

Package ‘grex’

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Type Package

Title Gene ID Mapping for Genotype-Tissue Expression (GTEx) Data

Version 1.8

Maintainer Nan Xiao <me@nanx.me>

Description Convert 'Ensembl' gene identifiers from Genotype-Tissue Expression (GTEx) data to identifiers in other annotation systems, including 'Entrez', 'HGNC', and 'UniProt'.

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LazyData TRUE

VignetteBuilder knitr

URL <https://nanx.me/grex/>, <https://github.com/road2stat/grex>

BugReports <https://github.com/road2stat/grex/issues>

Depends R (>= 3.0.2)

Suggests knitr, rmarkdown

Encoding UTF-8

RoxygenNote 6.0.1.9000

NeedsCompilation no

Author Nan Xiao [aut, cre] (<<https://orcid.org/0000-0002-0250-5673>>),
Gao Wang [aut],
Lei Sun [aut]

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R topics documented:

grex-package	2
cleanid	2
grex	3
gtexv6	4
gtexv6p	4
gtexv7	5

Index**6**

`grex-package`*Gene ID Mapping for Genotype-Tissue Expression (GTEx) Data*

Description

Gene ID Mapping for Genotype-Tissue Expression (GTEx) Data

DetailsOpened the vignette via `vignette("grex")`.

Package:	grex
Type:	Package
License:	GPL-3

Author(s)

Nan Xiao <<me@nanx.me>>, Gao Wang <<gaow@uchicago.edu>>, Lei Sun <<sunl@uchicago.edu>>

`cleanid`*Remove Version Numbers in Raw GTEx (GENCODE) Gene IDs*

DescriptionRemove the `‘.version’` part in raw GTEx (GENCODE) gene IDs to produce Ensembl IDs.**Usage**`cleanid(gtex_id)`**Arguments**`gtex_id` Character vector of GTEx (GENCODE) gene IDs**Value**

Character vector of Ensembl IDs

Examples

```
gtex_id = c("ENSG00000227232.4", "ENSG00000223972.4", "ENSG00000268020.2")
cleanid(gtex_id)
```

grex

Gene ID Mapping for Genotype-Tissue Expression (GTEx) Data

Description

Map Ensembl IDs to Entrez Gene ID, HGNC symbol, and UniProt ID, with basic annotation information such as gene type.

Usage

```
grex(ensembl_id)
```

Arguments

ensembl_id Character vector of Ensembl IDs

Value

This function returns a data frame with the same number of rows as the length of input Ensembl IDs, containing:

- ensembl_id - Input Ensembl ID
- entrez_id - Entrez Gene ID
- hgnc_symbol - HGNC gene symbol
- hgnc_name - HGNC gene name
- cyto_loc - Cytogenetic location
- uniprot_id - UniProt ID
- gene_biotype - Gene type

The elements that cannot be mapped will be NA.

Examples

```
# Ensembl IDs in GTEx v6p gene count data
data("gtexv6p")
# select 100 IDs as example
id = gtexv6p[101:200]
df = grex(id)
# Rows that have a mapped Entrez ID
df[!is.na(df$"entrez_id"),
  c("ensembl_id", "entrez_id", "gene_biotype")]
```

gtexv6

Ensembl IDs from GTEx V6 Gene Read Count Data

Description

A dataset containing the Ensembl IDs from GTEx (V6) gene read count data.

Usage

gtexv6

Format

A character vector with 56,318 Ensembl IDs.

Source

<https://www.gtexportal.org>

gtexv6p

Ensembl IDs from GTEx V6p Gene Read Count Data

Description

A dataset containing the Ensembl IDs from GTEx (V6p) gene read count data.

Usage

gtexv6p

Format

A character vector with 56,238 Ensembl IDs.

Source

<https://www.gtexportal.org>

`gtexv7`*Ensembl IDs from GTEx V7 Gene Read Count Data*

Description

A dataset containing the Ensembl IDs from GTEx (V7) gene read count data.

Usage`gtexv7`**Format**

A character vector with 56,202 Ensembl IDs.

Source

<https://www.gtexportal.org>

Index

*Topic **datasets**

gtexv6, [4](#)

gtexv6p, [4](#)

gtexv7, [5](#)

cleanid, [2](#)

grex, [3](#)

grex-package, [2](#)

gtexv6, [4](#)

gtexv6p, [4](#)

gtexv7, [5](#)