BSgenome.Mmulatta.UCSC.rheMac8

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`BSgenome.Mmulatta.UCSC.rheMac8`

Full genome sequences for Macaca mulatta (UCSC version rheMac8)

Description

Full genome sequences for Macaca mulatta (Rhesus) as provided by UCSC (rheMac8, Nov. 2015) and stored in Biostrings objects.

Note

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

```
rheMac8.2bit from http://hgdownload.soe.ucsc.edu/goldenPath/rheMac8/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.rheMac8
genome <- BSgenome.Mmulatta.UCSC.rheMac8
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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