

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 18, 2026

Pipelinier

RRID:SCR_003171

Type: Tool

Proper Citation

Pipelinier (RRID:SCR_003171)

Resource Information

URL: <https://github.com/brunonevado/Pipelinier>

Proper Citation: Pipelinier (RRID:SCR_003171)

Description: Software for evaluating the performance of bioinformatics pipelines for Next Generation re-Sequencing.

Resource Type: software resource

Defining Citation: [PMID:24890372](#)

Keywords: standalone software, c++, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: Pipelinier

Resource ID: SCR_003171

Alternate IDs: OMICS_04844, biotools:pipelinier

Alternate URLs: <https://bio.tools/pipelinier>

Record Creation Time: 20220129T080217+0000

Record Last Update: 20260912T195553+0000

Ratings and Alerts

No rating or validation information has been found for Pipelinier.

No alerts have been found for Pipelinier.

Data and Source Information

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Boudjadi S, et al. (2026) Involvement of the FGF8/FGF Receptor Signaling Pathway in the Maintenance and Progression of Fusion-Positive Rhabdomyosarcoma. *Molecular cancer therapeutics*, 25(3), 493.

Villamor-Pay?? M, et al. (2024) De novo TLK1 and MDM1 mutations in a patient with a neurodevelopmental disorder and immunodeficiency. *iScience*, 27(6), 109984.

Lim Y, et al. (2021) Exploration of alcohol use disorder-associated brain miRNA-mRNA regulatory networks. *Translational psychiatry*, 11(1), 504.

Smith RL, et al. (2021) Experimental *Babesia rossi* infection induces hemolytic, metabolic, and viral response pathways in the canine host. *BMC genomics*, 22(1), 619.

Tanwar S, et al. (2020) Type I IFN signaling in T regulatory cells modulates chemokine production and myeloid derived suppressor cells trafficking during EAE. *Journal of autoimmunity*, 115, 102525.

Federico A, et al. (2019) Pipeliner: A Nextflow-Based Framework for the Definition of Sequencing Data Processing Pipelines. *Frontiers in genetics*, 10, 614.

Bianco E, et al. (2015) A deep catalog of autosomal single nucleotide variation in the pig. *PloS one*, 10(3), e0118867.