

Resource Summary Report

Generated by [dkNET](#) on Sep 16, 2026

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: 20260912T195838+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 [dkNET](#) .

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.