

Resource Summary Report

Generated by T1D on Sep 20, 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](https://pubmed.ncbi.nlm.nih.gov/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: 20260919T195047+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 105 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Ray NR, et al. (2026) Genetic correlation analysis of Alzheimer's disease and stroke implicates PHLPP1 as a shared locus in individuals of African ancestry. *Alzheimer's & dementia : the journal of the Alzheimer's Association*, 22(4), e71433.

Enduru N, et al. (2026) PRISM-xQTL: Pleiotropic Relationships Integrated with System-level Multiomic QTL analysis for causal genes and molecular mediators in Alzheimer's disease. *Alzheimer's & dementia : the journal of the Alzheimer's Association*, 22(2), e71073.

Quinn-Bohmann N, et al. (2026) Metabolic modeling reveals determinants of prebiotic and probiotic treatment efficacy across multiple human intervention trials. *PLoS biology*, 24(2), e3003638.

Richmond GR, et al. (2026) Nutrient control enables metabolic reconstruction of *L. rhamnosus* GG and analysis of secretions. *bioRxiv : the preprint server for biology*.

Raethong N, et al. (2026) Modeling diet-gut microbiome interactions and prebiotic responses in Thai adults. *NPJ biofilms and microbiomes*, 12(1).

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*.

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.

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.

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.

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.

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.

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.

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.