

Resource Summary Report

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GET_HOMOLOGUES

RRID:SCR_015705

Type: Tool

Proper Citation

GET_HOMOLOGUES (RRID:SCR_015705)

Resource Information

URL: https://github.com/eead-csic-compbio/get_homologues

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Description: Software package for pan-genome analysis. This software is suitable for bacterial genomes and the study of intra-specific eukaryotic pan-genomes.

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

Defining Citation: [PMID:24096415](#), [PMID:28261241](#)

Keywords: pan-genome analysis, bacterial genome, intra-specific eukaryotic pan-genome, homologue

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Availability: Free, Available for download, Tutorial available

Resource Name: GET_HOMOLOGUES

Resource ID: SCR_015705

Alternate URLs: <http://www.eead.csic.es/compbio/soft/gethoms.php>,
<http://maya.ccg.unam.mx/soft/gethoms.php>

License: GPL

License URLs: https://github.com/eead-csic-compbio/get_homologues/blob/master/LICENSE.txt

Record Creation Time: 20220129T080327+0000

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Ratings and Alerts

No rating or validation information has been found for GET_HOMOLOGUES.

No alerts have been found for GET_HOMOLOGUES.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 268 mentions in open access literature.

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

Drebes Dörr NC, et al. (2026) Type VI-secretion system-mediated competition and virulence in clinical and environmental *Stenotrophomonas maltophilia*. *Microbiology spectrum*, 14(4), e0341125.

Sugiyama T, et al. (2026) Comparison of Predatory Phenotypes and Genotypes Between *Bdellovibrio* sp. BIS2 and *Bacteriovorax* sp. HI3 Isolated From the Same Freshwater Environment. *Environmental microbiology*, 28(1), e70243.

Rey C, et al. (2026) Comparative genomic analysis of *Sinorhizobium meliloti* LPU88: plasmid diversity and conjugative mechanisms. *Applied and environmental microbiology*, 92(6), e0199625.

Wang J, et al. (2026) Eco-evolutionary dynamics sustain a potent yet rare antibiotic gene cluster in *Streptomyces*. *The ISME journal*, 20(1).

García-Miranda N, et al. (2026) Gram-negative-staining Bacillaceae with thick cell wall and monoderm architecture uncover evolutionary diversity and challenge Gram-based classification. *Communications biology*, 9(1).

Chen X, et al. (2026) Metagenomic expansion of *Joyebacterota* identifies *Cavimicrobium*, a dominant sulfide-producing lineage in anoxic marine ecosystems. *ISME communications*, 6(1), ycag137.

Lau NS, et al. (2025) Comparative genomics and multiomics analyses reveal the evolution and physiological basis of rubber biosynthesis in *Hevea* species. *GigaScience*, 14.

Barcia-Cruz R, et al. (2025) Comparative genomics of *Vibrio toranzoniae* strains. *International microbiology : the official journal of the Spanish Society for Microbiology*, 28(3), 485.

Yacoub E, et al. (2025) A sweeping view of avian mycoplasmas biology drawn from comparative genomic analyses. *BMC genomics*, 26(1), 24.

Morris TC, et al. (2025) Phage-antibiotic synergy to combat multidrug resistant strains of Gram-negative ESKAPE pathogens. *Scientific reports*, 15(1), 17235.

Lin L, et al. (2025) Comparative Genomics Analysis Combined with Homologous Overexpression Reveals the Mechanism of Species-Specific Acid Stress Resistance in *Bifidobacterium animalis*. *Foods (Basel, Switzerland)*, 14(24).

Delbaje E, et al. (2025) *Aspergillus fumigatus* mitogenomes and their influence on azole-resistant and -susceptible populations. *npj antimicrobials and resistance*, 3(1), 15.

Terra LA, et al. (2025) Pangenome analysis indicates evolutionary origins and genetic diversity: emphasis on the role of nodulation in symbiotic *Bradyrhizobium*. *Frontiers in plant science*, 16, 1539151.

Timilsina S, et al. (2025) Diversification of an emerging bacterial plant pathogen; insights into the global spread of *Xanthomonas euvesicatoria* pv. *perforans*. *PLoS pathogens*, 21(4), e1013036.

Gumustop I, et al. (2025) Comparative genomics of *Lentilactobacillus buchneri* reveals strain-level hyperdiversity and broad-spectrum CRISPR immunity against human and livestock gut phages. *PloS one*, 20(6), e0325832.

Provenzano D, et al. (2025) *Vibrio cholerae* endemic to the lower Rio Grande Delta segregate into urban and rural phylotypes. *Scientific reports*, 15(1), 23430.

Acha Alarcon L, et al. (2025) Identification of *Streptococcus pneumoniae*-Specific Proteins by Surface-Shaving Proteomics. *Journal of proteome research*, 24(12), 6154.

Wang Q, et al. (2025) Genome analysis and machine learning-based feature selection strategy reveal potential drug-resistance determinants in *Nakaseomyces glabratus*. *Emerging microbes & infections*, 14(1), 2595789.

Vaccalluzzo A, et al. (2025) Strain-specific qPCR assay to track the vaginal colonization of the probiotic *Lactobacillus rhamnosus* TOM 22.8 strain orally administered. *BMC microbiology*, 25(1), 759.

Guillén-Navarro D, et al. (2025) Comparative genomics of carbapenem-resistant *Acinetobacter baumannii* isolated from pediatric patients in a tertiary care hospital. *Microbiology spectrum*, 13(11), e0167625.