Resource Summary Report

Generated by dkNET on Sep 18, 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

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: 20260912T195821+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 dkNET .

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.

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

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.

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

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

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).

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

Mangin CC, et al. (2025) Magnetotactic bacteria affiliated with diverse Pseudomonadota families biomineralize intracellular Ca-carbonate. The ISME journal, 19(1).

Duan X, et al. (2025) Exploration of the feasibility of clinical application of phage treatment for multidrug-resistant Serratia marcescens-induced pulmonary infection. Emerging microbes & infections, 14(1), 2451048.

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

O'Brien B, et al. (2025) Subtle genomic differences in Klebsiella pneumoniae sensu stricto isolates indicate host adaptation. One health (Amsterdam, Netherlands), 20, 100970.

Zhao K, et al. (2025) IS15DIV-flanked composite transposon harboring bla NDM-5 in multidrug-resistant Salmonella Typhimurium. iScience, 28(2), 111720.

Guo W, et al. (2025) In silico design of a multi-epitope vaccine against Mycobacterium avium subspecies paratuberculosis. Frontiers in immunology, 16, 1505313.