

Resource Summary Report

Generated by [Kravitz](#) on Sep 16, 2026

DeePhage

RRID:SCR_019243

Type: Tool

Proper Citation

DeePhage (RRID:SCR_019243)

Resource Information

URL: <http://cqb.pku.edu.cn/ZhuLab/DeePhage>

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Description: Software tool to distinguish virulent and temperate phage derived sequences in metavirome data with deep learning approach. Used to identify virome sequences as temperate phage derived or virulent phage derived fragments.

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

Keywords: Metavirome data, identify virome sequences, derived fragment, distinguish phage derived sequences, temperate phage sequences, virulent phage sequences, deep learning

Resource Name: DeePhage

Resource ID: SCR_019243

Alternate URLs: <https://github.com/shufangwu/DeePhage>

License: GNU GPLv3

Record Creation Time: 20220129T080344+0000

Record Last Update: 20260912T195911+0000

Ratings and Alerts

No rating or validation information has been found for DeePhage.

No alerts have been found for DeePhage.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Wang B, et al. (2026) Elevated temperature simulating heatwaves restructures active nitrifying communities and associated viruses in tidal flats and agricultural soils. The ISME journal, 20(1).

Liu Z, et al. (2026) Metagenomic analysis of the DNA virome communities in swine lungs. Frontiers in microbiology, 17, 1798033.

Fang L, et al. (2025) Ciprofloxacin-driven purifying selection on viral genomes accelerates soil N₂O production. Proceedings of the National Academy of Sciences of the United States of America, 122(29), e2503199122.

Wu S, et al. (2021) DeePhage: distinguishing virulent and temperate phage-derived sequences in metavirome data with a deep learning approach. GigaScience, 10(9).