

Resource Summary Report

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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

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: 20260801T190434+0000

Ratings and Alerts

No rating or validation information has been found for orthAgogue.

No alerts have been found for orthAgoque.

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 [ASWG](#).

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 Pseudobutyrvibrio 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).

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

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

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).

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

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

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.

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

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.