BSgenome.Musculus.UCSC.mm10

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**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)**

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.

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Examples

```r
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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