BSgenome.Hsapiens.UCSC.hs1

July 9, 2025

`BSgenome.Hsapiens.UCSC.hs1`

Full genomic sequences for UCSC genome hs1 (Homo sapiens)

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)

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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.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")
```

Index