

Package 'BSgenome.Mmusculus.Internal.mm10'

February 16, 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 Mus musculus

common_name Mouse

genome mm10

provider Internal

release_date 2022/01

source_url <https://www.example.com/>

biocViews AnnotationData, Genetics, BSgenome, Mus_musculus

NeedsCompilation no

R topics documented:

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Description

Internal BSGenome build

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.Mmusculus.Internal.mm10
genome <- BSgenome.Mmusculus.Internal.mm10
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")
```