

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

Optimus Pipeline

RRID:SCR_018908

Type: Tool

Proper Citation

Optimus Pipeline (RRID:SCR_018908)

Resource Information

URL: https://broadinstitute.github.io/warp/docs/Pipelines/Optimus_Pipeline/README

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Description: Optimus is a pipeline developed by the Data Coordination Platform (DCP) of the Human Cell Atlas (HCA) Project that supports processing of any 3' single-cell and single-nuclei expression data generated with the 10x Genomic v2 or v3 assay. It is an alignment and transcriptome quantification pipeline that corrects cell barcodes, aligns reads to the genome, corrects Unique Molecular Identifiers (UMIs), generates an expression matrix in a UMI-aware manner, calculates summary metrics for genes and cells, detects empty droplets, returns read outputs in BAM format, and returns gene counts in NumPy matrix and Loom matrix formats.

Synonyms: Optimus

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

Keywords: Data, single cell data, 10x technology data, cell bar code correction pipeline, reads alignment, genome, unique molecular identifier correction, mouse data sets analysis, human data sets analysis,

Availability: Free, Available for download, Freely available

Resource Name: Optimus Pipeline

Resource ID: SCR_018908

Old URLs: <https://github.com/broadinstitute/warp/tree/master/pipelines/skylab/optimus>

Record Creation Time: 20220129T080342+0000

Record Last Update: 20260731T043036+0000

Ratings and Alerts

No rating or validation information has been found for Optimus Pipeline.

No alerts have been found for Optimus Pipeline.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

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.