

Resource Summary Report

Generated by [NIF](#) on Aug 26, 2026

Smart-seq2 Multi-Sample Pipeline

RRID:SCR_018920

Type: Tool

Proper Citation

Smart-seq2 Multi-Sample Pipeline (RRID:SCR_018920)

Resource Information

URL: https://broadinstitute.github.io/warp/docs/Pipelines/Smart-seq2_Single_Nucleus_Multi_Sample_Pipeline/README

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Description: The Smart-seq2 Single Nucleus Multi-Sample (Multi-snSS2) pipeline was developed in collaboration with the BRAIN Initiative Cell Census Network (BICCN) to process single-nucleus RNAseq (snRNAseq) data generated by Smart-seq2 assays.

Resource Type: data processing software, software application, software resource, software toolkit

Keywords: Single cell data, Smart seq2 technology, scRNAseq data, Smart-seq2 assay data, data processing

Availability: Free, Available for download, Freely available

Resource Name: Smart-seq2 Multi-Sample Pipeline

Resource ID: SCR_018920

Old URLs:

https://github.com/broadinstitute/warp/tree/master/pipelines/skylab/smartseq2_multisample

Record Creation Time: 20220129T080342+0000

Record Last Update: 20260821T194136+0000

Ratings and Alerts

No rating or validation information has been found for Smart-seq2 Multi-Sample Pipeline.

No alerts have been found for Smart-seq2 Multi-Sample Pipeline.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

, et al. (2026) A Community Standard Multispecies Cell Atlas of the Basal Ganglia. bioRxiv : the preprint server for biology.

Palmeri JR, et al. (2024) CD8+ T cell priming that is required for curative intratumorally anchored anti-4-1BB immunotherapy is constrained by Tregs. Nature communications, 15(1), 1900.

Palmeri JR, et al. (2023) Tregs constrain CD8 + T cell priming required for curative intratumorally anchored anti-4-1BB immunotherapy. bioRxiv : the preprint server for biology.

Nilsson A, et al. (2022) Artificial neural networks enable genome-scale simulations of intracellular signaling. Nature communications, 13(1), 3069.