

Resource Summary Report

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OrthoVenn2

RRID:SCR_022504

Type: Tool

Proper Citation

OrthoVenn2 (RRID:SCR_022504)

Resource Information

URL: <https://orthovenn2.bioinfotoolkits.net/home>

Proper Citation: OrthoVenn2 (RRID:SCR_022504)

Description: Web server for whole genome comparison and annotation of orthologous clusters across multiple species. Works on any operating system with modern browser and Javascript enabled. Used to identify orthologous gene clusters and supports user define species to upload customized protein sequences. Interactive graphic tool which provides Venn diagram view for comparing multiple species protein sequences.

Resource Type: data access protocol, software resource, web service

Defining Citation: [PMID:31053848](https://pubmed.ncbi.nlm.nih.gov/31053848/)

Keywords: whole genome comparison and annotation, orthologous clusters across multiple species, identify orthologous gene clusters, comparing multiple species protein sequences

Funding: National Natural Science Foundation of China

Availability: Free, Freely available

Resource Name: OrthoVenn2

Resource ID: SCR_022504

Record Creation Time: 20220622T050139+0000

Record Last Update: 20250503T061006+0000

Ratings and Alerts

No rating or validation information has been found for OrthoVenn2.

No alerts have been found for OrthoVenn2.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 235 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Choi Y, et al. (2025) Analysis of the Genomes and Adaptive Traits of *Skermanella cutis* sp. nov., a Human Skin Isolate, and the Type Strains *Skermanella rosea* and *Skermanella mucosa*. *Microorganisms*, 13(1).

Sultan AB, et al. (2024) Divergent evolution of NLR genes in the genus *Glycine*: impacts of annuals and perennials' life history strategies. *Frontiers in plant science*, 15, 1383135.

Carneiro DG, et al. (2024) Genome sequencing and analysis of *Salmonella enterica* subsp. *enterica* serotype Enteritidis PT4 578: insights into pathogenicity and virulence. *Access microbiology*, 6(11).

Cunha-Ferreira IC, et al. (2024) Impact of *Paenibacillus elgii* supernatant on screening bacterial strains with potential for biotechnological applications. *Engineering microbiology*, 4(3), 100163.

Xie Y, et al. (2024) Comprehensive genome analysis of two novel *Saccharopolyspora* strains- *Saccharopolyspora montiporae* sp. nov. and *Saccharopolyspora galaxiae* sp. nov. isolated from stony corals in Hainan. *Frontiers in microbiology*, 15, 1432042.

Jiang S, et al. (2024) A high-quality haplotype genome of *Michelia alba* DC reveals differences in methylation patterns and flower characteristics. *Molecular horticulture*, 4(1), 23.

Singh RP, et al. (2024) First report on in-depth genome and comparative genome analysis of a metal-resistant bacterium *Acinetobacter pittii* S-30, isolated from environmental sample. *Frontiers in microbiology*, 15, 1351161.

Ma T, et al. (2024) High-quality genome assembly and genetic transformation system of *Lasioidiplodia theobromae* strain LTTK16-3, a fungal pathogen of Chinese hickory. *Microbiology spectrum*, 12(3), e0331123.

Mohan M, et al. (2024) The miniature genome of broad mite, *Polyphagotarsonemus latus*

(Tarsonemidae: Acari). Scientific data, 11(1), 748.

Hatmaker EA, et al. (2024) Pathogenicity is associated with population structure in a fungal pathogen of humans. bioRxiv : the preprint server for biology.

Yan S, et al. (2024) Endophytic strategies decoded by genome and transcriptome analysis of *Fusarium nematophilum* strain NQ8GII4. Frontiers in microbiology, 15, 1487022.

Vilela FP, et al. (2024) Comparative genomics reveals high genetic similarity among strains of *Salmonella enterica* serovar Infantis isolated from multiple sources in Brazil. PeerJ, 12, e17306.

Caña-Bozada VH, et al. (2024) Identifying potential drug targets in the kinomes of two monogenean species. Helminthologia, 61(2), 142.

Miao H, et al. (2024) Genomic evolution and insights into agronomic trait innovations of *Sesamum* species. Plant communications, 5(1), 100729.

Rodrigues SH, et al. (2024) First report of coexistence of blaKPC-2 and blaNDM-1 in carbapenem-resistant clinical isolates of *Klebsiella aerogenes* in Brazil. Frontiers in microbiology, 15, 1352851.

Hsu PC, et al. (2024) Protein moonlighting by a target gene dominates phenotypic divergence of the Sef1 transcriptional regulatory network in yeasts. Nucleic acids research, 52(22), 13914.

Barbosa RC, et al. (2024) Exploring the midgut physiology of the non-haematophagous mosquito *Toxorhynchites theobaldi*. Open biology, 14(7), 230437.

Borges KCM, et al. (2024) New antibacterial candidates against *Acinetobacter baumannii* discovered by in silico-driven chemogenomics repurposing. PloS one, 19(9), e0307913.

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.

Narula K, et al. (2024) Combining extracellular matrix proteome and phosphoproteome of chickpea and meta-analysis reveal novel proteoforms and evolutionary significance of clade-specific wall-associated events in plant. Plant direct, 8(3), e572.