

# Genome and assembly reports

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October 17, 2016

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. Additional 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")
```