

Resource Summary Report

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tRNAscan-SE

RRID:SCR_008637

Type: Tool

Proper Citation

tRNAscan-SE (RRID:SCR_008637)

Resource Information

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

Proper Citation: tRNAscan-SE (RRID:SCR_008637)

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).

Synonyms: Lowe Lab tRNAscan-SE

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

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

Keywords: bio.tools, tRNA genes, genomic sequence

Availability: Free, Freely available

Resource Name: tRNAscan-SE

Resource ID: SCR_008637

Alternate IDs: SCR_010835, OMICS_00385, nif-0000-32031, biotools:trnascan-se

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

Record Creation Time: 20220129T080248+0000

Record Last Update: 20260807T042715+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 2855 mentions in open access literature.

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

Bjornson S, et al. (2026) Stepwise evolutionary transitions in Cladophorales plastid genomes reveal origins of hairpin chromosomes. *Current biology : CB*, 36(7), 1659.

Shen F, et al. (2026) Capsule modulation enhances immunity and delays resistance in MDR *Acinetobacter baumannii*. *iScience*, 29(6), 115761.

Schlebusch SA, et al. (2026) Sex chromosome turnover and structural genome divergence shape meiotic outcomes in hybridizing *Cobitis*. *GigaScience*, 15.

Sharma M, et al. (2026) Improved reference assembly and core collection resequencing to facilitate exploration of important agronomical traits for the improvement of oilseed crop, *Carthamus tinctorius* L. *GigaScience*, 15.

Wu L, et al. (2026) Chromosome-level genome assembly of triploid *Cyperus rotundus* uncovers allelic expression patterns and herbicide resistance mechanisms. *Plant communications*, 7(2), 101624.

Sandholm RM, et al. (2026) Whole-genome assembly and annotation of the bumblebee wax moth, *Aphomia sociella*. *G3 (Bethesda, Md.)*, 16(2).

Wu B, et al. (2026) A chromosome-level genome assembly of *Coryphaenoides armatus*. *Scientific data*, 13(1).

Li Y, et al. (2026) Structural characterization of the plastid genome and comparative mitochondrial genomics of *Eupatorium lindleyanum* (Asteraceae): evolutionary dynamics and phylogenetic insights. *BMC plant biology*, 26(1).

Lin A, et al. (2026) Chromosome-level genome assembly of the stonefly *Rhopalopsale triangulispina* Mo and Li, 2025 (Plecoptera: Leuctridae). *Scientific data*, 13(1).

Yan Y, et al. (2026) *Bacillus subtilis* G01: A Multifunctional Agent with Broad-Spectrum Antimicrobial Activity and Digestive Enzymes for Sustainable Agriculture and Animal Husbandry. *Journal of microbiology and biotechnology*, 36, e2510049.

Wu H, et al. (2026) A high-quality chromosome-level genome assembly of the low chilling requirement mulberry, *Morus macroura*. *Scientific data*, 13(1).

Gao K, et al. (2026) Chromosome-level genome assembly and annotation of the schizothoracine fish *Gymnodiptychus pachycheilus*. *Scientific data*, 13(1).

Pan J, et al. (2026) Biocontrol potential and molecular basis of predation in a marine raptorial ciliate. *The ISME journal*, 20(1).

Kriti D, et al. (2026) Chromosome-scale genome assembly and characterization of *Saccharomycopsis schoenii*, a necrotrophic predatory yeast. *G3 (Bethesda, Md.)*, 16(5).

Zhang S, et al. (2026) The complete mitochondrial genome of *Alpheus digitalis* De Haan, 1844 (Decapoda: Alpheidae). *Mitochondrial DNA. Part B, Resources*, 11(4), 478.

Guerreiro MA, et al. (2026) Genomic and physiological signatures of adaptation in pathogenic fungi. *Nature communications*, 17(1), 748.

Chen SH, et al. (2026) Genome Assembly of *Spinifex sericeus* Provides Insights into Repetitive Content and Haplotype Variation in a Dioecious Coastal Grass. *Genome biology and evolution*, 18(3).

Lishai E, et al. (2026) The Liver Fluke *Opisthorchis felinus* Exosomal tRNA-Derived Small RNAs as Potential Mediators of Host Manipulation. *Biomolecules*, 16(2).

Sui B, et al. (2026) Intra-strain and inter-strain heterogeneity shape phage-host interactions and phenotypic adaptation in *Pseudomonas aeruginosa*. *Applied and environmental microbiology*, 92(4), e0005026.

Li R, et al. (2026) The chromosome-scale genome assembly and annotation of *Rosa bracteata* (Macartney Rose). *Scientific data*, 13(1).