

Resource Summary Report

Generated by SPARC SAWG on Sep 16, 2026

smashpp

RRID:SCR_018307

Type: Tool

Proper Citation

smashpp (RRID:SCR_018307)

Resource Information

URL: <https://github.com/smortezah/smashpp>

Proper Citation: smashpp (RRID:SCR_018307)

Description: Software tool to find and visualize rearrangements in DNA sequences.

Synonyms: Smash++

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

Keywords: Find sequence rearrangement, visualize sequence rearrangement, DNA, DNA sequence, DNA sequence rearrangement, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: smashpp

Resource ID: SCR_018307

Alternate IDs: biotools:smashpp, BioTools:smashpp

Alternate URLs: <https://bio.tools/smashpp>, <https://bio.tools/smashpp>, <https://bio.tools/smashpp>

License: GNU General Public License v3.0

Record Creation Time: 20220129T080339+0000

Record Last Update: 20260912T195859+0000

Ratings and Alerts

No rating or validation information has been found for smashpp.

No alerts have been found for smashpp.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Dieckmann AL, et al. (2021) Genome and Methylome analysis of a phylogenetic novel *Campylobacter coli* cluster with *C. jejuni* introgression. *Microbial genomics*, 7(10).

Hosseini M, et al. (2020) Smash++: an alignment-free and memory-efficient tool to find genomic rearrangements. *GigaScience*, 9(5).