Resource Summary Report

Generated by NIF on Apr 26, 2025

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

Funding:

Availability: MIT License

Resource Name: Snakemake

Resource ID: SCR_003475

Alternate IDs: OMICS_02299, biotools:snakemake

Alternate URLs: https://bio.tools/snakemake, https://sources.debian.org/src/snakemake/

Record Creation Time: 20220129T080219+0000

Record Last Update: 20250420T014144+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 286 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Keller MS, et al. (2025) Vitessce: integrative visualization of multimodal and spatially resolved single-cell data. Nature methods, 22(1), 63.

Naraharisetti R, et al. (2025) Timing of Infection as a Key Driver of Racial/Ethnic Disparities in Coronavirus Disease 2019 Mortality Rates During the Prevaccine Period. Open forum infectious diseases, 12(1), ofae636.

Kim DW, et al. (2025) Decoding Gene Networks Controlling Hypothalamic and Prethalamic Neuron Development. bioRxiv : the preprint server for biology.

Hassanpour A, et al. (2025) Optimization of breeding program design through stochastic simulation with evolutionary algorithms. G3 (Bethesda, Md.), 15(1).

Formichetti S, et al. (2025) Genetic gradual reduction of OGT activity unveils the essential role of O-GlcNAc in the mouse embryo. PLoS genetics, 21(1), e1011507.

Clark MS, et al. (2025) Assessing the impact of sewage and wastewater on antimicrobial resistance in nearshore Antarctic biofilms and sediments. Environmental microbiome, 20(1), 9.

Lee S, et al. (2025) Chromosome-scale genome assembly of Korean goosegrass (Eleusine indica). Scientific data, 12(1), 156.

Nevers Y, et al. (2025) Quality assessment of gene repertoire annotations with OMArk. Nature biotechnology, 43(1), 124.

Aguilar R, et al. (2024) Tigerfish designs oligonucleotide-based in situ hybridization probes targeting intervals of highly repetitive DNA at the scale of genomes. Nature communications, 15(1), 1027.

Gutzen R, et al. (2024) A modular and adaptable analysis pipeline to compare slow cerebral rhythms across heterogeneous datasets. Cell reports methods, 4(1), 100681.

Graelmann FJ, et al. (2024) Differential cell type-specific function of the aryl hydrocarbon receptor and its repressor in diet-induced obesity and fibrosis. Molecular metabolism, 85, 101963.

Paremskaia AI, et al. (2024) IAVCP (Influenza A Virus Consensus and Phylogeny): Automatic Identification of the Genomic Sequence of the Influenza A Virus from High-Throughput Sequencing Data. Viruses, 16(6).

Chacón RD, et al. (2024) Molecular characterization of the meq oncogene of Marek's disease virus in vaccinated Brazilian poultry farms reveals selective pressure on prevalent strains. The veterinary quarterly, 44(1), 1.

Moix S, et al. (2024) Breaking down causes, consequences, and mediating effects of telomere length variation on human health. Genome biology, 25(1), 125.

Mielnicka M, et al. (2024) Trim66's paternal deficiency causes intrauterine overgrowth. Life science alliance, 7(7).

Chen KY, et al. (2024) Massively parallel identification of sequence motifs triggering ribosome-associated mRNA quality control. Nucleic acids research, 52(12), 7171.

Bulka O, et al. (2024) Pangenomic insights into Dehalobacter evolution and acquisition of functional genes for bioremediation. Microbial genomics, 10(11).

Wilkins OG, et al. (2024) Creation of de novo cryptic splicing for ALS and FTD precision medicine. Science (New York, N.Y.), 386(6717), 61.

Dwarshuis N, et al. (2024) The GIAB genomic stratifications resource for human reference genomes. Nature communications, 15(1), 9029.

Iso-Touru T, et al. (2024) Genes and pathways revealed by whole transcriptome analysis of milk derived bovine mammary epithelial cells after Escherichia coli challenge. Veterinary research, 55(1), 13.