Resource Summary Report

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Smart-seq2 Multi-Sample Pipeline

RRID:SCR_018920 Type: Tool

Proper Citation

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

Resource Information

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

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Description: The Smart-seq2 Multi-Sample Pipeline is a wrapper around the Smart-seq2 Single Sample pipeline. It is developed by the Data Coordination Platform of the Human Cell Atlas to process single-cell RNAseq (scRNAseq) data generated by Smart-seq2 assays. The workflow processes multiple cells by importing and running the Smart-seq2 Single Sample workflow for each individual cell and then merging the resulting output matrices into a single cell-by-gene matrix that contains raw counts and TPMs for all cells.

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

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

Funding:

Availability: Free, Available for download, Freely available

Resource Name: Smart-seq2 Multi-Sample Pipeline

Resource ID: SCR_018920

Old URLs: https://github.com/HumanCellAtlas/skylab/tree/master/pipelines/smartseq2_multisample

Record Creation Time: 20220129T080342+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 3 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

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.