Resource Summary Report

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msigdbr

RRID:SCR_022870
Type: Tool

Proper Citation

msigdbr (RRID:SCR_022870)

Resource Information

URL: https://cran.r-project.org/package=msigdbr

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Description: Software R package contains Molecular Signatures Database (MSigDB) gene sets for multiple organisms in tidy data format. Gene sets in standard R data frame with key value pairs. Package includes human genes as well as corresponding symbols and IDs for frequently studied model organisms such as mouse, rat, pig, fly, and yeast.

Resource Type: software toolkit, software resource

Keywords: Standard R data frame, human genes as listed in MSigDB, corresponding symbols and IDs

Funding:

Availability: Free, Available for download, Freely available

Resource Name: msigdbr

Resource ID: SCR_022870

Alternate URLs: https://igordot.github.io/msigdbr/

License: MIT license

Record Creation Time: 20221013T050144+0000

Record Last Update: 20250426T060917+0000

Ratings and Alerts

No rating or validation information has been found for msigdbr.

No alerts have been found for msigdbr.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 19 mentions in open access literature.

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

Egea-Rodriguez S, et al. (2025) RECQL4 affects MHC class II-mediated signalling and favours an immune-evasive signature that limits response to immune checkpoint inhibitor therapy in patients with malignant melanoma. Clinical and translational medicine, 15(1), e70094.

Mass-Sanchez PB, et al. (2024) Perilipin 5 deletion protects against nonalcoholic fatty liver disease and hepatocellular carcinoma by modulating lipid metabolism and inflammatory responses. Cell death discovery, 10(1), 94.

Fournier M, et al. (2024) Reciprocal inhibition of NOTCH and SOX2 shapes tumor cell plasticity and therapeutic escape in triple-negative breast cancer. EMBO molecular medicine, 16(12), 3184.

Youssef KK, et al. (2024) Two distinct epithelial-to-mesenchymal transition programs control invasion and inflammation in segregated tumor cell populations. Nature cancer, 5(11), 1660.

Petralia F, et al. (2024) Pan-cancer proteogenomics characterization of tumor immunity. Cell, 187(5), 1255.

Kinyamu HK, et al. (2024) Proteasome Inhibition Reprograms Chromatin Landscape in Breast Cancer. Cancer research communications, 4(4), 1082.

Wei L, et al. (2024) Patient-specific analysis of co-expression to measure biological network rewiring in individuals. Life science alliance, 7(2).

Donahue KL, et al. (2024) Oncogenic KRAS-Dependent Stromal Interleukin-33 Directs the Pancreatic Microenvironment to Promote Tumor Growth. Cancer discovery, 14(10), 1964.

Zeng D, et al. (2024) Enhancing immuno-oncology investigations through multidimensional decoding of tumor microenvironment with IOBR 2.0. Cell reports methods, 4(12), 100910.

Tighanimine K, et al. (2024) A homoeostatic switch causing glycerol-3-phosphate and phosphoethanolamine accumulation triggers senescence by rewiring lipid metabolism. Nature metabolism, 6(2), 323.

Ziblat A, et al. (2024) Batf3+ DCs and the 4-1BB/4-1BBL axis are required at the effector phase in the tumor microenvironment for PD-1/PD-L1 blockade efficacy. Cell reports, 43(5), 114141.

Kwon DI, et al. (2024) Fc-fused IL-7 provides broad antiviral effects against respiratory virus infections through IL-17A-producing pulmonary innate-like T cells. Cell reports. Medicine, 5(1), 101362.

Kuo LW, et al. (2024) Blocking Tryptophan Catabolism Reduces Triple-Negative Breast Cancer Invasive Capacity. Cancer research communications, 4(10), 2699.

Wang W, et al. (2024) Identification of hypoxic macrophages in glioblastoma with therapeutic potential for vasculature normalization. Cancer cell, 42(5), 815.

Etoh K, et al. (2023) A web-based integrative transcriptome analysis, RNAseqChef, uncovers the cell/tissue type-dependent action of sulforaphane. The Journal of biological chemistry, 299(6), 104810.

Long D, et al. (2023) Integrated analysis of the ubiquitination mechanism reveals the specific signatures of tissue and cancer. BMC genomics, 24(1), 523.

D'Adamo GL, et al. (2023) Bacterial clade-specific analysis identifies distinct epithelial responses in inflammatory bowel disease. Cell reports. Medicine, 4(7), 101124.

He W, et al. (2023) Modeling breast cancer proliferation, drug synergies, and alternating therapies. iScience, 26(5), 106714.

Aso H, et al. (2022) Single-cell transcriptome analysis illuminating the characteristics of species-specific innate immune responses against viral infections. GigaScience, 12.