Package 'seq2pathway.data'

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Type Package

Title data set for R package seq2pathway

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Depends R (>= 2.10.0)

biocViews ExperimentData

Description Supporting data for the seq2patheway package. Includes
modified gene sets from MsigDB and org.Hs.eg.db; gene locus
definitions from GENCODE project.

License GPL (>= 2)

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R topics documented:

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 dara 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".

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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   *Description of GO term BP*

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 descritpion respectively.

Value

A list, list names are Go term BP's IDs, list elements are GO term BP's descritpion 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   *Description of GO term CC*

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 descritpion respectively.

Value

A list, list names are Go term CC's IDs, list elements are GO term CC's descritpion 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 *Description of GO term MF*

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 descritpion respectively.

Value

A list, list names are Go term MF's IDs, list elements are GO term MF's descritpion 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 *Gene symbol list of GO term BP*

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 *Gene symbol list of GO term CC*

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_v20   *intersection genes of GO terms and GENCODE 20*

Description

intersection genes of GO terms and GENCODE 20

Usage

```
data("GO_GENCODE_df_hg_v20")
```

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_v20)
head(GO_GENCODE_df_hg_v20)
```

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_vM3   *intersection genes of GO terms and GENCODE vM3*

Description

intersection genes of GO terms and GENCODE vM3

Usage

```
data("GO_GENCODE_df_mm_vM3")
```

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_vM3)
head(GO_GENCODE_df_mm_vM3)
```

GO_GENCODE_df_mm_vM4   *intersection genes of GO terms and GENCODE vM4*

Description

intersection genes of GO terms and GENCODE vM4 simply by gene symbol match

Usage

```
data("GO_GENCODE_df_mm_vM4")
```

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_vM4)
head(GO_GENCODE_df_mm_vM4)
```

GO_MF_list   *Gene symbol list of GO term MF*

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 *MsigDB data set*

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_v20

intersection genes of MSigDB collection and GENCODE 20

Description

intersection genes of MSigDB collection and GENCODE 20

Usage

```
data("Msig_GENCODE_df_hg_v20")
```

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_v20)
head(Msig_GENCODE_df_hg_v20)
```

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_vM3

intersection genes of MSigDB collection and GENCODE vM3

Description

intersection genes of MSigDB collection and GENCODE vM3

Usage

```
data("Msig_GENCODE_df_mm_vM3")
```

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_vM3)
head(Msig_GENCODE_df_mm_vM3)
```

Msig_GENCODE_df_mm_vM4

intersection genes of MSigDB collection and GENCODE vM4

Description

intersection genes of MSigDB collection and GENCODE vM4 simply by gene symbol match

Usage

```
data("Msig_GENCODE_df_mm_vM4")
```

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_vM4)
head(Msig_GENCODE_df_mm_vM4)
```

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