

# BSgenome.Celegans.UCSC.ce2

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Celegans

*Caenorhabditis elegans* (Worm) full genome (UCSC version ce2)

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## Description

*Caenorhabditis elegans* (Worm) 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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