

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. Official Python library (API) used to create, read, and manipulate .loom files, supporting out-of-memory operations to handle datasets larger than RAM.

Abbreviations: LoomPy

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

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

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

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 34 mentions in open access literature.

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

Pal S, et al. (2025) Cell-Type Specific Variation in X-Chromosome Dosage Compensation in Drosophila. microPublication biology, 2025.

Vinsland E, et al. (2025) Cell atlas of the developing human meninges reveals a dura origin of meningioma. bioRxiv : the preprint server for biology.

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.

Bui HV, et al. (2025) White and brown adipose tissue share a convergent fibro-adipogenic progenitor population. EMBO reports, 26(22), 5612.

Xu L, et al. (2025) Neuron-specific homologous coding genes and non-coding regulatory regions are the most conserved amongst amniotes despite neuron-specific cell size diversity. Scientific reports, 15(1), 43971.

Pech U, et al. (2025) Synaptic deregulation of cholinergic projection neurons causes olfactory dysfunction across five fly Parkinsonism models. eLife, 13.

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.

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

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).

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.

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.

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