

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

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: 20260815T182726+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 15 mentions in open access literature.

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

Anagho-Mattanovich M, et al. (2026) Protocol for integrating and interpreting multi-omics data combining unsupervised and supervised data integrating approaches. STAR protocols, 7(2), 104534.

Iperi C, et al. (2025) BiomiX, a user-friendly bioinformatic tool for democratized analysis and integration of multiomics data. BMC bioinformatics, 26(1), 8.

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.

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.

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.

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.

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.

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.

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.

Pinsach-Abuin ML, et al. (2021) Analysis of Brugada syndrome loci reveals that fine-mapping clustered GWAS hits enhances the annotation of disease-relevant variants. *Cell reports. Medicine*, 2(4), 100250.