

Resource Summary Report

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BioConda

RRID:SCR_018316

Type: Tool

Proper Citation

BioConda (RRID:SCR_018316)

Resource Information

URL: <https://bioconda.github.io/>

Proper Citation: BioConda (RRID:SCR_018316)

Description: Software distribution management for life sciences. Channel for Conda package manager specializing in bioinformatics software. Consists of repository of recipes hosted on GitHub, build system turning these recipes into conda packages, repository of packages containing bioinformatics packages ready to use with conda install.

Synonyms: Bioconda

Resource Type: software application, software resource

Defining Citation: [PMID:29967506](#)

Keywords: Software distribution management, bioinformatic software, package repository, GitHub, conda, bio.tools

Funding: German Research Foundation ;
Intramural Program of the National Institute of Diabetes and Digestive and Kidney Diseases ;
Netherlands Organisation for Scientific Research ;
NYU Abu Dhabi Research Institute

Availability: Free, Available for download, Freely available

Resource Name: BioConda

Resource ID: SCR_018316

Alternate IDs: biotools:bioconda

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

Record Creation Time: 20220129T080339+0000

Record Last Update: 20260905T133304+0000

Ratings and Alerts

No rating or validation information has been found for BioConda.

No alerts have been found for BioConda.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 73 mentions in open access literature.

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

Mendoza-Garcia P, et al. (2026) Omics-aided design genome editing strategy for challenging human immortalized cell models. PloS one, 21(2), e0341124.

Scott AT, et al. (2026) Hybrid capture RNA-seq defines temporal gene expression in Rickettsia. bioRxiv : the preprint server for biology.

Scott AT, et al. (2026) Hybrid capture RNA-seq defines temporal gene expression in Rickettsia. mSphere, 11(5), e0090125.

Pratt BM, et al. (2026) Single-cell gain-of-function mapping reveals latent regulatory programs governing CD8+ T cell fate. Research square.

Danner C, et al. (2025) Act1 out of Action: Identifying Reliable Reference Genes in Trichoderma reesei for Gene Expression Analysis. Journal of fungi (Basel, Switzerland), 11(5).

Blatnik AJ, et al. (2025) Sm-site containing mRNAs can accept Sm-rings and are downregulated in Spinal Muscular Atrophy. Nucleic acids research, 53(15).

Rojas WY, et al. (2025) Galaxy QCxMS for straightforward semi-empirical quantum mechanical EI-MS prediction. GigaByte (Hong Kong, China), 2025, gigabyte160.

Arnadottir AT, et al. (2025) Results from the IceGut study: tracking the gut microbiome development from mothers and infants up to five years of age. mSphere, 10(12), e0074525.

Freedman AH, et al. (2025) Building better genome annotations across the tree of life. Genome research, 35(5), 1261.

Schwarz EM, et al. (2025) Genomes of the entomopathogenic nematode *Steinernema hermaphroditum* and its associated bacteria. *Genetics*, 231(3).

Platt RN, et al. (2025) Efficient amplicon panels for evaluating hybridization and genetic structure in the *Schistosoma haematobium* species group. *bioRxiv : the preprint server for biology*.

Auchtung TA, et al. (2025) Evaluating Effects of Antibiotics Across Preclinical Models of the Human Gastrointestinal Microbiota. *MicrobiologyOpen*, 14(4), e70030.

Link JM, et al. (2025) Ongoing replication stress tolerance and clonal T cell responses distinguish liver and lung recurrence and outcomes in pancreatic cancer. *Nature cancer*, 6(1), 123.

Schraven AL, et al. (2025) Boost or Bust? The Impact of Supplementation on Functional Genetic Diversity and Selective Processes in Tasmanian Devils. *Molecular ecology*, 34(24), e70188.

Maaskant A, et al. (2025) AI for rapid identification of major butyrate-producing bacteria in rhesus macaques (*Macaca mulatta*). *Animal microbiome*, 7(1), 39.

B??kenkamp JE, et al. (2025) Proteogenomic analysis reveals adaptive strategies for alleviating the consequences of aneuploidy in cancer. *The EMBO journal*, 44(6), 1829.

Dai C, et al. (2024) quantms: a cloud-based pipeline for quantitative proteomics enables the reanalysis of public proteomics data. *Nature methods*, 21(9), 1603.

Bayarri G, et al. (2024) Using interactive Jupyter Notebooks and BioConda for FAIR and reproducible biomolecular simulation workflows. *PLoS computational biology*, 20(6), e1012173.

Roots CT, et al. (2024) CryptKeeper: a negative design tool for reducing unintentional gene expression in bacteria. *Synthetic biology (Oxford, England)*, 9(1), ysae018.

Lazovic B, et al. (2024) Human iPSC and CRISPR targeted gene knock-in strategy for studying the somatic TIE2L914F mutation in endothelial cells. *Angiogenesis*, 27(3), 523.