

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

Snakemake

RRID:SCR_003475

Type: Tool

Proper Citation

Snakemake (RRID:SCR_003475)

Resource Information

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

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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: 20260905T132504+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 [Kravitz](#) .

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.

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

- 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).
- Marques Silva B, et al. (2026) Pipeasm: a tool for automated large chromosome-scale genome assembly and evaluation. *Bioinformatics advances*, 6(1), vbaf326.
- Wissel D, et al. (2026) A systematic benchmark of high-accuracy PacBio long-read RNA sequencing for transcript-level quantification. *Genome biology*, 27(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).
- 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.
- Soria-Alcaide G, et al. (2026) crocketa: an automated Snakemake framework for integrated single-cell transcriptome and immune-repertoire analysis. *BMC genomics*, 27(1).
- 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.
- de Faria O, et al. (2026) Focal white matter lesions drive grey matter inflammation and synapse loss. *Nature*, 654(8120), 1033.
- Bimbocci A, et al. (2026) SnakeBITE: A SNAKEmake-Based Interface for Third-Generation Sequencing Data Analysis. *Biomolecules*, 16(2).