BSgenome.Scerevisiae.UCSC.sacCer3

April 10, 2016

`BSgenome.Scerevisiae.UCSC.sacCer3`
Saccharomyces cerevisiae (Yeast) full genome (UCSC version sacCer3)

Description

Saccharomyces cerevisiae (Yeast) full genome as provided by UCSC (sacCer3, April 2011) and stored in Biostrings objects.

Note

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

```
chromFa.tar.gz from http://hgdownload.cse.ucsc.edu/goldenPath/sacCer3/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

```
BSgenome.Scerevisiae.UCSC.sacCer3
genome <- BSgenome.Scerevisiae.UCSC.sacCer3
seqlengths(genome)
genome$chrI  # same as genome[["chrI"]]

## ---------------------------------------------------------------------
## 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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