

Resource Summary Report

Generated by T1D on Sep 4, 2026

Automated Microarray Pipeline

RRID:SCR_001219

Type: Tool

Proper Citation

Automated Microarray Pipeline (RRID:SCR_001219)

Resource Information

URL: <http://compbio.dfci.harvard.edu/amp/>

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Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented November 4, 2015. Web application based on the TM4 Microarray Software Suite to provide a means of normalization and analysis of microarray data. Users can upload data in the form of Affymetrix CEL files, and define an analysis pipeline by selecting several intuitive options. It performs data normalization (eg RMA), basic statistical analysis (eg t-test, ANOVA), and analysis of annotation using gene classification (eg Gene Ontology term assignment). The analysis are performed without user intervention and the results are presented in a web-based summary that allows data to be downloaded in a variety of formats compatible with further directed analysis.

Abbreviations: AMP

Synonyms: TM4 AMP, AMP: Automated Microarray Pipeline, AMP (TM4 Microarray Software Suite), TM4 Microarray Software Suite: Automated Microarray Pipeline, TM4 Microarray Software Suite: AMP

Resource Type: analysis service resource, data analysis service, production service resource, service resource

Keywords: microarray, normalization

Funding: NLM R01-LM008795

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Automated Microarray Pipeline

Resource ID: SCR_001219

Alternate IDs: OMICS_02125

Alternate URLs: <http://www.tm4.org/amp.html>

Record Creation Time: 20220129T080206+0000

Record Last Update: 20260904T000113+0000

Ratings and Alerts

No rating or validation information has been found for Automated Microarray Pipeline.

No alerts have been found for Automated Microarray Pipeline.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.