

Resource Summary Report

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Umap

RRID:SCR_018217

Type: Tool

Proper Citation

Umap (RRID:SCR_018217)

Resource Information

URL: <https://github.com/lmcinnes/umap>

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Description: Software package as dimension reduction technique that can be used for visualization similar to t-SNE, but also for general non-linear dimension reduction. Used for dimensionality reduction for visualizing single-cell data.

Abbreviations: UMAP

Synonyms: Uniform Manifold Approximation and Projection

Resource Type: data processing software, data visualization software, software application, software resource, software toolkit

Keywords: Dimension reduction technique, data visualization, singel cell data

Availability: Free, Available for download, Freely available

Resource Name: Umap

Resource ID: SCR_018217

Alternate URLs: <https://github.com/lmcinnes/umap>, <https://sources.debian.org/src/umap-learn/>

License: BSD 3-Clause New or Revised License

Record Creation Time: 20220129T080339+0000

Record Last Update: 20260821T194143+0000

Ratings and Alerts

No rating or validation information has been found for Umap.

No alerts have been found for Umap.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 179 mentions in open access literature.

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

Wang W, et al. (2026) Convergence-divergence circuits for multimodal integration of innate and learned opponent valences. *Frontiers in systems neuroscience*, 20, 1822122.

Goala P, et al. (2026) IFN- γ -driven skewing towards Th1 over Th17 differentiation underlies CRS and neutropenia in CAR-T therapy. *The Journal of clinical investigation*, 136(1).

López-Fuentes E, et al. (2026) Epigenetic and Transcriptional Programs Define Osteosarcoma Subtypes and Establish Targetable Vulnerabilities. *Cancer discovery*, 16(2), 296.

Yan C, et al. (2026) RAS/MEK/PI3K pathway inhibition augments response to CD40 agonism by targeting CD11b⁺ Bregs thereby overcoming melanoma PD1-resistance. *Nature communications*, 17(1), 162.

Yin J, et al. (2026) Chronic Hypoxia Disrupts Spermatogenesis Through ASXL2-EZH2-Mediated Microtubule Destabilization. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(26), e01266.

Aggrey-Fynn JE, et al. (2026) Epigenetic context defines the transcriptional activity of canonical and noncanonical NF- κ B signaling in pancreatic cancer. *Cell death discovery*, 12(1).

Dekker J, et al. (2026) An integrated view of the structure and function of the human 4D nucleome. *Nature*, 649(8097), 759.

Nam Y, et al. (2026) Cellular immunology data enable clinical severity prediction via supervised machine learning. *iScience*, 29(6), 116343.

Fu ZH, et al. (2026) Synthetic rewriting of the IGH locus. *Cell genomics*, 6(6), 101252.

Kelly B, et al. (2026) Sulfur partitioning from cysteine controls T cell proliferation and effector function. *Cell*, 189(12), 3669.

Adhikary U, et al. (2026) Cancer Susceptibility to Stapled Oncolytic Peptides Is Dictated by Membrane Cholesterol and Inflammatory Signaling. *Cancer research*, 86(11), 2810.

Roger E, et al. (2026) ATM Deficiency Induces TGF β -Mediated Stromal Programming in Pancreatic Cancer. *Cancer research*, 86(14), 3412.

Gao Y, et al. (2026) Conserved Cell Type Signatures Across the Brainstem and Spinal Cord in the Mouse Central Nervous System. *bioRxiv : the preprint server for biology*.

Romeo LR, et al. (2025) Correlations between biological markers of the perirenal adipose tissue and clinical features of patients with localized kidney cancer. *Frontiers in medicine*, 12, 1676630.

Song Z, et al. (2025) Mega-scale single-cell profiling reveals novel biomarkers associated with acute GvHD after allogeneic hematopoietic stem cell transplantation. *Biomarker research*, 13(1), 155.

Kumar S, et al. (2025) Characterizing Microglial Signaling Dynamics During Inflammation Using Single-Cell Mass Cytometry. *Glia*, 73(5), 1022.

Rask GC, et al. (2025) Seclidemstat (SP-2577) Induces Transcriptomic Reprogramming and Cytotoxicity in Multiple Fusion-Positive Sarcomas. *Cancer research communications*, 5(9), 1584.

Ghaneai P, et al. (2025) DeepBase: A Deep Learning-based Daily Baseflow Dataset across the United States. *Scientific data*, 12(1), 25.

Kamboj O, et al. (2025) From spots to cells: Cell segmentation in spatial transcriptomics with BOMS. *PloS one*, 20(6), e0311458.

Aramburu O, et al. (2025) Multiomics uncovers the epigenomic and transcriptomic response to viral and bacterial stimulation in turbot. *GigaScience*, 14.