

# Package: genomes (via r-universe)

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**Type** Package

**Title** Genome sequencing project metadata

**Version** 3.42.0

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**License** GPL-3

**Depends** readr, curl

**biocViews** Annotation, Genetics

**Description** Download genome and assembly reports from NCBI

**Config/pak/sysreqs** libssl-dev libx11-dev

**Repository** <https://bioc-release.r-universe.dev>

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**RemoteUrl** <https://github.com/bioc/genomes>

**RemoteRef** RELEASE\_3\_23

**RemoteSha** a918f3565010212be1c9f1f1775cc08256fa0448

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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 | <i>Genome and assembly reports</i> |
|---------|------------------------------------|

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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 | <i>Extract the species name</i> |
|---------|---------------------------------|

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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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