

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

SmashCommunity

RRID:SCR_013245

Type: Tool

Proper Citation

SmashCommunity (RRID:SCR_013245)

Resource Information

URL: <http://www.bork.embl.de/software/smash/>

Proper Citation: SmashCommunity (RRID:SCR_013245)

Description: A stand-alone metagenomic annotation and analysis pipeline suitable for data from Sanger and 454 sequencing technologies.

Abbreviations: SmashCommunity

Resource Type: software resource

Resource Name: SmashCommunity

Resource ID: SCR_013245

Alternate IDs: OMICS_01482

Record Creation Time: 20220129T080315+0000

Record Last Update: 20260725T190748+0000

Ratings and Alerts

No rating or validation information has been found for SmashCommunity.

No alerts have been found for SmashCommunity.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Yang B, et al. (2024) Analysis of the composition and function of rhizosphere microbial communities in plants with tobacco bacterial wilt disease and healthy plants. Microbiology spectrum, 12(12), e0055924.

Raj A, et al. (2021) Tapping the Role of Microbial Biosurfactants in Pesticide Remediation: An Eco-Friendly Approach for Environmental Sustainability. Frontiers in microbiology, 12, 791723.

Voigt AY, et al. (2015) Temporal and technical variability of human gut metagenomes. Genome biology, 16(1), 73.

Mandal RS, et al. (2015) Metagenomic surveys of gut microbiota. Genomics, proteomics & bioinformatics, 13(3), 148.

Thangam M, et al. (2015) CRCDA--Comprehensive resources for cancer NGS data analysis. Database : the journal of biological databases and curation, 2015.

Zeller G, et al. (2014) Potential of fecal microbiota for early-stage detection of colorectal cancer. Molecular systems biology, 10(11), 766.

Illegghems K, et al. (2012) Phylogenetic analysis of a spontaneous cocoa bean fermentation metagenome reveals new insights into its bacterial and fungal community diversity. PloS one, 7(5), e38040.

Prakash T, et al. (2012) Functional assignment of metagenomic data: challenges and applications. Briefings in bioinformatics, 13(6), 711.