

# Resource Summary Report

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## MicroArray and Gene Expression Markup Language

RRID:SCR\_003023

Type: Tool

### Proper Citation

MicroArray and Gene Expression Markup Language (RRID:SCR\_003023)

### Resource Information

**URL:** <http://www.mged.org/Workgroups/MAGE/mage-ml.html>

**Proper Citation:** MicroArray and Gene Expression Markup Language (RRID:SCR\_003023)

**Description:** A language / data exchange format designed to describe and communicate information about microarray based experiments that is based on XML and can describe microarray designs, microarray manufacturing information, microarray experiment setup and execution information, gene expression data and data analysis results. MAGE-ML has been automatically derived from Microarray Gene Expression Object Model (MAGE-OM), which is developed and described using the Unified Modelling Language (UML) -- a standard language for describing object models. Descriptions using UML have an advantage over direct XML document type definitions (DTDs), in many respects. First they use graphical representation depicting the relationships between different entities in a way which is much easier to follow than DTDs. Second, the UML diagrams are primarily meant for humans, while DTDs are meant for computers. Therefore MAGE-OM should be considered as the primary model, and MAGE-ML will be explained by providing simplified fragments of MAGE-OM, rather than XML DTD or XML Schema. (from the description by Ugis Sarkans) The field of gene expression experiments has several distinct technologies that a standard must include. These include single vs. dual channel experiments, cDNA vs. oligonucleotides. Because of these different technologies and different types of gene expression experiments, it is not expected that all aspects of the standard will be used by all organizations. Given the massive amount of data associated with a single set of experiments, it is felt that Extensible Markup Language (XML) is the best way to describe the data. The use of a Document Type Definition (DTD) allows a well-defined tag set, a vocabulary, to describe the domain of gene expression experiments. It also has the virtue of compressing very well so that files in an XML format compress to ten percent of their original size. XML is now widely accepted as a data exchange format across multiple platforms.

**Abbreviations:** MAGE-ML

**Synonyms:** MicroArray and Gene Expression Markup Language

**Resource Type:** data or information resource, interchange format, markup language, narrative resource, standard specification

**Keywords:** microarray, gene expression, bioinformatics

**Funding:** European Union ;  
TEMBLOR project

**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**Resource Name:** MicroArray and Gene Expression Markup Language

**Resource ID:** SCR\_003023

**Alternate IDs:** nif-0000-30390

**Record Creation Time:** 20220129T080216+0000

**Record Last Update:** 20260912T195550+0000

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## Ratings and Alerts

No rating or validation information has been found for MicroArray and Gene Expression Markup Language.

No alerts have been found for MicroArray and Gene Expression Markup Language.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Witney AA, et al. (2012) B??G@Sbase--a microbial gene expression and comparative genomic database. Nucleic acids research, 40(Database issue), D605.

Lyne R, et al. (2007) FlyMine: an integrated database for Drosophila and Anopheles genomics. Genome biology, 8(7), R129.

Freeman K, et al. (2004) Toxicogenomics data: the road to acceptance. Environmental health perspectives, 112(12), A678.

Spellman PT, et al. (2002) Design and implementation of microarray gene expression markup language (MAGE-ML). Genome biology, 3(9), RESEARCH0046.

Saal LH, et al. (2002) BioArray Software Environment (BASE): a platform for comprehensive management and analysis of microarray data. *Genome biology*, 3(8), SOFTWARE0003.