

Resource Summary Report

Generated by T1D on Jul 29, 2026

Conda

RRID:SCR_018317

Type: Tool

Proper Citation

Conda (RRID:SCR_018317)

Resource Information

URL: <https://docs.conda.io/en/latest/>

Proper Citation: Conda (RRID:SCR_018317)

Description: Software tool as cross platform, language agnostic binary package manager. Open source package management system and environment management system that runs on Windows, macOS and Linux. Can quickly install, run, and update packages and their dependencies. Package, dependency and environment management for any language—Python, R, Ruby, Lua, Scala, Java, JavaScript, C/ C++, FORTRAN, and more. Created for Python programs, but it can package and distribute software for any language. Conda can be combined with continuous integration systems such as Travis CI and AppVeyor to provide frequent, automated testing of your code. Conda package and environment manager is included in all versions of Anaconda and Miniconda.

Resource Type: software toolkit, software resource

Keywords: Package manager system, environment management system, software distribution, integration system, automated code testing

Availability: Free, Available for download, Freely available

Resource Name: Conda

Resource ID: SCR_018317

Alternate URLs: <https://conda.io/?>, <https://github.com/conda/conda>

License: 3-clause BSD license

License URLs: <https://docs.conda.io/en/latest/license.html>,
<https://github.com/conda/conda-docs>

Record Creation Time: 20220129T080339+0000

Record Last Update: 20260729T044444+0000

Ratings and Alerts

No rating or validation information has been found for Conda.

No alerts have been found for Conda.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 93 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

Lataretu M, et al. (2025) Targeted decontamination of sequencing data with CLEAN. NAR genomics and bioinformatics, 7(3), lqaf105.

Sanz-Robinson J, et al. (2025) Open-source platforms to investigate analytical flexibility in neuroimaging. Imaging neuroscience (Cambridge, Mass.), 3.

Sagar MAK, et al. (2025) MetaChrome: An Open-Source, User-Friendly Tool for Automated Metaphase Chromosome Analysis. bioRxiv : the preprint server for biology.

Rubalskii E, et al. (2025) Characterization and genome analysis of the novel virulent Burkholderia phage Bm1, which is active against pan-drug-resistant Burkholderia multivorans. Archives of virology, 170(5), 106.

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.

Beck AG, et al. (2025) Paddy: an evolutionary optimization algorithm for chemical systems and spaces. Digital discovery, 4(5), 1352.

Zirión-Martínez C, et al. (2025) WeavePop: A bioinformatics workflow to explore and analyze genomic variants of eukaryotic populations. bioRxiv : the preprint server for biology.

Offermanns A, et al. (2025) Developmental embedding of parvalbumin-positive interneurons drives local and crosshemispheric prefrontal gamma synchrony. Progress in neurobiology, 257, 102866.

Joubert PM, et al. (2024) Distinct genomic contexts predict gene presence-absence variation in different pathotypes of Magnaporthe oryzae. Genetics, 226(4).

Delavaux CS, et al. (2024) An updated LSU database and pipeline for environmental DNA identification of arbuscular mycorrhizal fungi. Mycorrhiza, 34(4), 369.

Zong P, et al. (2024) TSTA: thread and SIMD-based trapezoidal pairwise/multiple sequence-alignment method. GigaByte (Hong Kong, China), 2024, gigabyte141.

Yang C, et al. (2024) LRTK: a platform agnostic toolkit for linked-read analysis of both human genome and metagenome. GigaScience, 13.

Smith CC, et al. (2024) Kv2 channels do not function as canonical delayed rectifiers in spinal motoneurons. iScience, 27(8), 110444.

Markarian N, et al. (2024) Enrichment on steps, not genes, improves inference of differentially expressed pathways. PLoS computational biology, 20(3), e1011968.

Boulton W, et al. (2024) SWAMPy: simulating SARS-CoV-2 wastewater amplicon metagenomes. Bioinformatics (Oxford, England), 40(9).

Gutierrez-Castillo DE, et al. (2024) A recently collected *Xanthomonas translucens* isolate encodes TAL effectors distinct from older, less virulent isolates. Microbial genomics, 10(1).

Anneser L, et al. (2024) Molecular organization of neuronal cell types and neuromodulatory systems in the zebrafish telencephalon. Current biology : CB, 34(2), 298.

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

Giordano N, et al. (2024) Genome-scale community modelling reveals conserved metabolic cross-feedings in epipelagic bacterioplankton communities. Nature communications, 15(1), 2721.

Ardisson M, et al. (2024) GeCKO: user-friendly workflows for genotyping complex genomes using target enrichment capture. A use case on the large tetraploid durum wheat genome. Plant methods, 20(1), 103.