

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 8, 2026

Taxonomy

RRID:SCR_004299

Type: Tool

Proper Citation

Taxonomy (RRID:SCR_004299)

Resource Information

URL: <http://ftp://ftp.ebi.ac.uk/pub/databases/taxonomy>

Proper Citation: Taxonomy (RRID:SCR_004299)

Description: The taxonomy database of the International Sequence Database Collaboration contains the names of all organisms that are represented in the sequence databases with at least one nucleotide or protein sequence. The database is available via the EBI SRS server of ftp.

Abbreviations: Taxonomy

Synonyms: Taxonomy via SRS

Resource Type: data or information resource, database

Keywords: gold standard, FASEB list

Resource Name: Taxonomy

Resource ID: SCR_004299

Alternate IDs: nlx_31444

Old URLs: <http://srs.ebi.ac.uk/srsbin/cgi-bin/wgetz?-page=query+-libList+TAXONOMY>

Record Creation Time: 20220129T080223+0000

Record Last Update: 20260905T133123+0000

Ratings and Alerts

No rating or validation information has been found for Taxonomy.

No alerts have been found for Taxonomy.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 164 mentions in open access literature.

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

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

Cattelin C, et al. (2026) Searching for γ -solenoid proteins involved in organellar gene expression. *BMC genomics*, 27(1).

Azam MS, et al. (2026) Role of staphylococcal EzrA as a molecular organizer of cell division. *bioRxiv : the preprint server for biology*.

Wang H, et al. (2026) Multiple hypervariable markers improve mycobiome classification in metatranscriptome and metagenome data. *Communications biology*, 9(1).

Betow JY, et al. (2026) African Natural Products Database (ANPDB): A resource for exploring the therapeutic potential of natural compounds from Africa. *Nucleic acids research*, 54(D1), D1336.

Li K, et al. (2026) Telomere-to-Telomere Genomes Reveal that Multiscale Evolution Shapes the Largest Metabolic Arsenal of Diaporthe Fungi. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(27), e13287.

Basdani D, et al. (2026) De-novo assembly of 82 bacterial genomes using Nanopore sequencing and prediction of biosynthetic capacity. *Scientific data*, 13(1).

Wong KC, et al. (2026) A Scoping Review of Snail Antibacterial Peptides and Proteins: From Natural Defence to Translational Prospects. *Probiotics and antimicrobial proteins*, 18(3), 3671.

Yamakawa S, et al. (2026) Multiple losses of ecdysone receptor genes in nematodes: an alternative evolutionary scenario of molting regulation. *Molecular biology and evolution*, 43(5).

Sanchez SG, et al. (2026) A Spinster-like Transporter at the Inner Membrane Complex is critical for *Toxoplasma gondii* cytokinesis, motility and invasion. *PLoS pathogens*, 22(1), e1013886.

Zhu H, et al. (2025) Phosphorylation of PIP2;7 by CPK28 or Phytophthora kinase effectors dampens pattern-triggered immunity in Arabidopsis. *Plant communications*, 6(1), 101135.

Reyes G, et al. (2025) Mitogenome data sequence of a mangrove oyster of interest for cultivation in Ecuador: *Crassostrea* sp. (Bivalvia: Ostreidae). *Data in brief*, 59, 111330.

Phan ANT, et al. (2025) Rapid detection of Tulipalin A with SESI-Orbitrap MS: an exploration across spring flowers. *Plant methods*, 21(1), 14.

Kwon SL, et al. (2025) Exploring Multifaceted Roles of *Bambusicolous* *Apiospora* in *Phyllostachys bambusoides*. *Microbial ecology*, 88(1), 115.

Bukowski M, et al. (2025) Analysis of co-occurrence of type II toxin-antitoxin systems and antibiotic resistance determinants in *Staphylococcus aureus*. *mSystems*, 10(3), e0095724.

Sellés Vidal L, et al. (2025) Accurate, comprehensive database of group I introns and their homing endonucleases. *Bioinformatics advances*, 5(1), vbaf020.

Kharrat L, et al. (2025) Large-Scale Genomic Analysis of CpG-Mediated Immunogenicity in Bacteriophages and a Novel Predictive Risk Index. *bioRxiv : the preprint server for biology*.

Wu P, et al. (2025) TreeHub: a comprehensive dataset of phylogenetic trees. *Scientific data*, 12(1), 924.

Kim JW, et al. (2025) Standardizing the approach to clinical-based human microbiome research: from clinical information collection to microbiome profiling and human resource utilization. *Osong public health and research perspectives*, 16(3), 300.

Tziatzios G, et al. (2025) Third generation sequencing analysis detects significant differences in duodenal microbiome composition between functional dyspepsia patients and control subjects. *Neurogastroenterology and motility*, 37(1), e14955.