

Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

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.