

Resource Summary Report

Generated by [ASWG](#) on Aug 4, 2026

Transfer RNA database

RRID:SCR_008636

Type: Tool

Proper Citation

Transfer RNA database (RRID:SCR_008636)

Resource Information

URL: <http://trnadb.bioinf.uni-leipzig.de>

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Description: tRNAdb 2009 provides a powerful and fast search engine. Taxons can be identified by browsing the taxonomic tree or by using the search form. Queries can include DNA or RNA sequences, amino acid family, anticodon, references, Pubmed-ID of the reference, gene ID as well as comments. In addition, individual searches concerning sequence or structure characteristics are possible. The server accepts IDs of the new as well as the old tRNA database as queries and can perform BLAST searches. All sequences can be downloaded in several file- and alignment formats on the result list. This site is hosted and maintained in a cooperation between the universities of Leipzig (Germany), Marburg (Germany) and Strasbourg (France). Recent Visitors

Synonyms: tRNAdb

Resource Type: data or information resource, database

Resource Name: Transfer RNA database

Resource ID: SCR_008636

Alternate IDs: nif-0000-32030

Record Creation Time: 20220129T080248+0000

Record Last Update: 20260804T043352+0000

Ratings and Alerts

No rating or validation information has been found for Transfer RNA database.

No alerts have been found for Transfer RNA database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 78 mentions in open access literature.

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

Kompatscher M, et al. (2024) Contribution of tRNA sequence and modifications to the decoding preferences of E. coli and M. mycoides tRNAGlyUCC for synonymous glycine codons. Nucleic acids research, 52(3), 1374.

Kanwal N, et al. (2024) GPATCH4 regulates rRNA and snRNA 2'-O-methylation in both DHX15-dependent and DHX15-independent manners. Nucleic acids research, 52(4), 1953.

Bar O, et al. (2024) Reanalysis of Trio Whole-Genome Sequencing Data Doubles the Yield in Autism Spectrum Disorder: De Novo Variants Present in Half. International journal of molecular sciences, 25(2).

Ipas H, et al. (2024) ChemRAP uncovers specific mRNA translation regulation via RNA 5' phospho-methylation. EMBO reports, 25(3), 1570.

Kristen M, et al. (2024) DORQ-seq: high-throughput quantification of femtomol tRNA pools by combination of cDNA hybridization and Deep sequencing. Nucleic acids research, 52(18), e89.

Chen M, et al. (2024) Comprehensive Identification and Characterization of HML-9 Group in Chimpanzee Genome. Viruses, 16(6).

Herrmannová A, et al. (2024) Perturbations in eIF3 subunit stoichiometry alter expression of ribosomal proteins and key components of the MAPK signaling pathways. eLife, 13.

Lei HT, et al. (2023) tModBase: deciphering the landscape of tRNA modifications and their dynamic changes from epitranscriptome data. Nucleic acids research, 51(D1), D315.

Fuchs J, et al. (2023) TudS desulfidases recycle 4-thiouridine-5'-monophosphate at a catalytic [4Fe-4S] cluster. Communications biology, 6(1), 1092.

Guan L, et al. (2023) tatDB: a database of Ago1-mediated targets of transfer RNA fragments. Nucleic acids research, 51(D1), D297.

Brazane M, et al. (2023) The ribose methylation enzyme FTSJ1 has a conserved role in neuron morphology and learning performance. Life science alliance, 6(4).

Varenyk Y, et al. (2023) Modified RNAs and predictions with the ViennaRNA Package. Bioinformatics (Oxford, England), 39(11).

Jia L, et al. (2022) Comprehensive identification and characterization of the HERV-K (HML-9) group in the human genome. *Retrovirology*, 19(1), 11.

Jimenez J, et al. (2022) Protein-coding tRNA sequences? *Gene*, 814, 146154.

Chen X, et al. (2022) A new bacterial tRNA enhances antibiotic production in *Streptomyces* by circumventing inefficient wobble base-pairing. *Nucleic acids research*, 50(12), 7084.

Hoffmann A, et al. (2021) Changes of the tRNA Modification Pattern during the Development of *Dictyostelium discoideum*. *Non-coding RNA*, 7(2).

Guan L, et al. (2021) Large-Scale Computational Discovery of Binding Motifs in tRNA Fragments. *Frontiers in molecular biosciences*, 8, 647449.

Gulyaev AP, et al. (2021) Insertions of codons encoding basic amino acids in H7 hemagglutinins of influenza A viruses occur by recombination with RNA at hotspots near snoRNA binding sites. *RNA (New York, N.Y.)*, 27(2), 123.

Martinez Campos C, et al. (2021) Mapping of pseudouridine residues on cellular and viral transcripts using a novel antibody-based technique. *RNA (New York, N.Y.)*, 27(11), 1400.

Bayoumi A, et al. (2021) Mistranslation Drives Alterations in Protein Levels and the Effects of a Synonymous Variant at the Fibroblast Growth Factor 21 Locus. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 8(11), 2004168.