

GeneSummary

July 30, 2025

GeneSummary	<i>Version and source information</i>
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Description

Version and source information

Usage

```
GeneSummary
```

Examples

```
GeneSummary
```

loadGeneSummary	<i>Load gene summary table</i>
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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

<code>x</code>	A GeneSummary_info object.
<code>...</code>	Other arguments

Value

No value is returned.

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