Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 29, 2025

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

Defining Citation: PMID:15980563, PMID:9023104, DOI:10.1093/nar/25.5.0955

Keywords: bio.tools, tRNA genes, genomic sequence

Funding:

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: 20250429T055258+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 2206 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Zou X, et al. (2025) Chromosome-level genome assembly of the pine wood nematode carrier Arhopalus unicolor. Scientific data, 12(1), 111.

Yang G, et al. (2025) Chromosome-level genome assembly of Megachile sculpturalis Smith (Hymenoptera, Apoidea, Megachilidae). Scientific data, 12(1), 46.

Gu S, et al. (2025) Siderophore synthetase-receptor gene coevolution reveals habitat- and pathogen-specific bacterial iron interaction networks. Science advances, 11(3), eadq5038.

Guan DL, et al. (2025) A high-quality chromosome-level genome assembly of the mulberry looper, Phthonandria atrilineata. Scientific data, 12(1), 186.

Chen Y, et al. (2025) An improved chromosome-level genome assembly and annotation of Hong Kong catfish (Clarias fuscus). Scientific data, 12(1), 193.

Yakubovskij VI, et al. (2025) Phage vB_KlebPS_265 Active Against Resistant/MDR and Hypermucoid K2 Strains of Klebsiella pneumoniae. Viruses, 17(1).

Patil MP, et al. (2025) Complete Mitochondrial Genome of Niphon spinosus (Perciformes: Niphonidae): Genome Characterization and Phylogenetic Analysis. Biomolecules, 15(1).

Willemsen A, et al. (2025) Novel High-Quality Amoeba Genomes Reveal Widespread Codon Usage Mismatch Between Giant Viruses and Their Hosts. Genome biology and evolution, 17(1).

Öztoprak H, et al. (2025) Chromosome-scale genome dynamics reveal signatures of independent haplotype evolution in the ancient asexual mite Platynothrus peltifer. Science advances, 11(4), eadn0817.

Akdeniz Z, et al. (2025) The expanded genome of Hexamita inflata, a free-living diplomonad. Scientific data, 12(1), 192.

Zhang R, et al. (2025) Comparative organelle genomics in Daphniphyllaceae reveal phylogenetic position and organelle structure evolution. BMC genomics, 26(1), 40.

Das PJ, et al. (2025) Complete mitochondrial genome sequence analysis revealed double matrilineal components in Indian Ghoongroo pigs. Scientific reports, 15(1), 2219.

Kamilari E, et al. (2025) Bacillus safensis APC 4099 has broad-spectrum antimicrobial activity against both bacteria and fungi and produces several antimicrobial peptides, including the novel circular bacteriocin safencin E. Applied and environmental microbiology, 91(1), e0194224.

Xiao Z, et al. (2025) De novo assembly of the complete mitochondrial genomes of two Camellia-oil tree species reveals their multibranch conformation and evolutionary relationships. Scientific reports, 15(1), 2899.

Liu S, et al. (2025) Chromosome-level genome assembly and annotation of Japanese anchovy (Engraulis japonicus). Scientific data, 12(1), 134.

An M, et al. (2025) Chromosome-Level Genome Assembly and Annotation of the Highly Heterozygous Phallus echinovolvatus Provide New Insights into Its Genetics. Journal of fungi (Basel, Switzerland), 11(1).

Li X, et al. (2025) Chromosome-level genome assembly and annotation of largemouth bronze gudgeon (Coreius guichenoti). Scientific data, 12(1), 76.

Patel J, et al. (2025) Whole genome sequencing, assembly and annotation of the Southern Ground Hornbill - Bucorvus leadbeateri. Scientific data, 12(1), 58.

Sun L, et al. (2025) Association Analysis of the Genomic and Functional Characteristics of Halotolerant Glutamicibacter endophyticus J2-5-19 from the Rhizosphere of Suaeda salsa. Microorganisms, 13(1).

Xu T, et al. (2025) Discovery and characterization of complete genomes of 38 head-tailed proviruses in four predominant phyla of archaea. Microbiology spectrum, 13(1), e0049224.