

BSgenome.Mmulatta.UCSC.rheMac3

July 9, 2025

BSgenome.Mmulatta.UCSC.rheMac3

Full genome sequences for Macaca mulatta (UCSC version rheMac3)

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")
```

Index

- * **data**
 - BSgenome.Mmulatta.UCSC.rheMac3, [1](#)
- * **package**
 - BSgenome.Mmulatta.UCSC.rheMac3, [1](#)
- available.genomes, [1](#)
- BSgenome, [1](#)
- BSgenome.Mmulatta.UCSC.rheMac3, [1](#)
- BSgenome.Mmulatta.UCSC.rheMac3-package
 - (BSgenome.Mmulatta.UCSC.rheMac3),
[1](#)
- BSgenomeForge, [1](#)
- DNASTring, [1](#)
- Mmulatta
 - (BSgenome.Mmulatta.UCSC.rheMac3),
[1](#)