

# Package ‘msigdbr’

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**Type** Package

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

**Version** 7.0.1

**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. The package includes the original human gene symbols and NCBI/Entrez IDs as well as the equivalents for frequently studied model organisms such as mouse, rat, pig, fly, and yeast.

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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)

**Imports** magrittr, rlang, dplyr (>= 0.7.0), tibble

**Suggests** testthat, knitr, rmarkdown

**RoxygenNote** 6.1.1

**VignetteBuilder** knitr

**NeedsCompilation** no

**Author** Igor Dolgalev [aut, cre]

**Maintainer** Igor Dolgalev <igor.dolgalev@nyumc.org>

**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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