

Resource Summary Report

Generated by SPARC SAWG on Sep 14, 2026

Mayday

RRID:SCR_010945

Type: Tool

Proper Citation

Mayday (RRID:SCR_010945)

Resource Information

URL: <http://www-ps.informatik.uni-tuebingen.de/mayday/wp/>

Proper Citation: Mayday (RRID:SCR_010945)

Description: Software providing a workbench for visualization, analysis and storage of microarray data. It features a graphical user interface and supports the development and integration of existing and new analysis methods. Besides the infrastructural core functionality, Mayday offers a variety of plug-ins, such as various interactive viewers, a connection to the R statistical environment, a connection to SQL-based databases, and different clustering methods, including phylogenetic methods. In addition, so-called meta information objects are provided for annotation of the microarray data allowing integration of data from different sources. This meta information can be used to enhance visualizations, such as in the enhanced heatmap visualization. Written in the Java programming language, Mayday is extremely portable and runs on all platforms supporting the Java runtime environment 1.6.

Abbreviations: Mayday

Synonyms: Mayday - Microarray Data Analysis

Resource Type: software resource

Keywords: java

Availability: GNU General Public License, Plug-ins:, GNU Lesser General Public License

Resource Name: Mayday

Resource ID: SCR_010945

Alternate IDs: OMICS_00773

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260912T195726+0000

Ratings and Alerts

No rating or validation information has been found for Mayday.

No alerts have been found for Mayday.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Ferreira AF, et al. (2025) Blood DDIT4 and TRIM13 Transcript Levels Mark the Early Stages of Machado-Joseph Disease. *Annals of neurology*, 98(1), 107.

Lehmkuhl P, et al. (2021) Dysregulated immunity in PID??patients with low GARP expression on Tregs due to mutations in LRRC32. *Cellular & molecular immunology*, 18(7), 1677.

Sidisky JM, et al. (2021) Mayday sustains trans-synaptic BMP signaling required for synaptic maintenance with age. *eLife*, 10.

Rodrigues AS, et al. (2018) Comprehensive assembly and analysis of the transcriptome of maritime pine developing embryos. *BMC plant biology*, 18(1), 379.

Angelin A, et al. (2017) Foxp3 Reprograms T Cell Metabolism to Function in Low-Glucose, High-Lactate Environments. *Cell metabolism*, 25(6), 1282.

Nepal MP, et al. (2017) Comparative Genomics of Non-TNL Disease Resistance Genes from Six Plant Species. *Genes*, 8(10).

Huang J, et al. (2017) Histone/protein deacetylase 11 targeting promotes Foxp3+ Treg function. *Scientific reports*, 7(1), 8626.

Wang L, et al. (2016) Ubiquitin-specific Protease-7 Inhibition Impairs Tip60-dependent Foxp3+ T-regulatory Cell Function and Promotes Antitumor Immunity. *EBioMedicine*, 13, 99.

Miguel A, et al. (2015) Characterization of the cork oak transcriptome dynamics during acorn development. *BMC plant biology*, 15, 158.

Milanez-Almeida P, et al. (2015) CD11b(+)Ly6C(++)Ly6G(-) Cells with Suppressive Activity Towards T Cells Accumulate in Lungs of Influenza a Virus-Infected Mice. *European journal of microbiology & immunology*, 5(4), 246.

Mitschka S, et al. (2015) Co-existence of intact stemness and priming of neural differentiation programs in mES cells lacking Trim71. *Scientific reports*, 5, 11126.

Fengler S, et al. (2015) A whole-genome microarray study of *Arabidopsis thaliana* semisolid callus cultures exposed to microgravity and nonmicrogravity related spaceflight conditions for 5 days on board of Shenzhou 8. *BioMed research international*, 2015, 547495.

Ewald JA, et al. (2013) Expression microarray meta-analysis identifies genes associated with Ras/MAPK and related pathways in progression of muscle-invasive bladder transition cell carcinoma. *PloS one*, 8(2), e55414.

Nestler H, et al. (2012) Linking proteome responses with physiological and biochemical effects in herbicide-exposed *Chlamydomonas reinhardtii*. *Journal of proteomics*, 75(17), 5370.