

Resource Summary Report

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UNC Microarray Database

RRID:SCR_010979

Type: Tool

Proper Citation

UNC Microarray Database (RRID:SCR_010979)

Resource Information

URL: <https://genome.unc.edu/>

Proper Citation: UNC Microarray Database (RRID:SCR_010979)

Description: Database for microarray data storage, retrieval, analysis, and visualization.

Abbreviations: UNC MD, UNCMD

Synonyms: UNC-Chapel Hill Microarray Database

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

Keywords: microarray, FASEB list

Availability: Account required, The community can contribute to this resource

Resource Name: UNC Microarray Database

Resource ID: SCR_010979

Alternate IDs: OMICS_00872

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260729T044256+0000

Ratings and Alerts

No rating or validation information has been found for UNC Microarray Database.

No alerts have been found for UNC Microarray Database.

Data and Source Information

Usage and Citation Metrics

We found 31 mentions in open access literature.

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

Shi B, et al. (2023) Senescent Cells Accumulate in Systemic Sclerosis Skin. The Journal of investigative dermatology, 143(4), 661.

Büsselberg D, et al. (2017) Targeting Intracellular Calcium Signaling ([Ca²⁺]_i) to Overcome Acquired Multidrug Resistance of Cancer Cells: A Mini-Overview. Cancers, 9(5).

Qiu H, et al. (2016) JQ1 suppresses tumor growth via PTEN/PI3K/AKT pathway in endometrial cancer. Oncotarget, 7(41), 66809.

Patsialou A, et al. (2015) Autocrine CSF1R signaling mediates switching between invasion and proliferation downstream of TGF β in claudin-low breast tumor cells. Oncogene, 34(21), 2721.

Harrell JC, et al. (2014) Endothelial-like properties of claudin-low breast cancer cells promote tumor vascular permeability and metastasis. Clinical & experimental metastasis, 31(1), 33.

Makowski L, et al. (2014) Obesity increases tumor aggressiveness in a genetically engineered mouse model of serous ovarian cancer. Gynecologic oncology, 133(1), 90.

Huang CC, et al. (2013) Multiclass prediction with partial least square regression for gene expression data: applications in breast cancer intrinsic taxonomy. BioMed research international, 2013, 248648.

Li S, et al. (2013) Endocrine-therapy-resistant ESR1 variants revealed by genomic characterization of breast-cancer-derived xenografts. Cell reports, 4(6), 1116.

Sansores-Garcia L, et al. (2013) Mask is required for the activity of the Hippo pathway effector Yki/YAP. Current biology : CB, 23(3), 229.

Dong L, et al. (2013) Acidosis activation of the proton-sensing GPR4 receptor stimulates vascular endothelial cell inflammatory responses revealed by transcriptome analysis. PloS one, 8(4), e61991.

Prat A, et al. (2013) Genomic analyses across six cancer types identify basal-like breast cancer as a unique molecular entity. Scientific reports, 3, 3544.

Chen H, et al. (2012) Transcript profiling identifies dynamic gene expression patterns and an important role for Nrf2/Keap1 pathway in the developing mouse esophagus. PloS one, 7(5), e36504.

Vasilevsky N, et al. (2012) Research resources: curating the new eagle-i discovery system. Database : the journal of biological databases and curation, 2012, bar067.

Park YY, et al. (2012) Reconstruction of nuclear receptor network reveals that NR2E3 is a novel upstream regulator of ESR1 in breast cancer. EMBO molecular medicine, 4(1), 52.

Kumar P, et al. (2012) Cooperativity of Rb, Brca1, and p53 in malignant breast cancer evolution. PLoS genetics, 8(11), e1003027.

Harrell JC, et al. (2012) Genomic analysis identifies unique signatures predictive of brain, lung, and liver relapse. Breast cancer research and treatment, 132(2), 523.

Katz E, et al. (2011) An in vitro model that recapitulates the epithelial to mesenchymal transition (EMT) in human breast cancer. PloS one, 6(2), e17083.

Prat A, et al. (2011) Deconstructing the molecular portraits of breast cancer. Molecular oncology, 5(1), 5.

Cabanski CR, et al. (2010) SWISS MADE: Standardized WithIn Class Sum of Squares to evaluate methodologies and dataset elements. PloS one, 5(3), e9905.

Kim J, et al. (2010) A Myc network accounts for similarities between embryonic stem and cancer cell transcription programs. Cell, 143(2), 313.