

# BSgenome.Mmusculus.UCSC.mm10

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*Full genome sequences for Mus musculus (UCSC version mm10)*

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## Description

Full genome sequences for *Mus musculus* (Mouse) as provided by UCSC (mm10, Dec. 2011) and stored in Biostrings objects.

## Note

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

chr1.fa.gz chr2.fa.gz chr3.fa.gz chr4.fa.gz chr5.fa.gz chr6.fa.gz chr7.fa.gz chr8.fa.gz chr9.fa.gz chr10.fa.gz  
from <http://hgdownload.cse.ucsc.edu/goldenPath/mm10/chromosomes/>

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
seqlengths(genome)
genome$chr1 # same as genome[["chr1"]]

## 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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