

Resource Summary Report

Generated by [nidm-terms](#) on Jul 30, 2026

SMAGEXP

RRID:SCR_016360

Type: Tool

Proper Citation

SMAGEXP (RRID:SCR_016360)

Resource Information

URL: <https://github.com/sblanck/smagexp>

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Description: Software toolkit for transcriptomics data meta-analysis. It integrates metaMA and metaRNAseq packages into Galaxy, carries out meta-analysis of gene expression data, handles microarray data from Gene Expression Omnibus (GEO) database, and more.

Abbreviations: SMAGEXP

Synonyms: Statistical Meta Analysis for Gene EXpression

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

Defining Citation: [PMID:30698691](#)

Keywords: transcriptomics, data, meta, analysis, MicroArrays, RNA-Seq, Galaxy, gene, expression, next, generation, sequencing, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: SMAGEXP

Resource ID: SCR_016360

Alternate IDs: biotools:SMAGEXP

Alternate URLs: <https://bio.tools/SMAGEXP>

License: MIT License

Record Creation Time: 20220129T080330+0000

Record Last Update: 20260729T044417+0000

Ratings and Alerts

No rating or validation information has been found for SMAGEXP.

No alerts have been found for SMAGEXP.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Blanck S, et al. (2019) SMAGEXP: a galaxy tool suite for transcriptomics data meta-analysis. GigaScience, 8(2).

Forero DA, et al. (2019) Available Software for Meta-analyses of Genome-wide Expression Studies. Current genomics, 20(5), 325.