

# Genome and assembly reports

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April 10, 2025

The **genomes** package reads genome or assembly reports from the NCBI genomes FTP. The main function **reports** lists files in the GENOME\_REPORTS directory (or ASSEMBLY\_REPORTS if **assembly=TRUE**) and uses the **readr** package to download the tables. Additonal functions to download genome features and sequences in the genbank and ref-seq directories will be added soon (currently FTP paths in the prokaryotes.txt files are still missing).

```
R> reports()
```

```
R> proks <- reports("prokaryotes.txt")
```