

Resource Summary Report

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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., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Synonyms: Barrnap: Basic rapid ribosomal RNA predictor

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

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

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/>

License: GPL version 3.0

Record Creation Time: 20220129T080328+0000

Record Last Update: 20260728T043513+0000

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 568 mentions in open access literature.

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

Lemonnier C, et al. (2026) Comparison of Metabarcoding and Shotgun Sequencing Confirms the Relevance of Chloroplastic rRNA Genes to Assess Community Structure of Lake Phytoplankton. *Molecular ecology resources*, 26(1), e70077.

Liang H, et al. (2025) Efficiently constructing complete genomes with CycloneSEQ to fill gaps in bacterial draft assemblies. *GigaByte (Hong Kong, China)*, 2025, gigabyte154.

Choi J, et al. (2025) Accelerated Pseudogenization in the Ancient Endosymbionts of Giant Scale Insects. *Molecular biology and evolution*, 42(6).

Ticona ARP, et al. (2025) Functional Characterization, Genome Assembly, and Annotation of *Geobacillus* sp. G4 Isolated from a Geothermal Field in Tacna, Peru. *Microorganisms*, 13(6).

Wang G, et al. (2025) Genomic evidence for hybridization and introgression between blue peafowl and endangered green peafowl and molecular foundation of leucistic plumage of blue peafowl. *GigaScience*, 14.

Coelho MA, et al. (2025) Tracing the evolution and genomic dynamics of mating-type loci in *Cryptococcus* pathogens and closely related species. *bioRxiv : the preprint server for biology*.

Wang Z, et al. (2025) Biodegradation of high-molecular-weight polycyclic aromatic hydrocarbons by a novel species of the genus *Devosia* isolated from the deep-sea region of the Kermadec Trench. *Frontiers in microbiology*, 16, 1584496.

Sereika M, et al. (2025) Genome-resolved long-read sequencing expands known microbial diversity across terrestrial habitats. *Nature microbiology*, 10(8), 2018.

Wang J, et al. (2025) A haplotype-resolved genome assembly and gene expression map of Cushion willow. *Scientific data*, 12(1), 785.

??imek K, et al. (2025) New lineage of scuticociliates dominates the ciliate community and bacterivory in hypolimnetic waters of a freshwater reservoir. *The ISME journal*, 19(1).

Zhang C, et al. (2025) Chromosome-level genome assembly and annotation of *Gypsophila vaccaria*. *Scientific data*, 12(1), 818.

Lax G, et al. (2025) Divergent Plastid Genomes in the Deepest-Branching Apicomplexan Parasites. *Genome biology and evolution*, 17(6).

Muema EK, et al. (2025) *Mesorhizobium salmacidum* sp. nov. and *Mesorhizobium argentiipisi* sp. nov. are symbionts of the dry-land forage legumes *Lessertia diffusa* and *Calobota sericea*. *Antonie van Leeuwenhoek*, 118(3), 54.

Lu J, et al. (2025) Identification of a novel chromosome-encoded fosfomycin resistance gene *fosC3* in *Aeromonas caviae*. *Frontiers in microbiology*, 16, 1577167.

Tian Z, et al. (2025) Chromosome-level Genome Assembly of the Tibetan Medicinal Plant Duiyiwei (*Phlomis rotata*). *Scientific data*, 12(1), 1576.

Lei Y, et al. (2025) Deciphering functional landscapes of rumen microbiota unveils the role of *Prevotella bryantii* in milk fat synthesis in goats. *Genome biology*, 26(1), 311.

Kondrotaitė Z, et al. (2025) Ecophysiology and niche differentiation of three genera of polyphosphate-accumulating bacteria in a full-scale wastewater treatment plant. *mSystems*, 10(9), e0032225.

Liang H, et al. (2025) Metagenomics-based novel Caulimoviridae virus discovery and its development of identification markers in *Lilium lancifolium* thunb. *Virology journal*, 22(1), 221.

Puthumana MA, et al. (2025) Genome assembly and insights into globally invasive Red-vented Bulbul (*Pycnonotus cafer*). *DNA research : an international journal for rapid publication of reports on genes and genomes*, 32(6).

Liu G, et al. (2025) Comparative genomic analysis reveals the adaptive traits of *Ralstonia* spp. in aquatic environments. *Frontiers in microbiology*, 16, 1625651.