# BSgenome.Scerevisiae.UCSC.sacCer3

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

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## 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)

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.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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