BSgenome.Drerio.UCSC.danRer5
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BSgenome.Drerio.UCSC.danRer5

*Full genome sequences for Danio rerio (UCSC version danRer5)*

**Description**

Full genome sequences for Danio rerio (Zebrafish) as provided by UCSC (danRer5, Jul. 2007) and stored in Biostrings objects.

**Note**

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

danRer5.fa.gz from http://hgdownload.cse.ucsc.edu/goldenPath/danRer5/bigZips/

See [7BSgenomeForge](#) 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**

```r
BSgenome.Drerio.UCSC.danRer5
genome <- BSgenome.Drerio.UCSC.danRer5
seqlengths(genome)
genome$chr1 # same as genome["chr1"]
```

## Upstream sequences

```r
```
## Starting with BioC 3.0, the upstream1000, upstream2000, and
## upstream5000 sequences for danRer5 are not included in the BSgenome
## data package anymore. However they can easily be extracted from the
## full genome sequences with something like:

```r
library(GenomicFeatures)
txdb <- makeTranscriptDbFromUCSC("danRer5", "refGene")
gn <- sort(genes(txdb))
up1000 <- flank(gn, width=1000)
up1000seqs <- getSeq(genome, up1000)
```

## IMPORTANT: Make sure you use a TxDb package (or TranscriptDb object),
## that contains a gene model based on the exact same reference genome
## as the BSgenome object you pass to getSeq(). Note that you can make
## your own custom TranscriptDb object from various annotation resources.
## See the makeTranscriptDbFromUCSC(), makeTranscriptDbFromBiomart(),
## and makeTranscriptDbFromGFF() functions in the GenomicFeatures
## package.

## Genome-wide motif searching
```
if (interactive())
vignette("GenomeSearching", package="BSgenome")
```
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