BSgenome.Cfamiliaris.UCSC.canFam3

January 3, 2024

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Full genome sequences for Canis lupus familiaris (UCSC version can-Fam3)

Description

Full genome sequences for Canis lupus familiaris (Dog) as provided by UCSC (canFam3, Sep. 2011) and stored in Biostrings objects.

Note

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

canFam3.fa.gz from http://hgdownload.cse.ucsc.edu/goldenPath/canFam3/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

```r
BSgenome.Cfamiliaris.UCSC.canFam3
genome <- BSgenome.Cfamiliaris.UCSC.canFam3
seqlengths(genome)
genome$chr1 # same as genome["chr1"]

# Upstream sequences

## Starting with BioC 3.0, the upstream1000, upstream2000, and
## upstream5000 sequences for canFam3 are not included in the BSgenome
## data package anymore. However they can easily be extracted from the
## full genome sequences with something like:

library(GenomicFeatures)
txdb <- makeTranscriptDbFromUCSC("canFam3", "refGene")
up1000 <- flank(gn, width=1000)
up1000seqs <- getSeq(genome, up1000)

# Genome-wide motif searching

# See the GenomeSearching vignette in the BSgenome software
if (interactive())
  vignette("GenomeSearching", package="BSgenome")
```
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