

# GeneSummary

July 30, 2025

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|             |                                       |
|-------------|---------------------------------------|
| GeneSummary | <i>Version and source information</i> |
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## Description

Version and source information

## Usage

GeneSummary

## Examples

GeneSummary

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|                 |                                |
|-----------------|--------------------------------|
| 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](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)
```

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```
print.GeneSummary_info
```

*Print the GeneSummary\_info object*

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## 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

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