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.

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/GCF_000364345.1_Macaca_fascicularis_5.0/

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

The Bioconductor Dev Team

• 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

```r
geno <- BSgenome.Mfascicularis.NCBI.5.0
geno$MFA1 # same as geno["MFA1"]
```

---

# About the ordering of the sequences
---

The sequences in BSgenome object 'geno' are ordered like in the assembly report at the following URL:

```r
```

## 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:

```r
if (interactive())
  vignette("GenomeSearching", package="BSgenome")
```
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