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

Funding:

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: 20250420T014507+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 233 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

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.

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.

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.

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).

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.

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.

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).

Shigenobu S, et al. (2022) Genomic and transcriptomic analyses of the subterranean termite Reticulitermes speratus: Gene duplication facilitates social evolution. Proceedings of the National Academy of Sciences of the United States of America, 119(3).

Yadav S, et al. (2022) Whole Genome Sequencing and Comparative Genomics of Indian Isolates of Wheat Spot Blotch Pathogen Bipolaris sorokiniana Reveals Expansion of Pathogenicity Gene Clusters. Pathogens (Basel, Switzerland), 12(1).

Wooldridge TB, et al. (2022) An enhancer of Agouti contributes to parallel evolution of cryptically colored beach mice. Proceedings of the National Academy of Sciences of the United States of America, 119(27), e2202862119.