

BSgenome.Celegans.UCSC.ce2

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Full genome sequences for Caenorhabditis elegans (UCSC version ce2)

Description

Full genome sequences for *Caenorhabditis elegans* (Worm) as provided by UCSC (ce2, Mar. 2004) and stored in **Biostrings** objects.

Note

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

chromFa.zip from <http://hgdownload.cse.ucsc.edu/goldenPath/ce2/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

```

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genome <- BSgenome.Celegans.UCSC.ce2
seqlengths(genome)
genome$chrI # same as genome[["chrI"]]

## -----## Upstream sequences
## -----
## Starting with BioC 3.0, the upstream1000, upstream2000, and
## upstream5000 sequences for ce2 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("ce2", "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
## -----
## 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")

```

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