

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: 20260821T194216+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 [nidm-terms](#).

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.