

Resource Summary Report

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ALLPATHS-LG

RRID:SCR_010742

Type: Tool

Proper Citation

ALLPATHS-LG (RRID:SCR_010742)

Resource Information

URL: <https://www.broadinstitute.org/scientific-community/science/programs/genome-sequencing-and-analysis/computational-rd/computational->

Proper Citation: ALLPATHS-LG (RRID:SCR_010742)

Description: Software tool as whole genome shotgun assembler that can generate high quality genome assemblies using short reads (~100bp) such as those produced by the new generation of sequencers.

Abbreviations: ALLPATHS-LG

Resource Type: software resource

Defining Citation: [PMID:21187386](#)

Keywords: genome assembly, bio.tools

Resource Name: ALLPATHS-LG

Resource ID: SCR_010742

Alternate IDs: OMICS_00007, biotools:allpaths-lg

Alternate URLs: <https://bio.tools/allpaths-lg>

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260905T132645+0000

Ratings and Alerts

No rating or validation information has been found for ALLPATHS-LG.

No alerts have been found for ALLPATHS-LG.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 237 mentions in open access literature.

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

Dur??n-Fuentes JA, et al. (2025) Repeatome diversity in sea anemone genomics (Cnidaria: Actiniaria) based on the Actiniaria-REPlib library. BMC genomics, 26(1), 473.

Lord E, et al. (2025) Genome analyses suggest recent speciation and postglacial isolation in the Norwegian lemming. Proceedings of the National Academy of Sciences of the United States of America, 122(28), e2424333122.

Davis JT, et al. (2025) A chromosome-level genome assembly of the varied leaved jewelflower, *Streptanthus diversifolius*, reveals a recent whole genome duplication. G3 (Bethesda, Md.), 15(4).

Gajardo-Escobar F, et al. (2025) A recent and rapid genome expansion driven by the amplification of transposable elements in the Neotropical annual killifish *Garcialebias charrua*. Biological research, 59(1), 1.

Cohen AB, et al. (2024) The massive 340 megabase genome of *Anisogramma anomala*, a biotrophic ascomycete that causes eastern filbert blight of hazelnut. BMC genomics, 25(1), 347.

Jung H, et al. (2024) The identification of small molecule inhibitors with anthelmintic activities that target conserved proteins among ruminant gastrointestinal nematodes. mBio, 15(3), e0009524.

Vargas AM, et al. (2024) Morphological and dietary changes encoded in the genome of *Beroe ovata*, a ctenophore-eating ctenophore. NAR genomics and bioinformatics, 6(2), lqae072.

Sin SYW, et al. (2024) Genetic Basis and Evolution of Structural Color Polymorphism in an Australian Songbird. Molecular biology and evolution, 41(3).

Huynh S, et al. (2023) Whole-genome Analyses Reveal Past Population Fluctuations and Low Genetic Diversities of the North Pacific Albatrosses. Molecular biology and evolution, 40(7).

Fayyaz A, et al. (2023) Hiding in plain sight: Genome-wide recombination and a dynamic accessory genome drive diversity in *Fusarium oxysporum* f.sp. *ciceris*. Proceedings of the National Academy of Sciences of the United States of America, 120(27), e2220570120.

Barkdull M, et al. (2023) Worker Reproduction and Caste Polymorphism Impact Genome Evolution and Social Genes Across the Ants. Genome biology and evolution, 15(6).

Pang W, et al. (2023) Genomic Evidence for the Nonpathogenic State in HIV-1-Infected Northern Pig-Tailed Macaques. *Molecular biology and evolution*, 40(5).

Acosta K, et al. (2023) Optimization of Molecular Methods for Detecting Duckweed-Associated Bacteria. *Plants (Basel, Switzerland)*, 12(4).

Neverov AM, et al. (2023) Apoptotic gene loss in Cnidaria is associated with transition to parasitism. *Scientific reports*, 13(1), 8015.

Khalil S, et al. (2023) Testosterone Coordinates Gene Expression Across Different Tissues to Produce Carotenoid-Based Red Ornamentation. *Molecular biology and evolution*, 40(4).

Noh HJ, et al. (2022) The Antarctic Weddell seal genome reveals evidence of selection on cardiovascular phenotype and lipid handling. *Communications biology*, 5(1), 140.

Termignoni-Garcia F, et al. (2022) Comparative Population Genomics of Cryptic Speciation and Adaptive Divergence in Bicknell's and Gray-Cheeked Thrushes (Aves: *Catharus bicknelli* and *Catharus minimus*). *Genome biology and evolution*, 14(1).

Luo H, et al. (2022) Genes and evolutionary fates of the amanitin biosynthesis pathway in poisonous mushrooms. *Proceedings of the National Academy of Sciences of the United States of America*, 119(20), e2201113119.

Matos GM, et al. (2022) Microevolution of *Trypanosoma cruzi* reveals hybridization and clonal mechanisms driving rapid genome diversification. *eLife*, 11.

Thrimawithana AH, et al. (2022) The Genomics and Population Genomics of the Light Brown Apple Moth, *Epiphyas postvittana*, an Invasive Tortricid Pest of Horticulture. *Insects*, 13(3).