Resource Summary Report

Generated by NIF on Apr 26, 2025

Proteinortho

RRID:SCR_024177
Type: Tool

Proper Citation

Proteinortho (RRID:SCR_024177)

Resource Information

URL: https://gitlab.com/paulklemm_PHD/proteinortho

Proper Citation: Proteinortho (RRID:SCR_024177)

Description: Software tool to detect orthologous genes within different species. Stand-alone tool for large datasets for orthology analysis.

Resource Type: data analysis software, software application, software resource, data processing software

Defining Citation: PMID:21526987

Keywords: Stand-alone tool, detect orthologous genes, different species, large datasets, orthology analysis,

Funding:

Availability: Free, Available for download, Freely available,

Resource Name: Proteinortho

Resource ID: SCR_024177

Alternate IDs: OMICS_05355

Alternate URLs: https://sources.debian.org/src/proteinortho/

License: GNU General Public License v3.0 or later

Record Creation Time: 20230824T050212+0000

Record Last Update: 20250426T061005+0000

Ratings and Alerts

No rating or validation information has been found for Proteinortho.

No alerts have been found for Proteinortho.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 86 mentions in open access literature.

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

Pla?ková K, et al. (2024) Centromere drive may propel the evolution of chromosome and genome size in plants. Annals of botany, 134(6), 1067.

Unneberg P, et al. (2024) Ecological genomics in the Northern krill uncovers loci for local adaptation across ocean basins. Nature communications, 15(1), 6297.

Baroncelli R, et al. (2024) Genome evolution and transcriptome plasticity is associated with adaptation to monocot and dicot plants in Colletotrichum fungi. GigaScience, 13.

Zambounis A, et al. (2024) Pan-genome survey of Septoria pistaciarum, causal agent of Septoria leaf spot of pistachios, across three Aegean sub-regions of Greece. Frontiers in microbiology, 15, 1396760.

Fricke LC, et al. (2024) Identification of Parthenogenesis-Inducing Effector Proteins in Wolbachia. Genome biology and evolution, 16(4).

Velásquez C LF, et al. (2023) Identification of Cry toxin receptor genes homologs in a de novo transcriptome of Premnotrypes vorax (Coleoptera: Curculionidae). PloS one, 18(9), e0291546.

Martinez-Gutierrez CA, et al. (2023) A timeline of bacterial and archaeal diversification in the ocean. eLife, 12.

Ceron-Noriega A, et al. (2023) Nematode gene annotation by machine-learning-assisted proteotranscriptomics enables proteome-wide evolutionary analysis. Genome research, 33(1), 112.

Lin HC, et al. (2023) Key processes required for the different stages of fungal carnivory by a

nematode-trapping fungus. PLoS biology, 21(11), e3002400.

Fricke LC, et al. (2023) Identification of parthenogenesis-inducing effector proteins in Wolbachia. bioRxiv : the preprint server for biology.

Xiao M, et al. (2023) A high-quality chromosome-level Eutrema salsugineum genome, an extremophile plant model. BMC genomics, 24(1), 174.

Noecker C, et al. (2023) Systems biology elucidates the distinctive metabolic niche filled by the human gut microbe Eggerthella lenta. PLoS biology, 21(5), e3002125.

Buttimer C, et al. (2023) Temperate bacteriophages infecting the mucin-degrading bacterium Ruminococcus gnavus from the human gut. Gut microbes, 15(1), 2194794.

Foley S, et al. (2022) Evolutionary analyses of genes in Echinodermata offer insights towards the origin of metazoan phyla. Genomics, 114(4), 110431.

Aherfi S, et al. (2022) Incomplete tricarboxylic acid cycle and proton gradient in Pandoravirus massiliensis: is it still a virus? The ISME journal, 16(3), 695.

Chen SH, et al. (2022) A high-quality pseudo-phased genome for Melaleuca quinquenervia shows allelic diversity of NLR-type resistance genes. GigaScience, 12.

Eddie BJ, et al. (2022) Conservation of Energetic Pathways for Electroautotrophy in the Uncultivated Candidate Order Tenderiales. mSphere, 7(5), e0022322.

Jones MW, et al. (2022) Infection Dynamics of Cotransmitted Reproductive Symbionts Are Mediated by Sex, Tissue, and Development. Applied and environmental microbiology, 88(13), e0052922.

Larriba E, et al. (2022) Identification of Transcriptional Networks Involved in De Novo Organ Formation in Tomato Hypocotyl Explants. International journal of molecular sciences, 23(24).

Rolland C, et al. (2021) Clandestinovirus: A Giant Virus With Chromatin Proteins and a Potential to Manipulate the Cell Cycle of Its Host Vermamoeba vermiformis. Frontiers in microbiology, 12, 715608.