

# BSgenome.Celegans.UCSC.ce10

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BSgenome.Celegans.UCSC.ce10

*Full genome sequences for Caenorhabditis elegans (UCSC version ce10)*

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## Description

Full genome sequences for *Caenorhabditis elegans* (Worm) as provided by UCSC (ce10, Oct. 2010) and stored in Biostrings objects.

## Note

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

```
chromFa.tar.gz
upstream1000.fa.gz
upstream2000.fa.gz
upstream5000.fa.gz
from ftp://hgdownload.cse.ucsc.edu/goldenPath/ce10/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.Celegans.UCSC.ce10
genome <- BSgenome.Celegans.UCSC.ce10
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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