

# Resource Summary Report

Generated by PRECISE-TBI on Sep 8, 2026

## Smart-seq2 Multi-Sample Pipeline

RRID:SCR\_018920

Type: Tool

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### Proper Citation

Smart-seq2 Multi-Sample Pipeline (RRID:SCR\_018920)

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### Resource Information

**URL:** [https://broadinstitute.github.io/warp/docs/Pipelines/Smart-seq2\\_Single\\_Nucleus\\_Multi\\_Sample\\_Pipeline/README](https://broadinstitute.github.io/warp/docs/Pipelines/Smart-seq2_Single_Nucleus_Multi_Sample_Pipeline/README)

**Proper Citation:** Smart-seq2 Multi-Sample Pipeline (RRID:SCR\_018920)

**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](https://github.com/broadinstitute/warp/tree/master/pipelines/skylab/smartseq2_multisample)

**Record Creation Time:** 20220129T080342+0000

**Record Last Update:** 20260905T133056+0000

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### 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 [PRECISE-TBI](#) .

, 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.