Package ‘FGRepo’

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Type Package

Title Functional Genomics Repository for POST-GWAS Analysis

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Depends R (>= 3.5)

Description A collection of datasets essential for functional genomic analysis. Gene names, gene positions, cytoband information, sourced from Ensembl and phenotypes association graph prepared from GWAScatalog are included. Data is available in both GRCh37 and 38 builds. These datasets facilitate a wide range of genomic studies, including the identification of genetic variants, exploration of genomic features, and post-GWAS functional analysis.

Encoding UTF-8

LazyData true

LazyDataCompression xz

RoxygenNote 7.3.2

NeedsCompilation no

Repository CRAN

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Contents

`cytoband_grch37` *Cytoband information (GRCh37)*

Description

A dataset containing cytoband information based on GRCh37.

Usage

```
cytoband_grch37
```

Format

A data frame with 4 columns:

chr chromosome

start start position

end end position

band band name

Source

Ensembl, `https://www.ensembl.org`

References

Harrison, PW, et al. (2024). Ensembl 2024. Nucleic Acids Research, 52, Pages D891–D899. doi:10.1093/nar/gkad1049

Examples

```
data(cytoband_grch37)
```

`cytoband_grch38` *Cytoband information (GRCh38)*

Description

A dataset containing cytoband information based on GRCh38.

Usage

```
cytoband_grch38
```

Format

A data frame with 4 columns:

chr chromosome

start start position

end end position

band band name

Source

Ensembl, `https://www.ensembl.org`

References

Harrison, PW, et al. (2024). Ensembl 2024. Nucleic Acids Research, 52, Pages D891–D899. doi:10.1093/nar/gkad1049

Examples

```
data(cytoband_grch38)
```

`gene_names_grch37` *Gene Names (GRCh37)*

Description

A dataset containing gene names based on GRCh37.

Usage

```
gene_names_grch37
```

Format

A data frame with 6 columns:

id Gene identifier

name Gene name

chr Chromosome

start Start position

end End position

type Gene type

Source

Ensembl, `https://www.ensembl.org`

References

Harrison, PW, et al. (2024). Ensembl 2024. Nucleic Acids Research, 52, Pages D891–D899. doi:10.1093/nar/gkad1049

Examples

```
data(gene_names_grch37)
```

`gene_names_grch38` *Gene Names (GRCh38)*

Description

A dataset containing gene names based on GRCh38.

Usage

```
gene_names_grch38
```

Format

A data frame with 6 columns:

id Gene identifier

name Gene name

chr Gene name

start Gene name

end Gene name

type Gene name

Source

Ensembl, `https://www.ensembl.org`

References

Harrison, PW, et al. (2024). Ensembl 2024. Nucleic Acids Research, 52, Pages D891–D899. doi:10.1093/nar/gkad1049

Examples

```
data(gene_names_grch38)
```

`GWASCat_graph` *GWAScatalog graph*

Description

A graph object of GWAScatalog data. The association between variants and phenotypes are indicated.

Usage

```
GWASCat_graph
```

Format

An object of igraph class.

Source

GWAS Catalog, `https://www.ebi.ac.uk/gwas`

References

Sollis, E, et al. (2022). The NHGRI-EBI GWAS Catalog: knowledgebase and deposition resource. Nucleic Acids Research, 51, Pages D977–D985. doi:10.1093/nar/gkac1010

Examples

```
data(GWASCat_graph)
```

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