

Resource Summary Report

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GtRNADB - Genomic tRNA Database

RRID:SCR_006939

Type: Tool

Proper Citation

GtRNADB - Genomic tRNA Database (RRID:SCR_006939)

Resource Information

URL: <http://gtornadb.ucsc.edu>

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Description: This genomic tRNA database contains tRNA gene predictions made by the program tRNAscan-SE (Lowe & Eddy, Nucl Acids Res 25: 955-964, 1997) on complete or nearly complete genomes. Unless otherwise noted, all annotation is automated, and has not been inspected for agreement with published literature. Transfer RNAs (tRNAs) represent the single largest, best-understood class of non-protein coding RNA genes found in all living organisms. By far, the major source of new tRNAs is computational identification of genes within newly sequenced genomes. To organize the rapidly growing collection and enable systematic analyses, we created the Genomic tRNA Database (GtRNADB). The web resource provides overview statistics of tRNA genes within each analyzed genome, including information by isotype and genetic locus, easily downloadable primary sequences, graphical secondary structures and multiple sequence alignments. Direct links for each gene to UCSC eukaryotic and microbial genome browsers provide graphical display of tRNA genes in the context of all other local genetic information. The database can be searched by primary sequence similarity, tRNA characteristics or phylogenetic group. Inevitably with automated sequence analysis, we find exceptions to general identification rules, isoacceptor type predictions (esp. due to variable post-transcriptional anticodon modification), and questionable tRNA identifications (due to pseudogenes, SINES, or other tRNA-derived elements). We attempt to document all cases we come across, and welcome feedback on new or unrecognized discrepancies.

Abbreviations: GtRNADB

Synonyms: Genomic tRNA Database

Resource Type: analysis service resource, data analysis service, data or information resource, database, production service resource, service resource

Defining Citation: [PMID:18984615](#)

Keywords: trna, trna gene prediction, genome, gene, isotype, genetic locus, blast, secondary structure, sequence alignment, fasta, seq, eukaryotic, microbial, primary sequence, phylogenetic group, FASEB list

Funding: Hewlett-Packard

Resource Name: GtRNAdb - Genomic tRNA Database

Resource ID: SCR_006939

Alternate IDs: nif-0000-02932

Record Creation Time: 20220129T080239+0000

Record Last Update: 20260821T193816+0000

Ratings and Alerts

No rating or validation information has been found for GtRNAdb - Genomic tRNA Database.

No alerts have been found for GtRNAdb - Genomic tRNA Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 381 mentions in open access literature.

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

Lv J, et al. (2026) Tetrahedral DNA nanostructure-delivered suppressor tRNA ameliorates nephropathy in COL4A5 nonsense mutation-mediated Alport syndrome mice. NAR molecular medicine, 3(2), ugag029.

Rao H, et al. (2026) Ribosome Homeostasis Regulated by SETD2 Preserves Intestinal Epithelial Barrier. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(16), e08168.

Claus C, et al. (2026) Extracellular Small RNAs in Human Milk: Molecular Profiles, Stability and Fragment-Specific Responses in Cell-Based Assays. Non-coding RNA, 12(1).

Tan X, et al. (2026) Analysis of Codon Usage Bias in the Streptococcus pneumoniae Pneumolysin Gene. The Canadian journal of infectious diseases & medical microbiology = Journal canadien des maladies infectieuses et de la microbiologie medicale, 2026, 2707639.

Kutchuashvili A, et al. (2026) Anticodon loop remodeling and D-stem shape drive the specific recognition of ANN-decoding tRNAs for t6A modification. *Nucleic acids research*, 54(11).

Whittle CA, et al. (2026) Evidence for Non-optimal Codon Choice in Highly Transcribed Sex-Biased Genes of *Drosophila melanogaster*. *Genome biology and evolution*, 18(5).

Murphy GL, et al. (2026) Profiling of Small Noncoding RNAs During Bovine Conceptus Elongation Identifies Let-7 as a Candidate Regulator of Proliferation and Differentiation. *Animals : an open access journal from MDPI*, 16(8).

Wang Y, et al. (2026) Endogenous and Exogenous Small RNA Signatures as Novel Tools for Postmortem Interval Determination. *Biomolecules*, 16(3).

Shahi PK, et al. (2026) Engineered tRNA reduces vision loss in a mouse model of Leber congenital amaurosis. *Signal transduction and targeted therapy*, 11(1).

Ali RH, et al. (2025) A methyltransferase-independent role for METTL1 in tRNA aminoacylation and oncogenic transformation. *Molecular cell*, 85(5), 948.

Lin B, et al. (2025) WDR4-mediate tRNA m7G modification to promote mitophagy and browning of white adipose tissue for ameliorating obesity in male mice. *Adipocyte*, 14(1), 2588888.

Shirzad-Aski H, et al. (2025) Isolation, characterization, and genomic analysis of three novel Herelleviridae family lytic bacteriophages against uropathogenic isolates of *Staphylococcus saprophyticus*. *Virology journal*, 22(1), 87.

Fan R, et al. (2025) Spatially Resolved Panoramic in vivo CRISPR Screen via Perturb-DBiT. *Research square*.

Liao H, et al. (2025) The novel tRF-23 promotes osteogenic differentiation of hBMSCs and protects against bone loss in ovariectomized mice. *Stem cell reports*, 20(10), 102673.

Akyuz E, et al. (2025) Preventing vision loss in a mouse model of Leber Congenital Amaurosis by engineered tRNA. *bioRxiv : the preprint server for biology*.

van der Toorn W, et al. (2025) WarpDemuX-tRNA: barcode multiplexing for nanopore tRNA sequencing. *Nucleic acids research*, 53(17).

Staut J, et al. (2025) A map of integrated cis-regulatory elements enhances gene-regulatory analysis in maize. *Plant communications*, 6(7), 101376.

Zhang Y, et al. (2025) Phosphoglycerate dehydrogenase is required for kernel development and defines a predominant serine synthesis pathway in maize. *The Plant cell*, 37(6).

Seifert-D??vila W, et al. (2025) Structural and kinetic insights into tRNA promoter engagement by yeast general transcription factor TFIIIC. *Nucleic acids research*, 53(1).

Tan X, et al. (2025) Decoding codon usage in human papillomavirus type 59. *Virus genes*, 61(3), 313.