

Resource Summary Report

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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 resource, software toolkit

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

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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 116 mentions in open access literature.

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

Sacks B, et al. (2026) Protocol for automated analysis of biological images using Python code. STAR protocols, 7(1), 104368.

Placide A, et al. (2026) The de novo transcriptome of the freshwater copepod *Cyclops abyssorum taticus* reveals high-elevation adaptation. Scientific reports, 16(1).

Heumos L, et al. (2026) Pertpy: an end-to-end framework for perturbation analysis. Nature methods, 23(2), 350.

Fernandez Bonet D, et al. (2026) Computational protocol to assess the quality of sequencing-based microscopy networks using spatial coherence metrics. STAR protocols, 7(2), 104521.

Drouillard D, et al. (2026) Mutant KRAS promotes NF- κ B driven CCL20 chemokine expression in pancreatic ductal adenocarcinoma. bioRxiv : the preprint server for biology.

F?rat Y, et al. (2026) An explainable ensemble machine learning model using baseline blood transcriptomics to predict Parkinson's disease motor progression. Frontiers in digital health, 8, 1774436.

Aliyev E, et al. (2026) A comprehensive assessment of tandem repeat genotyping methods for Nanopore long-read genomes. bioRxiv : the preprint server for biology.

Lensing K, et al. (2026) A generic pipeline for CADD score generation: chickenCADD and turkeyCADD. G3 (Bethesda, Md.), 16(1).

Zirión-Martínez C, et al. (2026) WeavePop: a bioinformatics workflow to explore and analyze genomic variants of eukaryotic populations. G3 (Bethesda, Md.), 16(4).

Tóth AG, et al. (2026) Protocol for the assessment of the impact of mycotoxins and glyphosate residues on the gut microbiome and resistome of European fallow deer. STAR protocols, 7(2), 104498.

Güler BE, et al. (2026) The adhesion GPCR ADGRV1 controls glutamate homeostasis in hippocampal astrocytes supporting neurons. Acta neuropathologica communications,

14(1).

An C, et al. (2026) Pancreatic multi structure segmentation on CT using transformer and deep learning approaches. *Discover oncology*, 17(1).

Enabuele EE, et al. (2026) Misleading inference of schistosome epidemiology from ribosomal internal transcribed spacer (ITS) and mitochondrial DNA. *bioRxiv : the preprint server for biology*.

Calabrese FM, et al. (2026) GPCS Stratification of Exercise-Induced Gut Microbiota and Metabolome Remodeling in IBS: An Exploratory Multi-Omics Study. *Nutrients*, 18(12).

Zhang H, et al. (2026) Human milk oligosaccharide composition, concentrations and association with maternal factors in the multi-ethnic Asian GUSTO cohort. *Frontiers in nutrition*, 13, 1781871.

Yin X, et al. (2026) Predicting hormone receptor status in tumors: An innovative approach using breast ultrasound-radiomics combined model. *Medicine*, 105(8), e47576.

Schamber P, et al. (2026) SynAPSeg: A novel dataset and image analysis framework for deep learning-based synapse detection and quantification. *bioRxiv : the preprint server for biology*.

Escobar MA, et al. (2026) A municipality-level, monthly dataset of disappearance cases and outcomes in Mexico from the National Registry of Disappeared Persons, 2015-2025. *Data in brief*, 66, 112897.

Borbinha J, et al. (2026) Metabolic reprogramming regulates histone lactylation during zebrafish caudal fin regeneration. *iScience*, 29(2), 114792.

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