

BSgenome.Mmusculus.UCSC.mm10

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Full genome sequences for Mus musculus (UCSC version mm10)

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"]]

## -----
## Upstream sequences
## -----
## The upstream sequences for mm10 (i.e. the sequences 1000 bases
## upstream of annotated transcription starts) can easily be extracted
## from the full genome sequences with something like:

library(TxDb.Mmusculus.UCSC.mm10.knownGene)
txdb <- TxDb.Mmusculus.UCSC.mm10.knownGene
gn <- sort(genes(txdb))
up1000 <- flank(gn, width=1000)
up1000seqs <- getSeq(genome, up1000)

## 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.

## -----
## 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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