

# Resource Summary Report

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## AGORA

RRID:SCR\_005070

Type: Tool

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### Proper Citation

AGORA (RRID:SCR\_005070)

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### Resource Information

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

**Proper Citation:** AGORA (RRID:SCR\_005070)

**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

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### Ratings and Alerts

No rating or validation information has been found for AGORA.

No alerts have been found for AGORA.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 99 mentions in open access literature.

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

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).

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.

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.

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.