

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

Proper Citation: Bio++ (RRID:SCR_016055)

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., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

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

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

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

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

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 65 mentions in open access literature.

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

Nisson KA, et al. (2025) HIV Vpr activates a nucleolar-specific ATR pathway to degrade the nucleolar stress sensor CCDC137. *Nucleic acids research*, 53(11).

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

Näsval 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).

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).

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.

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.

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.

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.

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.

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.