

Resource Summary Report

Generated by T1D on Jul 31, 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 processing software, sequence analysis software, data analysis software, software resource, software application

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: 20260731T042915+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 4876 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

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*.

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.

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.

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.

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

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).

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

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

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.

- Pe?ka K, et al. (2025) Probiotic potential of *Bacillus* Isolates from Polish Bee Pollen and Bee Bread. *Probiotics and antimicrobial proteins*, 17(1), 364.
- 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.
- Wu Y, et al. (2025) Hotspots of genetic change in *Yersinia pestis*. *Nature communications*, 16(1), 388.
- An H, et al. (2025) Genomic and virulent characterization of a duck-associated *Salmonella* serovar Potsdam from China. *Poultry science*, 104(1), 104646.
- Banerjee G, et al. (2025) Deep sequencing-derived Metagenome Assembled Genomes from the gut microbiome of liver transplant patients. *Scientific data*, 12(1), 39.
- Gray HA, et al. (2025) Genomic epidemiology of extended-spectrum beta-lactamase-producing *Escherichia coli* from humans and a river in Aotearoa New Zealand. *Microbial genomics*, 11(1).
- Hamed SM, et al. (2025) *Pseudocitrobacter cyperus*, a novel bacterial species recovered from *Cyperus alternifolius* in Egypt. *BMC microbiology*, 25(1), 20.
- Xu ZS, et al. (2025) High-throughput analysis of microbiomes in a meat processing facility: are food processing facilities an establishment niche for persisting bacterial communities? *Microbiome*, 13(1), 25.
- Zhao K, et al. (2025) IS15DIV-flanked composite transposon harboring bla NDM-5 in multidrug-resistant *Salmonella* Typhimurium. *iScience*, 28(2), 111720.