

# BSgenome.Mmulatta.UCSC.rheMac10

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*Full genome sequences for Macaca mulatta (UCSC version rheMac10)*

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## Description

Full genome sequences for Macaca mulatta (Rhesus) as provided by UCSC (rheMac10, Feb. 2019) and stored in Biostrings objects.

## Note

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

rheMac10.2bit from <http://hgdownload.soe.ucsc.edu/goldenPath/rheMac10/bigZips/>

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.Mmulatta.UCSC.rheMac10
genome <- BSgenome.Mmulatta.UCSC.rheMac10
head(seqlengths(genome))
genome$chr1 # same as genome[["chr1"]]

## -----
## 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")
```

# Index

\* **data**

BSgenome.Mmulatta.UCSC.rheMac10, [1](#)

\* **package**

BSgenome.Mmulatta.UCSC.rheMac10, [1](#)

available.genomes, [1](#)

BSgenome, [1](#)

BSgenome.Mmulatta.UCSC.rheMac10, [1](#)

BSgenome.Mmulatta.UCSC.rheMac10-package  
(BSgenome.Mmulatta.UCSC.rheMac10),  
[1](#)

BSgenomeForge, [1](#)

DNAStrng, [1](#)

Mmulatta

(BSgenome.Mmulatta.UCSC.rheMac10),  
[1](#)