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: database, data or information resource

Keywords: FASEB list

Funding:

Resource Name: OrthoMCL DB: Ortholog Groups of Protein Sequences

Resource ID: SCR_007839

Alternate IDs: nif-0000-03230

Record Creation Time: 20220129T080244+0000

Record Last Update: 20250503T055951+0000

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: <u>SciCrunch Registry</u>

Usage and Citation Metrics

We found 994 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

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

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.

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

Cerqueira de Araujo A, et al. (2025) Genome sequences of four Ixodes species expands understanding of tick evolution. BMC biology, 23(1), 17.

Sanchez VA, et al. (2025) Genome evolution following an ecological shift in nectar-dwelling Acinetobacter. mSphere, 10(1), e0101024.

Abou-Kandil A, et al. (2025) The proteomic response of Aspergillus fumigatus to amphotericin B (AmB) reveals the involvement of the RTA-like protein RtaA in AmB resistance. microLife, 6, uqae024.

Krasi??ikova M, et al. (2025) Nanopore sequencing reveals that DNA replication compartmentalisation dictates genome stability and instability in Trypanosoma brucei. Nature communications, 16(1), 751.

Villarreal F, et al. (2024) Genome sequencing and analysis of black flounder (Paralichthys orbignyanus) reveals new insights into Pleuronectiformes genomic size and structure. BMC genomics, 25(1), 297.

Huang J, et al. (2024) Genome assembly provides insights into the genome evolution of Baccaurea ramiflora Lour. Scientific reports, 14(1), 4867.

Wan JN, et al. (2024) The rise of baobab trees in Madagascar. Nature, 629(8014), 1091.

Jiang M, et al. (2024) A comprehensive evaluation of the potential of three next-generation short-read-based plant pan-genome construction strategies for the identification of novel non-reference sequence. Frontiers in plant science, 15, 1371222.

Jia L, et al. (2024) Chromosome-level genome of Thymus mandschuricus reveals molecular mechanism of aroma compounds biosynthesis. Frontiers in plant science, 15, 1368869.

Acero-Pimentel D, et al. (2024) Study of an Enterococcus faecium strain isolated from an artisanal Mexican cheese, whole-genome sequencing, comparative genomics, and bacteriocin expression. Antonie van Leeuwenhoek, 117(1), 40.

Guerrero-Egido G, et al. (2024) bacLIFE: a user-friendly computational workflow for genome analysis and prediction of lifestyle-associated genes in bacteria. Nature communications, 15(1), 2072.

Wang Q, et al. (2024) A consensus genome of sika deer (Cervus nippon) and transcriptome analysis provided novel insights on the regulation mechanism of transcript factor in antler development. BMC genomics, 25(1), 617.

Shi K, et al. (2024) The chromosome-level assembly of the wild diploid alfalfa genome provides insights into the full landscape of genomic variations between cultivated and wild alfalfa. Plant biotechnology journal, 22(6), 1757.

Zhang H, et al. (2024) The Phylogeny and Metabolic Potentials of a Lignocellulosic Material-Degrading Aliiglaciecola Bacterium Isolated from Intertidal Seawater in East China Sea. Microorganisms, 12(1).

Xie WZ, et al. (2024) Two haplotype-resolved genome assemblies for AAB allotriploid bananas provide insights into banana subgenome asymmetric evolution and Fusarium wilt control. Plant communications, 5(2), 100766.

Liang J, et al. (2024) Integrated Genome Sequencing and Transcriptome Analysis Identifies Candidate Pathogenicity Genes from Ustilago crameri. Journal of fungi (Basel, Switzerland), 10(1).

Qian X, et al. (2024) Bifidobacteria with indole-3-lactic acid-producing capacity exhibit psychobiotic potential via reducing neuroinflammation. Cell reports. Medicine, 5(11), 101798.