

Resource Summary Report

Generated by [NIF](#) on Aug 29, 2026

Prokka

RRID:SCR_014732

Type: Tool

Proper Citation

Prokka (RRID:SCR_014732)

Resource Information

URL: <http://www.vicbioinformatics.com/software/prokka.shtml>

Proper Citation: Prokka (RRID:SCR_014732)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on February 28,2023. Software tool for the rapid annotation of prokaryotic genomes. It produces GFF3, GBK and SQN files that are ready for editing in Sequin and ultimately submitted to Genbank/DDJB/ENA. A typical 4 Mbp genome can be fully annotated in less than 10 minutes on a quad-core computer, and scales well to 32 core SMP systems., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

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

Defining Citation: [DOI:10.1093/bioinformatics/btu153](https://doi.org/10.1093/bioinformatics/btu153)

Keywords: annotation, prokaryote, genome, prokaryotic genome, sequence analysis software, annotation software, bio.tools

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Prokka

Resource ID: SCR_014732

Alternate IDs: OMICS_04220, biotools:prokka

Alternate URLs: <https://bio.tools/prokka>, <https://sources.debian.org/src/prokka/>, <https://sources.debian.org/src/prokka/>

License: General Public License version 2

Record Creation Time: 20220129T080322+0000

Record Last Update: 20260829T182502+0000

Ratings and Alerts

No rating or validation information has been found for Prokka.

No alerts have been found for Prokka.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4882 mentions in open access literature.

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

Withatanung P, et al. (2026) Genomic diversity and clade clustering of Burkholderia pseudomallei and B. thailandensis prophages with soil-derived phages. iScience, 29(2), 114658.

Modlin SJ, et al. (2026) Pervasive genome structure heterogeneity in Mycobacterium tuberculosis constitutively generates subpopulations with distinct clinical phenotypes. iScience, 29(5), 115045.

Lobel L, et al. (2026) Dietary sulfur amino acids enhance anti-tumor immunity in colon cancer via an NKT cell-XCL1-cDC1 circuit. Immunity, 59(6), 1708.

Lu Q, et al. (2026) Genomic characterization and pathogenicity validation of Mycoplasma ovipneumoniae strains from diseased sheep: insights into potential pathogenic mechanisms of GSWW364. Veterinary research, 57(1).

Villette R, et al. (2025) Human gut microbiome gene co-expression network reveals a loss in taxonomic and functional diversity in Parkinson's disease. NPJ biofilms and microbiomes, 11(1), 142.

Light-Maka I, et al. (2025) Bronze Age Yersinia pestis genome from sheep sheds light on hosts and evolution of a prehistoric plague lineage. Cell.

Levé M, et al. (2025) Metabolomics and metagenomics in mice reveal the role of the gut microbiota in tryptophan metabolism. iScience, 28(11), 113751.

Ono M, et al. (2025) Identifying genetic variations in emm89 Streptococcus pyogenes associated with severe invasive infections. eLife, 14.

Unitt A, et al. (2025) Neisseria gonorrhoeae LIN codes provide a robust, multi-resolution lineage nomenclature. eLife, 14.

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

Villette R, et al. (2025) Integrated multi-omics highlights alterations of gut microbiome functions in prodromal and idiopathic Parkinson's disease. *Microbiome*, 13(1), 200.

Sia CM, et al. (2025) Distinct adaptation and epidemiological success of different genotypes within *Salmonella enterica* serovar Dublin. *eLife*, 13.

Mehta I, et al. (2025) Control of pili synthesis and putrescine homeostasis in *Escherichia coli*. *eLife*, 13.

Scadden J, et al. (2025) The nisin O cluster: species dissemination, candidate leader peptide proteases and the role of regulatory systems. *Microbiology (Reading, England)*, 171(2).

Fernández-Fernández R, et al. (2025) Genomic Analysis of Bacteriocin-Producing *Staphylococci*: High Prevalence of Lanthipeptides and the Micrococцин P1 Biosynthetic Gene Clusters. *Probiotics and antimicrobial proteins*, 17(1), 159.

Chen J, et al. (2025) Adaptation for *Staphylococcus aureus* to hosts via insertion mutation in the accessory gene regulator *agrC* gene: decreased virulence and enhanced persistence capacity. *Microbiology spectrum*, 13(1), e0149724.

Hameed A, et al. (2025) *Neobacillus driksii* sp. nov. isolated from a Mars 2020 spacecraft assembly facility and genomic potential for lasso peptide production in *Neobacillus*. *Microbiology spectrum*, 13(1), e0137624.

Jiang Y, et al. (2025) GutMetaNet: an integrated database for exploring horizontal gene transfer and functional redundancy in the human gut microbiome. *Nucleic acids research*, 53(D1), D772.

Hamed SM, et al. (2025) *Pseudocitrobacter cyperus*, a novel bacterial species recovered from *Cyperus alternifolius* in Egypt. *BMC microbiology*, 25(1), 20.

Wu Y, et al. (2025) Hotspots of genetic change in *Yersinia pestis*. *Nature communications*, 16(1), 388.