

Resource Summary Report

Generated by RRID on Aug 4, 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: 20260804T043238+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 154 mentions in open access literature.

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

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.

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.

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.

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

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*.

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.

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.

Prince CR, et al. (2025) Conservation and evolution of the programmed ribosomal frameshift in *prfB* across the bacterial domain. *mBio*, 16(9), e0105525.

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

Bourgeois G, et al. (2025) Structures of *Saccharolobus solfataricus* initiation complexes with leaderless mRNAs highlight archaeal features and eukaryotic proximity. *Nature*

communications, 16(1), 348.

Su S, et al. (2025) Predicting viral host codon fitness and path shifting through tree-based learning on codon usage biases and genomic characteristics. Scientific reports, 15(1), 12251.

López Romo G, et al. (2025) The rhizosphere of *Phaseolus vulgaris* L. cultivars hosts a similar bacterial community in local agricultural soils. PloS one, 20(3), e0319172.

Das S, et al. (2024) Phylogenomics of *Psammodynastes* and *Bufo* (Elapidae: Serpentes), with the description of a new Asian snake family. Scientific reports, 14(1), 9489.

Prince CR, et al. (2024) The evolution and functional significance of the programmed ribosomal frameshift in *prfB*. bioRxiv : the preprint server for biology.

Gapińska M, et al. (2024) Structure-functional characterization of *Lactococcus* AbiA phage defense system. Nucleic acids research, 52(8), 4723.

Tangaro S, et al. (2024) Unraveling the microbiome-metabolome nexus: a comprehensive study protocol for personalized management of Behçet's disease using explainable artificial intelligence. Frontiers in microbiology, 15, 1341152.

Shi H, et al. (2024) RefMetaPlant: a reference metabolome database for plants across five major phyla. Nucleic acids research, 52(D1), D1614.