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: source code, data or information resource, software repository, software toolkit, wiki, software resource, narrative 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: Artistic License

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/

Record Creation Time: 20220129T080216+0000

Record Last Update: 20250426T055605+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 390 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

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

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

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

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.

Alburkat H, et al. (2024) Evolution and genetic characterization of Seoul virus in wild rats Rattus norvegicus from an urban park in Lyon, France 2020-2022. PLoS neglected tropical diseases, 18(5), e0012142.

Tournayre J, et al. (2024) MicroAnnot: A Dedicated Workflow for Accurate Microsporidian Genome Annotation. International journal of molecular sciences, 25(2).

Shangguan X, et al. (2024) Genome-Wide Identification and Expression Pattern of Sugar Transporter Genes in the Brown Planthopper, Nilaparvata lugens (Stål). Insects, 15(7).

Goodall J, et al. (2024) Evolution of fast-growing piscivorous herring in the young Baltic Sea. Nature communications, 15(1), 10707.

Moreira SM, et al. (2024) Diversification of the Rho transcription termination factor in bacteria. Nucleic acids research, 52(15), 8979.

Maheshwari N, et al. (2024) Insights into the production and evolution of lantibiotics from a computational analysis of peptides associated with the lanthipeptide cyclase domain. Royal Society open science, 11(7), 240491.

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.

Song Z, et al. (2024) Genome-Wide Identification and Comprehensive Analysis of the PPO Gene Family in Glycine max and Glycine soja. Genes, 16(1).

Nakahara K, et al. (2023) Gut microbiota of Parkinson's disease in an appendectomy cohort:

a preliminary study. Scientific reports, 13(1), 2210.

Jung H, et al. (2023) Comparative genomic analysis of Chryseobacterium species: deep insights into plant-growth-promoting and halotolerant capacities. Microbial genomics, 9(10).

Choquet M, et al. (2023) Comparative Population Transcriptomics Provide New Insight into the Evolutionary History and Adaptive Potential of World Ocean Krill. Molecular biology and evolution, 40(11).

Schoof M, et al. (2023) Lysis Cassette-Mediated Exoprotein Release in Yersinia entomophaga Is Controlled by a PhoB-Like Regulator. Microbiology spectrum, 11(2), e0036423.