

Resource Summary Report

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OrthoMCL DB: Ortholog Groups of Protein Sequences

RRID:SCR_007839

Type: Tool

Proper Citation

OrthoMCL DB: Ortholog Groups of Protein Sequences (RRID:SCR_007839)

Resource Information

URL: <http://www.orthomcl.org/cgi-bin/OrthoMclWeb.cgi>

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Description: OrthoMCL is a genome-scale algorithm for grouping orthologous protein sequences. It provides not only groups shared by two or more species/genomes, but also groups representing species-specific gene expansion families. OrthoMCL starts with reciprocal best hits within each genome as putative in-paralog/recent paralog pairs and reciprocal best hits across any two genomes as putative ortholog pairs. Related proteins are interlinked in a similarity graph. Then MCL (Markov Clustering algorithm, Van Dongen 2000; www.micans.org/mcl) is invoked to split mega-clusters. This process is analogous to the manual review in COG construction. MCL clustering is based on weights between each pair of proteins, so to correct for differences in evolutionary distance the weights are normalized before running MCL.

Synonyms: OrthoMCL DB

Resource Type: data or information resource, database

Keywords: FASEB list

Resource Name: OrthoMCL DB: Ortholog Groups of Protein Sequences

Resource ID: SCR_007839

Alternate IDs: r3d100012462, nif-0000-03230

Alternate URLs: <https://doi.org/10.17616/R3FZ27>

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Ratings and Alerts

No rating or validation information has been found for OrthoMCL DB: Ortholog Groups of Protein Sequences.

No alerts have been found for OrthoMCL DB: Ortholog Groups of Protein Sequences.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1051 mentions in open access literature.

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

Yang S, et al. (2025) Comparative Genomics Reveals Evidence of the Genome Reduction and Metabolic Potentials of *Alilineobacillus hadale* Isolated from Challenger Deep Sediment of the Mariana Trench. *Microorganisms*, 13(1).

Aspinwall J, et al. (2025) Behavioral Manipulation of *Ixodes scapularis* by *Ehrlichia muris euclairensis*: Implications for Tick-Borne Disease Transmission. *bioRxiv* : the preprint server for biology.

Kwak Y, et al. (2025) A dual insect symbiont and plant pathogen improves insect host fitness under arginine limitation. *mBio*, 16(4), e0358824.

He Y, et al. (2025) Comparative Genomic Analysis of *Campylobacter* Plasmids Identified in Food Isolates. *Microorganisms*, 13(1).

Huang M, et al. (2025) Goose multi-omics database: A comprehensive multi-omics database for goose genomics. *Poultry science*, 104(3), 104842.

Chen N, et al. (2025) Genome-wide identification of the AAP gene family and expression analysis under tissue-specific expression in five legumes. *BMC genomics*, 26(1), 173.

Salamzade R, et al. (2025) zol and fai: large-scale targeted detection and evolutionary investigation of gene clusters. *Nucleic acids research*, 53(3).

Guo L, et al. (2025) Duckweed: a starch-hyperaccumulating plant under cultivation with a combination of nutrient limitation and elevated CO₂. *Frontiers in plant science*, 16, 1531849.

Westaway JAF, et al. (2025) Genomic epidemiology of *Plasmodium knowlesi* reveals putative genetic drivers of adaptation in Malaysia. *PLoS neglected tropical diseases*, 19(3), e0012885.

Christel S, et al. (2025) Catabolic pathway acquisition by rhizosphere bacteria readily enables growth with a root exudate component but does not affect root colonization. *mBio*,

16(1), e0301624.

Wang Y, et al. (2025) Genome-Driven Functional Validation of *Bacillus amyloliquefaciens* Strain MEPW12: A Multifunctional Endophyte for Sustainable Sweet Potato Cultivation. *Microorganisms*, 13(6).

Bian C, et al. (2025) Chromosome-level genome assemblies of five *Sinocyclocheilus* species. *GigaByte* (Hong Kong, China), 2025, gigabyte155.

Sun R, et al. (2025) Chromosome-level genome assembly of a high-yield Chinese soybean variety Mengdou1137 unlocks genetic potential of disease and lodging resistance. *TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik*, 138(6), 119.

Ros-Lucas A, et al. (2025) Identification of novel compounds against *Trypanosoma cruzi* using AlphaFold structures. *Computational and structural biotechnology journal*, 27, 1838.

Adeniji AA, et al. (2025) Unveiling novel features and phylogenomic assessment of indigenous *Priestia megaterium* AB-S79 using comparative genomics. *Microbiology spectrum*, 13(4), e0146624.

Wang C, et al. (2025) Genomic-transcriptomic analysis identifies the Syrian hamster as a superior animal model for human diseases. *BMC genomics*, 26(1), 286.

Godinez-Macias KP, et al. (2025) Revisiting the *Plasmodium falciparum* druggable genome using predicted structures and data mining. *NPJ drug discovery*, 2(1), 3.

Cote-L'Heureux AE, et al. (2025) Lost in translation: conserved amino acid usage despite extreme codon bias in foraminifera. *mBio*, 16(4), e0391624.

Zangh?? G, et al. (2025) Genome-wide gene expression profiles throughout human malaria parasite liver stage development in humanized mice. *Nature microbiology*, 10(2), 569.

Qi Z, et al. (2025) Telomere-to-telomere genome assembly of *Electrophorus electricus* provides insights into the evolution of electric eels. *GigaScience*, 14.