

Resource Summary Report

Generated by [NIF](#) on Aug 22, 2026

SMD

RRID:SCR_004987

Type: Tool

Proper Citation

SMD (RRID:SCR_004987)

Resource Information

URL: <http://smd.princeton.edu/>

Proper Citation: SMD (RRID:SCR_004987)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on December 17, 2021. Database to store, annotate, view, analyze and share microarray data. It provides registered users access to their own data, provides users access to public data, and tools with which to analyze those data, to any public user anywhere in the world. The GenePattern software package has been incorporated directly into SMD, providing access to many new analysis tools, as well as a plug-in architecture that allows users to directly integrate and share additional tools through SMD. This extension is available with the SMD source code that is fully and freely available to others under an Open Source license, enabling other groups to create a local installation of SMD with an enriched data analysis capability. SMD search options allow the user to Search By Experiments, Search By Datasets, or Search By Gene Names. Web services are provided using common standards, such as Simple Object Access Protocol (SOAP). This enables both local and remote researchers to connect to an installation of the database and retrieve data using pre-defined methods, without needing to resort to use of a web browser.

Abbreviations: SMD

Synonyms: Stanford Microarray Database

Resource Type: analysis service resource, data analysis service, data or information resource, data repository, database, production service resource, service resource, storage service resource

Defining Citation: [PMID:18953035](#), [PMID:17182626](#), [PMID:15608265](#), [PMID:12519956](#), [PMID:11125075](#)

Keywords: data set, microarray, gene, image, gene expression, adenovirus disease, apoptosis, leukemia, source code, web service

Funding: NCI ;
Howard Hughes Medical Institute ;
Stanford University School of Medicine; California; USA ;
NHGRI R01 HG003469

Availability: Public, Open-source license, The community can contribute to this resource,
Acknowledgement requested, THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: SMD

Resource ID: SCR_004987

Alternate IDs: nlx_94141, OMICS_00870, r3d100010555

Alternate URLs: <https://doi.org/10.17616/R3DW40>

Old URLs: <http://genome-www.stanford.edu/microarray/>, <http://smd.stanford.edu/>

Record Creation Time: 20220129T080227+0000

Record Last Update: 20260821T193740+0000

Ratings and Alerts

No rating or validation information has been found for SMD.

No alerts have been found for SMD.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Kumar R, et al. (2019) Exploring the new horizons of drug repurposing: A vital tool for turning hard work into smart work. European journal of medicinal chemistry, 182, 111602.

Kim DK, et al. (2016) Identification of Molecular Signatures from Different Vaccine Adjuvants in Chicken by Integrative Analysis of Microarray Data. Asian-Australasian journal of animal sciences, 29(7), 1044.

Belean B, et al. (2015) Unsupervised image segmentation for microarray spots with irregular contours and inner holes. BMC bioinformatics, 16, 412.

Bermudez M, et al. (2015) CEMP1 Induces Transformation in Human Gingival Fibroblasts. PloS one, 10(5), e0127286.

Mori A, et al. (2014) Effect of photoperiod on the feline adipose transcriptome as assessed by RNA sequencing. BMC veterinary research, 10, 146.

Naderi E, et al. (2014) Network of microRNAs-mRNAs interactions in pancreatic cancer. BioMed research international, 2014, 534821.

Starmans MH, et al. (2011) A simple but highly effective approach to evaluate the prognostic performance of gene expression signatures. PloS one, 6(12), e28320.

Forsberg EC, et al. (2010) Molecular signatures of quiescent, mobilized and leukemia-initiating hematopoietic stem cells. PloS one, 5(1), e8785.

Mumcuoglu M, et al. (2010) The ability to generate senescent progeny as a mechanism underlying breast cancer cell heterogeneity. PloS one, 5(6), e11288.

Forsberg EC, et al. (2005) Differential expression of novel potential regulators in hematopoietic stem cells. PLoS genetics, 1(3), e28.

Budd A, et al. (2004) Bacterial alpha2-macroglobulins: colonization factors acquired by horizontal gene transfer from the metazoan genome? Genome biology, 5(6), R38.

Killion PJ, et al. (2003) The Longhorn Array Database (LAD): an open-source, MIAME compliant implementation of the Stanford Microarray Database (SMD). BMC bioinformatics, 4, 32.