

Resource Summary Report

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

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: 20260801T190516+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 [PRECISE-TBI](#) .

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.

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.

Oh JY, et al. (2025) Whole genome sequencing analysis of enteropathogenic *Escherichia coli* from human and companion animals in Korea. *Journal of veterinary science*, 26(1), e1.

Kamilari E, et al. (2025) *Bacillus safensis* APC 4099 has broad-spectrum antimicrobial activity against both bacteria and fungi and produces several antimicrobial peptides, including the novel circular bacteriocin safencin E. *Applied and environmental microbiology*, 91(1), e0194224.

An H, et al. (2025) Genomic and virulent characterization of a duck-associated *Salmonella* serovar Potsdam from China. *Poultry science*, 104(1), 104646.

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

Daussin A, et al. (2025) *Flavobacterium aerium* sp. nov., a bacterium isolated from the air of the Icelandic volcanic island Surtsey. *International journal of systematic and evolutionary microbiology*, 75(1).

Wang C, et al. (2025) Discovery of Novel Diagnostic Biomarkers for Common Pathogenic *Nocardia* Through Pan-Genome and Comparative Genome Analysis, with Preliminary Validation. *Pathogens (Basel, Switzerland)*, 14(1).

Leijon M, et al. (2025) Characterization of Esocid Herpesvirus 1 (EsHV1) from Europe. *Pathogens (Basel, Switzerland)*, 14(1).

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.