

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: web service, data access protocol, software resource

Defining Citation: [PMID: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: 20260804T043801+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 255 mentions in open access literature.

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

Jiang D, et al. (2025) The telomere-to-telomere genome of flowering cherry (*Prunus campanulata*) reveals genomic evolution of the subgenus *Cerasus*. *GigaScience*, 14.

Xu QZ, et al. (2025) Chromosome-level genome assembly and single-cell analysis unveil molecular mechanisms of arm regeneration in the ophiuroid *Ophiura sarsii vadicola*. *Genome biology*, 26(1), 82.

Banerjee G, et al. (2025) Whole genome sequence of multidrug-resistant *Staphylococcus haemolyticus* and *Enterococcus faecalis* isolates from public gymnasium equipment reveals evolving infection potential and resistance. *PloS one*, 20(10), e0324894.

Benhadj M, et al. (2025) Genomic Insights and Antimicrobial Potential of Newly *Streptomyces cavourensis* Isolated from a Ramsar Wetland Ecosystem. *Microorganisms*, 13(3).

Long M, et al. (2025) Characterization and comparative genomic analysis of *Pseudomonas aegiceratis* sp. nov., a new nitrogen-fixing bacterium from the sediments of mangrove plant *Aegiceras corniculatum*. *Microbiology spectrum*, 13(5), e0004125.

Pan K, et al. (2025) Genomic and metabolomic insights into the biocontrol potential of *Bacillus velezensis* ZHR0 against sugarcane smut. *Frontiers in microbiology*, 16, 1582763.

Sinichich AA, et al. (2025) Genome-Guided Metabolomic Profiling of Peptaibol-Producing *Trichoderma*. *International journal of molecular sciences*, 26(12).

Parvez S, et al. (2025) Tracing the path from conservation to expansion evolutionary insights into NLR genes in oleaceae. *BMC plant biology*, 25(1), 259.

Alborzi Z, et al. (2025) Tissue-specific transcriptomic and endocrine signatures of obligatory reproductive diapause in *Eurygaster integriceps*. *Scientific reports*, 15(1), 42999.

Cadavid S??nchez IC, et al. (2025) Harnessing genetic diversity: The genomic and transcriptomic insights of *Eugenia uniflora* for environmental resilience. *PloS one*, 20(11), e0333437.

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).

Gayathri M, et al. (2025) Genomic configuration of *Bacillus subtilis* (NMB01) unveils its antiviral activity against Orthospovirus arachnecrosis infecting tomato. *Frontiers in plant science*, 16, 1517157.

Kumari K, et al. (2025) In-depth genome and comparative genome analysis of a metal-resistant environmental isolate *Pseudomonas aeruginosa* S-8. *Frontiers in cellular and infection microbiology*, 15, 1511507.

Raj S, et al. (2025) Comparative genomic analysis of paired clinical isolates from a patient with recurrent melioidosis reveals a low within-host mutation rate. *Journal of medical microbiology*, 74(4).

Rai S, et al. (2025) Novel endophytic actinomycetes species *Streptomyces panacea* of *Panax sokpayensis* produce antimicrobial compounds against multidrug resistant *Staphylococcus aureus*. *Scientific reports*, 15(1), 19863.

Powell D, et al. (2025) The genome of the Australian water dragon (*Intellagama lesueurii*), an agamid model for urban adaptation. *The Journal of heredity*, 116(5), 571.

Auzane A, et al. (2025) A Novel Pathosystem With the Model Plant *Arabidopsis thaliana* for Defining the Molecular Basis of *Taphrina* Infections. *Environmental microbiology reports*, 17(3), e70118.

Fatima K, et al. (2025) PangenePro: an automated pipeline for rapid identification and classification of gene family members. *Bioinformatics advances*, 5(1), vbaf159.

Hashmi SS, et al. (2025) Exploring the role of ATP-binding cassette transporters in tomato (*Solanum lycopersicum*) under cadmium stress through genome-wide and transcriptomic analysis. *Frontiers in plant science*, 16, 1536178.

Yang X, et al. (2025) Lineage-specific targets of positive selection in three leaf beetles correspond with defence capacity against their shared parasitoid wasp. *Heredity*, 134(9), 567.