

# Package ‘seq2pathway.data’

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**Type** Package

**Title** data set for R package seq2pathway

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**Author** Bin Wang <binw@uchicago.edu>

**Maintainer** Arjun Kinstlick <akinstlick@uchicago.edu>

**Depends** R (>= 3.6.2)

**biocViews** ExperimentData

**Description** Supporting data for the seq2pathway package. Includes modified gene sets from MsigDB and org.Hs.eg.db; gene locus definitions from GENCODE project.

**License** GPL (>= 2)

**git\_url** <https://git.bioconductor.org/packages/seq2pathway.data>

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dat\_gene2path\_chip      *demo result of gene2pathway function from chip seq data*

### Description

demo result of gene2pathway function from chip seq data

### Usage

```
data("dat_gene2path_chip")
```

### Format

A list with 2 elements.

gene2pathway\_result.2 a list of gene2pathway test result, with 3 data frames(3 GO terms)

gene2pathway\_result.FET a list of fisher's test result, with 3 data frames(3 GO terms)

### Value

A list, with two sub lists. The name of one sub list is "gene2pathway\_result.2", with 3 data frames of GO\_BP, GO\_MF, and GO\_CC, another is "gene2pathway\_result.FET", with 3 data frames of GO\_BP, GO\_MF, and GO\_CC.

dat\_gene2path\_RNA      *demo result of gene2pathway function from RNA seq data*

### Description

demo result of gene2pathway function from RNA seq data

### Usage

```
data("dat_gene2path_RNA")
```

### Format

A list with 2 elements.

gene2pathway\_result.2 a data frame of gene2pathway test result

gene2pathway\_result.FET a data frame of fisher's test result

**Value**

A list, with two elements. one element is a data frame about "gene2pathway\_result.2"", another data frame is about "gene2pathway\_result.FET".

---

dat\_seq2pathway\_GOterms

*demo result of seq2pathway function from chip seq data*

---

**Description**

demo result of seq2pathway function from chip seq data

**Usage**

```
data("dat_seq2pathway_GOterms")
```

**Format**

A list with 3 elements.

seq2gene\_result a list with 2 annotation table

gene2pathway\_result.FAIME a list of gene2pathway test result, with 3 data frames(3 GO terms)

gene2pathway\_result.FET a list of fisher's test result, with 3 data frames(3 GO terms)

**Value**

A list, with three sub lists. The name of first sub list is seq2gene\_result, with 2 data frames of full and coding gene annotation respectively, the name of second sub list is "gene2pathway\_result.FAIME", with 3 data frames of GO\_BP, GO\_MF, and GO\_CC, the third is "gene2pathway\_result.FET", with 3 dara frames of GO\_BP, GO\_MF, and GO\_CC.

---

dat\_seq2pathway\_Msig

*demo result of seq2pathway function from chip seq data*

---

**Description**

demo result of seq2pathway function from chip seq data

**Usage**

```
data("dat_seq2pathway_Msig")
```

**Format**

A list with 3 elements.

seq2gene\_result a list with 2 annotation table

gene2pathway\_result.FAIME a data frame of gene2pathway test result by MsigDB C5 terms

gene2pathway\_result.FET a data frame of fisher's test resultby MsigDB C5 terms

**Value**

A list, with three elements. The name of first element is seq2gene\_result, with 2 data frames of full and coding gene annotation respectively, the second element is a data frame of "gene2pathway\_result.FAIME", the third is a data frame of "gene2pathway\_result.FET".

---

Des_BP_list	<i>Description of GO term BP</i>
-------------	----------------------------------

---

**Description**

Description of GO term BP

**Usage**

```
data("Des_BP_list")
```

**Format**

A list, list names are Go term BP's IDs, list elements are GO term BP's description respectively.

**Value**

A list, list names are Go term BP's IDs, list elements are GO term BP's description respectively.

**Source**

Carlson M. org.Hs.eg.db: Genome wide annotation for Human. R package version 3.0.0.

**Examples**

```
data(Des_BP_list)
head(names(Des_BP_list))
head(Des_BP_list)
```

---

Des_CC_list	<i>Description of GO term CC</i>
-------------	----------------------------------

---

**Description**

Description of GO term CC

**Usage**

```
data("Des_CC_list")
```

**Format**

A list, list names are Go term CC's IDs, list elements are GO term CC's description respectively.

**Value**

A list, list names are Go term CC's IDs, list elements are GO term CC's description respectively.

**Source**

Carlson M. org.Hs.eg.db: Genome wide annotation for Human. R package version 3.0.0.

**Examples**

```
data(Des_CC_list)
head(names(Des_CC_list))
head(Des_CC_list)
```

---

Des_MF_list	<i>Description of GO term MF</i>
-------------	----------------------------------

---

**Description**

Description of GO term MF

**Usage**

```
data("Des_MF_list")
```

**Format**

A list, list names are Go term MF's IDs, list elements are GO term MF's description respectively.

**Value**

A list, list names are Go term MF's IDs, list elements are GO term MF's description respectively.

**Source**

Carlson M. org.Hs.eg.db: Genome wide annotation for Human. R package version 3.0.0.

**Examples**

```
data(Des_MF_list)
head(names(Des_MF_list))
head(Des_MF_list)
```

gencode\_coding      *Coding gene list in GENCODE 20.*

---

**Description**

Coding gene list in GENCODE 20.

**Usage**

```
data("gencode_coding")
```

**Format**

A vector including all coding gene symbols in GENCODE version20.

**Value**

A character vector including all coding gene symbols in GENCODE version20.

**Source**

GENCODE 20

**References**

Harrow J, et al. (2012) GENCODE: The reference human genome annotation for The ENCODE Project

**Examples**

```
data(gencode_coding)
head(gencode_coding)
```

---

gene\_description      *demo data of adding gene description*

---

**Description**

demo data of adding gene description

**Usage**

```
data("gene_description")
```

**Format**

A data frame with 561 observations on the following 2 variables.

hgnc\_symbol a characteristic vector

description a characteristic vector

**Value**

A characteristic matrix of gene symbols and descriptions.

---

GO_BP_list	<i>Gene symbol list of GO term BP</i>
------------	---------------------------------------

---

**Description**

Gene symbol list of GO term BP

**Usage**

```
data("GO_BP_list")
```

**Format**

A list, list names are Go term BP's IDs, list elements are gene symbols in GO term BP.

**Value**

A list, list names are Go term BP's IDs, list elements are gene symbols in GO term BP.

**Source**

Carlson M. org.Hs.eg.db: Genome wide annotation for Human. R package version 3.0.0.

**Examples**

```
data(GO_BP_list)
head(GO_BP_list)
```

---

GO_CC_list	<i>Gene symbol list of GO term CC</i>
------------	---------------------------------------

---

**Description**

Gene symbol list of GO term CC

**Usage**

```
data("GO_CC_list")
```

**Format**

A list, list names are Go term CC's IDs, list elements are gene symbols in GO term CC.

**Value**

A list, list names are Go term CC's IDs, list elements are gene symbols in GO term CC.

**Source**

Carlson M. org.Hs.eg.db: Genome wide annotation for Human. R package version 3.0.0.

**Examples**

```
data(GO_CC_list)
head(GO_CC_list)
```

---

GO\_GENCODE\_df\_hg\_v19 *intersection genes of GO terms and GENCODE 19*

---

**Description**

intersection genes of GO terms and GENCODE 19

**Usage**

```
data("GO_GENCODE_df_hg_v19")
```

**Format**

A data frame.

**Value**

A data frame.

**Source**

Carlson M. org.Hs.eg.db: Genome wide annotation for Human. R package version 3.0.0.

**References**

Harrow J, et al. (2012) GENCODE: The reference human genome annotation for The ENCODE Project

**Examples**

```
data(GO_GENCODE_df_hg_v19)
head(GO_GENCODE_df_hg_v19)
```



---

GO\_GENCODE\_df\_hg\_v36 *intersection genes of GO terms and GENCODE 36*

---

**Description**

intersection genes of GO terms and GENCODE 36

**Usage**

```
data("GO_GENCODE_df_hg_v36")
```

**Format**

A data frame.

**Value**

A data frame.

**Source**

Carlson M. org.Hs.eg.db: Genome wide annotation for Human. R package version 3.0.0.

**References**

Harrow J, et al. (2012) GENCODE: The reference human genome annotation for The ENCODE Project

**Examples**

```
data(GO_GENCODE_df_hg_v36)  
head(GO_GENCODE_df_hg_v36)
```

---

GO\_GENCODE\_df\_mm\_vM1 *intersection genes of GO terms and GENCODE vM1*

---

**Description**

intersection genes of GO terms and GENCODE vM1

**Usage**

```
data("GO_GENCODE_df_mm_vM1")
```

**Format**

A data frame.

**Value**

A data frame.

**Source**

Carlson M. org.Hs.eg.db: Genome wide annotation for Human. R package version 3.0.0.

**References**

Harrow J, et al. (2012) GENCODE: The reference human genome annotation for The ENCODE Project

**Examples**

```
data(GO_GENCODE_df_mm_vM1)
head(GO_GENCODE_df_mm_vM1)
```

---

GO\_GENCODE\_df\_mm\_vM25 *intersection genes of GO terms and GENCODE vM25*

---

**Description**

intersection genes of GO terms and GENCODE vM25 simply by gene symbol match

**Usage**

```
data("GO_GENCODE_df_mm_vM25")
```

**Format**

A data frame.

**Value**

A data frame.

**Source**

Carlson M. org.Hs.eg.db: Genome wide annotation for Human. R package version 3.0.0.

**References**

Harrow J, et al. (2012) GENCODE: The reference human genome annotation for The ENCODE Project

**Examples**

```
data(GO_GENCODE_df_mm_vM25)
head(GO_GENCODE_df_mm_vM25)
```

---

GO_MF_list	<i>Gene symbol list of GO term MF</i>
------------	---------------------------------------

---

**Description**

Gene symbol list of GO term MF

**Usage**

```
data("GO_MF_list")
```

**Format**

A list, list names are Go term MF's IDs, list elements are gene symbols in GO term MF.

**Value**

A list, list names are Go term MF's IDs, list elements are gene symbols in GO term MF.

**Source**

Carlson M. org.Hs.eg.db: Genome wide annotation for Human. R package version 3.0.0.

**Examples**

```
data(GO_MF_list)
head(GO_MF_list)
```

---

MsigDB_C5	<i>MsigDB data set</i>
-----------	------------------------

---

**Description**

.gsa format data

**Usage**

```
data("MsigDB_C5")
```

**Format**

A list with 3 sub lists.

genesets a list of gene names

geneset.names a list of geneset names

geneset.descriptions a list of geneset descriptions

**Value**

A "GSA.genesets" object from GSA package.

---

Msig\_GENCODE\_df\_hg\_v19

*intersection genes of MSigDB collection and GENCODE 19*

---

**Description**

intersection genes of MSigDB collection and GENCODE 19

**Usage**

```
data("Msig_GENCODE_df_hg_v19")
```

**Format**

A data frame.

**Value**

A data frame.

**References**

Harrow J, et al. (2012) GENCODE: The reference human genome annotation for The ENCODE Project. Subramanian, Tamayo, et al. (2005, PNAS 102, 15545-15550).

**Examples**

```
data(Msig_GENCODE_df_hg_v19)
head(Msig_GENCODE_df_hg_v19)
```

---

Msig\_GENCODE\_df\_hg\_v36

*intersection genes of MSigDB collection and GENCODE 36*

---

**Description**

intersection genes of MSigDB collection and GENCODE 36

**Usage**

```
data("Msig_GENCODE_df_hg_v36")
```

**Format**

A data frame.

**Value**

A data frame.

**References**

Harrow J, et al. (2012) GENCODE: The reference human genome annotation for The ENCODE Project. Subramanian, Tamayo, et al. (2005, PNAS 102, 15545-15550).

**Examples**

```
data(Msig_GENCODE_df_hg_v36)
head(Msig_GENCODE_df)
```

---

Msig\_GENCODE\_df\_mm\_vM1

*intersection genes of MSigDB collection and GENCODE vM1*

---

**Description**

intersection genes of MSigDB collection and GENCODE vM1

**Usage**

```
data("Msig_GENCODE_df_mm_vM1")
```

**Format**

A data frame.

**Value**

A data frame.

**References**

Harrow J, et al. (2012) GENCODE: The reference human genome annotation for The ENCODE Project. Subramanian, Tamayo, et al. (2005, PNAS 102, 15545-15550).

**Examples**

```
data(Msig_GENCODE_df_mm_vM1)
head(Msig_GENCODE_df_mm_vM1)
```

---

Msig\_GENCODE\_df\_mm\_vM25

*intersection genes of MSigDB collection and GENCODE vM25*

---

**Description**

intersection genes of MSigDB collection and GENCODE vM25 simply by gene symbol match

**Usage**

```
data("Msig_GENCODE_df_mm_vM25")
```

**Format**

A data frame.

**Value**

A data frame.

**References**

Harrow J, et al. (2012) GENCODE: The reference human genome annotation for The ENCODE Project. Subramanian, Tamayo, et al. (2005, PNAS 102, 15545-15550).

**Examples**

```
data(Msig_GENCODE_df_mm_vM25)  
head(Msig_GENCODE_df)
```

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