BSgenome.Mfascicularis.NCBI.6.0

November 6, 2026

`BSgenome.Mfascicularis.NCBI.6.0`
Full genome sequences for Macaca fascicularis (Macaca_fascicularis_6.0)

Description

Full genome sequences for Macaca fascicularis (Crab-eating macaque) as provided by NCBI (assembly Macaca_fascicularis_6.0, assembly accession GCA_011100615.1) and stored in Biostrings objects.

Note

This BSgenome data package was made from the following source data files:

`GCA_011100615.1_Macaca_fascicularis_6.0_genomic.fna.gz` from `https://ftp.ncbi.nlm.nih.gov/genomes/`

See `?BSgenomeForge` and the BSgenomeForge vignette (`vignette("BSgenomeForge")`) in the **BSgenome** software package for how to make a BSgenome data package.

Author(s)

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See Also

- BSgenome objects and the `available.genomes` function in the **BSgenome** software package.
- DNAString objects in the **Biostrings** package.
- The BSgenomeForge vignette (`vignette("BSgenomeForge")`) in the **BSgenome** software package for how to make a BSgenome data package.

Examples

```
BSgenome.Mfascicularis.NCBI.6.0
genome <- BSgenome.Mfascicularis.NCBI.6.0
head(seqlengths(genome))
genome[["1"]]

## ---------------------------------------------------------------------
## Genome-wide motif searching
## ---------------------------------------------------------------------
## See the GenomeSearching vignette in the BSgenome software
## package for some examples of genome-wide motif searching using
## Biostrings and the BSgenome data packages:
if (interactive())
    vignette("GenomeSearching", package="BSgenome")
```

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