

BSgenome.Mmulatta.UCSC.rheMac10

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Full genome sequences for Macaca mulatta (UCSC version rheMac10)

Description

Full genome sequences for *Macaca mulatta* (Rhesus) as provided by UCSC (rheMac10, Feb. 2019) and stored in `Biostrings` objects.

Note

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

rheMac10.2bit from <http://hgdownload.soe.ucsc.edu/goldenPath/rheMac10/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

```
BSgenome.Mmulatta.UCSC.rheMac10
genome <- BSgenome.Mmulatta.UCSC.rheMac10
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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