

Resource Summary Report

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RNAmmmer

RRID:SCR_017075

Type: Tool

Proper Citation

RNAmmmer (RRID:SCR_017075)

Resource Information

URL: <http://www.cbs.dtu.dk/services/RNAmmmer/>

Proper Citation: RNAmmmer (RRID:SCR_017075)

Description: Software package to predict ribosomal RNA genes in full genome sequences by utilising two levels of Hidden Markov Models. Consistent and rapid annotation of ribosomal RNA genes.

Resource Type: software application, service resource, standalone software, data analysis software, data analysis service, data access protocol, data processing software, software resource, production service resource, web service, analysis service resource

Defining Citation: [PMID:17452365](#)

Keywords: predict, ribosomal, RNA, gene, full, genome, sequence, HMM, rRNA

Funding: EMBIO at the University of Oslo ;
Research Council of Norway ;
Danish Center for Scientific Computing ;
European Union

Availability: Restricted

Resource Name: RNAmmmer

Resource ID: SCR_017075

License: Academic Software Licence

Record Creation Time: 20220129T080333+0000

Record Last Update: 20260729T044426+0000

Ratings and Alerts

No rating or validation information has been found for RNAmmer.

No alerts have been found for RNAmmer.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 103 mentions in open access literature.

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

Li L, et al. (2025) Isolation, characterization, and genomic analysis of a novel phage WSPA with lytic activity against *Serratia marcescens*. *Microbiology spectrum*, 13(9), e0271624.

Liu H, et al. (2025) A telomere-to-telomere gapless genome reveals SIPRR1 control of circadian rhythm and photoperiodic flowering in tomato. *GigaScience*, 14.

Wang J, et al. (2025) Characterization and whole-genome sequencing data of a highly pathogenic group B *Streptococcus* strain related to stillbirth. *Data in brief*, 60, 111658.

Kumari K, et al. (2025) In-depth genome and comparative genome analysis of a metal-resistant environmental isolate *Pseudomonas aeruginosa* S-8. *Frontiers in cellular and infection microbiology*, 15, 1511507.

Yu T, et al. (2025) Evolution of KoRV-A transcriptional silencing in wild koalas. *Cell*, 188(8), 2081.

Feng R, et al. (2024) Characteristics of *Corynespora cassiicola*, the causal agent of tobacco *Corynespora* leaf spot, revealed by genomic and metabolic phenomic analysis. *Scientific reports*, 14(1), 18326.

Wang H, et al. (2024) The genomes of *Dahlia pinnata*, *Cosmos bipinnatus*, and *Bidens alba* in tribe Coreopsidae provide insights into polyploid evolution and inulin biosynthesis. *GigaScience*, 13.

Coles DW, et al. (2024) Functional genomics identifies a small secreted protein that plays a role during the biotrophic to necrotrophic shift in the root rot pathogen *Phytophthora medicaginis*. *Frontiers in plant science*, 15, 1439020.

Singh RP, et al. (2024) First report on in-depth genome and comparative genome analysis of a metal-resistant bacterium *Acinetobacter pittii* S-30, isolated from environmental sample. *Frontiers in microbiology*, 15, 1351161.

Wu L, et al. (2024) Construction of high-quality genomes and gene catalogue for culturable microbes of sugarcane (*Saccharum* spp.). *Scientific data*, 11(1), 534.

Huang YC, et al. (2024) The complete chloroplast genome of *Leonurus sibiricus* Linnaeus (Labiatae, *Leonurus* Miller). *Mitochondrial DNA. Part B, Resources*, 9(7), 934.

Li G, et al. (2024) Comparative analysis of chloroplast and mitochondrial genomes of sweet potato provides evidence of gene transfer. *Scientific reports*, 14(1), 4547.

Lyu ZY, et al. (2024) The first high-altitude autotetraploid haplotype-resolved genome assembled (*Rhododendron nivale* subsp. *boreale*) provides new insights into mountaintop adaptation. *GigaScience*, 13.

Molina D, et al. (2024) Genome characterization of a multi-drug resistant *Escherichia coli* strain, L1PEag1, isolated from commercial cape gooseberry fruits (*Physalis peruviana* L.). *Frontiers in microbiology*, 15, 1392333.

Lyu S, et al. (2024) Isolation and characterization of a novel temperate bacteriophage infecting *Aeromonas hydrophila* isolated from a *Macrobrachium rosenbergii* larvae pond. *Virus research*, 339, 199279.

Li XT, et al. (2024) *Acidithiobacillus acidisediminis* sp. nov., an acidophilic sulphur-oxidizing chemolithotroph isolated from acid mine drainage sediment. *International journal of systematic and evolutionary microbiology*, 74(5).

Cheng C, et al. (2024) A *Bacillus velezensis* strain isolated from oats with disease-preventing and growth-promoting properties. *Scientific reports*, 14(1), 12950.

Zhang Y, et al. (2024) Comparison of organelle genomes between endangered mangrove plant *Dolichandrone spathacea* to terrestrial relative provides insights into its origin and adaptative evolution. *Frontiers in plant science*, 15, 1442178.

Yuan L, et al. (2024) The genomes of 5 underutilized Papilionoideae crops provide insights into root nodulation and disease resistance. *GigaScience*, 13.

Herliana L, et al. (2023) A chromosome-level genome assembly of *Plantago ovata*. *Scientific reports*, 13(1), 1528.