

# Resource Summary Report

Generated by [dkNET](#) on Apr 24, 2025

## 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:** production service resource, data analysis service, analysis 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:** 20250424T064450+0000

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## Ratings and Alerts

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

No alerts have been found for Automated Microarray Pipeline.

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## Data and Source Information

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

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## Usage and Citation Metrics

We have not found any literature mentions for this resource.