

Genome and assembly reports

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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 refseq directories will be added soon (currently FTP paths in the prokaryotes.txt files are still missing).

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