

# GeneSummary

January 1, 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.

*print.GeneSummary\_info*

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### **Examples**

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