

Resource Summary Report

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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 processing software, data analysis software, software application, software resource

Defining Citation: [PMID:21526987](#)

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

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: 20260801T190815+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 97 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#).

Proença M, et al. (2025) Prophage dynamics in gastric and enterohepatic environments: unraveling ecological barriers and adaptive transitions. *ISME communications*, 5(1), ycaf017.

Mendonça-Santos T, et al. (2025) Integrative genomic analyses support the division of the extended Asfarviridae clade into multiple viral families. *Journal of virology*, 99(12), e0133725.

Reyes Loaiciga C, et al. (2025) Comprehensive profiling of ribo-seq detected small sequences in yeast reveals robust conservation patterns and their potential mechanisms of origin. *BMC genomics*, 26(1), 856.

Colombi E, et al. (2025) Adaptative and ancient co-evolution of integrons with *Xanthomonas* genomes. *Microbial genomics*, 11(9).

Wong BC, et al. (2025) *Shigella sonnei* and *Shigella flexneri* infection in *Caenorhabditis elegans* led to species-specific regulatory responses in the host and pathogen. *Microbial genomics*, 11(1).

Korla PK, et al. (2025) Isolation and Characterization of *Rickettsia finnyi*, Novel Pathogenic Spotted Fever Group *Rickettsia* in Dogs, United States. *Emerging infectious diseases*, 31(11), 2118.

Martinez-Hernandez JE, et al. (2025) Comparative and systems analyses of *Leishmania* spp. non-coding RNAs through developmental stages. *PLoS neglected tropical diseases*, 19(5), e0013108.

Sepúlveda-Rebolledo P, et al. (2025) Comparative Genomics of Sigma Factors in *Acidithiobacillia* Sheds Light into the Transcriptional Regulatory Networks Involved in Biogeochemical Dynamics in Extreme Acidic Environments. *Microorganisms*, 13(6).

Shi T, et al. (2025) Resolving phylogenetic conflicts in Pandanales: the dual roles of gene flow and whole-genome duplication. *Frontiers in plant science*, 16, 1511582.

Zaman SAU, et al. (2025) Whole genome of petroleum hydrocarbon degrading *Rhodococcus indonesiensis* isolated from Nacharam, Hyderabad, India. *Scientific reports*,

16(1), 165.

Bian C, et al. (2025) Telomere-to-telomere chromosome-scale genome assemblies of black and golden koi carp variants support construction of an ancient karyotype of Cypriniformes. *GigaScience*, 14.

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

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

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).

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

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

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

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