

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

Aragorn

RRID:SCR_015974

Type: Tool

Proper Citation

Aragorn (RRID:SCR_015974)

Resource Information

URL: <http://mbio-serv2.mbioekol.lu.se/ARAGORN/>

Proper Citation: Aragorn (RRID:SCR_015974)

Description: Software that detects tRNA genes and tmRNA genes in nucleotide sequences. The program employs heuristic algorithms to predict tRNA secondary structure, based on homology with recognized tRNA consensus sequences and ability to form a base-paired cloverleaf., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Resource Type: data processing software, sequence analysis software, data analysis software, software resource, software application

Defining Citation: [PMID:14704338](#), [DOI:10.1093/nar/gkh152](#)

Keywords: software, program, nucleotide, sequence, detect, tmRNA, tRNA

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Aragorn

Resource ID: SCR_015974

Alternate IDs: OMICS_04227

Alternate URLs: <https://sources.debian.org/src/arden/>

License: GPLv3

Record Creation Time: 20220129T080328+0000

Record Last Update: 20260731T043004+0000

Ratings and Alerts

No rating or validation information has been found for Aragorn.

No alerts have been found for Aragorn.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 472 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#).

Janssen AB, et al. (2025) PneumoBrowse 2: an integrated visual platform for curated genome annotation and multiomics data analysis of *Streptococcus pneumoniae*. *Nucleic acids research*, 53(D1), D839.

Takita K, et al. (2025) Distribution and functional analysis of two types of quorum sensing gene pairs, *glaI1/glaR1* and *glaI2/glaR2*, in *Burkholderia gladioli*. *FEMS microbiology letters*, 372.

Nawrocki EP, et al. (2025) Expansion of the tmRNA sequence database and new tools for search and visualization. *NAR genomics and bioinformatics*, 7(1), lqaf019.

Zou T, et al. (2025) Chloroplast whole genome assembly and phylogenetic analysis of *Persicaria criopolitana* reveals its new taxonomic status. *Scientific reports*, 15(1), 19890.

Stevens-Green R, et al. (2025) Organellar Genomes of Three Globally Important Nanoplanktonic Diatoms Refine Their Taxon-Specific Distribution and Succession Patterns in the Northwest Atlantic. *The Journal of eukaryotic microbiology*, 72(5), e70033.

Rivas-Santisteban J, et al. (2025) Metagenomic analysis of heavy water-adapted bacterial communities. *Microbial genomics*, 11(5).

Liu L, et al. (2025) Complete chloroplast genome sequencing of *Pseudocodon convolvulaceus*, a medicinal herb from Qinghai-Tibet Plateau in China. *PloS one*, 20(8), e0328307.

Washington JM, et al. (2025) Expanding the Diversity of Actinobacterial Tectiviridae: A Novel Genus from *Microbacterium*. *Viruses*, 17(1).

Cui H, et al. (2025) Branched-chain amino acid metabolism supports *Roseobacteraceae* positive interactions in marine biofilms. *Applied and environmental microbiology*, 91(3), e0241124.

Guo W, et al. (2025) Transcriptomic analysis of *Virescentia guangxiensis* (Rhodophyta: Batrachospermales) revealed differential expression of genes in gametophyte and chlamydomonas life phases. *BMC genomics*, 26(1), 202.

Rubalskii E, et al. (2025) Characterization and genome analysis of the novel virulent Burkholderia phage Bm1, which is active against pan-drug-resistant Burkholderia multivorans. Archives of virology, 170(5), 106.

Li X, et al. (2025) Analysis of synonymous codon usage bias in the chloroplast genome of five Caragana. BMC plant biology, 25(1), 322.

Li Y, et al. (2025) PlasmidScope: a comprehensive plasmid database with rich annotations and online analytical tools. Nucleic acids research, 53(D1), D179.

Ruang-Areerate P, et al. (2025) Comparative Chloroplast Genomes and Phylogenetic Relationships of True Mangrove Species Brownlowia tersa and Brownlowia argentata (Malvaceae). Current issues in molecular biology, 47(2).

Záhonová K, et al. (2025) Comparative genomic analysis of trypanosomatid protists illuminates an extensive change in the nuclear genetic code. mBio, 16(6), e0088525.

Maurya S, et al. (2025) Comparative plastome evaluation, phylogenomic analysis, and DNA signatures of medicinally important malvaceous genera and their adulterants. Scientific reports, 15(1), 24285.

Daundasekara KC, et al. (2025) Plastomic studies inform the mechanisms of edaphic adaptation in North American species in the tribe Thelypodieae (Brassicaceae). American journal of botany, 112(7), e70071.

Supina BSI, et al. (2025) A flagella-dependent Burkholderia jumbo phage controls rice seedling rot and steers Burkholderia glumae toward reduced virulence in rice seedlings. mBio, 16(3), e0281424.

Ranta K, et al. (2025) Isolation and characterization of fMGyn-Pae01, a phiKZ-like jumbo phage infecting Pseudomonas aeruginosa. Virology journal, 22(1), 55.

Harrison RL, et al. (2025) The Genome Sequences of Baculoviruses from the Tufted Apple Bud Moth, Platynota idaeusalis, Reveal Recombination Between an Alphabaculovirus and a Betabaculovirus from the Same Host. Viruses, 17(2).