

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 19, 2026

MergeMaid

RRID:SCR_001221

Type: Tool

Proper Citation

MergeMaid (RRID:SCR_001221)

Resource Information

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

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Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on August 18, 2025. R extension whose functions are intended for cross-study comparison of gene expression array data. Required from the user is gene expression matrices, their corresponding gene-id vectors and other useful information, and they could be "list", "matrix", or "ExpressionSet". The main function is "mergeExprs" which transforms the input objects into data in the merged format, such that common genes in different datasets can be easily found. And the function "intcor" calculate the correlation coefficients. Other functions use the output from "modelOutcome" to graphically display the results and cross-validate associations of gene expression data with survival.

Abbreviations: MergeMaid

Synonyms: Merge Maid

Resource Type: software resource

Defining Citation: [PMID:16646808](#)

Keywords: differential expression, microarray, visualization, gene expression

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: MergeMaid

Resource ID: SCR_001221

Alternate IDs: OMICS_02124

Record Creation Time: 20220129T080206+0000

Record Last Update: 20260912T195521+0000

Ratings and Alerts

No rating or validation information has been found for MergeMaid.

No alerts have been found for MergeMaid.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Marzec J, et al. (2021) The Transcriptomic Landscape of Prostate Cancer Development and Progression: An Integrative Analysis. *Cancers*, 13(2).

Alam T, et al. (2020) Comparative transcriptomics of primary cells in vertebrates. *Genome research*, 30(7), 951.

Isella C, et al. (2017) Selective analysis of cancer-cell intrinsic transcriptional traits defines novel clinically relevant subtypes of colorectal cancer. *Nature communications*, 8, 15107.