

Package ‘GIGSEAdata’

November 13, 2025

Type Package

Title Gene set collections for the GIGSEA package

Version 1.28.0

Author Shijia Zhu

Maintainer Shijia Zhu <shijia.zhu@mssm.edu>

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_22

git_last_commit 6b89d9c

git_last_commit_date 2025-10-29

Repository Bioconductor 3.22

Date/Publication 2025-11-13

Contents

Fantom5.TF	2
org.Hs.eg.GO	2
Index	3

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" in R.](#)

Index

* **datasets**

Fantom5.TF, [2](#)

org.Hs.eg.G0, [2](#)

Fantom5.TF, [2](#)

org.Hs.eg.G0, [2](#)