

BSgenome.Celegans.UCSC.ce2

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Celegans

Caenorhabditis elegans full genome (UCSC version ce2)

Description

Caenorhabditis elegans full genome 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-class](#), [DNAString-class](#), [available.genomes](#), [BSgenomeForge](#)

Examples

```
Celegans
seqlengths(Celegans)
Celegans$chrI # same as Celegans[["chrI"]]

if ("AGAPS" %in% masknames(Celegans)) {

  ## Check that the assembly gaps contain only Ns:
  checkOnlyNsInGaps <- function(seq)
```

```
{
  ## Replace all masks by the inverted AGAPS mask
  masks(seq) <- gaps(masks(seq)["AGAPS"])
  unique_letters <- uniqueLetters(seq)
  if (any(unique_letters != "N"))
    stop("assembly gaps contain more than just Ns")
}

## A message will be printed each time a sequence is removed
## from the cache:
options(verbose=TRUE)

for (seqname in seqnames(Celegans)) {
  cat("Checking sequence", seqname, "... ")
  seq <- Celegans[[seqname]]
  checkOnlyNsInGaps(seq)
  cat("OK\n")
}

## 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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