

Resource Summary Report

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FastANI

RRID:SCR_021091

Type: Tool

Proper Citation

FastANI (RRID:SCR_021091)

Resource Information

URL: <https://github.com/ParBLiSS/FastANI>

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Description: Software tool for fast alignment free computation of whole genome Average Nucleotide Identity . Supports pairwise comparison of both complete and draft genome assemblies. to calculate the average nucleotide identity (ANI) between your samples.

Synonyms: Fast Whole Genome Similarity Estimation

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

Keywords: whole genome, Average Nucleotide Identity, ANI, alignment identity estimates, whole genome, similarity estimation

Availability: Free, Available for download, Freely available

Resource Name: FastANI

Resource ID: SCR_021091

License: Apache License 2.0

Record Creation Time: 20220129T080353+0000

Record Last Update: 20260812T044407+0000

Ratings and Alerts

No rating or validation information has been found for FastANI.

No alerts have been found for FastANI.

Data and Source Information

Usage and Citation Metrics

We found 336 mentions in open access literature.

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

Rahimian M, et al. (2026) Genomic landscape of biosynthetic gene clusters in Iranian extremophiles reveals prolific metabolite potential, prophage associations, and integrated defensive-metabolic islands. BMC microbiology, 26(1).

Kocsub?? S, et al. (2026) Pseudomonas rhizozeae sp. nov., originated from rhizosphere soil of corn field. Scientific reports, 16(1).

Ge G, et al. (2026) Isolation, identification and genomic analysis of Mycobacterium caprae strain SY-1 from Chinese sika deer (Cervus nippon). BMC genomics, 27(1), 184.

Protic IA, et al. (2026) Comparative genomic analyses shed light on the introduction routes of rice-pathogenic Burkholderia gladioli strains into Bangladesh. BMC genomics, 27(1), 121.

Li M, et al. (2026) Intricate chemosymbiosis in a widespread shallow-water thyasirid clam. Science advances, 12(10), eadw8163.

Quan K, et al. (2026) Machine learning-based prediction of BV-relevant probiotic functional potential in vaginal-derived Lactobacillus crispatus strains. BMC microbiology, 26(1).

Huang J, et al. (2026) RejuAgro A as an antimicrobial for fire blight control of pome fruits and beyond. Nature communications, 17(1).

Delbaje E, et al. (2026) Evidence that increased azole persistence and stress resistance precede the in vivo evolution of azole resistance in Aspergillus fumigatus. Microbiology spectrum, 14(4), e0402125.

Achudhan AB, et al. (2026) Metagenome Sequencing and Recovery of 52 Microbial Genomes from Plastic-Polluted Coastal Sediment. Scientific data, 13(1).

Azour A, et al. (2026) Plasmid-Driven Resistome Diversity in 9700 Escherichia coli Genomes Across Phylogroups and Sequence Types. Antibiotics (Basel, Switzerland), 15(3).

Payne CJ, et al. (2026) Are the genomes of motile Aeromonas species from the aquatic environment shaped by local geography and host species? Microbial genomics, 12(4).

Zhou J, et al. (2026) Ornithinibacillus liuyingii sp. nov.: a novel multidrug-resistant and potentially pathogenic bacterium isolated from Apodemus chevrieri lung tissue. BMC microbiology, 26(1).

Schwarzthans A, et al. (2026) Stable association of a chlamydial symbiont with the freshwater predator hydra suggests broad host potential. *The ISME journal*, 20(1).

Huang J, et al. (2026) Comparative genomic analysis of antimicrobial resistance and virulence in *Escherichia coli* isolated from pigeons and chickens in live poultry markets, Guiyang, China. *Poultry science*, 105(8), 107119.

Jehanne Q, et al. (2026) Contributions of whole-genome sequencing to the epidemiological monitoring of *Campylobacter* spp. in France. *Antimicrobial agents and chemotherapy*, 70(7), e0019326.

Fan F, et al. (2026) Meropenem stress drives lipid remodeling and resistance gene dissemination via outer membrane vesicles in carbapenem-resistant *Klebsiella pneumoniae*. *Current research in microbial sciences*, 11, 100616.

Zhou K, et al. (2026) vClassifier: a toolkit for high-resolution phylogenetic classification of prokaryotic viruses. *Bioinformatics advances*, 6(1), vbag149.

Ozawa M, et al. (2026) Evidence for Genotype-Associated Differences in Disease Severity and Limitations of Serotype-Based Classification in *Glaesserella parasuis* Revealed by Whole-Genome Sequencing in Japan. *Pathogens (Basel, Switzerland)*, 15(6).

Maeno S, et al. (2026) Discordance Between 16S rRNA Similarity and Genome-Based Species Boundaries in *Gluconobacter*. *MicrobiologyOpen*, 15(3), e70335.

Garcia-Candela E, et al. (2026) Phylogenomic and comparative genomic analyses of *Aeromonas* spp. from South American aquatic systems reveal extensive genomic diversity, antimicrobial resistance, and predicted human pathogenicity. *Frontiers in microbiology*, 17, 1823138.