

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

Microarray Literature-based Annotation

RRID:SCR_008206

Type: Tool

Proper Citation

Microarray Literature-based Annotation (RRID:SCR_008206)

Resource Information

URL: <http://bioinformatics.ekmd.huji.ac.il/milano/>

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Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented August 23, 2016. MILANO provides a useful tool for the automatic custom annotation of microarray results which is based on all the available literature. It has two major advances over similar tools: the ability to expand gene names to include all their informative synonyms while removing synonyms that are not informative and access to the GeneRIF database which provides short summaries of curated articles relevant to known genes. MILANO allows annotation of lists of genes derived from microarray results by user defined terms. The annotation strategy is based on counting the number of literature co-occurrences of each gene on the list with a user defined term. This strategy allows the customization of the annotation procedure and thus overcomes one of the major limitations of the functional annotations usually provided with microarray results. MILANO expands the gene names to include all their informative synonyms while filtering out gene symbols that are likely to be less informative as literature searching terms. It supports searching two literature databases: GeneRIF and Medline (through PubMed), allowing retrieval of both quick and comprehensive results. MILANO's ability can improve microarray analysis by analyzing a list of 150 genes that were affected by p53 overproduction. This analysis reveals that it enables immediate identification of known p53 target genes on this list and assists in sorting the list into genes known to be involved in p53 related pathways, apoptosis and cell cycle arrest. This program performs automatic searches in PubMed or the GeneRIF collection for articles containing co-occurrences of search terms with a list of genes (e.g. from a microarray experiment). The program is used by pasting the list of Gene ID's or symbols in the Primary Search Term field, and the list of cross-reference search terms in the Secondary Search Term field. The output is a table containing the number of hits for each pair of search terms. Sample input is provided in the fields, so you can just click submit and see what happens. If you want to run data of your own, delete the sample input first.

Abbreviations: MILANO

Resource Type: data processing software, software application, data analysis software, software resource

Keywords: gene, annotation, apoptosis, arrest, cell, cycle, literature, microarray, gene expression, p53, symbol

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Microarray Literature-based Annotation

Resource ID: SCR_008206

Alternate IDs: nif-0000-21264

Alternate URLs: <http://milano.md.huji.ac.il/>

Record Creation Time: 20220129T080246+0000

Record Last Update: 20260731T042745+0000

Ratings and Alerts

No rating or validation information has been found for Microarray Literature-based Annotation.

No alerts have been found for Microarray Literature-based Annotation.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.