

# Package ‘msigdb’

October 9, 2018

**Type** Package

**Title** MSigDB Gene Sets for Multiple Organisms in a Tidy Data Format

**Version** 6.2.1

**Description** Provides the 'Molecular Signatures Database' (MSigDB) gene sets typically 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>) in a standard R data frame with key-value pairs. Included are the original human gene symbols and Entrez IDs as well as the equivalents for various frequently studied model organisms such as mouse, rat, pig, fly, and yeast.

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**Encoding** UTF-8

**URL** <https://github.com/igordot/msigdb>

**BugReports** <https://github.com/igordot/msigdb/issues>

**LazyData** true

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

**Imports** magrittr, rlang

**Suggests** testthat, knitr, rmarkdown

**RoxygenNote** 6.1.0

**VignetteBuilder** knitr

**NeedsCompilation** no

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**Repository** CRAN

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msigdb	<i>Retrieve the msigdb data frame</i>
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**Description**

Retrieve the 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")
```

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

List the species available in the msigdb package

**Usage**

```
msigdb_show_species()
```

**Value**

a vector of possible species

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