

Resource Summary Report

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Loupe Browser

RRID:SCR_018555

Type: Tool

Proper Citation

Loupe Browser (RRID:SCR_018555)

Resource Information

URL: <https://support.10xgenomics.com/single-cell-gene-expression/software/visualization/latest/what-is-loupe-cell-browser>

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Description: Desktop application that provides interactive visualization functionality to analyze data from different 10x Genomics solutions. Used to interrogate different views of 10x data to gain insights into underlying biology.

Synonyms: Loupe Cell Browser 4.0

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

Keywords: Interactive visualization, data analysis, 10x Genomics solutions, data

Availability: Restricted

Resource Name: Loupe Browser

Resource ID: SCR_018555

License URLs: <https://support.10xgenomics.com/single-cell-gene-expression/software/downloads/latest#loupe>

Record Creation Time: 20220129T080340+0000

Record Last Update: 20260821T194130+0000

Ratings and Alerts

No rating or validation information has been found for Loupe Browser.

No alerts have been found for Loupe Browser.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 187 mentions in open access literature.

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

Gridley J, et al. (2026) iHALT unlocks liver functionality as a surrogate secondary lymphoid organ. *Nature*, 649(8098), 991.

Plumbom I, et al. (2026) circVDJ-seq for T cell clonotype detection in single-cell and spatial multi-omics. *Genome medicine*, 18(1).

Margolin G, et al. (2026) Differential expression analysis in single-cell and spatial RNA-seq without model assumptions. *Cell reports methods*, 6(5), 101383.

Fernandez KJ, et al. (2026) Endocrine therapy reprogramming of breast cancer facilitates metastatic escape via upregulation of P-Rex1/Rac1 signalling. *Nature communications*, 17(1).

Cheng X, et al. (2026) Interleukin-34-Induced Arg1+ Macrophages Play a Key Role in Breast Cancer Brain Metastasis. *Cancer research communications*, 6(6), 1388.

Ziemia??ska M, et al. (2026) Risperidone regulates the expression of schizophrenia-related genes in the forebrain of adult male mice. *Frontiers in molecular neuroscience*, 19, 1844705.

Chung BK, et al. (2026) Multimodal transcriptomics identifies metallothionein as a novel pathway in primary sclerosing cholangitis. *Hepatology (Baltimore, Md.)*, 83(5), 1066.

Hirose K, et al. (2026) Pathogenic mechanism of extracranial arteriovenous malformations: insights from clinical, pathological, and genetic analyses. *Virchows Archiv : an international journal of pathology*, 488(5), 1137.

Williams EC, et al. (2026) Spatially resolved integrative analysis of transcriptomic and metabolomic changes in tissue injury studies. *Nature communications*, 17(1), 205.

Funagura N, et al. (2026) Histone demethylase KDM7A negatively regulates fibrotic macrophage polarization and lung fibrosis progression. *Communications biology*, 9(1).

Sochodolsky K, et al. (2026) BDNF Regulates Pituitary Stem Cell Engagement towards precursor state. *bioRxiv : the preprint server for biology*.

Sasagawa S, et al. (2026) Spatial profiling of chronic liver disease: a pilot spatial case series. *Scientific reports*, 16(1).

Jamroze A, et al. (2026) Single-cell imaging analysis, therapeutic modeling and a Phase Ib trial validate BCL-2 as a target across heterogeneous castration-resistant prostate

cancer. *Signal transduction and targeted therapy*, 11(1).

Sumii M, et al. (2026) Plasminogen Activator Inhibitor-1 Mediates Tolerance to Anti-PD-1 Immunotherapy in Non-Small Cell Lung Cancer. *Molecular cancer therapeutics*, 25(3), 435.

Cerezo-Wallis D, et al. (2026) Architecture of the neutrophil compartment. *Nature*, 649(8098), 1003.

Haga S, et al. (2026) Spatial transcriptomics of urothelial carcinoma with basal/squamous differentiation identifies Galectin-7 as a specific marker of squamous lineage commitment. *Discover oncology*, 17(1).

Iwabuchi S, et al. (2026) Single-Cell Analysis Identified a Recurrent Malignant-Associated Transcriptional State in Colorectal Cancer. *Cancer science*, 117(5), 1397.

F Sousa J, et al. (2026) Comparative multi-omic analysis reveals conserved and derived mechanisms of fin and limb regeneration. *Nature communications*, 17(1).

Sierra-Rodero B, et al. (2026) Decoding B-cell Signatures of Complete Pathologic Response to Perioperative Chemoimmunotherapy in Non-Small Cell Lung Cancer. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(8), 1499.

Wanchai V, et al. (2026) A transcriptomic-driven segmentation and cell simulation framework for high-resolution spatial transcriptomics and cell-cell communication. *bioRxiv : the preprint server for biology*.