

Resource Summary Report

Generated by [PRECISE-TBI](#) on Aug 9, 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: 20260808T185954+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 [PRECISE-TBI](#) .

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.

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

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

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

Illeghems 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.