

Resource Summary Report

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BioPerl

RRID:SCR_002989

Type: Tool

Proper Citation

BioPerl (RRID:SCR_002989)

Resource Information

URL: <http://www.bioperl.org>

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Description: BioPerl is a community effort to produce Perl code which is useful in biology. This toolkit of perl modules is useful in building bioinformatics solutions in Perl. It is built in an object-oriented manner so that many modules depend on each other to achieve a task. The collection of modules in the bioperl-live repository consist of the core of the functionality of bioperl. Additionally auxiliary modules for creating graphical interfaces (bioperl-gui), persistent storage in RDMBS (bioperl-db), running and parsing the results from hundreds of bioinformatics applications (Run package), software to automate bioinformatic analyses (bioperl-pipeline) are all available as Git modules in our repository. The BioPerl toolkit provides a library of hundreds of routines for processing sequence, annotation, alignment, and sequence analysis reports. It often serves as a bridge between different computational biology applications assisting the user to construct analysis pipelines. This chapter illustrates how BioPerl facilitates tasks such as writing scripts summarizing information from BLAST reports or extracting key annotation details from a GenBank sequence record. BioPerl includes modules written by Sohel Merchant of the GO Consortium for parsing and manipulating OBO ontologies. Platform: Windows compatible, Mac OS X compatible, Linux compatible, Unix compatible

Abbreviations: BioPerl

Resource Type: software toolkit, wiki, narrative resource, source code, software repository, data or information resource, software resource

Defining Citation: [PMID:12368254](#), [DOI:10.1101/gr.361602](#)

Keywords: perl, biology, ontology, library, sequence, analysis, computational, application, pipeline, bioinformatics, sequence, annotation, module, life science, python, java, genome, software library, parse, manipulate, bio.tools

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NHGRI K22 HG00056;
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NHGRI HG00739;
NHGRI P41HG02223

Availability: Free, Available for download, Freely available

Resource Name: BioPerl

Resource ID: SCR_002989

Alternate IDs: OMICS_04849, nif-0000-30188, biotools:bioperl

Alternate URLs: <https://bio.tools/bioperl>, <https://sources.debian.org/src/bioperl/>

License: Artistic License

Record Creation Time: 20220129T080216+0000

Record Last Update: 20260804T043210+0000

Ratings and Alerts

No rating or validation information has been found for BioPerl.

No alerts have been found for BioPerl.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 402 mentions in open access literature.

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

Bulzu PA, et al. (2025) Lineage-specific expansions of polinton-like viruses in photosynthetic cryptophytes. *Microbiome*, 13(1), 154.

Manzano-Alvarez J, et al. (2025) Virome profiling of *Culex tarsalis* through small RNA-seq: A challenge of suboptimal samples. *PLoS neglected tropical diseases*, 19(11), e0013611.

Park S, et al. (2025) Comparative genome-wide characterization and evolutionary insights into the AP2/ERF gene family in three *Coffea* species (*C. canephora*, *C. eugenoides*, and *C. arabica*). *BMC genomics*, 26(1), 653.

Guo F, et al. (2025) Insight into the codon usage patterns and adaptation of Tembusu Virus. *Poultry science*, 104(1), 104651.

Rojas-Villalobos C, et al. (2025) MOBHunter: a data integration platform for identification and classification of mobile genetic elements in microbial genomes. *Nucleic acids research*, 53(W1), W398.

Wang Y, et al. (2025) A modulatory role of CG methylation on gene expression in soybean implicates its potential utility in breeding. *Plant biotechnology journal*, 23(5), 1585.

Maul JE, et al. (2025) Genomic and mutational analysis of *Pseudomonas syringae* pv. *tagetis* EB037 pathogenicity on sunflower. *BMC microbiology*, 25(1), 43.

Zhang Y, et al. (2025) Genetic Differentiation of Chinese Fir Populations From Mainland China and Taiwan as Revealed by Genotyping-By-Sequencing Analysis, With Implication for Taxonomic Position of the Species. *Ecology and evolution*, 15(4), e71270.

Bush NG, et al. (2025) Insights into antibiotic resistance promoted by quinolone exposure. *Antimicrobial agents and chemotherapy*, 69(1), e0099724.

Fu C, et al. (2025) Genome-Wide Identification of the Potato GGPS Gene Family and Analysis of Its Response to Abiotic Stress. *Genes*, 16(6).

Manzano-Alvarez J, et al. (2025) Virome profiling of *Culex tarsalis* through small RNA-seq: A challenge of suboptimal samples. *bioRxiv : the preprint server for biology*.

Shi C, et al. (2025) Characterization and functional analysis of the BAM gene family in peanut (*Arachis hypogaea* L.). *Frontiers in plant science*, 16, 1599610.

Zhang X, et al. (2025) Genome-Wide identification and expression profiles of the WRKY transcription factor family in *Artocarpus nanchuanensis*. *BMC plant biology*, 25(1), 922.

Fonseca PLC, et al. (2025) Integrative multi-omics approach identified emerging viral threat in *Theobroma cacao* plants. *BMC plant biology*, 25(1), 1425.

Gallego-Parrilla JJ, et al. (2024) Identification of novel tail-anchored membrane proteins integrated by the bacterial twin-arginine translocase. *Microbiology (Reading, England)*, 170(2).

Chuzel L, et al. (2024) High-throughput nanopore DNA sequencing of large insert fosmid clones directly from bacterial colonies. *Applied and environmental microbiology*, 90(6), e0024324.

Xin X, et al. (2024) Temperature-dependent jumonji demethylase modulates flowering time by targeting H3K36me2/3 in *Brassica rapa*. *Nature communications*, 15(1), 5470.

Haas D, et al. (2024) Synteruptor: mining genomic islands for non-classical specialized metabolite gene clusters. *NAR genomics and bioinformatics*, 6(2), lqae069.

Nazziwa J, et al. (2024) Higher HIV-1 evolutionary rate is associated with cytotoxic T lymphocyte escape mutations in infants. *Journal of virology*, 98(7), e0007224.

Delgado S, et al. (2024) Impact of the chemical modification of tRNAs anticodon loop on the variability and evolution of codon usage in proteobacteria. *Frontiers in microbiology*, 15, 1412318.