**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)**

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

```r
## 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:

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

## 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:

```r
if (interactive())
vignette("GenomeSearching", package="BSgenome")
```
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