

Resource Summary Report

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AGORA

RRID:SCR_005070

Type: Tool

Proper Citation

AGORA (RRID:SCR_005070)

Resource Information

URL: <http://www.biomedcentral.com/1471-2105/13/189>

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Description: An algorithm to use optical map information directly within the de Bruijn graph framework to help produce an accurate assembly of a genome that is consistent with the optical map information provided. AGORA takes as input two data structures: OpMap ? an ordered list of fragment sizes representing the optical map; and Edges ? a list of de Bruijn graph edges with their corresponding sequences.

Abbreviations: AGORA

Synonyms: Assembly Guided by Optical Restriction Alignment

Resource Type: software resource

Defining Citation: [PMID:22856673](#)

Keywords: genome assembly, genome, reconstruction

Funding:

Resource Name: AGORA

Resource ID: SCR_005070

Alternate IDs: OMICS_00039

Record Creation Time: 20220129T080228+0000

Record Last Update: 20250420T014243+0000

Ratings and Alerts

No rating or validation information has been found for AGORA.

No alerts have been found for AGORA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 79 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Nychas E, et al. (2025) Discovery of robust and highly specific microbiome signatures of non-alcoholic fatty liver disease. *Microbiome*, 13(1), 10.

Qian Y, et al. (2025) A data-driven modeling framework for mapping genotypes to synthetic microbial community functions. *bioRxiv : the preprint server for biology*.

Carr A, et al. (2024) Personalized *Clostridioides difficile* engraftment risk prediction and probiotic therapy assessment in the human gut. *bioRxiv : the preprint server for biology*.

Al-Nijir M, et al. (2024) Metabolic modelling uncovers the complex interplay between fungal probiotics, poultry microbiomes, and diet. *Microbiome*, 12(1), 267.

Vavougios GD, et al. (2024) SARS-CoV-2-Induced Type I Interferon Signaling Dysregulation in Olfactory Networks Implications for Alzheimer's Disease. *Current issues in molecular biology*, 46(5), 4565.

Gelbach PE, et al. (2024) Flux sampling in genome-scale metabolic modeling of microbial communities. *BMC bioinformatics*, 25(1), 45.

Xu Q, et al. (2024) Simulate Scientific Reasoning with Multiple Large Language Models: An Application to Alzheimer's Disease Combinatorial Therapy. *medRxiv : the preprint server for health sciences*.

Zhu J, et al. (2024) Integrative analysis with microbial modelling and machine learning uncovers potential alleviators for ulcerative colitis. *Gut microbes*, 16(1), 2336877.

Yu W, et al. (2024) Disease-Associated Neurotoxic Astrocyte Markers in Alzheimer Disease Based on Integrative Single-Nucleus RNA Sequencing. *Cellular and molecular neurobiology*,

44(1), 20.

Wright CJ, et al. (2024) Comparative genomics reveals the dynamics of chromosome evolution in Lepidoptera. *Nature ecology & evolution*, 8(4), 777.

Najer T, et al. (2024) Mitochondrial genome fragmentation is correlated with increased rates of molecular evolution. *PLoS genetics*, 20(5), e1011266.

Tassoulas LJ, et al. (2024) Insights into the action of the pharmaceutical metformin: Targeted inhibition of the gut microbial enzyme agmatinase. *iScience*, 27(2), 108900.

Groen In 't Woud S, et al. (2024) Genetic and environmental factors driving congenital solitary functioning kidney. *Nephrology, dialysis, transplantation : official publication of the European Dialysis and Transplant Association - European Renal Association*, 39(3), 463.

Park T, et al. (2024) Genome-wide transcriptome analysis of A β deposition on PET in a Korean cohort. *Alzheimer's & dementia : the journal of the Alzheimer's Association*, 20(12), 8787.

Hedin KA, et al. (2024) *Saccharomyces boulardii* enhances anti-inflammatory effectors and AhR activation via metabolic interactions in probiotic communities. *The ISME journal*, 18(1).

Balzerani F, et al. (2024) q2-metnet: QIIME2 package to analyse 16S rRNA data via high-quality metabolic reconstructions of the human gut microbiota. *Bioinformatics (Oxford, England)*, 40(11).

Srinak N, et al. (2024) Metabolic cross-feeding interactions modulate the dynamic community structure in microbial fuel cell under variable organic loading wastewaters. *PLoS computational biology*, 20(10), e1012533.

Román L, et al. (2024) Genome-scale metabolic modeling of the human milk oligosaccharide utilization by *Bifidobacterium longum* subsp. *infantis*. *mSystems*, 9(3), e0071523.

Zhang Z, et al. (2024) Complete telomere-to-telomere genomes uncover virulence evolution conferred by chromosome fusion in oomycete plant pathogens. *Nature communications*, 15(1), 4624.

Wang Y, et al. (2024) The association between circulating CD34+CD133+ endothelial progenitor cells and reduced risk of Alzheimer's disease in the Framingham Heart Study. *Exploration of medicine*, 5(2), 193.