

Resource Summary Report

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Anvi'o

RRID:SCR_021802

Type: Tool

Proper Citation

Anvi'o (RRID:SCR_021802)

Resource Information

URL: <https://anvio.org>

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Description: Open source software analysis and visualization platform for microbial omics including genomics, metagenomics, metatranscriptomics, pangenomics, metapangenomics, phylogenomics, and microbial population genetics in integrated fashion through extensive interactive visualization capabilities.

Synonyms: Anvi'o

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

Keywords: analysis, visualization, integrated omics, metagenomics, pangenomics, phylogenomics, microbial omics

Funding: Alfred P. Sloan Foundation ;
Helmholtz Institute for Functional Marine Biodiversity ;
Marine Biological Laboratory ;
Simons Foundation ;
University of Chicago ;
W. M. Keck Foundation

Availability: Free, Available for download, Freely available

Resource Name: Anvi'o

Resource ID: SCR_021802

Alternate IDs: biotools:anvio

Alternate URLs: <https://github.com/merenlab/anvio>, <https://bio.tools/anvio>

License: GNU General Public License v3.0

Record Creation Time: 20220129T080357+0000

Record Last Update: 20260912T200001+0000

Ratings and Alerts

No rating or validation information has been found for Anvi'o.

No alerts have been found for Anvi'o.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 21 mentions in open access literature.

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

Thygesen VFDF, et al. (2026) The genomic history of Streptococcus mutans from the Mesolithic until modern times. Genome biology, 27(1).

Lean SS, et al. (2025) The Road Less Traveled: Exploring the Genomic Characteristics and Antimicrobial Resistance Potential of Acinetobacter baumannii From the Indigenous Orang Asli Community in Peninsular Malaysia. MicrobiologyOpen, 14(5), e70073.

Kananen K, et al. (2025) Adaptive adjustment of profile HMM significance thresholds improves functional and metabolic insights into microbial genomes. Bioinformatics advances, 5(1), vbaf039.

Velo-Suarez L, et al. (2025) Genomic diversity in Porphyromonas: evidence of Porphyromonas catoniae commensality in lungs. Microbial genomics, 11(6).

Xu CCY, et al. (2025) Pre-exposure to stress reduces loss of community and genetic diversity following severe environmental disturbance. Current biology : CB, 35(5), 1061.

Bech PK, et al. (2024) Succession of microbial community composition and secondary metabolism during marine biofilm development. ISME communications, 4(1), ycae006.

Veseli I, et al. (2024) Digital Microbe: a genome-informed data integration framework for team science on emerging model organisms. Scientific data, 11(1), 967.

Kiefl E, et al. (2023) Structure-informed microbial population genetics elucidate selective pressures that shape protein evolution. Science advances, 9(8), eabq4632.

Gilroy R, et al. (2023) An initial genomic blueprint of the healthy human oesophageal microbiome. Access microbiology, 5(6).

Baker JL, et al. (2023) Illuminating the oral microbiome and its host interactions: recent advancements in omics and bioinformatics technologies in the context of oral microbiome research. *FEMS microbiology reviews*, 47(5).

Fogarty EC, et al. (2023) A highly conserved and globally prevalent cryptic plasmid is among the most numerous mobile genetic elements in the human gut. *bioRxiv : the preprint server for biology*.

Chan DTC, et al. (2023) Revealing the Host-Dependent Nature of an Engineered Genetic Inverter in Concordance with Physiology. *Biodesign research*, 5, 0016.

Gaïa M, et al. (2023) Mirusviruses link herpesviruses to giant viruses. *Nature*, 616(7958), 783.

Hochart C, et al. (2023) Ecology of Endozoicomonadaceae in three coral genera across the Pacific Ocean. *Nature communications*, 14(1), 3037.

O'Banion BS, et al. (2023) Plant myo-inositol transport influences bacterial colonization phenotypes. *Current biology : CB*, 33(15), 3111.

Cornet L, et al. (2022) The GEN-ERA toolbox: unified and reproducible workflows for research in microbial genomics. *GigaScience*, 12.

McCauley KE, et al. (2022) Heritable vaginal bacteria influence immune tolerance and relate to early-life markers of allergic sensitization in infancy. *Cell reports. Medicine*, 3(8), 100713.

Vanni C, et al. (2022) Unifying the known and unknown microbial coding sequence space. *eLife*, 11.

Nanjani S, et al. (2022) Genome analysis uncovers the prolific antagonistic and plant growth-promoting potential of endophyte *Bacillus velezensis* K1. *Gene*, 836, 146671.

Bulankova P, et al. (2021) Mitotic recombination between homologous chromosomes drives genomic diversity in diatoms. *Current biology : CB*, 31(15), 3221.