

# BSgenome.Drerio.UCSC.danRer10

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BSgenome.Drerio.UCSC.danRer10

*Full genome sequences for Danio rerio (UCSC version danRer10)*

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## Description

Full genome sequences for Danio rerio (Zebrafish) as provided by UCSC (danRer10, Sep. 2014) and stored in Biostrings objects.

## Note

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

danRer10.2bit from <http://hgdownload.soe.ucsc.edu/goldenPath/danRer10/bigZips/>

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.Drerio.UCSC.danRer10
genome <- BSgenome.Drerio.UCSC.danRer10
head(seqlengths(genome))
genome$chr1 # same as genome[["chr1"]]

## -----
## Extract the upstream sequences
## -----
## The upstream sequences located in
## http://hgdownload.cse.ucsc.edu/goldenPath/danRer10/bigZips/
## are based on RefSeq genes (RefSeq Genes track in the Genome Browser).
## These can easily be extracted from the full genome sequences with:

library(GenomicFeatures)
refGene_txdb <- suppressWarnings(makeTxDbFromUCSC("danRer10", "refGene"))
refGene_up1000seqs <- extractUpstreamSeqs(genome, refGene_txdb)

## 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.
## IMPORTANT: Make sure you use a TxDb package (or TxDb object) that
## contains a gene model based on danRer10 or on a compatible genome
## (i.e. a genome with sequences identical to the sequences in
## danRer10). See ?extractUpstreamSeqs 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")
```

# Index

**\* data**

BSgenome.Drerio.UCSC.danRer10, 1

**\* package**

BSgenome.Drerio.UCSC.danRer10, 1

`available.genomes`, 1

`BSgenome`, 1

`BSgenome.Drerio.UCSC.danRer10`, 1

`BSgenome.Drerio.UCSC.danRer10-package`  
(`BSgenome.Drerio.UCSC.danRer10`),  
1

`BSgenomeForge`, 1

`DNASTring`, 1

`Drerio` (`BSgenome.Drerio.UCSC.danRer10`),  
1