

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: 20260801T190416+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 [dkNET](#) .

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).

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.

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.

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.

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.

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).

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).

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.

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

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.

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).

Di Genova A, et al. (2022) Genome sequencing and transcriptomic analysis of the Andean killifish *Orestias ascotanensis* reveals adaptation to high-altitude aquatic life. *Genomics*, 114(1), 305.