

Resource Summary Report

Generated by [Kravitz](#) on Sep 13, 2026

[inSilicoMerging](#)

RRID:SCR_012829

Type: Tool

Proper Citation

inSilicoMerging (RRID:SCR_012829)

Resource Information

URL: <http://www.bioconductor.org/packages/release/bioc/html/inSilicoMerging.html>

Proper Citation: inSilicoMerging (RRID:SCR_012829)

Description: Collection of techniques to remove inter-study bias when combining gene expression data originating from different studies.

Abbreviations: inSilicoMerging

Resource Type: software resource

Resource Name: inSilicoMerging

Resource ID: SCR_012829

Alternate IDs: OMICS_00859

Record Creation Time: 20220129T080312+0000

Record Last Update: 20260912T195753+0000

Ratings and Alerts

No rating or validation information has been found for inSilicoMerging.

No alerts have been found for inSilicoMerging.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 41 mentions in open access literature.

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

Ma W, et al. (2026) FOS Knockdown Alleviates Helicobacter pylori-Infected Gastritis by Suppressing Mast Cell Activation and Treg Polarization. Mediators of inflammation, 2026(1), e4596288.

Wang Y, et al. (2026) Integrated transcriptomic analysis and experimental validation identify ACADL as a mitochondrial tumor suppressor via the FOXO3a/PUMA axis in lung adenocarcinoma. European journal of medical research, 31(1), 202.

Zheng X, et al. (2026) Multi-omics data mining combined with experimental validation reveals ferroptosis- and autophagy-associated hub genes as diagnostic candidates and immune modulators in atherosclerosis. Animal models and experimental medicine, 9(4), 652.

Zhang Z, et al. (2025) Identification of CCNB1 as a biomarker for cellular senescence in hepatocellular carcinoma: a bioinformatics and experimental validation study. Discover oncology, 16(1), 384.

Guo H, et al. (2025) LAX1 as a core biomarker in Alzheimer's disease and periodontitis via the STAT signaling pathway. BMC geriatrics, 26(1), 69.

Zou YF, et al. (2025) Roles of JUN and MMP1 in lung cancer brain metastases. Medicine, 104(31), e42254.

Xuan D, et al. (2025) Identification of CD36 as a contributor in inflammatory response of rheumatoid arthritis and screening of feasible bioactive drugs targeting it. Hereditas, 162(1), 95.

Zhang H, et al. (2024) Identification of core genes in intervertebral disc degeneration using bioinformatics and machine learning algorithms. Frontiers in immunology, 15, 1401957.

Zhang YY, et al. (2024) Screening of coexpression genes of immune cells in breast cancer tissues. Medicine, 103(1), e36211.

Chen Q, et al. (2024) MAP7 drives EMT and cisplatin resistance in ovarian cancer via wnt/??-catenin signaling. Heliyon, 10(9), e30409.

Liang X, et al. (2024) Exploration of PVT1 as a biomarker in prostate cancer. Medicine, 103(34), e39406.

Cheng F, et al. (2024) Exploration and identification of diabetes targets in nursing: CDH1 and DVL1. Medicine, 103(44), e40002.

Lin Z, et al. (2023) Comprehensive analysis of copper-metabolism-related genes about prognosis and immune microenvironment in osteosarcoma. Scientific reports, 13(1), 15059.

Wang X, et al. (2023) Identification and verification of ferroptosis-related genes in diabetic foot using bioinformatics analysis. International wound journal, 20(8), 3191.

Ma C, et al. (2023) A novel defined risk signature of cuproptosis-related long non-coding RNA for predicting prognosis, immune infiltration, and immunotherapy response in lung adenocarcinoma. *Frontiers in pharmacology*, 14, 1146840.

Sousa LG, et al. (2022) ISA101 and nivolumab for HPV-16+ cancer: updated clinical efficacy and immune correlates of response. *Journal for immunotherapy of cancer*, 10(2).

Bertucci F, et al. (2021) Immune landscape of inflammatory breast cancer suggests vulnerability to immune checkpoint inhibitors. *Oncoimmunology*, 10(1), 1929724.

Tian Y, et al. (2021) Significance of CD8+ T cell infiltration-related biomarkers and the corresponding prediction model for the prognosis of kidney renal clear cell carcinoma. *Aging*, 13(19), 22912.

Cangelosi D, et al. (2020) Hypoxia Predicts Poor Prognosis in Neuroblastoma Patients and Associates with Biological Mechanisms Involved in Telomerase Activation and Tumor Microenvironment Reprogramming. *Cancers*, 12(9).

Wu M, et al. (2020) Development and validation of a metastasis-related Gene Signature for predicting the Overall Survival in patients with Pancreatic Ductal Adenocarcinoma. *Journal of Cancer*, 11(21), 6299.