

Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

[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

Resource Name: AGORA

Resource ID: SCR_005070

Alternate IDs: OMICS_00039

Record Creation Time: 20220129T080228+0000

Record Last Update: 20260801T190245+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 99 mentions in open access literature.

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

Wang G, et al. (2025) Genomic evidence for hybridization and introgression between blue peafowl and endangered green peafowl and molecular foundation of leucistic plumage of blue peafowl. *GigaScience*, 14.

Ray NR, et al. (2025) Local genetic covariance analysis with lipid traits identifies novel loci for early-onset Alzheimer's Disease. *PLoS genetics*, 21(3), e1011631.

Eissman JM, et al. (2025) Sex-Specific Genetic Drivers of Memory, Executive Functioning, and Language Performance in Older Adults. *medRxiv : the preprint server for health sciences*.

Bernard C, et al. (2025) EdgeHOG: a method for fine-grained ancestral gene order inference at large scale. *Nature ecology & evolution*, 9(10), 1951.

Lorenz A, et al. (2025) The effect of Alzheimer's disease genetic factors on limbic white matter microstructure. *Alzheimer's & dementia : the journal of the Alzheimer's Association*, 21(4), e70130.

Temple SD, et al. (2025) Multiple-testing corrections in case-control studies using identity-by-descent segments. *bioRxiv : the preprint server for biology*.

Martínez-González MA, et al. (2025) Recent advances in precision nutrition and cardiometabolic diseases. *Revista espanola de cardiologia (English ed.)*, 78(3), 263.

Huang J, et al. (2025) The impact of blood MCP-1 levels on Alzheimer's disease with genetic variation at the NAV3 and UNC5C loci. *Translational psychiatry*, 15(1), 296.

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

Mofidifar S, et al. (2025) Reducing redundancy and enhancing accuracy through a phylogenetically-informed microbial community metabolic modeling approach. *Bioinformatics (Oxford, England)*, 41(7).

Genc DE, et al. (2025) Exploring the role of gut microbiota in rheumatoid arthritis: the effects of diet and drug supplementation. *BMC rheumatology*, 9(1), 71.

Ovalle A, et al. (2025) A rationally designed microbial consortium modulates neurodegeneration in a *Drosophila melanogaster* model of Parkinson's disease. *NPJ*

biofilms and microbiomes, 11(1), 185.

Jiang B, et al. (2025) Neuronal subtype-specific metabolic changes in neurodegenerative and neuropsychiatric diseases predicted via a systems biology-based approach. bioRxiv : the preprint server for biology.

Fässler D, et al. (2025) Characterising functional redundancy in microbiome communities via relative entropy. Computational and structural biotechnology journal, 27, 1482.

Du Z, et al. (2025) Genome architecture evolution in an invasive copepod species complex. Nature communications, 16(1), 10312.

Gutierrez MW, et al. (2025) Early-life gut mycobiome core species modulate metabolic health in mice. Nature communications, 16(1), 1467.

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

Bekris F, et al. (2025) Vintage and terroir are the strongest determinants of grapevine carposphere microbiome in the viticultural zone of Drama, Greece. FEMS microbiology ecology, 101(2).

Tian Q, et al. (2025) Plasma proteomic signatures of dual cognitive and mobility decline in older adults. EBioMedicine, 118, 105858.

Molina Ortiz JP, et al. (2025) Genome-scale metabolic modelling of human gut microbes to inform rational community design. Gut microbes, 17(1), 2534673.