

Resource Summary Report

Generated by [T1D](#) on Sep 5, 2026

tRNAscan-SE

RRID:SCR_010835

Type: Tool

Proper Citation

tRNAscan-SE (RRID:SCR_010835)

Resource Information

URL: <http://lowelab.ucsc.edu/tRNAscan-SE/>

Proper Citation: tRNAscan-SE (RRID:SCR_010835)

Description: Web server to search for tRNA genes in genomic sequence. If you would like to run tRNAscan-SE locally, you can get the UNIX source code (gzip'd tar file).

Abbreviations: tRNAscan-SE

Resource Type: software resource, production service resource, service resource, analysis service resource, data analysis service

Defining Citation: [PMID:15980563](#), [PMID:9023104](#), [DOI:10.1093/nar/25.5.0955](#)

Keywords: bio.tools

Availability: Acknowledgement requested

Resource Name: tRNAscan-SE

Resource ID: SCR_010835

Alternate IDs: OMICS_00385, biotools:trnascan-se

Alternate URLs: <https://bio.tools/trnascan-se>, <https://sources.debian.org/src/trnascan-se/>

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260903T235055+0000

Ratings and Alerts

No rating or validation information has been found for tRNAscan-SE.

No alerts have been found for tRNAscan-SE.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1695 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

Mohanta TK, et al. (2023) Anticodon table of the chloroplast genome and identification of putative quadruplet anticodons in chloroplast tRNAs. *Scientific reports*, 13(1), 760.

Xuan G, et al. (2023) Characterization of the newly isolated *Pseudomonas* phage vB_Pae_LC3I3. *Virus research*, 323, 198978.

Soorni A, et al. (2023) Genome-wide screening and characterization of long noncoding RNAs involved in flowering/bolting of *Lactuca sativa*. *BMC plant biology*, 23(1), 3.

Ali S, et al. (2023) Characterization, genome analysis and antibiofilm efficacy of lytic *Proteus* phages RP6 and RP7 isolated from university hospital sewage. *Virus research*, 326, 199049.

Herliana L, et al. (2023) A chromosome-level genome assembly of *Plantago ovata*. *Scientific reports*, 13(1), 1528.

Zhang D, et al. (2023) Analysis of the chloroplast genome and phylogenetic evolution of *Bidens pilosa*. *BMC genomics*, 24(1), 113.

Yang Y, et al. (2023) Genome sequencing of *Sitopsis* species provides insights into their contribution to the B??subgenome of bread wheat. *Plant communications*, 4(4), 100567.

Qi Y, et al. (2023) Chromosome-level genome assembly of *Phrynocephalus forsythii* using third-generation DNA sequencing and Hi-C analysis. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 30(2).

Guo Y, et al. (2023) Hologenome analysis reveals independent evolution to chemosymbiosis by deep-sea bivalves. *BMC biology*, 21(1), 51.

Zhang Y, et al. (2023) Chromosome-level genome assembly and annotation of the prickly nightshade *Solanum rostratum* Dunal. *Scientific data*, 10(1), 341.

Guo X, et al. (2023) The *Sapria himalayana* genome provides new insights into the lifestyle of endoparasitic plants. *BMC biology*, 21(1), 134.

Bandla A, et al. (2023) Genome-resolved carbon processing potential of tropical peat microbiomes from an oil palm plantation. *Scientific data*, 10(1), 373.

Deng J, et al. (2023) Genome Comparison Reveals Inversions and Alternative Evolutionary History of Nutritional Endosymbionts in Planthoppers (Hemiptera: Fulgoromorpha). *Genome biology and evolution*, 15(7).

Rao YZ, et al. (2023) Metagenomic Discovery of "Candidatus Parvarchaeales"-Related Lineages Sheds Light on Adaptation and Diversification from Neutral-Thermal to Acidic-Mesothermal Environments. *mSystems*, 8(2), e0125222.

Zhang YJ, et al. (2023) Mitochondrial genome of *Cordyceps blackwelliae*: organization, transcription, and evolutionary insights into *Cordyceps*. *IMA fungus*, 14(1), 13.

Honeker LK, et al. (2023) Drought re-routes soil microbial carbon metabolism towards emission of volatile metabolites in an artificial tropical rainforest. *Nature microbiology*, 8(8), 1480.

Wang C, et al. (2023) Population genomic analysis provides evidence of the past success and future potential of South China tiger captive conservation. *BMC biology*, 21(1), 64.

Zhang L, et al. (2023) Phenotypic, Genomic, and Transcriptomic Comparison of Industrial *Aspergillus oryzae* Used in Chinese and Japanese Soy Sauce: Analysis of Key Proteolytic Enzymes Produced by Koji Molds. *Microbiology spectrum*, 11(2), e0083622.

Chen Y, et al. (2023) Isolation and characterization of a novel phage belonging to a new genus against *Vibrio parahaemolyticus*. *Virology journal*, 20(1), 81.

Liu C, et al. (2023) Comparative Genomic Analysis of *Sphingomonas morindae* sp. NBD5 and *Sphingopyxis* sp. USTB-05 for Producing Macular Pigment. *Microorganisms*, 11(2).