

# Package ‘msigdbr’

May 5, 2021

**Type** Package

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

**Version** 7.4.1

**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 human genes as listed in MSigDB as well as the corresponding symbols and IDs for frequently studied model organisms such as mouse, rat, pig, fly, and yeast.

**License** MIT + file LICENSE

**Encoding** UTF-8

**URL** <https://igordot.github.io/msigdbr/>

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

**Depends** R (>= 3.3.0)

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

**Suggests** knitr, rmarkdown, testthat

**RoxygenNote** 7.1.1

**VignetteBuilder** knitr

**NeedsCompilation** no

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

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

**Repository** CRAN

**Date/Publication** 2021-05-05 16:10:02 UTC

## R topics documented:

msigdb . . . . .	2
msigdb_collections . . . . .	3
msigdb_show_species . . . . .	3
msigdb_species . . . . .	4

<b>Index</b>	<b>5</b>
--------------	----------

---

msigdb	<i>Retrieve the gene sets data frame</i>
--------	--

---

### Description

Retrieve a data frame of gene sets and their member genes. The available species and collections can be checked with `msigdb_species()` and `msigdb_collections()`.

### Usage

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

### Arguments

species	Species name, such as Homo sapiens or Mus musculus.
category	MSigDB collection abbreviation, such as H or C1.
subcategory	MSigDB sub-collection abbreviation, such as CGP or BP.

### Value

A data frame of gene sets with one gene per row.

### References

<https://www.gsea-msigdb.org/gsea/msigdb/collections.jsp>

### Examples

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

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

---

`msigdbr_collections` *List the collections available in the msigdbr package*

---

**Description**

List the collections available in the msigdbr package

**Usage**

```
msigdbr_collections()
```

**Value**

A data frame of the available collections.

**Examples**

```
msigdbr_collections()
```

---

`msigdbr_show_species` *List the species available in the msigdbr package*

---

**Description**

This function is being deprecated and replaced by `msigdbr_species()`.

**Usage**

```
msigdbr_show_species()
```

**Value**

A vector of possible species.

---

msigdbr_species	<i>List the species available in the msigdbr package</i>
-----------------	--

---

**Description**

List the species available in the msigdbr package

**Usage**

```
msigdbr_species()
```

**Value**

A data frame of the available species.

**Examples**

```
msigdbr_species()
```

# Index

msigdb, [2](#)  
msigdb\_collections, [3](#)  
msigdb\_show\_species, [3](#)  
msigdb\_species, [4](#)