

Resource Summary Report

Generated by [RRID](#) on Aug 15, 2026

Pharokka

RRID:SCR_026017

Type: Tool

Proper Citation

Pharokka (RRID:SCR_026017)

Resource Information

URL: <https://github.com/gbouras13/pharokka>

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Description: Software fast scalable bacteriophage genome annotation tool. Used to annotate bacteriophage genomes easily, rapidly and consistently with standards compliant outputs.

Resource Type: data processing software, software application, data analysis software, source code, software resource

Defining Citation: [PMID:36453861](#)

Keywords: bacteriophage genome, annotation, bacteriophage genome annotation,

Funding: National Health and Medical Research Council Investigator

Availability: Free, Available for download, Freely available

Resource Name: Pharokka

Resource ID: SCR_026017

License: MIT license

Record Creation Time: 20241106T053253+0000

Record Last Update: 20260815T042945+0000

Ratings and Alerts

No rating or validation information has been found for Pharokka.

No alerts have been found for Pharokka.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Black KA, et al. (2026) Resolution of a T1-Like Bacteriophage Outbreak by Receptor Engineering. *Molecular biotechnology*, 68(3), 1411.

Mancini A, et al. (2026) Genomic and functional analysis of stress-responsive prophages in *Lactobacillus helveticus*. *Frontiers in microbiology*, 17, 1819103.

Chong Q, et al. (2026) Systematic evaluation of phage cocktail-ciprofloxacin combination therapy against multidrug-resistant *Salmonella* Typhimurium induced gut dysbiosis. *Microbiology spectrum*, 14(5), e0264025.

Ramirez AL, et al. (2026) Metagenomic analysis of the human gut virome reveals functional signatures and viral stability across hospitalized and non-hospitalized diarrheal and non-diarrheal individuals. *Gut pathogens*, 18(1).

Barchi Y, et al. (2025) Characterization of strictly lytic phages infecting *Oenococcus oeni* from Merlot wines and proposal of a new genus. *Microbiology spectrum*, 13(9), e0258824.

Tian Y, et al. (2024) Role of hypothetical protein PA1-LRP in antibacterial activity of endolysin from a new *Pantoea* phage PA1. *Frontiers in microbiology*, 15, 1463192.

Kosmopoulos JC, et al. (2024) Viromes vs. mixed community metagenomes: choice of method dictates interpretation of viral community ecology. *Microbiome*, 12(1), 195.

Chen H, et al. (2024) A *Klebsiella*-phage cocktail to broaden the host range and delay bacteriophage resistance both in vitro and in vivo. *NPJ biofilms and microbiomes*, 10(1), 127.

Shao B, et al. (2024) A long-context language model for deciphering and generating bacteriophage genomes. *Nature communications*, 15(1), 9392.

Kosmopoulos JC, et al. (2023) Viromes vs. mixed community metagenomes: choice of method dictates interpretation of viral community ecology. *bioRxiv : the preprint server for biology*.