

# BSgenome.Mmusculus.UCSC.mm10

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BSgenome.Mmusculus.UCSC.mm10

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

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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

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.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")
```

# Index

**\* data**

BSgenome.Mmusculus.UCSC.mm10, [1](#)

**\* package**

BSgenome.Mmusculus.UCSC.mm10, [1](#)

available.genomes, [1](#)

BSgenome, [1](#)

BSgenome.Mmusculus.UCSC.mm10, [1](#)

BSgenome.Mmusculus.UCSC.mm10-package  
(BSgenome.Mmusculus.UCSC.mm10),  
[1](#)

BSgenomeForge, [1](#)

DNAStrng, [1](#)

Mmusculus

(BSgenome.Mmusculus.UCSC.mm10),  
[1](#)