

# Package ‘genomes’

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**Type** Package  
**Title** Genome sequencing project metadata  
**Version** 3.39.0  
**Date** 2015-12-21  
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**License** GPL-3  
**Depends** readr, curl  
**biocViews** Annotation, Genetics  
**Description** Download genome and assembly reports from NCBI  
**git\_url** <https://git.bioconductor.org/packages/genomes>  
**git\_branch** devel  
**git\_last\_commit** 52cdcc6  
**git\_last\_commit\_date** 2025-04-15  
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|       |                               |
|-------|-------------------------------|
| genus | <i>Extract the genus name</i> |
|-------|-------------------------------|

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## Description

Extracts the genus name from a scientific name

## Usage

genus(x)

**Arguments**

x                      A vector of scientific names

**Details**

Removes single quotes, brackets and candidate qualifiers.

**Value**

A vector of genus names

**Author(s)**

Chris Stubben

**See Also**

[species](#)

**Examples**

```
genus("[Bacillus] selenitireducens")
```

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reports

*Genome and assembly reports*

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**Description**

Genome and assembly reports from the NCBI genomes FTP

**Usage**

```
reports(file, assembly = FALSE, ...)
```

**Arguments**

file                      file name, if missing then the files in the FTP directory are listed  
assembly                  use ASSEMBLY\_REPORTS directory, default is GENOME\_REPORTS  
...                        additional options passed to read\_delim

**Details**

Uses read\_delim in the readr package to read genome or assembly reports in the genomes FTP

**Value**

A list of files if file name is missing, otherwise a data.frame with class c("tbl\_df", "tbl", "data.frame").  
If dplyr is loaded, then printing will return the first ten rows and not the first 10,000.

**Author(s)**

Chris Stubben

**References**

See [ftp://ftp.ncbi.nih.gov/genomes/GENOME\\_REPORTS](ftp://ftp.ncbi.nih.gov/genomes/GENOME_REPORTS) and [ftp://ftp.ncbi.nih.gov/genomes/ASSEMBLY\\_REPORTS](ftp://ftp.ncbi.nih.gov/genomes/ASSEMBLY_REPORTS)

**Examples**

```
reports()
## Not run:
proks <- reports("prokaryotes.txt")

## End(Not run)
```

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species

*Extract the species name*

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**Description**

Extracts the species name from a scientific name

**Usage**

```
species(x)
```

**Arguments**

x                      A vector of scientific names

**Details**

Removes single quotes, brackets and candidate qualifiers.

**Value**

A vector of species names

**Author(s)**

Chris Stubben

**See Also**

[genus](#)

**Examples**

```
species("Candidatus Carsonella ruddii PV")
```

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