

Resource Summary Report

Generated by [ASWG](#) on Aug 2, 2026

MAGE-TAB

RRID:SCR_003222

Type: Tool

Proper Citation

MAGE-TAB (RRID:SCR_003222)

Resource Information

URL: <http://www.mged.org/mage-tab/>

Proper Citation: MAGE-TAB (RRID:SCR_003222)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on July 27,2023. A simple tab-delimited, spreadsheet-based format which will become a part of the MAGE microarray data standard that can be used for annotating and communicating microarray data in a MIAME compliant fashion. MAGE-TAB will enable laboratories without bioinformatics experience or support to manage, exchange and submit well-annotated microarray data in a standard format using a spreadsheet. The MAGE-TAB format is self-contained, and does not require an understanding of MAGE-ML or XML.

Abbreviations: MAGE-TAB

Resource Type: standard specification, narrative resource, data or information resource

Defining Citation: [PMID:17087822](#)

Keywords: microarray, bio.tools

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: MAGE-TAB

Resource ID: SCR_003222

Alternate IDs: nlx_157259, biotools:tab2mage

Alternate URLs: <https://bio.tools/tab2mage>

Record Creation Time: 20220129T080217+0000

Record Last Update: 20260803T040356+0000

Ratings and Alerts

No rating or validation information has been found for MAGE-TAB.

No alerts have been found for MAGE-TAB.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Skrzypiec AE, et al. (2013) Stress-induced lipocalin-2 controls dendritic spine formation and neuronal activity in the amygdala. PLoS one, 8(4), e61046.

Kristoffersen SM, et al. (2012) Global mRNA decay analysis at single nucleotide resolution reveals segmental and positional degradation patterns in a Gram-positive bacterium. Genome biology, 13(4), R30.

Wang X, et al. (2012) Inactivation of a novel FGF23 regulator, FAM20C, leads to hypophosphatemic rickets in mice. PLoS genetics, 8(5), e1002708.

Byrne M, et al. (2012) VarioML framework for comprehensive variation data representation and exchange. BMC bioinformatics, 13, 254.

Washington NL, et al. (2011) The modENCODE Data Coordination Center: lessons in harvesting comprehensive experimental details. Database : the journal of biological databases and curation, 2011, bar023.