BSgenome.Scerevisiae.UCSC.sacCer1

November 11, 2026

`BSgenome.Scerevisiae.UCSC.sacCer1`
Saccharomyces cerevisiae (Yeast) full genome (UCSC version sacCer1)

Description

Saccharomyces cerevisiae (Yeast) full genome as provided by UCSC (sacCer1, Oct. 2003) and stored in Biostrings objects.

Note

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

`chromFa.zip from http://hgdownload.cse.ucsc.edu/goldenPath/sacCer1/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.sacCer1
genome <- BSgenome.Scerevisiae.UCSC.sacCer1
seqlengths(genome)
genome$chr1  # same as genome[["chr1"]]

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