BSgenome.Mmusculus.UCSC.mm10

November 11, 2026

`BSgenome.Mmusculus.UCSC.mm10`
Full genome sequences for Mus musculus (UCSC version mm10, based on GRCm38.p6)

Description

Full genome sequences for Mus musculus (Mouse) as provided by UCSC (mm10, based on GRCm38.p6) and stored in Biostrings objects.

Note

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

`mm10.p6.2bit, downloaded from https://hgdownload.soe.ucsc.edu/goldenPath/mm10/bigZips/p6/ on July 1st`

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.Mmusculus.UCSC.mm10
genome <- BSgenome.Mmusculus.UCSC.mm10
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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