

Resource Summary Report

Generated by [NIF](#) on Jul 31, 2026

Umap

RRID:SCR_018217

Type: Tool

Proper Citation

Umap (RRID:SCR_018217)

Resource Information

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

Proper Citation: Umap (RRID:SCR_018217)

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, software toolkit, data visualization software, software resource, software application

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: 20260731T043020+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 158 mentions in open access literature.

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

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).

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.

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.

Sullivan KE, et al. (2025) Quantification and analysis of multiplexed fluorescence insitu hybridization data using open-source tools. STAR protocols, 6(4), 104127.

Umeda M, et al. (2025) Fusion oncoproteins and cooperating mutations define disease phenotypes in NUP98-rearranged leukemia. medRxiv : the preprint server for health sciences.

Donovan LJ, et al. (2025) Aging and injury drive neuronal senescence in the dorsal root ganglia. Nature neuroscience, 28(5), 985.

Kim NJ, et al. (2025) Genetic Insights into Brain Morphology: a Genome-Wide Association Study of Cortical Thickness and T1-Weighted MRI Gray Matter-White Matter Intensity Contrast. *Neuroinformatics*, 23(2), 26.

van Velthoven CTJ, et al. (2025) Transcriptomic and spatial organization of telencephalic GABAergic neurons. *Nature*, 647(8088), 143.

Burendei B, et al. (2025) Structure-guided discovery of Otopetrin 1 inhibitors reveals druggable binding sites at the intrasubunit interface. *Nature communications*, 16(1), 9362.

Wang K, et al. (2025) Exploring the Role of Ccn3 in Type III Cell of Mice Taste Buds. *Journal of neurochemistry*, 169(1), e16291.

Kakoulidis P, et al. (2025) Comparative structural insights and functional analysis for the distinct unbound states of Human AGO proteins. *Scientific reports*, 15(1), 9432.

Lanzar ZR, et al. (2025) De-coupling immune parameters and toxicity associated with IL-12 agonism. *Cell reports*, 44(6), 115840.

Stupichev D, et al. (2025) AI-driven multimodal algorithm predicts immunotherapy and targeted therapy outcomes in clear cell renal cell carcinoma. *Cell reports. Medicine*, 6(8), 102299.

Wu Y, et al. (2025) BEEEx Is an Open-Source Tool That Evaluates Batch Effects in Medical Images to Enable Multicenter Studies. *Cancer research*, 85(2), 218.

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

Schaeffer SM, et al. (2025) Hypertension-induced neurovascular and cognitive dysfunction at single-cell resolution. *Neuron*.