

Resource Summary Report

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LoomPy

RRID:SCR_016666

Type: Tool

Proper Citation

LoomPy (RRID:SCR_016666)

Resource Information

URL: <https://loompy.org>

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Description: Python implementation of the Loom file format to store and organize very large omics datasets, consisting of a main matrix, optional additional layers, a variable number of row and column annotations and sparse graph objects. Used to store single-cell gene expression data. Created in HDF5 file format and can be opened from programming languages, including Python, R, C, C++, Java, MATLAB, Mathematica, and Julia.

Abbreviations: LoomPy

Synonyms: Loompy v2.0, Loompy v2.0.14, Loom Python, LoomPy, LoomPython

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

Keywords: Python, Loom, file, format, store, organize, omics, dataset, single, cell, expression, data, HDF5

Funding:

Availability: Free, Available for download, Freely available

Resource Name: LoomPy

Resource ID: SCR_016666

Alternate URLs: <https://linnarssonlab.org/loompy/>, <https://github.com/linnarsson-lab/loompy>

License: BSD 2-Clause

Record Creation Time: 20220129T080331+0000

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Ratings and Alerts

No rating or validation information has been found for LoomPy.

No alerts have been found for LoomPy.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 29 mentions in open access literature.

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

De Vriendt S, et al. (2025) Single-cell transcriptome atlas of male mouse pituitary across postnatal life highlighting its stem cell landscape. *iScience*, 28(2), 111708.

Walsh RM, et al. (2024) Generation of human cerebral organoids with a structured outer subventricular zone. *Cell reports*, 43(4), 114031.

Zanini F, et al. (2024) Hyperoxia prevents the dynamic neonatal increases in lung mesenchymal cell diversity. *Scientific reports*, 14(1), 2033.

Zenk F, et al. (2024) Single-cell epigenomic reconstruction of developmental trajectories from pluripotency in human neural organoid systems. *Nature neuroscience*, 27(7), 1376.

Vanheer L, et al. (2023) Inferring regulators of cell identity in the human adult pancreas. *NAR genomics and bioinformatics*, 5(3), lqad068.

Grochowska MM, et al. (2023) deCLUTTER2+ - a pipeline to analyze calcium traces in a stem cell model for ventral midbrain patterned astrocytes. *Disease models & mechanisms*, 16(6).

Upchurch S, et al. (2023) RNAget: an API to securely retrieve RNA quantifications. *Bioinformatics (Oxford, England)*, 39(4).

Fleck JS, et al. (2023) Inferring and perturbing cell fate regulomes in human brain organoids. *Nature*, 621(7978), 365.

Li C, et al. (2023) Single-cell brain organoid screening identifies developmental defects in autism. *Nature*, 621(7978), 373.

Barruet E, et al. (2023) Loss of transcriptional heterogeneity in aged human muscle stem cells. *PloS one*, 18(5), e0285018.

Savary C, et al. (2023) Fusion-negative rhabdomyosarcoma 3D organoids to predict effective drug combinations: A proof-of-concept on cell death inducers. *Cell reports. Medicine*, 4(12), 101339.

Vanova T, et al. (2023) Cerebral organoids derived from patients with Alzheimer's disease with PSEN1/2 mutations have defective tissue patterning and altered development. *Cell reports*, 42(11), 113310.

, et al. (2022) A blood atlas of COVID-19 defines hallmarks of disease severity and specificity. *Cell*, 185(5), 916.

Putri GH, et al. (2022) Analysing high-throughput sequencing data in Python with HTSeq 2.0. *Bioinformatics (Oxford, England)*, 38(10), 2943.

Liu Y, et al. (2022) Hedgehog signaling reprograms hair follicle niche fibroblasts to a hyper-activated state. *Developmental cell*, 57(14), 1758.

Feng H, et al. (2022) scDIOR: single cell RNA-seq data IO software. *BMC bioinformatics*, 23(1), 16.

Fernández-García J, et al. (2022) CD8+ T cell metabolic rewiring defined by scRNA-seq identifies a critical role of ASNS expression dynamics in T cell differentiation. *Cell reports*, 41(7), 111639.

Di Persio S, et al. (2021) Single-cell RNA-seq unravels alterations of the human spermatogonial stem cell compartment in patients with impaired spermatogenesis. *Cell reports. Medicine*, 2(9), 100395.

Legeth O, et al. (2021) CellexaVR: A virtual reality platform to visualize and analyze single-cell omics data. *iScience*, 24(11), 103251.

Duan L, et al. (2021) Follicular dendritic cells restrict interleukin-4 availability in germinal centers and foster memory B cell generation. *Immunity*, 54(10), 2256.