

# BSgenome.Mfascicularis.NCBI.6.0

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*Full genome sequences for Macaca fascicularis  
(Macaca\_fascicularis\_6.0)*

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## 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/all>

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

## Author(s)

The Bioconductor Dev Team

## 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
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## 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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