# BSgenome.Mfascicularis.NCBI.5.0

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`BSgenome.Mfascicularis.NCBI.5.0`
*Full genome sequences for Macaca fascicularis (Macaca_fascicularis_5.0)*

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## Description

Full genome sequences for Macaca fascicularis (long-tailed macaque) as provided by NCBI (Macaca_fascicularis_5.0, 2013-06-12) and stored in Biostrings objects.

## Note

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

`GCF_000364345.1_Macaca_fascicularis_5.0_genomic.fna.gz from ftp://ftp.ncbi.nlm.nih.gov/genomes/all/G`

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.5.0
genome <- BSgenome.Mfascicularis.NCBI.5.0
head(seqlengths(genome))
genome$MFA1  # same as genome[["MFA1"]]

## ---------------------------------------------------------------------
## About the ordering of the sequences
## ---------------------------------------------------------------------
## The sequences in BSgenome object 'genome' are ordered like in the
## assembly report at the following URL
url <- "ftp://ftp.ncbi.nlm.nih.gov/genomes/ASSEMBLY_REPORTS/All/GCF_000364345.1.assembly.txt"
## except that the MT sequence was moved from the last position to the
## position between the chromosomes (MFA* sequences) and the scaffolds
## (Scaffold* sequences):
SequenceName <- read.table(url, sep="\t", stringsAsFactors=FALSE)[[1]]
target_seqlevels <- SequenceName[c(1:21, 7601, 22:7600)]
stopifnot(identical(seqlevels(genome), target_seqlevels))

## ---------------------------------------------------------------------
## 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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