Resource Summary Report

Generated by dkNET on Apr 29, 2025

Barrnap

RRID:SCR_015995
Type: Tool

Proper Citation

Barrnap (RRID:SCR_015995)

Resource Information

URL: http://www.vicbioinformatics.com/software.barrnap.shtml

Proper Citation: Barrnap (RRID:SCR_015995)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on February 28,2023. Software to predict the location of ribosomal RNA genes in genomes. It supports bacteria, archaea, mitochondria, and eukaryotes. It takes FASTA DNA sequence as input, writes GFF3 as output, and supports multithreading.

Synonyms: Barrnap: Basic rapid ribosomal RNA predictor

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

Keywords: multithreading, fasta, sequencing, software, predict, location, ribosomal, gene, genome, RNA, prediction, bacteria, archaea, mitochondria, eukaryote, bio.tools

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Barrnap

Resource ID: SCR_015995

Alternate IDs: biotools:barrnap, OMICS_13988

Alternate URLs: https://github.com/tseemann/barrnap, https://bio.tools/barrnap, https://sources.debian.org/src/barrnap/

Record Creation Time: 20220129T080328+0000

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Ratings and Alerts

No rating or validation information has been found for Barrnap.

No alerts have been found for Barrnap.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 470 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Hu H, et al. (2025) Metagenome-assembled microbial genomes (n?=?3,448) of the oral microbiomes of Tibetan and Duroc pigs. Scientific data, 12(1), 141.

Byers AK, et al. (2025) Whole genome sequencing of Penicillium and Burkholderia strains antagonistic to the causal agent of kauri dieback disease (Phytophthora agathidicida) reveals biosynthetic gene clusters related to antimicrobial secondary metabolites. Molecular ecology resources, 25(2), e13810.

Krabberød AK, et al. (2025) The Ribosomal Operon Database: A Full-Length rDNA Operon Database Derived From Genome Assemblies. Molecular ecology resources, 25(1), e14031.

Wolf S, et al. (2025) Microbial carbon oxidation in seawater below the hypoxic threshold. Scientific reports, 15(1), 2838.

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

White OW, et al. (2025) A Snakemake Toolkit for the Batch Assembly, Annotation and Phylogenetic Analysis of Mitochondrial Genomes and Ribosomal Genes From Genome Skims of Museum Collections. Molecular ecology resources, 25(1), e14036.

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.

Wang X, et al. (2025) Chromosome-level haplotype-resolved genome of the tropical loach (Oreonectes platycephalus). Scientific data, 12(1), 29.

Yang S, et al. (2025) Comparative Genomics Reveals Evidence of the Genome Reduction and Metabolic Potentials of Aliineobacillus hadale Isolated from Challenger Deep Sediment of the Mariana Trench. Microorganisms, 13(1).

Hong L, et al. (2024) Construction and analysis of telomere-to-telomere genomes for 2 sweet oranges: Longhuihong and Newhall (Citrus sinensis). GigaScience, 13.

Luo Z, et al. (2024) Haplotype-phased genome assemblies and annotation of the northern white-cheeked gibbon (Nomascus leucogenys). Scientific data, 11(1), 1279.

Ritz NL, et al. (2024) The gut virome is associated with stress-induced changes in behaviour and immune responses in mice. Nature microbiology, 9(2), 359.

Coelho MA, et al. (2024) Comparative genomics of Cryptococcus and Kwoniella reveals pathogenesis evolution and contrasting karyotype dynamics via intercentromeric recombination or chromosome fusion. bioRxiv : the preprint server for biology.

Khoeri MM, et al. (2024) Whole genome sequencing data of Streptococcus pneumoniae isolated from Indonesian population. Data in brief, 53, 110251.

Li T, et al. (2024) The American Cherimoya Genome Reveals Insights into the Intra-Specific Divergence, the Evolution of Magnoliales, and a Putative Gene Cluster for Acetogenin Biosynthesis. Plants (Basel, Switzerland), 13(5).

Martin? J, et al. (2024) Highly Resolved Genomes of Two Closely Related Lineages of the Rodent Louse Polyplax serrata with Different Host Specificities. Genome biology and evolution, 16(3).

Lax G, et al. (2024) Phylogenomic diversity of archigregarine apicomplexans. Open biology, 14(9), 240141.

Wang T, et al. (2024) Complete genome sequence and anti-obesity potential of Lactiplantibacillus plantarum HOM2217 in 3T3-L1 cells and high-fat diet-fed rats. Frontiers in microbiology, 15, 1436378.

Liao H, et al. (2024) Prophage-encoded antibiotic resistance genes are enriched in human-impacted environments. Nature communications, 15(1), 8315.

Gu F, et al. (2024) Genome-wide comparative analysis of CC1 Staphylococcus aureus between colonization and infection. European journal of medical research, 29(1), 474.