

Resource Summary Report

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Annotree

RRID:SCR_018980

Type: Tool

Proper Citation

Annotree (RRID:SCR_018980)

Resource Information

URL: <http://annotree.uwaterloo.ca/>

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Description: Web tool for visualization of genome annotations across large phylogenetic trees. Used for visualization and exploration of functionally annotated microbial tree of life. Integrates taxonomic, phylogenetic and functional annotation data from bacterial and archaeal genomes.

Synonyms: AnnoTree 1.2

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

Defining Citation: [PMID:31081040](#)

Keywords: Genome annotation, genome visualization, phylogenetic tree, functionally annotated tree, microbial tree of life, taxonomic data, phylogenetic data, functionally annotated data, bacterial genome, archaeal genome, genome distribution, data, bio.tools

Funding: Ontario Early Researcher award ;
NSERC Discovery Grant ;
Australian Research Council Laureate Fellowship ;
Tier II Canada Research Chair ;
Natural Sciences and Engineering Research Council of Canada

Availability: Free, Freely available

Resource Name: Annotree

Resource ID: SCR_018980

Alternate IDs: biotools:Annotree

Alternate URLs: <https://bio.tools/AnnoTree>

Record Creation Time: 20220129T080342+0000

Record Last Update: 20260815T182600+0000

Ratings and Alerts

No rating or validation information has been found for Annotree.

No alerts have been found for Annotree.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 25 mentions in open access literature.

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

Huang ZC, et al. (2026) The growth and pathogenesis of *Citrobacter rodentium* are compromised when multiple mucin sugar utilization pathways are disrupted, leading to accumulation of N-acetylglucosamine 6-phosphate. *Infection and immunity*, 94(4), e0054525.

Duret M, et al. (2025) Diversity and functional features of the root-associated bacteriome are dependent on grapevine susceptibility to *Plasmopara viticola*. *Environmental microbiome*, 20(1), 30.

Hernández-Rocamora VM, et al. (2025) A novel peptidoglycan deacetylase modulates daughter cell separation in *E. coli*. *PLoS genetics*, 21(9), e1011626.

Smith ME, et al. (2025) Uncovering functional deterioration in the rhizosphere microbiome associated with post-green revolution wheat cultivars. *Environmental microbiome*, 20(1), 64.

Pi HW, et al. (2025) Nitrogen-fixing microbes gain genes in diverse types of living environments. *Proceedings of the National Academy of Sciences of the United States of America*, 122(48), e2523106122.

Ali S, et al. (2025) Comparative proteomics of biofilm development in *Pseudoalteromonas tunicata* discovers a distinct family of Ca²⁺-dependent adhesins. *mBio*, 16(6), e0106925.

Amikura K, et al. (2025) Evolutionary Flexibility of Ribosome Biogenesis in Bacteria. *Molecular biology and evolution*, 42(11).

Berry MA, et al. (2024) Diverse domain architectures of CheA histidine kinase, a central component of bacterial and archaeal chemosensory systems. *Microbiology spectrum*,

12(1), e0346423.

Bollinger KW, et al. (2024) Identification of a new family of peptidoglycan transpeptidases reveals atypical crosslinking is essential for viability in *Clostridioides difficile*. *bioRxiv : the preprint server for biology*.

Nishihara A, et al. (2024) Illuminating the coevolution of photosynthesis and Bacteria. *Proceedings of the National Academy of Sciences of the United States of America*, 121(25), e2322120121.

Bollinger KW, et al. (2024) Identification of a family of peptidoglycan transpeptidases reveals that *Clostridioides difficile* requires noncanonical cross-links for viability. *Proceedings of the National Academy of Sciences of the United States of America*, 121(34), e2408540121.

Diao M, et al. (2023) Global diversity and inferred ecophysiology of microorganisms with the potential for dissimilatory sulfate/sulfite reduction. *FEMS microbiology reviews*, 47(5).

Berry MA, et al. (2023) Diverse domain architectures of CheA histidine kinase, a central component of bacterial and archaeal chemosensory systems. *bioRxiv : the preprint server for biology*.

Somee MR, et al. (2022) Genome-resolved analyses show an extensive diversification in key aerobic hydrocarbon-degrading enzymes across bacteria and archaea. *BMC genomics*, 23(1), 690.

Pi HW, et al. (2022) Origin and Evolution of Nitrogen Fixation in Prokaryotes. *Molecular biology and evolution*, 39(9).

Wang F, et al. (2022) Archaeal bundling pili of *Pyrobaculum calidifontis* reveal similarities between archaeal and bacterial biofilms. *Proceedings of the National Academy of Sciences of the United States of America*, 119(26), e2207037119.

Winkle M, et al. (2021) DpaA Detaches Braun's Lipoprotein from Peptidoglycan. *mBio*, 12(3).

Chen Y, et al. (2021) Nitrogen-fixing Ability and Nitrogen Fixation-related Genes of Thermophilic Fermentative Bacteria in the Genus *Caldicellulosiruptor*. *Microbes and environments*, 36(2).

Londei P, et al. (2021) Ribosome Biogenesis in Archaea. *Frontiers in microbiology*, 12, 686977.

Liu J, et al. (2021) Bacterial Vipp1 and PspA are members of the ancient ESCRT-III membrane-remodeling superfamily. *Cell*, 184(14), 3660.