

Resource Summary Report

Generated by T1D on Sep 5, 2026

Snakemake

RRID:SCR_003475

Type: Tool

Proper Citation

Snakemake (RRID:SCR_003475)

Resource Information

URL: <https://bitbucket.org/johanneskoester/snakemake/wiki/>

Proper Citation: Snakemake (RRID:SCR_003475)

Description: A Python based language and execution environment for make-like workflows. The system supports the use of automatically inferred multiple named wildcards (or variables) in input and output filenames.

Abbreviations: Snakemake

Synonyms: snakemake - A Python based language and execution environment for make-like workflows

Resource Type: software resource

Defining Citation: [PMID:22908215](#), [DOI:10.1093/bioinformatics/bts480](#)

Keywords: python, workflow, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: Snakemake

Resource ID: SCR_003475

Alternate IDs: OMICS_02299, biotools:snakemake

Alternate URLs: <https://snakemake.github.io/>

Record Creation Time: 20220129T080219+0000

Record Last Update: 20260903T234617+0000

Ratings and Alerts

No rating or validation information has been found for Snakemake.

No alerts have been found for Snakemake.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 465 mentions in open access literature.

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

Ravindran D, et al. (2026) High-throughput evaluation of cardiac-specific promoters for adeno-associated virus mediated cardiac gene therapy. *Gene therapy*, 33(2), 203.

Langstein-Skora I, et al. (2026) Sequence and chemical specificity define the functional landscape of intrinsically disordered regions. *Nature cell biology*, 28(2), 323.

Gameiro PA, et al. (2026) Meta-unstable mRNAs in activated CD8⁺ T cells are defined by interlinked AU-rich elements and m6A mRNA methylation. *Nature communications*, 17(1), 160.

Schmidt A, et al. (2026) Host control of persistent Epstein-Barr virus infection. *Nature*, 653(8114), 444.

Bhattacharyya S, et al. (2026) EpiExpr: Predicting gene expression using epigenetic data and chromatin interactions. *bioRxiv : the preprint server for biology*.

Mendez M, et al. (2026) Segzoo: a turnkey system that summarizes genome annotations. *Bioinformatics (Oxford, England)*, 42(5).

Xu Z, et al. (2026) Single-cell multimodal profiling of pan-cancer cell lines uncovers gene regulatory principles underlying intrinsic cell states and environmental features. *bioRxiv : the preprint server for biology*.

Otwinowska A, et al. (2026) Capsular specificity in temperate phages of *Klebsiella pneumoniae* is driven by diverse receptor-binding enzymes. *PLoS biology*, 24(4), e3003716.

Hernandez JB, et al. (2026) Mapping the metagenomic landscape: combined shotgun sequencing and quantitative PCR to profile gut metagenome-assembled genomes in marmosets following treatment with a broad-spectrum antibiotic cocktail. *Gut microbes*, 18(1), 2687925.

Dupas SJ, et al. (2026) Splice isoform-perturbation coupled to single cell transcriptome profiling reveals functions of microexons in neurogenesis and autism-linked pathways. *Nature communications*, 17(1), 1217.

Klitting R, et al. (2026) Genomic Epidemiology of West Nile Virus in Paris. JAMA network open, 9(2), e2559588.

Bacon WA, et al. (2026) Ten common misconceptions about Galaxy (and why they are wrong!). PLoS computational biology, 22(2), e1013869.

Marques Silva B, et al. (2026) Pipeasm: a tool for automated large chromosome-scale genome assembly and evaluation. Bioinformatics advances, 6(1), vbaf326.

Dvořáková L, et al. (2026) Secondary thalamic neuroinflammation associates with disturbed corticothalamic connectivity in a model of severe traumatic brain injury in male rats-a longitudinal study. Cerebral cortex (New York, N.Y. : 1991), 36(1).

Kulikov N, et al. (2026) The Chromosome-Scale Genome Assembly of the Redlip Blenny, *Ophioblennius macclurei* (Blenniidae). Genome biology and evolution, 18(1).

Trimbour R, et al. (2026) CIRCE: a scalable Python package to predict cis-regulatory DNA interactions from single-cell chromatin accessibility data. Bioinformatics (Oxford, England), 42(3).

Wissel D, et al. (2026) A systematic benchmark of high-accuracy PacBio long-read RNA sequencing for transcript-level quantification. Genome biology, 27(1).

Bimbocci A, et al. (2026) SnakeBITE: A SNAKEmake-Based Interface for Third-Generation Sequencing Data Analysis. Biomolecules, 16(2).

Soria-Alcaide G, et al. (2026) crocketa: an automated Snakemake framework for integrated single-cell transcriptome and immune-repertoire analysis. BMC genomics, 27(1).

de Faria O, et al. (2026) Focal white matter lesions drive grey matter inflammation and synapse loss. Nature, 654(8120), 1033.