

Resource Summary Report

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Smart-seq2 Single Sample Pipeline

RRID:SCR_021228

Type: Tool

Proper Citation

Smart-seq2 Single Sample Pipeline (RRID:SCR_021228)

Resource Information

URL:

https://github.com/broadinstitute/warp/blob/master/pipelines/skylab/smartseq2_single_sample/Smart-seq2_Single_Sample_Pipeline/README

Proper Citation: Smart-seq2 Single Sample Pipeline (RRID:SCR_021228)

Description: Software tool designed by Data Coordination Platform of Human Cell Atlas to process single-cell RNAseq data generated by Smart-seq2 assays. Processes stranded or unstranded, paired- or single-end, scRNA-seq data from an individual cell.

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

Keywords: scRNAseq data, Smart-seq2 assays, processing scRNA-seq data from individual cell

Availability: Free, Freely available

Resource Name: Smart-seq2 Single Sample Pipeline

Resource ID: SCR_021228

Alternate URLs: https://broadinstitute.github.io/warp/docs/Pipelines/Smart-seq2_Single_Sample_Pipeline/README

Old URLs:

https://github.com/broadinstitute/warp/tree/master/pipelines/skylab/smartseq2_single_sample

Record Creation Time: 20220129T080354+0000

Record Last Update: 20260919T195611+0000

Ratings and Alerts

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

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

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Nayak PK, et al. (2025) Transcriptome profiling of tendon fibroblasts at the onset of embryonic muscle contraction reveals novel force-responsive genes. eLife, 14.

Wu H, et al. (2024) Simultaneous single-cell three-dimensional genome and gene expression profiling uncovers dynamic enhancer connectivity underlying olfactory receptor choice. Nature methods, 21(6), 974.

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.