Package 'seq2pathway.data'

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

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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 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".

`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_v36 *intersection genes of GO terms and GENCODE 36*

Description

intersection genes of GO terms and GENCODE 36

Usage

```
data("GO_GENECODE_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_GENECODE_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_GENECODE_df_mm_vM25)
head(GO_GENCODE_df_mm_vM25)
```

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_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_GENECODE_df_hg_v36)
head(Msig_GENECODE_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_GENECODE_df_mm_vM25)
head(Msig_GENECODE_df)
```

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