

# BSgenome.Mmulatta.UCSC.rheMac3

February 26, 2025

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*Full genome sequences for Macaca mulatta (UCSC version rheMac3)*

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## Description

Full genome sequences for *Macaca mulatta* (Rhesus) as provided by UCSC (rheMac3, Oct. 2010) and stored in Biostrings objects.

## Note

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

rheMac3.fa.gz from <http://hgdownload.soe.ucsc.edu/goldenPath/rheMac3/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.rheMac3
genome <- BSgenome.Mmulatta.UCSC.rheMac3
seqlengths(genome)
genome$chr1 # same as genome[["chr1"]]
```

```
## -----
## Upstream sequences
```

```
## -----  
## Starting with BioC 3.0, the upstream1000, upstream2000, and  
## upstream5000 sequences for rheMac3 are not included in the BSgenome  
## data package anymore. However they can easily be extracted from the  
## full genome sequences with something like:  
  
library(GenomicFeatures)  
txdb <- makeTranscriptDbFromUCSC("rheMac3", "refGene")  
gn <- sort(genes(txdb))  
up1000 <- flank(gn, width=1000)  
up1000seqs <- getSeq(genome, up1000)  
  
## IMPORTANT: Make sure you use a TxDb package (or TranscriptDb object),  
## that contains a gene model based on the exact same reference genome  
## as the BSgenome object you pass to getSeq(). Note that you can make  
## your own custom TranscriptDb object from various annotation resources.  
## See the makeTranscriptDbFromUCSC(), makeTranscriptDbFromBiomart(),  
## and makeTranscriptDbFromGFF() functions in the GenomicFeatures  
## package.  
  
## -----  
## 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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