

Resource Summary Report

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Bio++

RRID:SCR_016055

Type: Tool

Proper Citation

Bio++ (RRID:SCR_016055)

Resource Information

URL: http://biopp.univ-montp2.fr/wiki/index.php/Main_Page

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Description: Software providing a set of ready-to-use C++ libraries as re-usable tools to visualize, edit, print and output data for bioinformatics. It uses sequence analysis, phylogenetics, molecular evolution and population genetics to help to write programs.

Synonyms: Bppsuite, Bppphyview, Bio++ program suite, Bio++ Phylogenetic Viewer

Resource Type: software library, software resource, software development tool, software toolkit, software application

Keywords: phylogenetic, molecular evolution, genetic, program, write, tool, visualize, edit, print, data, bioinformatic, sequence analysis, bio.tools

Funding:

Availability: Free, Available for download

Resource Name: Bio++

Resource ID: SCR_016055

Alternate IDs: OMICS_15696, biotools:biopp

Alternate URLs: <https://sources.debian.org/src/bppsuite/>,
<https://groups.google.com/forum/#!categories/biopp-help-forum/all-questions>,
<https://github.com/BioPP>, <https://bio.tools/biopp>,

License: GNU GPL, CeCILL (from CEA CNRS INRIA Logiciel Libre)

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Ratings and Alerts

No rating or validation information has been found for Bio++.

No alerts have been found for Bio++.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 64 mentions in open access literature.

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

Gálvez-Morante A, et al. (2024) Dollo Parsimony Overestimates Ancestral Gene Content Reconstructions. *Genome biology and evolution*, 16(4).

Reboud EL, et al. (2023) Genomics, Population Divergence, and Historical Demography of the World's Largest and Endangered Butterfly, The Queen Alexandra's Birdwing. *Genome biology and evolution*, 15(4).

Näsvalk K, et al. (2023) Base Composition, Codon Usage, and Patterns of Gene Sequence Evolution in Butterflies. *Genome biology and evolution*, 15(8).

Farrell AA, et al. (2023) Early Divergence and Gene Exchange Highways in the Evolutionary History of Mesoaciditogales. *Genome biology and evolution*, 15(9).

Jacques F, et al. (2023) Roadmap to the study of gene and protein phylogeny and evolution- A practical guide. *PloS one*, 18(2), e0279597.

Awal RP, et al. (2023) Experimental analysis of diverse actin-like proteins from various magnetotactic bacteria by functional expression in *Magnetospirillum gryphiswaldense*. *mBio*, 14(5), e0164923.

Meteyer CU, et al. (2022) Plant pathogens provide clues to the potential origin of bat white-nose syndrome *Pseudogymnoascus destructans*. *Virulence*, 13(1), 1020.

Chaurasia S, et al. (2022) The Structural Determinants of Intra-Protein Compensatory

Substitutions. *Molecular biology and evolution*, 39(4).

Ralph DK, et al. (2022) Inference of B cell clonal families using heavy/light chain pairing information. *PLoS computational biology*, 18(11), e1010723.

Chiou KL, et al. (2022) Genomic signatures of high-altitude adaptation and chromosomal polymorphism in geladas. *Nature ecology & evolution*, 6(5), 630.

Cariou M, et al. (2022) Distinct evolutionary trajectories of SARS-CoV-2-interacting proteins in bats and primates identify important host determinants of COVID-19. *Proceedings of the National Academy of Sciences of the United States of America*, 119(35), e2206610119.

Moutinho AF, et al. (2022) Strong evidence for the adaptive walk model of gene evolution in *Drosophila* and *Arabidopsis*. *PLoS biology*, 20(9), e3001775.

Ritchie AM, et al. (2021) Inferring the number and position of changes in selective regime in a non-equilibrium mutation-selection framework. *BMC ecology and evolution*, 21(1), 39.

Allio R, et al. (2021) High-quality carnivoran genomes from roadkill samples enable comparative species delineation in aardwolf and bat-eared fox. *eLife*, 10.

Allio R, et al. (2021) Genome-wide macroevolutionary signatures of key innovations in butterflies colonizing new host plants. *Nature communications*, 12(1), 354.

Picard L, et al. (2020) DGINN, an automated and highly-flexible pipeline for the detection of genetic innovations on protein-coding genes. *Nucleic acids research*, 48(18), e103.

Rousselle M, et al. (2020) Is adaptation limited by mutation? A timescale-dependent effect of genetic diversity on the adaptive substitution rate in animals. *PLoS genetics*, 16(4), e1008668.

Saclier N, et al. (2020) Bedrock radioactivity influences the rate and spectrum of mutation. *eLife*, 9.

Wang D, et al. (2020) *Pyropia yezoensis* genome reveals diverse mechanisms of carbon acquisition in the intertidal environment. *Nature communications*, 11(1), 4028.

Koutsovoulos GD, et al. (2020) Population genomics supports clonal reproduction and multiple independent gains and losses of parasitic abilities in the most devastating nematode pest. *Evolutionary applications*, 13(2), 442.