

Package: FGRepo (via r-universe)

November 9, 2024

Type Package

Title Functional Genomics Repository for POST-GWAS Analysis

Version 1.3.2.0

Date 2024-11-07

Author Alireza Ani [aut, cre], Ahmad Vaez [aut]

Maintainer Alireza Ani <a.ani@umcg.nl>

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.

License GPL-3

Encoding UTF-8

LazyData true

LazyDataCompression xz

RoxygenNote 7.3.2

NeedsCompilation no

Repository CRAN

Date/Publication 2024-11-08 15:10:12 UTC

Contents

cytoband_grch37	2
cytoband_grch38	3
gene_names_grch37	3
gene_names_grch38	4
GWASCat_graph	5

cytoband_grch37	<i>Cytoband information (GRCh37)</i>
-----------------	--------------------------------------

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](https://doi.org/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](https://doi.org/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](https://doi.org/10.1093/nar/gkad1049)

Examples

```
data(gene_names_grch37)
```

gene_names_grch38	<i>Gene Names (GRCh38)</i>
-------------------	----------------------------

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](https://doi.org/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](https://doi.org/10.1093/nar/gkac1010)

Examples

```
data(GWASCat_graph)
```

Index

* datasets

- cytoband_grch37, [2](#)
- cytoband_grch38, [3](#)
- gene_names_grch37, [3](#)
- gene_names_grch38, [4](#)
- GWASCat_graph, [5](#)

- cytoband_grch37, [2](#)
- cytoband_grch38, [3](#)

- gene_names_grch37, [3](#)
- gene_names_grch38, [4](#)
- GWASCat_graph, [5](#)