Resource Summary Report

Generated by NIF on May 16, 2025

orthAgogue

RRID:SCR_011979
Type: Tool

Proper Citation

orthAgogue (RRID:SCR_011979)

Resource Information

URL: https://code.google.com/p/orthagogue/

Proper Citation: orthAgogue (RRID:SCR_011979)

Description: A software tool for high speed estimation of homology relations within and between species in massive data sets.

Abbreviations: orthAgogue

Synonyms: orthAgogue: a tool for high speed estimation of homology relations within and between species in massive data sets.

Resource Type: software resource

Defining Citation: PMID:24115168

Keywords: unix/linux

Funding:

Availability: GNU General Public License, v3

Resource Name: orthAgogue

Resource ID: SCR_011979

Alternate IDs: OMICS_01691

Record Creation Time: 20220129T080307+0000

Record Last Update: 20250420T014603+0000

Ratings and Alerts

No rating or validation information has been found for orthAgogue.

No alerts have been found for orthAgogue.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 31 mentions in open access literature.

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

Thatcher S, et al. (2023) The NLRomes of Zea mays NAM founder lines and Zea luxurians display presence-absence variation, integrated domain diversity, and mobility. Molecular plant pathology, 24(7), 742.

Wang Y, et al. (2023) Divergent Evolution of Early Terrestrial Fungi Reveals the Evolution of Mucormycosis Pathogenicity Factors. Genome biology and evolution, 15(4).

van Beveren F, et al. (2022) Independent Size Expansions and Intron Proliferation in Red Algal Plastid and Mitochondrial Genomes. Genome biology and evolution, 14(4).

Pidcock SE, et al. (2021) Phylogenetic systematics of Butyrivibrio and Pseudobutyrivibrio genomes illustrate vast taxonomic diversity, open genomes and an abundance of carbohydrate-active enzyme family isoforms. Microbial genomics, 7(10).

Foulongne-Oriol M, et al. (2021) Mating-Type Locus Organization and Mating-Type Chromosome Differentiation in the Bipolar Edible Button Mushroom Agaricus bisporus. Genes, 12(7).

Alkema W, et al. (2021) Charting host-microbe co-metabolism in skin aging and application to metagenomics data. PloS one, 16(11), e0258960.

De Witte C, et al. (2021) Presence of Broad-Spectrum Beta-Lactamase-Producing Enterobacteriaceae in Zoo Mammals. Microorganisms, 9(4).

Garrison NL, et al. (2020) Shifting evolutionary sands: transcriptome characterization of the Aptostichus atomarius species complex. BMC evolutionary biology, 20(1), 68.

Dulovic A, et al. (2020) Rhabditophanes diutinus a parthenogenetic clade IV nematode with dauer larvae. PLoS pathogens, 16(12), e1009113.

Mugal CF, et al. (2020) Polymorphism Data Assist Estimation of the Nonsynonymous over

Synonymous Fixation Rate Ratio ? for Closely Related Species. Molecular biology and evolution, 37(1), 260.

Rödelsperger C, et al. (2019) Crowdsourcing and the feasibility of manual gene annotation: A pilot study in the nematode Pristionchus pacificus. Scientific reports, 9(1), 18789.

Beckerson WC, et al. (2019) Cause and Effectors: Whole-Genome Comparisons Reveal Shared but Rapidly Evolving Effector Sets among Host-Specific Plant-Castrating Fungi. mBio, 10(6).

Van de Weyer AL, et al. (2019) A Species-Wide Inventory of NLR Genes and Alleles in Arabidopsis thaliana. Cell, 178(5), 1260.

Kooyman FNJ, et al. (2019) Whole-genome sequencing of dog-specific assemblages C and D of Giardia duodenalis from single and pooled cysts indicates host-associated genes. Microbial genomics, 5(12).

Bayjanov JR, et al. (2019) Enterococcus faecium genome dynamics during long-term asymptomatic patient gut colonization. Microbial genomics, 5(7).

Weinstein DJ, et al. (2019) The genome of a subterrestrial nematode reveals adaptations to heat. Nature communications, 10(1), 5268.

Wang Y, et al. (2019) Molecular Dating of the Emergence of Anaerobic Rumen Fungi and the Impact of Laterally Acquired Genes. mSystems, 4(4).

Dhaygude K, et al. (2019) The first draft genomes of the ant Formica exsecta, and its Wolbachia endosymbiont reveal extensive gene transfer from endosymbiont to host. BMC genomics, 20(1), 301.

Rödelsperger C, et al. (2018) Phylotranscriptomics of Pristionchus Nematodes Reveals Parallel Gene Loss in Six Hermaphroditic Lineages. Current biology : CB, 28(19), 3123.

Prabh N, et al. (2018) Deep taxon sampling reveals the evolutionary dynamics of novel gene families in Pristionchus nematodes. Genome research, 28(11), 1664.