

Package ‘msigdbr’

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Type Package

Title MSigDB for Multiple Organisms in a Tidy Data Format

Version 6.1.1

Description Provides the 'Molecular Signatures Database' (MSigDB) gene sets used with the 'Gene Set Enrichment Analysis' (GSEA) software (Subramanian et al. 2005 <doi:10.1073/pnas.0506580102>, Liberzon et al. 2015 <doi:10.1016/j.cels.2015.12.004>) for various frequently studied model organisms in a standard R data frame with key-value pairs.

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Encoding UTF-8

URL <https://github.com/igordot/msigdbr>

BugReports <https://github.com/igordot/msigdbr/issues>

LazyData true

Depends R (>= 3.2.0), dplyr (>= 0.7.0), tibble

Imports magrittr, rlang

Suggests testthat, knitr, rmarkdown

RoxygenNote 6.0.1

VignetteBuilder knitr

NeedsCompilation no

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Repository CRAN

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msigdb	<i>Retrieve msigdb data frame.</i>
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Description

Retrieve msigdb data frame.

Usage

```
msigdb(species = "Homo sapiens", category = NULL, subcategory = NULL)
```

Arguments

species	species name, such as Homo sapiens, Mus musculus, etc.
category	collection, such as H, C1, C2, C3, C4, C5, C6, C7.
subcategory	sub-collection, such as CGP, MIR, BP, etc.

Value

a data frame of gene sets with one gene per row

Examples

```
# all human gene sets
m = msigdb(species = "Homo sapiens")

# mouse C2 (curated) CGP (chemical and genetic perturbations) gene sets
m = msigdb(species = "Mus musculus", category = "C2", subcategory = "CGP")
```

msigdb_show_species	<i>List the species available in msigdb.</i>
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Description

List the species available in msigdb.

Usage

```
msigdb_show_species()
```

Value

a vector of possible species

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