

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>

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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.

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.

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

Urban-Olivares J, et al. (2026) The Copepoda mitogenome as a dynamic evolutionary landscape. *PloS one*, 21(6), e0350115.

Sun H, et al. (2026) The chromosome-level genome assembly and annotation of *Parabotia bimaculata* (Cypriniformes: Cobitidae: Botiinae). *Scientific data*, 13(1).

Tahir MS, et al. (2026) Chromosome-level genome and transcriptome analysis of *Trichophyton verrucosum* reveals pathogenicity mechanisms and antifungal response. *Virulence*, 17(1), 2677294.

White K, et al. (2026) Diversity and prevalence of dairy streptococcal phages in two European dairy fermentation facilities over a one-year period. *Microbial genomics*, 12(5).

Liu M, et al. (2026) A chromosome-scale nuclear genome and complete mitogenome of the bio-control fungus *Cordyceps cateniannulata*. *Scientific data*, 13(1).

Wang J, et al. (2026) The chromosome-level genome assembly of *Sitobion avenae* Fabricius (Hemiptera: Aphididae). *Scientific data*, 13(1).

Lin F, et al. (2026) A chromosome-level genome assembly of the panda loach (*Yaoshania pachychilus*). *Scientific data*, 13(1).

Hu X, et al. (2026) Chromosome-level genome assembly and annotation of the moon jellyfish *Aurelia coerulea*. *Scientific data*, 13(1).

Safi H, et al. (2026) Elucidating the protein interaction network of one of the largest icosahedral capsids in the virosphere. *The EMBO journal*, 45(10), 3514.

Chihara K, et al. (2026) Phage homing endonuclease amplifies anti-defense genes to evade bacterial immunity. *Nature communications*, 17(1).

Perdon DM, et al. (2026) Genomic analysis reveals recent population decline and exceptionally low genome-wide heterozygosity of the critically endangered Philippine eagle, *Pithecophaga jefferyi* (Aves: Accipitridae). *BMC genomics*, 27(1).

Hu YF, et al. (2026) Chromosome-level genome assembly of *Phoebe chekiangensis*, an endemic and endangered tree in east Asia. *Scientific data*, 13(1).

Wang L, et al. (2026) Chromosome-level genome assembly, annotation, evolutionary analysis, and establishment of transformation systems in *Carex rigescens*. *Plant cell reports*, 45(5).

N??jera-Peso A, et al. (2026) Transfer RNA (tRNA) Genes, Codon Usage and Translational Efficiency in *Leishmania infantum*. *Genes*, 17(6).