

# BSgenome.Mmulatta.UCSC.rheMac8

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BSgenome.Mmulatta.UCSC.rheMac8

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

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## 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")
```

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