BSgenome.Mmulatta.UCSC.rheMac2

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*Full genome sequences for Macaca mulatta (UCSC version rheMac2)*

Description

Full genome sequences for *Macaca mulatta* (Rhesus) as provided by UCSC (rheMac2, Jan. 2006) and stored in Biostrings objects.

Note

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

chromFa.tar.gz from http://hgdownload.cse.ucsc.edu/goldenPath/rheMac2/bigZips/

See [BSgenomeForge](#) and the BSgenomeForge vignette (vignette("BSgenomeForge")) in the BSgenome software package for how to make a BSgenome data package.

Author(s)

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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

```r
BSgenome.Mmulatta.UCSC.rheMac2
genome <- BSgenome.Mmulatta.UCSC.rheMac2
seqlengths(genome)
genome$chr1 # same as genome["chr1"]
```

```r
## Upstream sequences
```
## Starting with BioC 3.0, the upstream1000, upstream2000, and upstream5000 sequences for rheMac2 are not included in the BSgenome data package anymore. However they can easily be extracted from the full genome sequences with something like:

```r
library(GenomicFeatures)
txdb <- makeTranscriptDbFromUCSC("rheMac2", "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.

## Genome-wide motif searching

```
if (interactive())
  vignette("GenomeSearching", package="BSgenome")
```
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