

# Package ‘GIGSEAdata’

November 26, 2020

**Type** Package

**Title** Gene set collections for the GIGSEA package

**Version** 1.8.0

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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\_12

**git\_last\_commit** ca487c4

**git\_last\_commit\_date** 2020-10-27

**Date/Publication** 2020-11-26

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Fantom5.TF

*Fantom5.TF*

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### 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>

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org.Hs.eg.GO

*org.Hs.eg.GO*

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### 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.](#)

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