# BSgenome.Sscrofa.UCSC.susScr3

## March 4, 2026

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BSgenome.Sscrofa.UCSC.susScr3

*Full genome sequences for Sus scrofa (UCSC version susScr3)*

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### Description

Full genome sequences for Sus scrofa (Pig) as provided by UCSC (susScr3, Aug. 2011) and stored in Biostrings objects.

### Note

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

susScr3.fa.gz from http://hgdownload.soe.ucsc.edu/goldenPath/susScr3/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.Sscrofa.UCSC.susScr3
genome <- BSgenome.Sscrofa.UCSC.susScr3
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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