**NCBI Taxonomy**

RRID:SCR_003256  
Type: Tool

**Proper Citation**

NCBI Taxonomy (RRID:SCR_003256)

**Resource Information**


**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:** Taxonomy Browser, Entrez Taxonomy Browser, NCBI Taxonomy Database, NCBI Taxonomy Browser

**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:** Acknowledgement requested
**Resource Name:** NCBI Taxonomy

**Resource ID:** SCR_003256

**Alternate IDs:** nif-0000-03179

**Alternate URLs:** http://www.ncbi.nlm.nih.gov/Taxonomy/taxonomyhome.html

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**Ratings and Alerts**

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

No alerts have been found for NCBI Taxonomy.

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**Data and Source Information**

**Source:** SciCrunch Registry

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**Usage and Citation Metrics**

We found 212 mentions in open access literature.

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


Yang P, et al. (2023) Microbiome-based enrichment pattern mining has enabled a deeper understanding of the biome-species-function relationship. Communications biology, 6(1), 391.


Ilyukhin E, et al. (2023) Cytospora paraplurivora sp. nov. isolated from orchards with fruit tree decline syndrome in Ontario, Canada. PloS one, 18(1), e0279490.

Zhang X, et al. (2022) TreeTuner: A pipeline for minimizing redundancy and complexity in large phylogenetic datasets. STAR protocols, 3(1), 101175.


Hubert B, et al. (2022) SkewDB, a comprehensive database of GC and 10 other skews for over 30,000 chromosomes and plasmids. Scientific data, 9(1), 92.


Dunham SJB, et al. (2022) Longitudinal Analysis of the Microbiome and Metabolome in the 5xfAD Mouse Model of Alzheimer's Disease. mBio, 13(6), e0179422.


Bray JE, et al. (2022) Ribosomal MLST nucleotide identity (rMLST-NI), a rapid bacterial species identification method: application to Klebsiella and Raoultella genomic species validation. Microbial genomics, 8(9).