BSgenome.Dmelanogaster.UCSC.dm3

May 8, 2024

BSgenome.Dmelanogaster.UCSC.dm3

*Full genome sequences for Drosophila melanogaster (UCSC version dm3)*

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**Description**

Full genome sequences for Drosophila melanogaster (Fly) as provided by UCSC (dm3, Apr. 2006) and stored in Biostrings objects.

**Note**

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


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.dm3
genome <- BSgenome.Dmelanogaster.UCSC.dm3
seqlengths(genome)
genome$chr2L # same as genome[["chr2L"]]

### Upstream sequences
### Starting with BioC 3.0, the upstream1000, upstream2000, and
### upstream5000 sequences for dm3 are not included in the BSgenome data
### package anymore. However they can easily be extracted from the full
### genome sequences with something like:

library(TxDb.Dmelanogaster.UCSC.dm3.ensGene)
txdb <- TxDb.Dmelanogaster.UCSC.dm3.ensGene
gn <- sort(genes(txdb))
up1000 <- flank(gn, width=1000)
up1000seqs <- getSeq(genome, up1000)

### Genome-wide motif searching
### See the GenomeSearching vignette in the BSgenome software
### 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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