

Resource Summary Report

Generated by [kravitz2](#) on Sep 4, 2026

Mash

RRID:SCR_019135

Type: Tool

Proper Citation

Mash (RRID:SCR_019135)

Resource Information

URL: <https://github.com/marbl/Mash>

Proper Citation: Mash (RRID:SCR_019135)

Description: Software tool for genome and metagenome distance estimation using MinHash. Reduces large sequences and sequence sets to small, representative sketches, from which global mutation distances can be rapidly estimated.

Resource Type: data analytics software, software application, software resource

Defining Citation: [PMID:27323842](#)

Keywords: Genome distance estimation, metagenome distance estimation, MinHash, mutation distance, sequence, sequence set

Funding: NHGRI ;
NIH

Availability: Free, Available for download, Freely available

Resource Name: Mash

Resource ID: SCR_019135

Alternate IDs: OMICS_10468

Alternate URLs: <https://mash.readthedocs.io/en/latest/>,
<https://sources.debian.org/src/mash/>

License: BSD license

Record Creation Time: 20220129T080343+0000

Record Last Update: 20260904T000546+0000

Ratings and Alerts

No rating or validation information has been found for Mash.

No alerts have been found for Mash.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 75 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Sauerborn E, et al. (2026) Resolving plasmid-encoded carbapenem resistance dynamics and reservoirs in a hospital setting through nanopore sequencing. *Microbial genomics*, 12(2).

van Gorp E, et al. (2026) Ambler class C-type β -lactamases and porin alterations in *Enterobacter cloacae* complex and *Klebsiella aerogenes* in the Netherlands, 2012-2023. *BMC microbiology*, 26(1).

Yu Q, et al. (2026) Diversity and evolution of a phase-variable multi-locus antigen in *Neisseria gonorrhoeae*. *bioRxiv : the preprint server for biology*.

Tao J, et al. (2026) Identification of a novel SXT/R391 integrative and conjugative element harboring bla NDM-1 in a clinical *Providencia huaxiensis* isolate. *Frontiers in microbiology*, 17, 1818759.

Hernández-Velázquez R, et al. (2026) Metagenomic insight into the diversity and biogeochemical functions of microbial communities in the maar tropical Lake Atexcac. *Microbiology (Reading, England)*, 172(6).

Mbwana JR, et al. (2026) Molecular characterisation of extended-Spectrum-Beta-lactamase-producing *Klebsiella pneumoniae* among children and chicken in the rural Korogwe District, Tanzania. *One health (Amsterdam, Netherlands)*, 23, 101472.

Kim DD, et al. (2026) Metagenomic strain tracking reveals patterns of bacterial spread and the impact of water chlorination. *medRxiv : the preprint server for health sciences*.

Diop A, et al. (2026) Genomic Characterization of *Salmonella* Isolates Causing Infections in Children with Sickle Cell Disease in Dakar, Senegal. *Microorganisms*, 14(2).

Karama I, et al. (2026) Asymptomatic Carriage and Antimicrobial Resistance of *Salmonella* in Humans and Poultry in Rural Burkina Faso: Phenotypic and Genotypic Profiles and Associated Risk Factors. *Microorganisms*, 14(2).

Cavka M, et al. (2026) Phenotypic and Whole-Genome Sequencing-Based Profiling of Antimicrobial Resistance and Virulence in *Pseudomonas aeruginosa* Isolated from Patients with Ventilator-Associated Pneumonia and Ventilator-Associated Tracheobronchitis in a Croatian Intensive Care Unit. *Genes*, 17(2).

Vatansever C, et al. (2026) Emergence of carbapenem-resistant putative hypervirulent *Klebsiella pneumoniae* ST147 with a distinct hybrid plasmid in Türkiye. *Emerging microbes & infections*, 15(1), 2653280.

Yu Q, et al. (2026) Diversity and evolution of a phase-variable multi-locus antigen in *Neisseria gonorrhoeae*. *PLoS pathogens*, 22(5), e1013962.

Huang X, et al. (2026) Conformations and sequence determinants in the lipid binding of an adhesive peptide derived from *Vibrio cholerae* biofilms. *PLoS pathogens*, 22(2), e1013990.

McClain HM, et al. (2026) Integrase-On-Demand: bioprospecting integrases for targeted genomic insertion of genetic cargo. *Nucleic acids research*, 54(4).

Valverde G, et al. (2026) An ancient genome of *Streptococcus pyogenes* from a pre-Columbian Bolivian mummy. *Nature communications*, 17(1).

Kidenya BR, et al. (2025) Multidrug resistant hypervirulent ST307 clone from genomic surveillance of extended spectrum beta-lactamase-producing *Klebsiella pneumoniae* species complex in East Africa. *BMC microbiology*, 25(1), 755.

Kavanagh NL, et al. (2025) Co-carriage of diverse vancomycin-resistant *Enterococcus faecium* ST80-lineages by 70% of patients in an Irish hospital. *JAC-antimicrobial resistance*, 7(3), dlaf065.

Azam S, et al. (2025) Advancing the Indian cattle pangenome: characterizing non-reference sequences in *Bos indicus*. *Journal of animal science and biotechnology*, 16(1), 21.

Xu Z, et al. (2025) PISAD: reference-free intraspecies sample anomalies detection tool based on k-mer counting. *GigaScience*, 14.

Aguilar-Bultet L, et al. (2025) Genetic Cluster of Extended-Spectrum β -lactamase-Producing *Klebsiella pneumoniae* in Humans and Food, Switzerland, 2018-2019. *Emerging infectious diseases*, 31(10), 2017.