

Resource Summary Report

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Rtsne

RRID:SCR_016342

Type: Tool

Proper Citation

Rtsne (RRID:SCR_016342)

Resource Information

URL: <https://github.com/jkrijthe/Rtsne>

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Description: Software as R wrapper for Van der Maaten's Barnes-Hut implementation of t-Distributed Stochastic Neighbor Embedding. Used for high-dimensional data visualisation.

Synonyms: , R t-distributed stochastic neighbor embedding, R t-Distributed Stochastic Neighbor Embedding

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

Keywords: data, visualisation, high-dimensional, van der Maaten, Barnes-Hut, implementation, distribution, stochastic, neighbor, embedding

Funding: European Union Seventh Framework Program ; the Netherlands Organization for Scientific Research (NWO)

Availability: Free, Available for download, Freely available

Resource Name: Rtsne

Resource ID: SCR_016342

Alternate IDs: SCR_016900

Alternate URLs: <https://cran.r-project.org/web/packages/Rtsne/index.html>

License URLs: <https://github.com/jkrijthe/Rtsne/blob/master/LICENSE>

Record Creation Time: 20220129T080330+0000

Record Last Update: 20260821T194045+0000

Ratings and Alerts

No rating or validation information has been found for Rtsne.

No alerts have been found for Rtsne.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 190 mentions in open access literature.

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

Chen K, et al. (2026) Liquid?liquid phase separation of PHLDB2 promotes oral squamous cell carcinoma metastasis through regulating epithelial mesenchymal transition and PIK3CA expression. *Molecular medicine reports*, 33(1).

Marter P, et al. (2026) The microbiome of marine mat-forming cyanobacteria-a microcosm of taxonomic novelty and phototrophic diversity. *ISME communications*, 6(1), ycag041.

Wu Q, et al. (2026) Refined phenotyping of vaccine responses reveals transcriptomic determinants of neutralizing antibody heterogeneity. *NPJ vaccines*, 11(1).

Pan X, et al. (2026) Multi-Tissue Genetic Regulation of RNA Editing in Pigs. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(17), e18238.

Hofvander J, et al. (2026) Transcriptomic Subgroups in Soft Tissue Tumors Correlate with Morphologic Subtype, Genomic Features, and Outcome. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(9), 1825.

Autio M, et al. (2025) Spatial Analysis of the Tumor Microenvironment in Diffuse Large B-cell Lymphoma Reveals Clinically Relevant Cell Interactions and Recurrent Cellular Neighborhoods. *Cancer immunology research*, 13(10), 1674.

Duckett D, et al. (2025) Development, validation, and utility of a clinically applicable methylation classifier for recurrence risk prediction in meningiomas. *Acta neuropathologica communications*, 13(1), 259.

Tisza MJ, et al. (2025) Longitudinal phage-bacteria dynamics in the early life gut microbiome. *Nature microbiology*, 10(2), 420.

Chen CY, et al. (2025) Integrative brain omics approach highlights sn-1 lysophosphatidylethanolamine in Alzheimer's dementia. *Nature communications*, 16(1), 9627.

Hu H, et al. (2025) Super enhancer lncRNA RP11-54O7.17 regulates the proliferation and metastasis of triple-negative breast cancer by targeting lysosomal degradation of S100A4.

Cell death & disease, 16(1), 773.

Panzeri I, et al. (2025) TRIM28-dependent developmental heterogeneity determines cancer susceptibility through distinct epigenetic states. *Nature cancer*, 6(2), 385.

Tan J, et al. (2025) Alternative promoter usage during organ development. *PLoS genetics*, 21(3), e1011635.

Gan Y, et al. (2025) Exploration of Epigenetic Mechanisms and Biomarkers Among Patients with Very-Late-Onset Schizophrenia-Like Psychosis. *Neuropsychiatric disease and treatment*, 21, 927.

Le Rhun E, et al. (2025) The clinical and molecular landscape of diffuse hemispheric glioma, H3 G34-mutant. *Neuro-oncology*, 27(6), 1519.

Strakova-Peterikova A, et al. (2025) Calcifying nested stromal-epithelial tumor of the liver: Report of two cases revealing novel WT1 mutation and distinct epigenetic features. *Virchows Archiv : an international journal of pathology*.

Duan B, et al. (2025) Widespread epistasis shapes RNA polymerase II active site function and evolution. *Nature communications*, 16(1), 7993.

Jiang J, et al. (2025) Functional consequences of reductive protein evolution in a minimal eukaryotic genome. *Cell reports*, 44(10), 116333.

George AF, et al. (2025) Anatomical, subset, and HIV-dependent expression of viral sensors and restriction factors. *Cell reports*, 44(1), 115202.

Morais LH, et al. (2024) α -synuclein overexpression and the microbiome shape the gut and brain metabolome in mice. *NPJ Parkinson's disease*, 10(1), 208.

Inoue M, et al. (2024) Genomic alterations in two patients with esophageal carcinosarcoma identified by whole genome sequencing: a case report. *Surgical case reports*, 10(1), 191.