

# Package ‘FIs’

April 25, 2024

**Title** Human Functional Interactions (FIs) for splineTimeR package

**Version** 1.31.0

**Date** 2020-04-14

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**Depends** R (>= 3.3)

**Description** Data set containing two complete lists of identified functional interaction partners in Human. Data are derived from Reactome and BioGRID databases.

**License** GPL-3

**biocViews** PathwayInteractionDatabase, Homo\_sapiens\_Data

**NeedsCompilation** no

**git\_url** <https://git.bioconductor.org/packages/FIs>

**git\_branch** devel

**git\_last\_commit** 183305b

**git\_last\_commit\_date** 2023-10-24

**Repository** Bioconductor 3.19

**Date/Publication** 2024-04-25

## Contents

FIs . . . . .	2
<b>Index</b>	<b>4</b>

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FIs

*Human Functional Interactions (FIs)*

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### Description

Data set with two complete lists of identified functional interaction partners in Human. Data are derived from Reactome and BioGRID databases.

### Usage

```
data(FIs)
```

### Format

A list of two data frames with two columns describing interaction partners.

FIs\_Reactome functional interactions derived from Reactome database

FIs\_BioGRID functional interactions derived from BioGRID database

### Details

The data sets contain unique interaction pairs. Self-loops are not considered.

### Value

A list of two data frames.

### Source

Reactome functional interaction pairs. Retrieved December 3, 2015 from <http://www.reactome.org/pages/download-data/>

BioGRID functional interaction pairs. Retrieved December 3, 2015 from <http://thebiogrid.org/download.php>

### References

Croft, D., Mundo, A. F., Haw R., Milacic, M., Weiser, J., Wu, G., Caudy, M., Garapati, P., Gillespie, M., Kamdar, M. R., Jassal, B., Jupe, S., Matthews, L., May, B., Palatnik, S., Rothfels, K., Shamovsky, V., Song, H., Williams, M., Birney, E., Hermjakob, H., Stein, L., D'Eustachio, P. (2014). The Reactome pathway knowledgebase. *Nucleic Acids Research* 42(Database issue), 472-477.

Stark, C., Breitkreutz, B.-J., Reguly, T. Boucher, L., Breitkreutz, A., Tyers, M. (2006). BioGRID: a general repository for interaction datasets. *Nucleic Acids Research* 34(Database issue), 535-539.

**Examples**

```
data(FIs)
names(FIs)
head(FIs$FIs_Reactome)
head(FIs$FIs_BioGRID)
```

# Index

\* **datasets**

FIs, [2](#)

FIs, [2](#)