transfer. Communications biology, 8(1), 407.

Schoenstein M, et al. (2025) Profylo: A Python Package for Phylogenetic Profile Comparison and Analysis. Journal of molecular evolution, 93(6), 806.

Cai H, et al. (2025) Molecular defense strategy of volatile organic compound-emitting plants (order Piperales) against herbivorous mammals. Communications biology, 9(1), 19.

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

Li FL, et al. (2025) Identification of novel rodent and shrew orthohepeviruses sheds light on hepatitis E virus evolution. Zoological research, 46(1), 103.

Testone G, et al. (2025) The molecular pathways leading to GABA and lactic acid accumulation in florets of organic broccoli rabe (*Brassica rapa* subsp. *sylvestris*) stored as fresh or as minimally processed product. Horticulture research, 12(1), uhae274.

Bachler A, et al. (2025) Disruption of HaVipR1 confers Vip3Aa resistance in the moth crop pest *Helicoverpa armigera*. PLoS biology, 23(5), e3003165.

Wang B, et al. (2025) Genetic Diversity and Molecular Evolution of Hepatitis E Virus Within the Genus *Chirohepevirus* in Bats. Viruses, 17(3).

Timinskas K, et al. (2025) Common themes in architecture and interactions of prokaryotic PolB2 and Pol V mutasomes inferred from in silico studies. Computational and structural biotechnology journal, 27, 401.

Dandare SU, et al. (2025) Diversity and distribution of the lanthanome in aerobic methane-oxidising bacteria. Environmental microbiome, 20(1), 120.

Niu K, et al. (2025) Development of a Multiplexed qPCR Kit for the Detection of Bloodstream Infection. Journal of clinical laboratory analysis, 39(10), e70037.