

# Resource Summary Report

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## Smart-seq2 Single Nucleus Multi Sample Pipeline

RRID:SCR\_021312

Type: Tool

### Proper Citation

Smart-seq2 Single Nucleus Multi Sample Pipeline (RRID:SCR\_021312)

### 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 Single Nucleus Multi Sample Pipeline (RRID:SCR\_021312)

**Description:** Software pipeline for single-nucleus RNAseq data generated by Smart-seq2 assays. Used to simultaneously process multiple libraries of single nuclei Smart-seq2 and Smart-seq4 data. For each library (nucleus), the pipeline trims paired FASTQ files, aligns trimmed reads to the genome, counts intronic and exonic reads, and calculates quality control metrics. Counts and metrics for all libraries are combined into merged Loom formatted count matrix.

**Synonyms:** Multi-snSS2, Smart-seq2 Single Nucleus Multi-Sample Pipeline

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

**Keywords:** snRNAseq data, Smart-seq2 assays, single nucleus, multi sample, WARP repository

**Availability:** Free, Freely available

**Resource Name:** Smart-seq2 Single Nucleus Multi Sample Pipeline

**Resource ID:** SCR\_021312

**Alternate URLs:** [https://app.terra.bio/#workspaces/warp-pipelines/Smart-seq2\\_Single\\_Nucleus\\_Multi-Sample](https://app.terra.bio/#workspaces/warp-pipelines/Smart-seq2_Single_Nucleus_Multi-Sample)

**Old URLs:**

[https://github.com/broadinstitute/warp/tree/master/pipelines/skylab/smartseq2\\_single\\_nucleus\\_multi](https://github.com/broadinstitute/warp/tree/master/pipelines/skylab/smartseq2_single_nucleus_multi)

**Record Creation Time:** 20220129T080354+0000

**Record Last Update:** 20260821T194153+0000

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## Ratings and Alerts

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

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

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Hawrylycz M, et al. (2023) A guide to the BRAIN Initiative Cell Census Network data ecosystem. PLoS biology, 21(6), e3002133.

Ament SA, et al. (2023) The Neuroscience Multi-Omic Archive: a BRAIN Initiative resource for single-cell transcriptomic and epigenomic data from the mammalian brain. Nucleic acids research, 51(D1), D1075.