Package 'BSgenome.Cporcellus.Internal.cavPor3'

February 17, 2022

Title Internal

Description Internal BSGenome build

Version 1.0.0

Author The Bioconductor Dev Team

Maintainer Bioconductor Package Maintainer <maintainer@bioconductor.org>

Depends R (>= 3.5.0), BSgenome (>= 1.62.0)

Imports BSgenome

Suggests

License Artistic-2.0

organism Cavia porcellus

common_name Guinea pig

genome cavPor3

provider Internal

release_date 2022/01

source_url https://www.example.com/

biocViews AnnotationData, Genetics, BSgenome, Cavia_porcellus

NeedsCompilation no

R topics documented:

BSgenome.Cporcellus.Internal.cavPor3

Internal

Description

Internal BSGenome build

1

Note

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

```
-- information not available --
```

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.Cporcellus.Internal.cavPor3
genome <- BSgenome.Cporcellus.Internal.cavPor3
head(seqlengths(genome))


## ---------------------------------------------------------------------
## 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")
```