

Resource Summary Report

Generated by [RRID](#) on Aug 15, 2026

MOFA2

RRID:SCR_028488

Type: Tool

Proper Citation

MOFA2 (RRID:SCR_028488)

Resource Information

URL: <https://github.com/bioFAM/MOFA2>

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Description: Software statistical framework for comprehensive integration of multi-modal single-cell data. Used for integration of multi-omic data sets in unsupervised fashion.

Synonyms: , MOFA+, Multi-Omics Factor Analysis v2

Resource Type: source code, software application, software resource

Defining Citation: [PMID:32393329](#)

Keywords: reconstructs low-dimensional representation, variational inference, flexible sparsity constraints, jointly model variation, multiple sample groups and data modalities,

Availability: Free, Available for download, Freely available

Resource Name: MOFA2

Resource ID: SCR_028488

License: LGPL-3.0

Record Creation Time: 20260529T042811+0000

Record Last Update: 20260815T183315+0000

Ratings and Alerts

No rating or validation information has been found for MOFA2.

No alerts have been found for MOFA2.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 18 mentions in open access literature.

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

Cheng Y, et al. (2026) Aligned cross-modal integration and regulatory heterogeneity characterization of single-cell multiomic data with deep contrastive learning. *Genome medicine*, 18(1), 10.

Feeney AK, et al. (2026) Early multi-omic signatures and machine learning models predict cardiomyocyte differentiation efficiency and enable robust hPSC differentiation to cardiomyocytes. *bioRxiv : the preprint server for biology*.

Mosquim Junior S, et al. (2026) Multiomic profiling of ER-positive HER2-negative breast cancer reveals markers associated with metastatic spread. *Breast cancer research : BCR*, 28(1), 12.

Kutscherauer RK, et al. (2026) Csf1r-mediated depletion of myeloid cells prevents dopaminergic neuron loss during chronic colitis. *Journal of neuroinflammation*, 23(1).

Botey-Bataller J, et al. (2025) Genetic and molecular landscape of comorbidities in people living with HIV. *Nature medicine*, 31(10), 3350.

Liu RP, et al. (2025) Multi-organ multi-omic and gut microbiome markers of fat and sucrose dietary oversupply in cardiometabolic disease. *iScience*, 28(4), 111887.

Manurung MD, et al. (2025) Systems analysis unravels a common rural-urban gradient in immunological profile, function, and metabolic dependencies. *Science advances*, 11(18), eadu0419.

Keele GR, et al. (2025) Genetic architecture of the murine red blood cell proteome reveals central role of hemoglobin beta cysteine 93 in maintaining redox balance. *Cell genomics*, 101069.

Tkach VV, et al. (2025) Combined neocortical protein and morphological profiling of reactive microglia across Alzheimer's and Creutzfeldt-Jakob disease. *Acta neuropathologica communications*, 13(1), 244.

Li X, et al. (2025) Genetic mapping of lifespan and mitochondrial stress response in *C. elegans*. *bioRxiv : the preprint server for biology*.

Kostopoulou A, et al. (2025) Impact of Oxygen Availability on the Organelle-Specific Redox Potentials and Stress in Recombinant Protein Producing *Komagataella phaffii*. *Microbial biotechnology*, 18(2), e70106.

Ban M, et al. (2024) Expression profiling of cerebrospinal fluid identifies dysregulated antiviral mechanisms in multiple sclerosis. *Brain : a journal of neurology*, 147(2), 554.

Ponce-de-Leon M, et al. (2024) Stool and blood metabolomics in the metabolic syndrome: a cross-sectional study. *Metabolomics : Official journal of the Metabolomic Society*, 20(5), 105.

Ghazanfar S, et al. (2024) Stabilized mosaic single-cell data integration using unshared features. *Nature biotechnology*, 42(2), 284.

Borgmästars E, et al. (2024) Multi-omics profiling to identify early plasma biomarkers in pre-diagnostic pancreatic ductal adenocarcinoma: a nested case-control study. *Translational oncology*, 48, 102059.

Zheng Y, et al. (2024) Multi-omics data integration using ratio-based quantitative profiling with Quartet reference materials. *Nature biotechnology*, 42(7), 1133.

Esplin ED, et al. (2024) Multiomic analysis of familial adenomatous polyposis reveals molecular pathways associated with early tumorigenesis. *Nature cancer*, 5(11), 1737.

Palou-Márquez G, et al. (2021) DNA methylation and gene expression integration in cardiovascular disease. *Clinical epigenetics*, 13(1), 75.