GeneSummary

April 1, 2026

`GeneSummary` *Version and source information*

Description

Version and source information

Usage

```
GeneSummary
```

Examples

```
GeneSummary
```

`loadGeneSummary` *Load gene summary table*

Description

Load gene summary table

Usage

```
loadGeneSummary(organism = 9606,
    status = c("reviewed", "predicted", "inferred", "validated", "provisional"))
```

Arguments

`organism`	Name of the organism (e.g. "Homo sapiens") or the corresponding taxon ID (e.g. 9606).
`status`	Status of the review of the genes.

Details

The gene summaries are extracted from RefSeq database (`https://ftp.ncbi.nih.gov/refseq/release/complete/*.rna.gbff.gz`). Gene summaries are available in the "COMMENT" section of the `*rna.gbff.gz` files.

The Perl script used to parse `*rna.gbff.gz` files is available in `system.file("extdata", "parse_refseq.pl", package = "GeneSummary")`.

Value

A data frame with the following columns:

RefSeq_accession RefSeq accession. Note there is also the version number after the accession.

Organism Full organism name.

Taxon_ID Taxon ID of the organism.

Gene_ID Entrez gene ID.

Review_status Status of the review of the gene.

Gene_summary A long description of the gene.

Examples

```
df = loadGeneSummary(9606)
dim(df)
head(df)
```

`print.GeneSummary_info`

Print the GeneSummary_info object

Description

Print the GeneSummary_info object

Usage

```
## S3 method for class 'GeneSummary_info'
print(x, ...)
```

Arguments

`x`	A `GeneSummary_info` object.
`...`	Other arguments

Value

No value is returned.

Examples

```
GeneSummary
```

Index