**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

from [http://hgdownload.cse.ucsc.edu/goldenPath/mm10/chromosomes/](http://hgdownload.cse.ucsc.edu/goldenPath/mm10/chromosomes/)

See [BSgenomeForge](http://example.com) 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

```r
BSgenome.Musculus.UCSC.mm10
genome <- BSgenome.Musculus.UCSC.mm10
seqlengths(genome)
genome$chr1 # same as genome["chr1"]
```

```r
# Upstream sequences
library(TxDb.Musculus.UCSC.mm10.knownGene)
txdb <- TxDb.Musculus.UCSC.mm10.knownGene
gn <- sort(genes(txdb))
up1000 <- flank(gn, width=1000)
up1000seqs <- getSeq(genome, up1000)
```

```r
# IMPORTANT: Make sure you use a TxDb package (or TranscriptDb object),
# that contains a gene model based on the exact same reference genome
# as the BSgenome object you pass to getSeq(). Note that you can make
# your own custom TranscriptDb object from various annotation resources.
# See the makeTranscriptDbFromUCSC(), makeTranscriptDbFromBiomart(),
# and makeTranscriptDbFromGFF() functions in the GenomicFeatures
# package.
```

```r
# Genome-wide motif searching
if (interactive())
  vignette("GenomeSearching", package="BSgenome")
```
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