

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 17, 2026

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

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: 20260912T195833+0000

Ratings and Alerts

No rating or validation information has been found for Barnnap.

No alerts have been found for Barnnap.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 722 mentions in open access literature.

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

Sharma M, et al. (2026) Improved reference assembly and core collection resequencing to facilitate exploration of important agronomical traits for the improvement of oilseed crop, *Carthamus tinctorius* L. *GigaScience*, 15.

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.

Li J, et al. (2026) Telomere-to-telomere genome assembly and a mutant library empower functional genomics and genetic improvement in *Cucurbita moschata*. *Plant communications*, 7(5), 101836.

Chen D, et al. (2026) Insights into karyotype evolution and flower color variation from the genome assembly of wallflower (*Erysimum cheiri*). *Plant physiology*, 200(4).

Zhen Z, et al. (2026) Genome-wide characteristics, antibiotic resistance, and pathogenicity analysis of *Streptococcus parasuis* strains isolated from diseased pigs. *BMC microbiology*, 26(1).

Lee J, et al. (2026) MlrROR release 02: Expanded and refined 16S-ITS-23S rRNA operon dataset. *Scientific data*, 13(1).

Zhang S, et al. (2026) The complete mitochondrial genome of *Alpheus digitalis* De Haan, 1844 (Decapoda: Alpheidae). *Mitochondrial DNA. Part B, Resources*, 11(4), 478.

Nishimura Y, et al. (2026) Molecular evolution and diversity of isomerase-reductase clusters involved in the bacterial metabolism of glycosaminoglycans. *mSphere*, 11(1), e0081725.

Niu Z, et al. (2026) Genome-Guided Identification of an OTA-Degrading Amidohydrolase AMH2102 from *Acinetobacter kookii* AK4 with Enhanced Soluble Expression in *Escherichia coli*. *Toxins*, 18(2).

Toki S, et al. (2026) Genomic and evolutionary factors influencing the prediction accuracy of optimal growth temperature in prokaryotes. *mSystems*, 11(5), e0006226.

Sun J, et al. (2026) A chromosome-level genome assembly of *Rhizopus stolonifer* associated with passion fruit flower rot. *Frontiers in microbiology*, 17, 1757919.

Nguyen CV, et al. (2026) A chromosome-scale reference genome and integrative transcriptome provide insight into tissue- and stress-specific responses in tetraploid sainfoin (*Onobrychis viciifolia*). *Planta*, 263(6).

Wang H, et al. (2026) *Candidatus Dermatophostum* as a novel genus of polyphosphate-accumulating organisms for high-strength wastewater treatment. *The ISME journal*, 20(1).

Shi X, et al. (2026) Comprehensive catalog of gut microbial genomes in Asian elephants: insights from shotgun metagenomics. *Animal microbiome*, 8(1).

Sun M, et al. (2026) Virus-encoded metabolism may support environmental stress adaptation of microbial hosts in an estuarine hypoxic zone. *Frontiers in microbiology*, 17, 1785655.

Hagenbeek A, et al. (2026) Genome-resolved metagenomics reveals unexpected diversity and host range of *Candidatus Lariskella* (Rickettsiales: Midichloriaceae). *BMC genomics*, 27(1).

Hu Y, et al. (2026) Probiotic-driven microbiome remodeling is associated with coordinated immune and metabolic responses, improving growth and disease resistance in farmed tongue sole (*Cynoglossus semilaevis*). *Current research in microbial sciences*, 10, 100600.

Salengros A, et al. (2026) Uncovering the ecophysiological potential of *Motilimonas* through genomic profiling analysis. *BMC genomics*, 27(1).

Mohammadi P, et al. (2026) Genome-wide identification of eQTL-associated lncRNAs in melon and their role in fruit cracking. *Scientific reports*, 16(1).

Li N, et al. (2026) Large-scale multi-omics unveils host-microbiome interactions driving root development and nitrogen acquisition. *Nature plants*, 12(2), 319.