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://gtrnadb.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: production service resource, data or information resource, database, service resource, data analysis service, analysis 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: 20260803T040447+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 336 mentions in open access literature.

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

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.

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.

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).

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

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

Rao J, et al. (2025) A 6-tsRNA signature for early detection, treatment response monitoring, and prognosis prediction in diffuse large B cell lymphoma. Blood cancer journal, 15(1), 79.

Biela AD, et al. (2025) Determining the effects of pseudouridine incorporation on human tRNAs. The EMBO journal, 44(13), 3553.

Wang J, et al. (2025) Characterization and whole-genome sequencing data of a highly pathogenic group B Streptococcus strain related to stillbirth. Data in brief, 60, 111658.

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

Chen YT, et al. (2025) Intratumoral amino acid insufficiency limits CD8+ T-cell effector function. bioRxiv : the preprint server for biology.

Zhang YY, et al. (2025) A cohort of mRNAs undergo high-stoichiometry NSUN6-mediated site-specific m5C modification. Nature communications, 16(1), 6119.

Meng X, et al. (2025) A novel tsRNA signature -tRF-58:76-Tyr-GTA-2-M3 as potential biomarker and therapeutic target for duodenal atresia. Cell biology and toxicology, 41(1), 88.

Wang Z, et al. (2025) A reference-guided iterative approach to polish the nanopore sequencing basecalling for therapeutic RNA quality control. Communications biology, 8(1), 1406.

Kim A, et al. (2025) Exploring Organ-Specific Extracellular Vesicles in Metabolic Improvements Following Bariatric Surgery in Youth With Obesity. Obesity (Silver Spring, Md.), 33(11), 2181.

Mathavan S, et al. (2025) Aptamer based immunotherapy: a potential solid tumor therapeutic. Frontiers in immunology, 16, 1536569.

Elahi R, et al. (2025) tRNA lysidinylation is essential for the minimal translation system in the Plasmodium falciparum apicoplast. EMBO reports, 26(9), 2300.

Vaz C, et al. (2025) Short-term diet intervention comprising of olive oil, vitamin D, and omega-3 fatty acids alters the small non-coding RNA (sncRNA) landscape of human sperm. Scientific reports, 15(1), 7790.