

# BSgenome.Dmelanogaster.UCSC.dm2

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Dmelanogaster

*Drosophila melanogaster (Fly) full genome (UCSC version dm2)*

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## Description

*Drosophila melanogaster* (Fly) full genome as provided by UCSC (dm2, Apr. 2004) and stored in Biostrings objects.

## Note

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

```
sequences: chromFa.zip, upstream1000.fa.gz, upstream2000.fa.gz, upstream5000.fa.gz
from http://hgdownload.cse.ucsc.edu/goldenPath/dm2/bigZips/
AGAPS masks: all the chr*_gap.txt.gz files from ftp://hgdownload.cse.ucsc.edu/goldenPath/dm2/bigZips/chr*_gap.txt.gz
RM masks: http://hgdownload.cse.ucsc.edu/goldenPath/dm2/bigZips/chromOut.zip
TRF masks: http://hgdownload.cse.ucsc.edu/goldenPath/dm2/bigZips/chromTrf.zip
```

See [?BSgenomeForge](#) and the BSgenomeForge vignette (`vignette("BSgenomeForge")`) in the BSgenome software package for how to make a BSgenome data package.

## Author(s)

H. Pages

## See Also

[BSgenome-class](#), [DNAString-class](#), [available.genomes](#), [BSgenomeForge](#)

## Examples

```
Dmelanogaster
seqlengths(Dmelanogaster)
Dmelanogaster$chr2L # same as Dmelanogaster[["chr2L"]]

if ("AGAPS" %in% masknames(Dmelanogaster)) {

  ## Check that the assembly gaps contain only Ns:
  checkOnlyNsInGaps <- function(seq)
```

```
{
  ## Replace all masks by the inverted AGAPS mask
  masks(seq) <- gaps(masks(seq)["AGAPS"])
  unique_letters <- uniqueLetters(seq)
  if (any(unique_letters != "N"))
    stop("assembly gaps contain more than just Ns")
}

## A message will be printed each time a sequence is removed
## from the cache:
options(verbose=TRUE)

for (seqname in seqnames(Dmelanogaster)) {
  cat("Checking sequence", seqname, "... ")
  seq <- Dmelanogaster[[seqname]]
  checkOnlyNsInGaps(seq)
  cat("OK\n")
}

## 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")
```

# Index

## \*Topic **data**

Dmelanogaster, [1](#)

## \*Topic **package**

Dmelanogaster, [1](#)

available.genomes, [1](#)

BSgenome-class, [1](#)

BSgenome.Dmelanogaster.UCSC.dm2

(*Dmelanogaster*), [1](#)

BSgenome.Dmelanogaster.UCSC.dm2-package

(*Dmelanogaster*), [1](#)

BSgenomeForge, [1](#)

Dmelanogaster, [1](#)

DNASTring-class, [1](#)