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
upstream1000.zip
upstream2000.zip
upstream5000.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.

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Examples

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

## 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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