

# BSgenome.Mmulatta.UCSC.rheMac3

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BSgenome.Mmulatta.UCSC.rheMac3

*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, upstream1000.fa.gz, upstream2000.fa.gz, upstream5000.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"]]

## 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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