

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

SwiftOrtho

RRID:SCR_017122

Type: Tool

Proper Citation

SwiftOrtho (RRID:SCR_017122)

Resource Information

URL: <https://github.com/Rinoahu/SwiftOrtho>

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Description: Software tool for orthology analysis to identify orthologs, paralogs and co orthologs for genomes. Used to perform homology classification across genomes of different species in large genomic datasets.

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

Defining Citation: [DOI:10.1101/543223](https://doi.org/10.1101/543223)

Keywords: orthology, analysis, identify, ortholog, paralog, co ortholog, genome, homology, different, species, large, dataset, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: SwiftOrtho

Resource ID: SCR_017122

Alternate IDs: OMICS_30890, biotools:SwiftOrtho

Alternate URLs: <https://bio.tools/SwiftOrtho>

License: GNU GPL v3

Record Creation Time: 20220129T080333+0000

Record Last Update: 20260905T132819+0000

Ratings and Alerts

No rating or validation information has been found for SwiftOrtho.

No alerts have been found for SwiftOrtho.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

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

Beatman TR, et al. (2021) A nomenclature for echinoderm genes. Database : the journal of biological databases and curation, 2021.

Deutekom ES, et al. (2021) Benchmarking orthology methods using phylogenetic patterns defined at the base of Eukaryotes. Briefings in bioinformatics, 22(3).

Hu X, et al. (2019) SwiftOrtho: A fast, memory-efficient, multiple genome orthology classifier. GigaScience, 8(10).