BSgenome.Mmusculus.UCSC.mm9

April 10, 2024

Full genome sequences for Mus musculus (UCSC version mm9)

Description

Full genome sequences for Mus musculus (Mouse) as provided by UCSC (mm9, Jul. 2007) and stored in Biostrings objects.

Note

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

chromFa.tar.gz from http://hgdownload.cse.ucsc.edu/goldenPath/mm9/bigZips/

See ?BSgenomeForge 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

BSgenome.Mmuscus.UCSC.mm9

gene <- BSgenome.Mmuscus.UCSC.mm9
seqlengths(genome)

 genome$chr1  # same as genome["chr1"]

## Upstream sequences

library(TxDb.Mmuscus.UCSC.mm9.knownGene)
txdb <- TxDb.Mmuscus.UCSC.mm9.knownGene
gn <- sort(genes(txdb))
up1000 <- flank(gn, width=1000)
up1000seqs <- getSeq(genome, up1000)

## Genome-wide motif searching

if (interactive())
vignette("GenomeSearching", package="BSgenome")
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