

Resource Summary Report

Generated by SPARC SAWG on Aug 9, 2026

SpikeHunter

RRID:SCR_024831

Type: Tool

Proper Citation

SpikeHunter (RRID:SCR_024831)

Resource Information

URL: <https://github.com/nlm-irp-jianglab/SpikeHunter>

Proper Citation: SpikeHunter (RRID:SCR_024831)

Description: Software deep learning tool for identifying phage tailspike proteins. Used to identify phage tailspike proteins.

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

Defining Citation: [PMID:37503040](#)

Keywords: identifying phage tailspike proteins, phage tailspike protein, depolymerase, right-handed beta-helix,

Funding: NLM ;
NSF

Availability: Free, Available for download, Freely available

Resource Name: SpikeHunter

Resource ID: SCR_024831

License: MIT license

Record Creation Time: 20240104T050329+0000

Record Last Update: 20260808T190714+0000

Ratings and Alerts

No rating or validation information has been found for SpikeHunter.

No alerts have been found for SpikeHunter.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Yang Y, et al. (2024) Large-scale genomic survey with deep learning-based method reveals strain-level phage specificity determinants. GigaScience, 13.