

# BSgenome.Scerevisiae.UCSC.sacCer2

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BSgenome.Scerevisiae.UCSC.sacCer2

*Saccharomyces cerevisiae* (Yeast) full genome (UCSC version sacCer2)

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## Description

*Saccharomyces cerevisiae* (Yeast) full genome as provided by UCSC (sacCer2, June 2008) 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/sacCer2/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.Scerevisiae.UCSC.sacCer2
genome <- BSgenome.Scerevisiae.UCSC.sacCer2
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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