

Resource Summary Report

Generated by dkNET on Apr 29, 2025

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.

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

Funding:

Availability: Free, Freely available, Available for download

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: 20250429T055800+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 446 mentions in open access literature.

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

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, glal1/glaR1 and glal2/glaR2, in *Burkholderia gladioli*. FEMS microbiology letters, 372.

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

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

Denoeud F, et al. (2024) Evolutionary genomics of the emergence of brown algae as key components of coastal ecosystems. Cell, 187(24), 6943.

Wang M, et al. (2024) ICEberg 3.0: functional categorization and analysis of the integrative and conjugative elements in bacteria. Nucleic acids research, 52(D1), D732.

Wang W, et al. (2024) The complete chloroplast genome sequence of *Melochia corchorifolia* Linnaeus, 1753 (Sterculiaceae). Mitochondrial DNA. Part B, Resources, 9(1), 153.

Zhan Q, et al. (2024) Comparative chloroplast genomics and phylogenetic analysis of *Oreomecon nudicaulis* (Papaveraceae). BMC genomic data, 25(1), 49.

Cho HS, et al. (2024) Taxonomic reinvestigation of the genus *Tetraedesmus* (Scenedesmaceae; Sphaeropleales) based on morphological characteristics and chloroplast genomes. *Frontiers in plant science*, 15, 1303175.

Nagy NA, et al. (2024) The updated genome of the Hungarian population of *Aedes koreicus*. *Scientific reports*, 14(1), 7545.

Willner DL, et al. (2024) Transcriptional dynamics during *Rhodococcus erythropolis* infection with phage WC1. *BMC microbiology*, 24(1), 107.

Hulatt CJ, et al. (2024) The genome of the Arctic snow alga *Limnomonas spitsbergensis* (Chlamydomonadales). *G3 (Bethesda, Md.)*, 14(7).

Sosa-Jiménez VM, et al. (2024) Discovery of a novel symbiotic lineage associated with a hematophagous leech from the genus *Haementeria*. *Microbiology spectrum*, 12(7), e0428623.

Amarillas L, et al. (2024) Isolation and Characterization of a Bacteriophage with Potential for the Control of Multidrug-Resistant *Salmonella* Strains Encoding Virulence Factors Associated with the Promotion of Precancerous Lesions. *Viruses*, 16(11).

Cho MS, et al. (2024) Plastid phylogenomics of *Robinsonia* (Senecioneae; Asteraceae), endemic to the Juan Fernández Islands: insights into structural organization and molecular evolution. *BMC plant biology*, 24(1), 1016.

Li X, et al. (2024) Genomic diversity of phages infecting the globally widespread genus *Sulfurimonas*. *Communications biology*, 7(1), 1428.

Zhang J, et al. (2024) Viral Communities Contribute More to the Lysis of Antibiotic-Resistant Bacteria than the Transduction of Antibiotic Resistance Genes in Anaerobic Digestion Revealed by Metagenomics. *Environmental science & technology*, 58(5), 2346.

Vitt AR, et al. (2024) Diverse bacteriophages for biocontrol of ESBL- and AmpC-?-lactamase-producing *E. coli*. *iScience*, 27(2), 108826.

Silva EC, et al. (2024) Molecular Characterization and Genome Mechanical Features of Two Newly Isolated Polyvalent Bacteriophages Infecting *Pseudomonas syringae* pv. *garcae*. *Genes*, 15(1).

Svanberga K, et al. (2024) Isolation and Characterization of a Novel *Aeromonas salmonicida*-Infecting Studiervirinae Bacteriophage, JELG-KS1. *Microorganisms*, 12(3).