

# Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

## Barrnap

RRID:SCR\_015995

Type: Tool

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### Proper Citation

Barrnap (RRID:SCR\_015995)

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### 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

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## Ratings and Alerts

No rating or validation information has been found for Barnnap.

No alerts have been found for Barnnap.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## 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.

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*.

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.

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.

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

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

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.

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

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

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

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).

??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).

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.

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.

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

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).

Chakraborty A, et al. (2025) Life inside a bag: multiomics insights into the bagworm species *Eumeta crameri*. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 32(6).

Karbstein K, et al. (2025) Assembling genomes of non-model plants: A case study with evolutionary insights from *Ranunculus* (Ranunculaceae). *The Plant journal : for cell and molecular biology*, 123(6), e70390.