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, data processing software, data storage software, software application

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

Record Last Update: 20250513T061806+0000

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), Iqad068.

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.

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.

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

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 hyperactivated 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.

Legetth O, et al. (2021) CellexalVR: 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.