Resource Summary Report

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GeneSigDB

RRID:SCR_013275
Type: Tool

Proper Citation

GeneSigDB (RRID:SCR_013275)

Resource Information

URL: http://www.genesigdb.org

Proper Citation: GeneSigDB (RRID:SCR_013275)

Description: Database of traceable, standardized, annotated gene signatures which have been manually curated from publications that are indexed in PubMed. The Advanced Gene Search will perform a One-tailed Fisher Exact Test (which is equivalent to Hypergeometric Distribution) to test if your gene list is over-represented in any gene signature in GeneSigDB. Gene expression studies typically result in a list of genes (gene signature) which reflect the many biological pathways that are concurrently active. We have created a Gene Signature Data Base (GeneSigDB) of published gene expression signatures or gene sets which we have manually extracted from published literature. GeneSigDB was creating following a thorough search of PubMed using defined set of cancer gene signature search terms. We would be delighted to accept or update your gene signature. Please fill out the form as best you can. We will contact you when we get it and will be happy to work with you to ensure we accurately report your signature. GeneSigDB is capable of providing its functionality through a Java RESTful web service.

Abbreviations: GeneSigDB

Synonyms: Gene Signature Data Base, GeneSigDB - Curated Gene Signatures Database

Resource Type: storage service resource, web service, data or information resource, analysis service resource, service resource, data access protocol, database, production service resource, data analysis service, data repository, software resource

Defining Citation: PMID:22110038

Keywords: gene, gene signature, curated gene signature, gene expression, gene

expression signature, bio.tools

Related Condition: Cancer

Funding: Genome Research Institute ;
Dana-Farber Cancer Institute ;
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NLM 1R01 LM010129;
NCI 1U19 CA148065;
NHGRI 1P50 HG004233

Resource Name: GeneSigDB

Resource ID: SCR_013275

Alternate IDs: biotools:genesigdb, nlx_149342

Alternate URLs: https://bio.tools/genesigdb

Record Creation Time: 20220129T080315+0000

Record Last Update: 20250509T060027+0000

Ratings and Alerts

No rating or validation information has been found for GeneSigDB.

No alerts have been found for GeneSigDB.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 24 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Li T, et al. (2024) PMAIP1, a novel diagnostic and potential therapeutic biomarker in osteoporosis. Aging, 16(4), 3694.

Marcoux P, et al. (2023) Modeling RET-Rearranged Non-Small Cell Lung Cancer (NSCLC): Generation of Lung Progenitor Cells (LPCs) from Patient-Derived Induced Pluripotent Stem Cells (iPSCs). Cells, 12(24).

Miryala SK, et al. (2022) Organ-specific host differential gene expression analysis in systemic candidiasis: A systems biology approach. Microbial pathogenesis, 169, 105677.

Nguyen T, et al. (2021) Linking clinotypes to phenotypes and genotypes from laboratory test results in comprehensive physical exams. BMC medical informatics and decision making, 21(Suppl 3), 51.

Yang Y, et al. (2020) Identification of prognostic chromatin-remodeling genes in clear cell renal cell carcinoma. Aging, 12(24), 25614.

Seo MK, et al. (2020) An Improved, Assay Platform Agnostic, Absolute Single Sample Breast Cancer Subtype Classifier. Cancers, 12(12).

Stephenson S, et al. (2019) Growth Factor-like Gene Regulation Is Separable from Survival and Maturation in Antibody-Secreting Cells. Journal of immunology (Baltimore, Md. : 1950), 202(4), 1287.

Chen YA, et al. (2019) The TargetMine Data Warehouse: Enhancement and Updates. Frontiers in genetics, 10, 934.

Jose V, et al. (2018) Feasibility of developing reliable gene expression modules from FFPE derived RNA profiled on Affymetrix arrays. PloS one, 13(8), e0203346.

Yue Z, et al. (2018) PAGER 2.0: an update to the pathway, annotated-list and gene-signature electronic repository for Human Network Biology. Nucleic acids research, 46(D1), D668.

Rahmati S, et al. (2017) pathDIP: an annotated resource for known and predicted human gene-pathway associations and pathway enrichment analysis. Nucleic acids research, 45(D1), D419.

Paquet ER, et al. (2017) Detecting gene signature activation in breast cancer in an absolute, single-patient manner. Breast cancer research : BCR, 19(1), 32.

Avgustinova A, et al. (2016) Tumour cell-derived Wnt7a recruits and activates fibroblasts to promote tumour aggressiveness. Nature communications, 7, 10305.

Huang X, et al. (2015) Molecular portrait of breast cancer in China reveals comprehensive transcriptomic likeness to Caucasian breast cancer and low prevalence of luminal A subtype. Cancer medicine, 4(7), 1016.

Care MA, et al. (2015) Gene expression meta-analysis reveals immune response convergence on the IFN?-STAT1-IRF1 axis and adaptive immune resistance mechanisms in lymphoma. Genome medicine, 7(1), 96.

Aramburu A, et al. (2015) Combined clinical and genomic signatures for the prognosis of early stage non-small cell lung cancer based on gene copy number alterations. BMC genomics, 16, 752.

Pappa KI, et al. (2015) Profiling of Discrete Gynecological Cancers Reveals Novel Transcriptional Modules and Common Features Shared by Other Cancer Types and Embryonic Stem Cells. PloS one, 10(11), e0142229.

Kohlscheen S, et al. (2015) Inhibition of Thrombopoietin/Mpl Signaling in Adult Hematopoiesis Identifies New Candidates for Hematopoietic Stem Cell Maintenance. PloS one, 10(7), e0131866.

Bihani T, et al. (2015) Resistance to everolimus driven by epigenetic regulation of MYC in ER+ breast cancers. Oncotarget, 6(4), 2407.

Speakman CM, et al. (2014) Elevated O-GlcNAc levels activate epigenetically repressed genes and delay mouse ESC differentiation without affecting naïve to primed cell transition. Stem cells (Dayton, Ohio), 32(10), 2605.