

Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

[nmf](#)

RRID:SCR_024284

Type: Tool

Proper Citation

nmf (RRID:SCR_024284)

Resource Information

URL: <https://cran.r-project.org/web/packages/NMF/index.html>

Proper Citation: nmf (RRID:SCR_024284)

Description: Software R package provides framework to perform Non-negative Matrix Factorization.Used for nonnegative matrix factorization.Implements set of already published algorithms and seeding methods, and provides framework to test, develop and plug new/custom algorithms. Most of the built-in algorithms have been optimized in C++, and the main interface function provides an easy way of performing parallel computations on multicore machines.

Resource Type: software resource, software toolkit

Defining Citation: [PMID:20598126](#)

Keywords: perform Non-negative Matrix Factorization, nonnegative matrix factorization,

Availability: Free, Available for download, Freely available,

Resource Name: nmf

Resource ID: SCR_024284

Alternate URLs: <https://sources.debian.org/src/r-cran-nmf/>

License: GPL-2 | GPL-3 [expanded from: GPL (? 2)]

Record Creation Time: 20230830T050217+0000

Record Last Update: 20260801T190901+0000

Ratings and Alerts

No rating or validation information has been found for nmf.

No alerts have been found for nmf.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Hecker J, et al. (2025) Serum microRNA expression quantitative trait loci in children with asthma colocalize with asthma-related GWAS results. NPJ genomic medicine, 10(1), 55.

Jansma A, et al. (2025) High order expression dependencies finely resolve cryptic states and subtypes in single cell data. Molecular systems biology, 21(2), 173.

Suda K, et al. (2025) Low OLFM1 and BMP6 Expression Predicts Recurrence in Early-Stage Nonsquamous NSCLC with Pure Solid Tumor Appearance. Cancer research communications, 5(12), 2186.

Krull JE, et al. (2024) Follicular lymphoma B cells exhibit heterogeneous transcriptional states with associated somatic alterations and tumor microenvironments. Cell reports. Medicine, 5(3), 101443.

Liu B, et al. (2024) Distinctive multicellular immunosuppressive hubs confer different intervention strategies for left- and right-sided colon cancers. Cell reports. Medicine, 5(6), 101589.

He S, et al. (2024) Elucidating immune-related gene transcriptional programs via factorization of large-scale RNA-profiles. iScience, 27(6), 110096.

Liu W, et al. (2024) Multiomics analysis reveals metabolic subtypes and identifies diacylglycerol kinase ?? (DGKA) as a potential therapeutic target for intrahepatic cholangiocarcinoma. Cancer communications (London, England), 44(2), 226.

Plitt G, et al. (2024) The Genomic Landscape of Benign and Malignant Thyroid Tumors from Individuals Carrying Germline PTEN Variants Is Distinct from Sporadic Thyroid Cancers. Cancer research, 84(21), 3657.

Hacking JPR, et al. (2023) Deriving a continuum score for group 3 and 4 medulloblastoma tumor samples analyzed via RNA-sequencing or DNA methylation microarray. STAR protocols, 4(3), 102509.

Xing X, et al. (2023) Integrated omics landscape of hepatocellular carcinoma suggests proteomic subtypes for precision therapy. Cell reports. Medicine, 4(12), 101315.

Lou N, et al. (2023) Proteomics Identifies Circulating TIMP-1 as a Prognostic Biomarker for Diffuse Large B-Cell Lymphoma. *Molecular & cellular proteomics : MCP*, 22(9), 100625.

Qin P, et al. (2023) Cancer-associated fibroblasts undergoing neoadjuvant chemotherapy suppress rectal cancer revealed by single-cell and spatial transcriptomics. *Cell reports. Medicine*, 4(10), 101231.