Package 'GIGSEAdata'

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Type Package

Title Gene set collections for the GIGSEA package

Version 1.26.0

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Description The gene set collection used for the GIGSEA package.

License LGPL-3

Encoding UTF-8

LazyData true

Depends R (>= 3.5)

Suggests GIGSEA, knitr, rmarkdown

VignetteBuilder knitr

RoxygenNote 6.0.1

NeedsCompilation no

biocViews ExperimentData, Homo_sapiens_Data

git_url https://git.bioconductor.org/packages/GIGSEAdata

git_branch RELEASE_3_21

git_last_commit 4e9bfb3

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`Fantom5.TF` *Fantom5.TF*

Description

The human transcript promoter locations were obtained from Fantom5. Based on the promoter locations, the tool MotEvo was used to predict the human transcriptional factor (TF) target sites.

Usage

```
Fantom5.TF
```

Format

A list with two items:

net a sparse matrix, the connectivity between terms and genes, comprising 500 Positional Weight Matrices (PWM) and 21964 genes

annot a data frame, description of terms ...

Source

http://www.swissregulon.unibas.ch

`org.Hs.eg.GO` *org.Hs.eg.GO*

Description

Gene sets that contain genes annotated by the same Gene Ontology (GO) term. For each GO term, we not only incorporate its own gene sets, but also incorporate the gene sets belonging to its offsprings.

Usage

```
org.Hs.eg.GO
```

Format

A list with two items:

net a sparse matrix, the connectivity between terms and genes

annot a data frame, description of terms ...

Source

Seethedatabase"org.Hs.eg.db"and"GO.db"inR.

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