

Resource Summary Report

Generated by T1D on Jul 28, 2026

Mfuzz

RRID:SCR_000523

Type: Tool

Proper Citation

Mfuzz (RRID:SCR_000523)

Resource Information

URL: <http://mfuzz.sysbiolab.eu/>

Proper Citation: Mfuzz (RRID:SCR_000523)

Description: Software package for noise-robust soft clustering of gene expression time-series data (including a graphical user interface)., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Synonyms: Mfuzz - Soft clustering of time series gene expression data

Resource Type: software resource

Defining Citation: [PMID:18084642](https://pubmed.ncbi.nlm.nih.gov/18084642/)

Keywords: r, time series, gene expression, clustering, microarray, preprocessing, time course, visualization, bio.tools

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Mfuzz

Resource ID: SCR_000523

Alternate IDs: biotools:mfuzz, OMICS_02012

Alternate URLs: <https://bio.tools/mfuzz>

Old URLs: <http://itb.biologie.hu-berlin.de/~futschik/software/R/Mfuzz/>

License: GNU General Public License, v2

Record Creation Time: 20220129T080202+0000

Record Last Update: 20260725T190446+0000

Ratings and Alerts

No rating or validation information has been found for Mfuzz.

No alerts have been found for Mfuzz.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 14 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

Paloviita P, et al. (2025) Integrated transcriptomic analysis reveals metabolic remodeling and gene expression networks related to human 8-cell-stage embryo-like cells. *Cell reports*, 45(1), 116748.

Zhang G, et al. (2025) Genomic and transcriptomic analyses of *Heteropoda venatoria* reveal the expansion of P450 family for starvation resistance in spiders. *GigaScience*, 14.

Taoka H, et al. (2025) Transcriptional dynamics uncover the role of BNIP3 in mitophagy during muscle remodeling in *Drosophila*. *eLife*, 14.

Yu Z, et al. (2024) Thermal facial image analyses reveal quantitative hallmarks of aging and metabolic diseases. *Cell metabolism*, 36(7), 1482.

Lan Q, et al. (2024) Mesenchyme instructs growth while epithelium directs branching in the mouse mammary gland. *eLife*, 13.

Li X, et al. (2023) Lifespan changes in cannabinoid 1 receptor mRNA expression in the female C57BL/6J mouse brain. *The Journal of comparative neurology*, 531(2), 294.

Rudjord-Levann AM, et al. (2023) Galectin-1 induces a tumor-associated macrophage phenotype and upregulates indoleamine 2,3-dioxygenase-1. *iScience*, 26(7), 106984.

Lyu Q, et al. (2022) A small proportion of X-linked genes contribute to X chromosome upregulation in early embryos via BRD4-mediated transcriptional activation. *Current biology : CB*, 32(20), 4397.

Janas JA, et al. (2022) Tip60-mediated H2A.Z acetylation promotes neuronal fate specification and bivalent gene activation. *Molecular cell*, 82(24), 4627.

Wang S, et al. (2019) Epigenetic Compensation Promotes Liver Regeneration. *Developmental cell*, 50(1), 43.

Sumigray KD, et al. (2018) Morphogenesis and Compartmentalization of the Intestinal Crypt. *Developmental cell*, 45(2), 183.

Li Z, et al. (2018) Co-sequencing and novel delayed anti-correlation identify function for pancreatic enriched microRNA biomarkers in a rat model of acute pancreatic injury. BMC genomics, 19(1), 297.

Sardina JL, et al. (2018) Transcription Factors Drive Tet2-Mediated Enhancer Demethylation to Reprogram Cell Fate. Cell stem cell, 23(5), 727.

Apostolopoulou M, et al. (2017) Non-monotonic Changes in Progenitor Cell Behavior and Gene Expression during Aging of the Adult V-SVZ Neural Stem Cell Niche. Stem cell reports, 9(6), 1931.