

Resource Summary Report

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RNAmmer

RRID:SCR_017075

Type: Tool

Proper Citation

RNAmmer (RRID:SCR_017075)

Resource Information

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

Proper Citation: RNAmmer (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: data analysis software, service resource, web service, standalone software, data processing software, data access protocol, software application, data analysis service, analysis service resource, software resource, production 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: RNAmmer

Resource ID: SCR_017075

License: Academic Software Licence

Record Creation Time: 20220129T080333+0000

Record Last Update: 20260810T040656+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 120 mentions in open access literature.

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

Teng Y, et al. (2026) Complete mitochondrial sequencing reveals the horizontal transfer and gene rearrangement of *Passiflora edulis*. *Frontiers in plant science*, 17, 1851081.

Xu T, et al. (2026) Isolation and therapeutic potential of phage vB_EcoM_GXW16 against a drug-resistant avian pathogenic *Escherichia coli* strain. *Poultry science*, 105(6), 106701.

Zheng C, et al. (2026) Biological characteristics and genetics differentiation of smut fungi in *Coix L*. *Frontiers in microbiology*, 17, 1746178.

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

Li XY, et al. (2025) Whole genome analysis of *Shigella* sp. JZ001: a novel strain isolated from diarrheic suckling mice. *Frontiers in veterinary science*, 12, 1686554.

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.

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.

Huang T, et al. (2025) Induced Mutagenesis and Comparative Genomics of *Raoultella* sp. 64 for Enhanced Antimony Resistance and Biosorption. *Microorganisms*, 13(4).

Huang H, et al. (2025) Complete Genome Sequencing of *Erwinia phyllosphaerae* ZX-13, a Novel Biocontrol Agent to Against the Stem Blight Pathogen *Pseudocryphonectria elaeocarpicola* in *Elaeocarpus* spp. *Microorganisms*, 13(12).

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 Coreopsideae 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.

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

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.

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.

Kong Q, et al. (2024) The Whole-Genome Sequencing and Probiotic Profiling of *Lactobacillus reuteri* Strain TPC32 Isolated from Tibetan Pig. *Nutrients*, 16(12).

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.

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.