

BSgenome.Cjacchus.UCSC.calJac3

May 14, 2025

BSgenome.Cjacchus.UCSC.calJac3

Full genome sequences for Callithrix jacchus (UCSC version calJac3)

Description

Full genome sequences for *Callithrix jacchus* (Marmoset) as provided by UCSC (calJac3, Mar. 2009) and stored in Biostrings objects.

Note

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

calJac3.2bit from <http://hgdownload.cse.ucsc.edu/goldenPath/calJac3/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.Cjacchus.UCSC.calJac3
genome <- BSgenome.Cjacchus.UCSC.calJac3
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")
```

Index

* **data**

BSgenome.Cjacchus.UCSC.calJac3, [1](#)

* **package**

BSgenome.Cjacchus.UCSC.calJac3, [1](#)

available.genomes, [1](#)

BSgenome, [1](#)

BSgenome.Cjacchus.UCSC.calJac3, [1](#)

BSgenome.Cjacchus.UCSC.calJac3-package
(BSgenome.Cjacchus.UCSC.calJac3),
[1](#)

BSgenomeForge, [1](#)

Cjacchus

(BSgenome.Cjacchus.UCSC.calJac3),
[1](#)

DNAStrng, [1](#)