

# BSgenome.Mmulatta.UCSC.rheMac8

September 18, 2024

---

BSgenome.Mmulatta.UCSC.rheMac8

*Full genome sequences for Macaca mulatta (UCSC version rheMac8)*

---

## Description

Full genome sequences for Macaca mulatta (Rhesus) as provided by UCSC (rheMac8, Nov. 2015) and stored in Biostrings objects.

## Note

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

rheMac8.2bit from <http://hgdownload.soe.ucsc.edu/goldenPath/rheMac8/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.rheMac8
genome <- BSgenome.Mmulatta.UCSC.rheMac8
head(seqlengths(genome))
genome$chr1 # same as genome[["chr1"]]

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

# Index

\* **data**

BSgenome.Mmulatta.UCSC.rheMac8, [1](#)

\* **package**

BSgenome.Mmulatta.UCSC.rheMac8, [1](#)

available.genomes, [1](#)

BSgenome, [1](#)

BSgenome.Mmulatta.UCSC.rheMac8, [1](#)

BSgenome.Mmulatta.UCSC.rheMac8-package  
(BSgenome.Mmulatta.UCSC.rheMac8),  
[1](#)

BSgenomeForge, [1](#)

DNAStrng, [1](#)

Mmulatta

(BSgenome.Mmulatta.UCSC.rheMac8),  
[1](#)