

# BSgenome.Hsapiens.UCSC.hs1

December 11, 2024

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BSgenome.Hsapiens.UCSC.hs1

*Full genomic sequences for UCSC genome hs1 (Homo sapiens)*

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## Description

Full genomic sequences for UCSC genome hs1 (the hs1 genome is based on assembly T2T-CHM13v2.0, with GenBank assembly accession GCA\_009914755.4). The sequences are stored in DNASTring objects.

## Note

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

hs1.2bit, downloaded from <https://hgdownload.soe.ucsc.edu/goldenPath/hs1/bigZips/> on 2023-01-03

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.Hsapiens.UCSC.hs1
genome <- BSgenome.Hsapiens.UCSC.hs1
head(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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