BSgenome.Cjacchus.UCSC.calJac4

November 11, 2026

`BSgenome.Cjacchus.UCSC.calJac4`

Full genome sequences for Callithrix jacchus (UCSC version calJac4)

Description

Full genome sequences for Callithrix jacchus (Marmoset) as provided by UCSC (calJac4, May 2020) and wrapped in a BSgenome object.

Note

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

`calJac4.2bit from http://hgdownload.cse.ucsc.edu/goldenPath/calJac4/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.Cjacchus.UCSC.calJac4
genome <- BSgenome.Cjacchus.UCSC.calJac4
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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