

BSgenome.Drerio.UCSC.danRer7

October 7, 2014

BSgenome.Drerio.UCSC.danRer7

Full genome sequences for Danio rerio (UCSC version danRer7)

Description

Full genome sequences for Danio rerio (Zebrafish) as provided by UCSC (danRer7, Jul. 2010) and stored in Biostrings objects.

Note

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

danRer7.fa.gz, upstream1000.fa.gz, upstream2000.fa.gz and upstream5000.fa.gz files from <http://hgdownload.cse.ucsc.edu/goldenPath/danRer7/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.danRer7
genome <- BSgenome.Drerio.UCSC.danRer7
seqlengths(genome)
genome$chr1 # same as genome[["chr1"]]

## 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**

BSgenome.Drerio.UCSC.danRer7, [1](#)

*Topic **package**

BSgenome.Drerio.UCSC.danRer7, [1](#)

available.genomes, [1](#)

BSgenome, [1](#)

BSgenome.Drerio.UCSC.danRer7, [1](#)

BSgenome.Drerio.UCSC.danRer7-package
(BSgenome.Drerio.UCSC.danRer7),
[1](#)

BSgenomeForge, [1](#)

DNAStrng, [1](#)

Drerio (BSgenome.Drerio.UCSC.danRer7), [1](#)