BSgenome.Dmelanogaster.UCSC.dm6

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`BSgenome.Dmelanogaster.UCSC.dm6`
Full genome sequences for Drosophila melanogaster (UCSC version dm6)

Description

Full genome sequences for Drosophila melanogaster (Fly) as provided by UCSC (dm6, Aug. 2014) and stored in Biostrings objects.

Note

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

```
dm6.2bit from http://hgdownload.cse.ucsc.edu/goldenPath/dm6/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.Dmelanogaster.UCSC.dm6
genome <- BSgenome.Dmelanogaster.UCSC.dm6
seqlengths(genome)
genome$chr2L  # same as genome[["chr2L"]]

## ---------------------------------------------------------------------
## Extract the upstream sequences
## ---------------------------------------------------------------------
## The upstream sequences can easily be extracted from the full genome
## sequences with something like:

library(GenomicFeatures)
txdb <- makeTxDbFromUCSC("dm6", tablename="refGene")
up1000seqs <- extractUpstreamSeqs(genome, txdb, width=1000)

## IMPORTANT: Make sure you use a TxDb package (or TxDb object) that
## contains a gene model based on dm6 or on a compatible genome (i.e.
## a genome with sequences identical to the sequences in dm6). Note
## that you can make a TxDb object from various annotation resources.
## See the makeTxDbFromUCSC(), makeTxDbFromBiomart(), and
## makeTxDbFromGFF() functions in the GenomicFeatures package for more
## information.

## ---------------------------------------------------------------------
## 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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