

Resource Summary Report

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MOFA

RRID:SCR_022992

Type: Tool

Proper Citation

MOFA (RRID:SCR_022992)

Resource Information

URL: <https://biofam.github.io/MOFA2/>

Proper Citation: MOFA (RRID:SCR_022992)

Description: Software framework for unsupervised integration of multi-omics data sets. Used for discovering principal sources of variation in multi omics data sets.

Abbreviations: MOFA

Synonyms: Multi Omics Factor Analysis

Resource Type: software resource, data processing software, software application, data analysis software

Defining Citation: [PMID:29925568](#)

Keywords: factor analysis model, integration of multi-omic data sets, unsupervised integration, variation in multi omics data sets discovery.

Funding: European Union

Availability: Free, Available for download, Freely available

Resource Name: MOFA

Resource ID: SCR_022992

Alternate URLs: <https://github.com/bioFAM/MOFA2>

License: LGPL-3.0 license

Record Creation Time: 20221124T050201+0000

Record Last Update: 20260804T043752+0000

Ratings and Alerts

No rating or validation information has been found for MOFA.

No alerts have been found for MOFA.

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](#) .

Alakwaa F, et al. (2025) Leveraging complementary multi-omics data integration methods for mechanistic insights in kidney diseases. JCI insight, 10(5).

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.

Villette R, et al. (2025) Integrated multi-omics highlights alterations of gut microbiome functions in prodromal and idiopathic Parkinson's disease. Microbiome, 13(1), 200.

Shi Y, et al. (2025) Dynamic Synthesis of Multi-Modal Representations for CITE-seq Data Integration and Analysis. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(44), e09247.

Anagho-Mattanovich M, et al. (2025) Multi-omics analysis of thermogenic lipolysis in brown adipocytes. iScience, 28(9), 113382.

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.

Zhou M, et al. (2024) Protocol to perform integrative analysis of high-dimensional single-cell multimodal data using an interpretable deep learning technique. STAR protocols, 5(2), 103066.

Borgm??stars 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.

Cortez Cardoso Penha R, et al. (2024) Understanding the biological processes of kidney carcinogenesis: an integrative multi-omics approach. Molecular systems biology, 20(12), 1282.

Zhou M, et al. (2023) Single-cell multi-omics topic embedding reveals cell-type-specific and COVID-19 severity-related immune signatures. Cell reports methods, 3(8), 100563.

Brown BC, et al. (2023) Multiset correlation and factor analysis enables exploration of multi-omics data. *Cell genomics*, 3(8), 100359.

Di Genova A, et al. (2022) A molecular phenotypic map of malignant pleural mesothelioma. *GigaScience*, 12.