

# Resource Summary Report

Generated by [kravitz2](#) on Sep 5, 2026

## Rtsne

RRID:SCR\_016900

Type: Tool

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### Proper Citation

Rtsne (RRID:SCR\_016900)

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### Resource Information

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

**Proper Citation:** Rtsne (RRID:SCR\_016900)

**Description:** R wrapper for Van der Maaten's Barnes-Hut implementation of t-Distributed Stochastic Neighbor Embedding.

**Abbreviations:** t-SNE

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

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

**Keywords:** wrapper, implementation, t-distributed, stochastic, neighbor, embedding, data, visualization

**Funding:** Dutch Scientific Organization ;  
Google ;  
Microsoft

**Availability:** Free, Available for download, Freely available

**Resource Name:** Rtsne

**Resource ID:** SCR\_016900

**License:** BSD licence

**Record Creation Time:** 20220129T080332+0000

**Record Last Update:** 20260903T235400+0000

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### Ratings and Alerts

No rating or validation information has been found for Rtsne.

No alerts have been found for Rtsne.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 85 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [kravitz2](#) .

Duan B, et al. (2023) Widespread epistasis shapes RNA Polymerase II active site function and evolution. bioRxiv : the preprint server for biology.

Nakamura M, et al. (2023) Molecular genetic positioning of small intestine and papilla of Vater carcinomas including clinicopathological classification. Cancer medicine.

Ajuyah P, et al. (2023) Histone H3-wild type diffuse midline gliomas with H3K27me3 loss are a distinct entity with exclusive EGFR or ACVR1 mutation and differential methylation of homeobox genes. Scientific reports, 13(1), 3775.

Hancock SE, et al. (2023) FACS-assisted single-cell lipidome analysis of phosphatidylcholines and sphingomyelins in cells of different lineages. Journal of lipid research, 64(3), 100341.

Subkhankulova T, et al. (2023) Zebrafish pigment cells develop directly from persistent highly multipotent progenitors. Nature communications, 14(1), 1258.

Ross KE, et al. (2023) Network models of protein phosphorylation, acetylation, and ubiquitination connect metabolic and cell signaling pathways in lung cancer. PLoS computational biology, 19(3), e1010690.

Tu J, et al. (2022) Sensitivity to copy number variation analysis in single cell genomics. Gene, 808, 145995.

Martinek J, et al. (2022) Transcriptional profiling of macrophages in situ in metastatic melanoma reveals localization-dependent phenotypes and function. Cell reports. Medicine, 3(5), 100621.

Angst P, et al. (2022) Genetic Drift Shapes the Evolution of a Highly Dynamic Metapopulation. Molecular biology and evolution, 39(12).

Ebrahimi A, et al. (2022) Pleomorphic xanthoastrocytoma is a heterogeneous entity with pTERT mutations prognosticating shorter survival. Acta neuropathologica communications, 10(1), 5.

Gabay O, et al. (2022) Landscape of adenosine-to-inosine RNA recoding across human tissues. *Nature communications*, 13(1), 1184.

Zhang Y, et al. (2022) A novel ferroptosis-related gene signature for overall survival prediction and immune infiltration in patients with breast cancer. *International journal of oncology*, 61(6).

Gill PA, et al. (2022) A randomized dietary intervention to increase colonic and peripheral blood SCFAs modulates the blood B- and T-cell compartments in healthy humans. *The American journal of clinical nutrition*, 116(5), 1354.

Molina L, et al. (2022) Bi-allelic hydroxymethylbilane synthase inactivation defines a homogenous clinico-molecular subtype of hepatocellular carcinoma. *Journal of hepatology*, 77(4), 1038.

Zipper L, et al. (2022) The MicroRNA miR-277 Controls Physiology and Pathology of the Adult *Drosophila* Midgut by Regulating the Expression of Fatty Acid  $\beta$ -Oxidation-Related Genes in Intestinal Stem Cells. *Metabolites*, 12(4).

Williamson D, et al. (2022) Medulloblastoma group 3 and 4 tumors comprise a clinically and biologically significant expression continuum reflecting human cerebellar development. *Cell reports*, 40(5), 111162.

Aramaki M, et al. (2022) Transcriptional control of cone photoreceptor diversity by a thyroid hormone receptor. *Proceedings of the National Academy of Sciences of the United States of America*, 119(49), e2209884119.

Perico CP, et al. (2022) Genomic landscape of the SARS-CoV-2 pandemic in Brazil suggests an external P.1 variant origin. *Frontiers in microbiology*, 13, 1037455.

Li R, et al. (2022) Metabolic incorporation of electron-rich ribonucleosides enhances APEX-seq for profiling spatially restricted nascent transcriptome. *Cell chemical biology*, 29(7), 1218.

Roncalli V, et al. (2021) Post-diapause transcriptomic restarts: insight from a high-latitude copepod. *BMC genomics*, 22(1), 409.